Suppl. Table III: List of all transcripts detected as present by array analysis in FACS purified rat β-cells

				IL+IFN 6h		IL+IFN 24h		TNF+IFN 6h		TNF+IFN 24h	
Probe Set ID	**GeneBank**	**Gene Title**	**Gene Symbol**	**FC**	**Pval**	**FC**	**Pval**	**FC**	**Pval**	**FC**	**Pval**
1371748_at	BI284306	1-acylglycerol-3-phosphate O-acyltransferase 1	Agpat1	0.987	0.511	0.799	0.054	1.200	0.163	0.959	0.553
1374570_at	AI012474	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta) (predicted)	Agpat2_predicted	0.912	0.761	1.606	0.067	0.687	0.140	1.193	0.093
1382041_at	BI290161	1-acylglycerol-3-phosphate O-acyltransferase 3 (predicted)	Agpat3_predicted	0.463	0.030	0.552	0.424	0.385	0.122	0.478	0.189
1380480_at	AI711263	1-acylglycerol-3-phosphate O-acyltransferase 3 (predicted)	Agpat3_predicted	0.998	0.984	0.967	0.965	0.999	0.995	0.999	0.995
1368194_at	NM_133406	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)	Agpat4	1.335	0.456	2.211	0.000	1.063	0.258	1.803	0.004
1378284_at	BI292067	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) (predicted)	Agpat5_predicted	0.976	0.159	0.345	0.023	0.728	0.077	0.494	0.183
1373169_at	AI175416	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) (predicted)	Agpat5_predicted	1.034	0.917	0.881	0.199	0.878	0.933	0.971	0.564
1390966_at	BE111759	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta)	Agpat6	1.126	0.399	0.440	0.012	1.780	0.348	0.893	0.379
1384383_at	BF557230	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta)	Agpat6	1.003	0.874	0.997	0.992	0.998	0.882	0.999	0.992
1391754_at	BM391818	2 ' -5 ' oligoadenylate synthetase 1I	Oas1i	5.638	0.000	2.784	0.008	7.759	0.000	4.644	0.002
1388544_at	BI294941	2,3-bisphosphoglycerate mutase	Bpgm	2.394	0.018	1.420	0.172	3.097	0.004	1.997	0.005
1367777_at	NM_057197	2,4-dienoyl CoA reductase 1, mitochondrial	Decr1	0.452	0.013	0.357	0.000	0.404	0.027	0.445	0.000
1371152_a_at	Z18877	2',5'-oligoadenylate synthetase 1, 40/46kDa	Oas1	9.701	0.038	6.207	0.001	41.425	0.001	13.217	0.002
1372012_at	BF417479	24-dehydrocholesterol reductase	Dhcr24	0.278	0.048	0.900	0.036	0.470	0.085	0.687	0.013
1370818_at	AF044574	2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	Decr2	0.655	0.003	0.787	0.109	0.778	0.073	0.809	0.253
1388056_at	AF068268	2-5 oligoadenylate synthetase 1B	Oas1b	7.331	0.003	2.070	0.039	23.474	0.000	6.535	0.010
1377497_at	BF419319	2'-5' oligoadenylate synthetase-like 1	Oasl1	8.938	0.052	1.956	0.034	41.181	0.000	17.648	0.000
1391755_at	AI535177	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	Hmgcl	1.020	0.311	0.999	0.993	1.007	0.373	1.000	0.933
1367767_at	NM_024386	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	Hmgcl	1.244	0.996	1.322	0.210	0.401	0.022	1.141	0.221
1375852_at	BM390399	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	Hmgcr	0.684	0.057	0.818	0.032	0.779	0.382	0.677	0.010
1387848_at	NM_013134	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	Hmgcr	0.702	0.132	0.590	0.024	0.589	0.105	0.809	0.056
1367932_at	NM_017268	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	Hmgcs1	0.851	0.289	0.572	0.015	0.879	0.747	0.581	0.048
1382260_at	AW531471	3-hydroxybutyrate dehydrogenase, type 1	Bdh1	0.999	0.726	0.702	0.141	1.036	0.849	0.781	0.318
1388118_at	AI176586	3-hydroxyisobutyrate dehydrogenase	Hibadh	0.548	0.001	0.897	0.117	0.474	0.044	0.687	0.076
1373564_at	AI410548	3-hydroxyisobutyryl-Coenzyme A hydrolase	Hibch	0.940	0.762	1.502	0.172	0.411	0.035	1.156	0.505
1371850_at	AA892829	3'-phosphoadenosine 5'-phosphosulfate synthase 1 (predicted)	Papss1_predicted	0.466	0.020	0.729	0.001	0.583	0.063	0.699	0.071
1370052_at	NM_031081	3-phosphoinositide dependent protein kinase-1	Pdpk1	1.108	0.886	0.805	0.912	0.972	0.146	0.742	0.241
1369799_at	U29701	4-aminobutyrate aminotransferase	Abat	0.538	0.014	0.631	0.018	0.590	0.086	0.512	0.109
1375321_at	BF393840	4-aminobutyrate aminotransferase	Abat	0.901	0.081	0.987	0.902	0.899	0.765	0.889	0.617
1391365_at	BF416465	4-aminobutyrate aminotransferase	Abat	0.953	0.757	0.401	0.007	1.807	0.522	0.428	0.064
1388537_at	BF554891	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. elegans)	Nipsnap1	0.611	0.257	0.732	0.031	0.828	0.841	0.687	0.217
1390454_at	BI289807	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. elegans)	Nipsnap1	0.936	0.978	0.835	0.038	0.827	0.344	0.832	0.334
1384112_at	BI289470	5' nucleotidase, ecto	Nt5e	1.719	0.053	0.760	0.198	0.708	0.317	0.788	0.704
1369200_at	NM_021576	5' nucleotidase, ecto	Nt5e	0.964	0.446	1.111	0.830	0.972	0.840	0.939	0.759
1392719_at	AA957588	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)	Mthfs	0.848	0.793	1.349	0.039	0.702	0.083	1.409	0.132
1384370_at	BF542664	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)	Mthfs	1.002	0.918	1.500	0.033	0.843	0.172	1.118	0.022
1381768_at	AW535082	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)	Mthfs	1.024	0.945	2.303	0.006	0.845	0.270	2.034	0.009
1385254_at	BE104427	5'-3' exoribonuclease 1 (predicted)	Xrn1_predicted	1.178	0.011	1.010	0.971	0.997	0.545	0.998	0.829
1391107_at	BI275784	5'-3' exoribonuclease 1 (predicted)	Xrn1_predicted	4.020	0.019	1.789	0.061	3.504	0.030	2.692	0.048
1378759_at	BE102644	5'-3' exoribonuclease 1 (predicted)	Xrn1_predicted	2.006	0.020	1.458	0.052	1.636	0.163	1.193	0.070
1391412_at	AA996841	5'-3' exoribonuclease 2 (predicted)	Xrn2_predicted	1.103	0.711	2.564	0.005	1.377	0.025	1.828	0.004
1393702_at	BF397290	5'-3' exoribonuclease 2 (predicted)	Xrn2_predicted	0.911	0.884	1.343	0.069	1.223	0.167	1.214	0.107
1369962_at	NM_031014	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	Atic	0.499	0.243	1.616	0.011	0.513	0.002	1.677	0.004
1388631_at	AI177093	5-azacytidine induced gene 2	Azi2	1.619	0.108	1.905	0.030	2.267	0.002	1.654	0.061
1369456_at	NM_017250	5-hydroxytryptamine (serotonin) receptor 2B	Htr2b	0.991	0.604	0.996	0.286	1.452	0.118	1.015	0.043
1388219_at	L10073	5-hydroxytryptamine (serotonin) receptor 5B	Htr5b	0.919	0.550	0.936	0.387	1.001	0.221	0.940	0.343
1387545_at	NM_030864	5-methyltetrahydrofolate-homocysteine methyltransferase	Mtr	1.122	0.862	2.146	0.015	0.861	0.614	1.417	0.871
1398642_at	BI279274	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	Mtrr	0.728	0.059	1.250	0.275	1.481	0.670	0.656	0.067
1384423_at	AW140661	5'-nucleotidase, cytosolic II (predicted)	Nt5c2_predicted	0.398	0.087	0.671	0.073	0.507	0.086	0.791	0.026
1373412_at	AI409146	5'-nucleotidase, cytosolic III (predicted)	Nt5c3_predicted	1.083	0.726	0.494	0.007	3.082	0.001	1.222	0.048
1389131_at	BF412799	5'-nucleotidase, cytosolic III-like	Nt5c3l	0.797	0.178	0.662	0.369	0.642	0.726	0.788	0.290
1391306_at	AI070952	5-oxoprolinase (ATP-hydrolysing)	Oplah	0.630	0.395	1.169	0.436	0.412	0.048	0.973	0.904
1378976_x_at	AI070952	5-oxoprolinase (ATP-hydrolysing)	Oplah	0.714	0.465	1.136	0.324	0.425	0.009	1.078	0.192
1388044_at	L27084	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	Pfkfb2	1.131	0.142	0.516	0.001	0.959	0.448	0.490	0.023
1382712_at	AI044245	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	Pfkfb2	0.790	0.512	0.510	0.012	0.676	0.171	0.283	0.002
1374523_at	AI231339	6-phosphogluconolactonase (predicted)	Pgls_predicted	0.645	0.097	0.597	0.248	0.633	0.352	0.484	0.017
1369304_at	NM_017220	6-pyruvoyl-tetrahydropterin synthase	Pts	1.000	0.626	0.992	0.828	0.997	0.984	0.981	0.646

1368189_at	NM_022389	7-dehydrocholesterol reductase	Dhcr7	0.697	0.083	0.955	0.490	0.487	0.383	0.794	0.185
1370040_at	NM_030870	8-oxoguanine DNA-glycosylase 1	Ogg1	0.947	0.627	0.997	0.991	0.674	0.659	0.999	0.980
1371420_at	AI412054	92Aa-Protein	LOC494529	0.633	0.048	0.670	0.247	0.590	0.208	0.616	0.235
1387135_at	NM_020308	a disintegrin and metallopeptidase domain 15 (metargidin)	Adam15	0.780	0.079	0.387	0.021	0.640	0.118	0.243	0.041
1387256_at	NM_020078	a disintegrin and metallopeptidase domain 1a	Adam1a	1.001	0.433	0.981	0.590	0.972	0.607	0.700	0.134
1388161_at	BI300565	a disintegrin and metalloprotease domain 10	Adam10	0.983	0.249	0.791	0.086	1.044	0.481	0.848	0.105
1369833_at	NM_020077	a disintegrin and metalloprotease domain 2	Adam2	1.261	0.872	1.154	0.241	2.816	0.030	1.018	0.448
1369832_at	NM_020302	a disintegrin and metalloprotease domain 3 (cyritestin)	Adam3	1.099	0.820	1.167	0.942	1.247	0.278	1.112	0.978
1394612_at	AW535206	A disintegrin and metalloprotease domain 4	Adam4	0.934	0.534	0.438	0.011	1.225	0.272	0.754	0.041
1390046_at	BI288110	a disintegrin and metalloprotease domain 8 (predicted)	Adam8_predicted	0.826	0.725	5.739	0.000	1.163	0.775	1.259	0.208
1367922_at	NM_020306	a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)	Adam17	3.586	0.000	2.035	0.004	3.598	0.001	2.089	0.022
1375337_at	AI011712	a disintegrin and metalloproteinase domain 9 (meltrin gamma) (predicted)	Adam9_predicted	1.376	0.441	0.551	0.081	1.499	0.327	0.577	0.061
1394518_at	BF284436	A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (predicted)	Adamts9_predicted	0.797	0.115	0.953	0.952	1.330	0.774	1.001	0.979
1368869_at	BG663107	A kinase (PRKA) anchor protein (gravin) 12	Akap12	13.725	0.000	3.964	0.016	17.530	0.000	3.450	0.008
1368868_at	NM_057103	A kinase (PRKA) anchor protein (gravin) 12	Akap12	1.980	0.008	0.991	0.077	1.445	0.345	1.002	0.155
1383151_at	AI011474	A kinase (PRKA) anchor protein (yotiao) 9	Akap9	1.452	0.223	0.716	0.105	1.266	0.896	0.866	0.140
1384857_at	AI145240	A kinase (PRKA) anchor protein (yotiao) 9	Akap9	0.973	0.972	0.966	0.433	1.102	0.596	0.715	0.231
1383358_at	AI072577	A kinase (PRKA) anchor protein 1	Akap1	1.533	0.339	2.037	0.002	1.234	0.788	1.576	0.004
1395278_at	BI299865	A kinase (PRKA) anchor protein 10 (predicted)	Akap10_predicted	1.614	0.976	1.350	0.051	1.013	0.963	1.535	0.008
1368427_at	NM_012773	A kinase (PRKA) anchor protein 11	Akap11	1.208	0.157	1.204	0.242	1.119	0.157	1.220	0.071
1390883_at	AI501759	A kinase (PRKA) anchor protein 11	Akap11	0.834	0.274	0.311	0.003	0.864	0.485	0.591	0.026
1392049_at	BF411767	A kinase (PRKA) anchor protein 11	Akap11	0.921	0.753	0.685	0.113	1.240	0.674	0.617	0.049
1381842_at	AI511309	A kinase (PRKA) anchor protein 13	Akap13	0.699	0.321	0.887	0.940	1.084	0.253	1.098	0.145
1382268_at	AW526712	A kinase (PRKA) anchor protein 13	Akap13	0.778	0.525	0.470	0.058	0.748	0.187	0.581	0.011
1386521_at	AI511291	A kinase (PRKA) anchor protein 2	Akap2	3.138	0.041	1.984	0.058	18.776	0.000	10.157	0.012
1382206_a_at	BF398063	A kinase (PRKA) anchor protein 2	Akap2	1.151	0.181	0.993	0.882	16.586	0.000	1.560	0.354
1391548_at	AA955786	A kinase (PRKA) anchor protein 5	Akap5	2.089	0.009	0.932	0.600	1.776	0.001	0.698	0.236
1380914_at	AI175405	A kinase (PRKA) anchor protein 5	Akap5	1.312	0.152	1.328	0.073	1.827	0.050	1.508	0.128
1378880_at	AW532591	A kinase (PRKA) anchor protein 5	Akap5	1.542	0.397	1.277	0.046	1.815	0.065	1.636	0.003
1381619_at	BE116003	A kinase (PRKA) anchor protein 5	Akap5	1.338	0.707	1.133	0.856	1.257	0.242	1.019	0.376
1389496_at	BI300893	A kinase (PRKA) anchor protein 7	Akap7	0.347	0.033	0.719	0.015	0.259	0.003	0.579	0.074
1392079_at	AW526264	A kinase (PRKA) anchor protein 7	Akap7	0.852	0.099	0.843	0.588	0.847	0.448	0.662	0.536
1370911_at	U01914	A kinase (PRKA) anchor protein 8	Akap8	0.804	0.047	0.992	0.667	1.024	0.181	1.018	0.448
1385713_at	BF392577	A kinase (PRKA) anchor protein 8-like	Akap8l	0.521	0.303	0.589	0.148	1.004	0.829	0.583	0.015
1375813_at	BE102687	A kinase (PRKA) anchor protein 8-like	Akap8l	1.029	0.711	1.857	0.194	1.023	0.369	0.943	0.614
1390375_at	BF414692	A kinase (PRKA) anchor protein 8-like	Akap8l	0.980	0.805	0.769	0.100	0.985	0.907	0.654	0.051
1376720_at	BG376414	aarF domain containing kinase 2 (predicted)	Adck2_predicted	0.770	0.515	0.816	0.263	0.789	0.038	0.876	0.150
1389043_at	AI101347	aarF domain containing kinase 4	Adck4	1.646	0.519	3.266	0.004	1.339	0.450	1.645	0.047
1398194_at	BF405720	AarF domain containing kinase 4	Adck4	1.217	0.769	0.966	0.354	1.295	0.187	1.003	0.997
1374746_at	AA891922	Ab1-152	LOC500877	1.496	0.005	1.519	0.001	1.485	0.005	1.992	0.010
1385397_at	AA859085	Ab1-219	LOC499991	17.424	0.000	2.444	0.000	16.680	0.000	1.471	0.359
1390662_at	AW435169	Ab2-427	LOC500084	2.378	0.003	1.957	0.003	2.508	0.001	2.069	0.002
1382981_at	AI138017	Abelson helper integration site 1	Ahi1	0.349	0.022	0.529	0.076	0.420	0.111	0.705	0.261
1379594_at	AW524408	Abelson helper integration site 1	Ahi1	0.937	0.671	0.995	0.956	1.005	0.258	1.017	0.860
1372976_at	BI294842	abhydrolase domain containing 14A	Abhd14a	0.995	0.970	0.955	0.528	0.738	0.960	0.958	0.532
1377900_at	BF409560	abhydrolase domain containing 14b	Abhd14b	0.939	0.130	0.464	0.012	0.623	0.326	0.365	0.021
1388988_at	AI175070	abhydrolase domain containing 14b	Abhd14b	0.660	0.800	0.389	0.001	0.557	0.124	0.420	0.015
1390455_at	AI013474	abhydrolase domain containing 2 (predicted)	Abhd2_predicted	6.338	0.025	20.377	0.000	1.159	0.656	7.093	0.001
1382137_at	BG662490	abhydrolase domain containing 3 (predicted)	Abhd3_predicted	0.962	0.825	0.500	0.001	0.900	0.345	0.571	0.036
1393028_at	BM383152	Abhydrolase domain containing 4 (predicted)	Abhd4_predicted	0.669	0.010	1.152	0.518	0.398	0.002	1.632	0.098
1399019_at	AI407868	abhydrolase domain containing 4 (predicted)	Abhd4_predicted	0.297	0.166	1.328	0.112	0.397	0.023	1.673	0.067
1390155_at	AA924793	abhydrolase domain containing 6	Abhd6	1.315	0.062	1.344	0.011	0.875	0.277	1.210	0.013
1380332_at	BF411794	Abhydrolase domain containing 6	Abhd6	1.934	0.084	0.539	0.105	1.110	0.702	0.422	0.067
1393197_at	BG376055	abhydrolase domain containing 8 (predicted)	Abhd8_predicted	0.970	0.749	0.553	0.031	0.997	0.926	0.554	0.014
1367958_at	NM_024397	abl-interactor 1	Abi1	1.054	0.498	1.292	0.229	1.479	0.071	1.559	0.066
1383147_at	AW526373	Abl-interactor 2	Abi2	0.583	0.039	0.167	0.000	0.770	0.224	0.352	0.030
1393031_at	BI297075	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)	Abo	0.753	0.105	0.898	0.353	0.753	0.097	0.899	0.359
1375036_at	AI172146	Ac1158	LOC302898	0.722	0.000	0.597	0.012	0.780	0.044	0.802	0.322
1394397_at	BF522734	Ac1158	LOC302898	0.724	0.043	1.215	0.437	0.413	0.004	1.178	0.498
1385212_at	AI603192	Ac1158	LOC302898	0.637	0.568	0.462	0.096	0.945	0.740	0.987	0.962

1383607_at	BG377487	Ac1158	LOC302898	1.076	0.657	0.346	0.000	1.134	0.751	0.766	0.245
1397100_at	BF403835	Ac1258	LOC361230	1.055	0.258	1.918	0.056	1.002	0.846	1.001	0.955
1371405_at	BE109143	Ac2-193	---	0.442	0.466	0.617	0.000	0.619	0.113	0.736	0.011
1385889_at	AA893212	Ac2-193	---	0.988	0.992	0.461	0.091	1.000	1.000	0.453	0.081
1368126_at	NM_023104	acetoacetyl-CoA synthetase	Aacs	1.362	0.335	0.750	0.080	1.386	0.988	0.573	0.026
1367763_at	D13921	acetyl-coenzyme A acetyltransferase 1	Acat1	0.471	0.002	0.303	0.001	0.589	0.016	0.229	0.001
1383416_at	AA899304	Acetyl-coenzyme A acetyltransferase 1	Acat1	0.322	0.010	0.358	0.006	0.390	0.117	0.345	0.003
1376226_at	BG377636	Acetyl-Coenzyme A acetyltransferase 2	Acat2	0.738	0.243	0.839	0.944	0.710	0.091	0.913	0.196
1372462_at	AI412322	acetyl-Coenzyme A acetyltransferase 2	Acat2	0.913	0.742	1.203	0.178	0.838	0.192	0.970	0.637
1387783_a_at	NM_012489	acetyl-Coenzyme A acyltransferase 1 /// similar to 3-ketoacyl-CoA thiolase B, peroxisomal precursor (Beta-ketothiolase B) (predicted)	Acaa1 /// RGD1562373_predicted	0.967	0.883	0.620	0.048	0.972	0.890	0.853	0.059
1386880_at	NM_130433	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	Acaa2	0.610	0.424	0.422	0.105	0.551	0.028	0.362	0.036
1370893_at	BI296153	acetyl-coenzyme A carboxylase alpha	Acaca	0.629	0.161	1.000	0.721	1.169	0.461	0.998	0.750
1367735_at	NM_012819	acetyl-Coenzyme A dehydrogenase, long-chain	Acadl	0.908	0.997	1.555	0.044	0.631	0.232	1.405	0.057
1367702_at	NM_016986	acetyl-Coenzyme A dehydrogenase, medium chain	Acadm	0.307	0.011	0.444	0.032	0.865	0.681	0.521	0.041
1367828_at	NM_022512	acetyl-Coenzyme A dehydrogenase, short chain	Acads	0.466	0.053	0.621	0.198	0.483	0.081	0.695	0.291
1372228_at	BF420745	acetylserotonin O-methyltransferase-like (predicted)	Asmtl_predicted	0.562	0.305	0.719	0.151	0.953	0.619	0.572	0.392
1376037_at	BF283385	achalasia, adrenocortical insufficiency, alacrimia (Allgrove, triple-A) (predicted)	Aaas_predicted	0.920	0.965	1.009	0.933	1.001	0.995	1.593	0.026
1398938_at	AI170780	acid phosphatase 1, soluble	Acp1	0.703	0.010	1.516	0.001	0.674	0.025	1.553	0.027
1387840_at	NM_021262	acid phosphatase 1, soluble	Acp1	0.708	0.635	1.310	0.019	0.604	0.545	1.080	0.685
1367906_at	NM_016988	acid phosphatase 2, lysosomal	Acp2	0.629	0.086	0.916	0.052	0.486	0.066	0.755	0.047
1373732_at	BM386224	acid phosphatase 6, lysophosphatidic	Acp6	0.927	0.668	0.730	0.010	0.928	0.747	0.745	0.000
1389229_at	AI113146	acid phosphatase-like 2	Acpl2	0.582	0.248	0.516	0.033	0.655	0.181	0.702	0.034
1369063_at	NM_012903	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	Anp32a	0.551	0.211	2.050	0.273	0.514	0.031	1.714	0.462
1372620_at	AI008642	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	Anp32e	0.841	0.141	1.883	0.003	0.913	0.541	1.662	0.005
1371873_at	AA850735	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	Anp32e	0.612	0.413	0.457	0.002	0.662	0.109	0.580	0.010
1386915_at	NM_131911	acidic nuclear phosphoprotein 32 family, member B	Anp32b	0.607	0.612	2.058	0.006	0.596	0.022	1.730	0.001
1367560_at	NM_022402	acidic ribosomal phosphoprotein P0	Arbp	0.892	0.574	1.151	0.073	0.724	0.053	0.987	0.879
1389363_at	AA997430	acireductone dioxygenase 1	Adi1	0.510	0.251	0.541	0.013	0.614	0.010	0.562	0.011
1372847_at	AW524458	ACN9 homolog (S. cerevisiae)	Acn9	0.558	0.449	1.512	0.390	0.680	0.262	1.290	0.180
1386916_at	NM_017321	aconitase 1	Aco1	0.228	0.009	0.413	0.000	0.377	0.019	0.558	0.038
1367589_at	NM_024398	aconitase 2, mitochondrial	Aco2	0.446	0.090	0.614	0.001	0.532	0.005	0.565	0.004
1378945_at	AI638990	Aconitase 2, mitochondrial	Aco2	1.471	0.285	1.313	0.188	1.108	0.863	1.497	0.060
1396474_at	AW254078	Acrosin binding protein	Acrbp	0.944	0.934	0.824	0.488	1.002	0.995	0.774	0.717
1370856_at	AA800705	actin alpha cardiac 1	Actc1	1.005	0.375	1.017	0.995	1.008	0.343	0.998	0.846
1398779_at	NM_031146	actin related protein 2/3 complex, subunit 1A	Arpc1a	0.935	0.966	0.743	0.022	0.886	0.254	0.787	0.011
1386925_at	NM_019289	actin related protein 2/3 complex, subunit 1B	Arpc1b	1.014	0.399	1.110	0.375	0.804	0.074	1.016	0.498
1371511_at	AI009775	actin related protein 2/3 complex, subunit 2 (predicted)	Arpc2_predicted	0.998	0.254	1.181	0.014	0.872	0.835	1.174	0.075
1371977_at	BG381477	actin related protein 2/3 complex, subunit 3 (predicted)	Arpc3_predicted	0.871	0.946	0.829	0.193	0.834	0.090	0.769	0.018
1372577_at	AI411582	actin related protein 2/3 complex, subunit 4 (predicted)	Arpc4_predicted	0.845	0.783	1.043	0.122	0.793	0.016	0.977	0.187
1390022_at	AA946538	actin related protein 2/3 complex, subunit 5	Arpc5	1.708	0.000	1.013	0.355	1.373	0.026	0.982	0.733
1371457_at	BI291468	Actin related protein 2/3 complex, subunit 5-like	Arpc5l	0.534	0.092	0.924	0.654	0.440	0.062	1.353	0.527
1398835_at	NM_031144	actin, beta	Actb	1.381	0.213	1.953	0.006	1.282	0.954	1.857	0.080
1398836_s_at	NM_031144	actin, beta	Actb	1.423	0.468	2.066	0.018	1.223	0.317	2.020	0.219
1371327_a_at	BG666668	actin, gamma, cytoplasmic 1 /// similar to Actin, cytoplasmic 2 (Gamma-actin)	Actg1 /// LOC295810	1.725	0.013	4.404	0.000	1.247	0.097	3.078	0.000
1384581_at	BI850151	actin, gamma, cytoplasmic 1 /// similar to Actin, cytoplasmic 2 (Gamma-actin) /// similar to put. type 5 nonmuscle actin (predicted)	Actg1 /// LOC295810 /// RGD1563410_predicted	1.322	0.790	2.529	0.013	1.000	0.994	2.178	0.001
1367962_at	NM_133424	actinin alpha 3	Actn3	0.954	0.827	0.919	0.510	0.956	0.836	0.944	0.484
1369942_at	NM_031675	actinin alpha 4	Actn4	1.219	0.079	2.849	0.000	0.566	0.848	2.412	0.010
1389189_at	BF555956	actinin, alpha 1	Actn1	2.572	0.005	2.004	0.006	2.191	0.002	1.440	0.002
1396539_at	BE119221	Actinin, alpha 1	Actn1	1.593	0.011	1.264	0.052	1.182	0.121	1.213	0.080
1398294_at	NM_031005	actinin, alpha 1	Actn1	3.668	0.098	5.427	0.012	5.164	0.309	2.167	0.035
1373849_at	AI102978	actin-like 6A	Actl6a	0.716	0.389	0.971	0.641	0.892	0.429	0.970	0.258
1379781_at	BE120508	Actin-like 6A	Actl6a	1.111	0.630	0.886	0.844	0.801	0.370	0.994	0.970
1382608_at	BI281712	actin-like 6B (predicted)	Actl6b_predicted	0.898	0.610	0.439	0.046	0.924	0.487	0.496	0.050
1382294_at	AI576111	Activated leukocyte cell adhesion molecule	Alcam	3.015	0.001	0.885	0.502	3.065	0.001	0.890	0.132
1370043_at	NM_031753	activated leukocyte cell adhesion molecule	Alcam	2.029	0.006	0.947	0.673	2.548	0.001	0.939	0.125
1375263_at	BI296498	Activated leukocyte cell adhesion molecule	Alcam	0.615	0.725	1.166	0.684	1.245	0.126	0.754	0.001
1395981_at	AW919934	activating signal cointegrator 1 complex subunit 3 (predicted)	Ascc3_predicted	1.197	0.111	0.990	0.761	1.065	0.266	0.946	0.968
1388354_at	BE349703	activating signal cointegrator 1 complex subunit 3-like 1	Ascc3l1	0.951	0.139	1.367	0.109	0.932	0.520	1.405	0.008
1389623_at	AA849092	activating transcription factor 1	Atf1	1.020	0.336	1.347	0.020	0.966	0.256	1.443	0.001

1369472_a_at	NM_031018	activating transcription factor 2	Atf2	0.995	0.990	3.241	0.034	1.006	0.704	1.983	0.131
1369268_at	NM_012912	activating transcription factor 3	Atf3	15.734	0.003	53.891	0.004	23.273	0.003	26.593	0.002
1367624_at	NM_024403	activating transcription factor 4	Atf4	1.332	0.064	2.325	0.000	1.072	0.410	2.160	0.003
1372601_at	BM391471	activating transcription factor 5	Atf5	0.694	0.089	1.118	0.652	0.700	0.006	1.091	0.382
1384957_at	AI059385	activating transcription factor 6 (predicted)	Atf6_predicted	0.834	0.976	1.846	0.227	0.978	0.999	0.998	0.990
1384498_at	BI274185	Activating transcription factor 7 (predicted)	Atf7_predicted	1.142	0.778	0.902	0.491	0.721	0.051	1.027	0.848
1382380_at	AI176317	Activating transcription factor 7 (predicted)	Atf7_predicted	1.001	0.996	0.941	0.765	0.999	0.279	0.957	0.841
1382070_at	AA819758	activating transcription factor 7 interacting protein (predicted)	Atf7ip_predicted	2.041	0.006	1.564	0.007	1.406	0.054	1.162	0.028
1388601_at	AI598410	activator of basal transcription 1	Abt1	0.365	0.011	1.222	0.209	0.518	0.184	1.060	0.669
1373215_at	BI282699	active BCR-related gene (predicted)	Abr_predicted	0.740	0.998	0.668	0.006	0.999	0.999	0.646	0.037
1381220_at	BM383968	activin receptor IIA	Acvr2a	1.280	0.109	2.249	0.012	0.583	0.445	2.124	0.008
1376125_at	BI289112	Activity and neurotransmitter-induced early gene 11 (ania-11) mRNA, 3' UTR	---	1.651	0.057	1.729	0.038	2.002	0.026	1.008	0.964
1383306_at	AI013468	Activity and neurotransmitter-induced early gene 2 (ania-2) mRNA, 3'UTR	---	0.732	0.066	0.894	0.794	0.639	0.033	0.902	0.066
1389346_at	BI274136	activity-dependent neuroprotective protein	Adnp	0.464	0.026	0.235	0.016	0.540	0.025	0.395	0.005
1389088_at	AI600029	activity-dependent neuroprotective protein	Adnp	0.989	0.913	0.889	0.103	0.825	0.078	0.885	0.193
1397389_at	BF398664	Activity-dependent neuroprotective protein	Adnp	0.979	0.934	1.023	0.066	0.674	0.184	0.840	0.106
1370939_at	D90109	acyl-CoA synthetase long-chain family member 1	Acsl1	0.779	0.508	0.613	0.002	1.451	0.005	1.224	0.108
1388153_at	BI277523	acyl-CoA synthetase long-chain family member 1	Acsl1	0.972	0.858	0.981	0.393	1.753	0.264	1.462	0.680
1368177_at	NM_057107	acyl-CoA synthetase long-chain family member 3	Acsl3	0.784	0.108	1.917	0.005	0.510	0.038	1.341	0.127
1387101_at	NM_053623	acyl-CoA synthetase long-chain family member 4	Acsl4	1.538	0.275	0.844	0.164	1.388	0.340	0.885	0.203
1386926_at	NM_053607	acyl-CoA synthetase long-chain family member 5	Acsl5	1.669	0.011	2.354	0.000	1.413	0.042	2.167	0.000
1368182_at	NM_130739	acyl-CoA synthetase long-chain family member 6	Acsl6	0.679	0.177	0.367	0.013	1.099	0.471	0.498	0.040
1370313_at	D88891	acyl-CoA thioesterase 7	Acot7	0.834	0.333	0.846	0.734	0.887	0.037	0.895	0.987
1368206_at	NM_130756	acyl-CoA thioesterase 8	Acot8	0.742	0.321	1.208	0.221	0.506	0.000	1.306	0.013
1372552_at	AI102273	acyl-Coenzyme A binding domain containing 3	Acbd3	0.814	0.055	0.962	0.587	0.835	0.006	0.856	0.083
1394734_at	BE120590	acyl-Coenzyme A binding domain containing 3	Acbd3	0.836	0.277	1.675	0.039	0.782	0.255	1.755	0.062
1373347_at	BF419134	acyl-Coenzyme A binding domain containing 3	Acbd3	0.944	0.778	0.913	0.597	1.106	0.873	1.354	0.133
1395913_at	AI136400	Acyl-Coenzyme A binding domain containing 4	Acbd4	1.236	0.162	1.067	0.350	1.257	0.175	1.210	0.439
1373507_at	AI232810	acyl-Coenzyme A binding domain containing 5	Acbd5	0.662	0.031	0.369	0.000	0.749	0.227	0.505	0.004
1374555_at	AI501425	acyl-Coenzyme A binding domain containing 6	Acbd6	1.222	0.513	1.666	0.011	0.823	0.416	1.384	0.218
1390789_at	BI296347	acyl-Coenzyme A dehydrogenase family, member 11 (predicted)	Acad11_predicted	0.474	0.231	0.715	0.056	0.374	0.018	0.797	0.590
1373389_at	BM391807	acyl-Coenzyme A dehydrogenase family, member 9	Acad9	0.516	0.002	0.639	0.005	0.719	0.103	0.861	0.230
1367897_at	NM_012891	acyl-Coenzyme A dehydrogenase, very long chain	Acadvl	0.696	0.546	0.865	0.299	0.941	0.208	0.958	0.724
1367680_at	NM_017340	acyl-Coenzyme A oxidase 1, palmitoyl	Acox1	0.696	0.150	0.852	0.018	0.630	0.003	0.959	0.181
1377887_at	AI013044	Acyl-Coenzyme A oxidase 3, pristanoyl	Acox3	1.149	0.402	0.634	0.082	1.317	0.294	0.784	0.407
1398815_at	NM_012500	acylpeptide hydrolase	Apeh	0.628	0.451	0.416	0.003	0.639	0.130	0.487	0.196
1373448_at	AI413052	acylphosphatase 1, erythrocyte (common) type (predicted)	Acyp1_predicted	0.874	0.451	0.905	0.266	0.854	0.306	1.396	0.034
1371923_at	BG380281	acyltransferase like 2 (predicted)	Aytl2_predicted	0.706	0.722	0.119	0.006	0.811	0.898	0.232	0.001
1367872_at	NM_017277	adaptor protein complex AP-1, beta 1 subunit	Ap1b1	1.052	0.995	0.923	0.147	0.910	0.630	0.883	0.112
1374305_at	AI408613	adaptor protein complex AP-1, gamma 2 subunit (predicted)	Ap1g2_predicted	0.939	0.881	0.701	0.337	1.343	0.364	0.736	0.842
1371858_at	BM385719	adaptor protein complex AP-1, sigma 1 (predicted)	Ap1s1_predicted	0.572	0.020	1.119	0.320	0.616	0.002	0.824	0.855
1377769_at	AA955775	adaptor protein complex AP-1, sigma 1 (predicted)	Ap1s1_predicted	0.570	0.989	0.918	0.841	0.567	0.054	0.769	0.110
1371493_at	BI285640	Adaptor protein complex AP-2, alpha 2 subunit	Ap2a2	0.650	0.454	0.509	0.059	0.469	0.070	0.453	0.011
1369982_at	NM_031008	adaptor protein complex AP-2, alpha 2 subunit	Ap2a2	0.710	0.487	1.093	0.031	0.513	0.017	0.893	0.312
1373816_at	BM383443	adaptor-related protein complex 1, gamma 1 subunit	Ap1g1	1.102	0.638	1.779	0.008	1.367	0.066	1.384	0.030
1384187_at	BF551686	adaptor-related protein complex 1, sigma 2 subunit (predicted)	Ap1s2_predicted	0.601	0.050	0.528	0.018	0.557	0.005	0.641	0.071
1398616_at	AI045228	adaptor-related protein complex 1, sigma 2 subunit (predicted)	Ap1s2_predicted	0.539	0.057	0.580	0.008	0.996	0.724	0.809	0.123
1396217_at	BF542447	Adaptor-related protein complex 1, sigma 2 subunit (predicted)	Ap1s2_predicted	0.517	0.129	0.312	0.008	0.485	0.031	0.201	0.060
1384703_at	AI228602	Adaptor-related protein complex 1, sigma 2 subunit (predicted)	Ap1s2_predicted	0.934	0.732	1.023	0.995	0.607	0.183	0.800	0.288
1367704_at	NM_080583	adaptor-related protein complex 2, beta 1 subunit	Ap2b1	1.006	0.129	0.692	0.004	1.041	0.431	0.664	0.051
1398765_at	NM_053837	adaptor-related protein complex 2, mu 1 subunit	Ap2m1	1.078	0.345	1.056	0.052	1.025	0.664	1.176	0.027
1386877_at	NM_022952	adaptor-related protein complex 2, sigma 1 subunit	Ap2s1	0.582	0.086	0.741	0.252	0.616	0.081	0.950	0.271
1373888_at	BE113312	adaptor-related protein complex 3, beta 1 subunit (predicted)	Ap3b1_predicted	0.899	0.727	0.884	0.045	1.214	0.854	0.835	0.797
1393359_at	AW534487	adaptor-related protein complex 3, beta 2 subunit (predicted)	Ap3b2_predicted	1.224	0.021	0.531	0.019	1.654	0.069	0.770	0.131
1367549_a_at	BI282757	adaptor-related protein complex 3, delta 1 subunit	Ap3d1	0.733	0.012	1.247	0.140	0.969	0.210	1.146	0.008
1393562_at	BF564312	adaptor-related protein complex 3, mu 1 subunit	Ap3m1	0.555	0.029	0.382	0.010	0.658	0.024	0.474	0.046
1368062_at	NM_133593	adaptor-related protein complex 3, mu 1 subunit	Ap3m1	0.547	0.181	0.447	0.006	0.622	0.003	0.632	0.102
1368246_at	NM_133305	adaptor-related protein complex 3, mu 2 subunit	Ap3m2	2.191	0.009	1.003	0.987	2.113	0.001	1.017	0.930
1373024_at	BI296511	adaptor-related protein complex 3, sigma 1 subunit (predicted)	Ap3s1_predicted	0.731	0.510	0.672	0.008	0.801	0.964	0.694	0.138
1372045_at	BE112941	adaptor-related protein complex AP-1, mu subunit 1	Ap1m1	0.806	0.188	1.320	0.023	1.065	0.324	1.300	0.006
1376874_a_at	BF560100	adaptor-related protein complex AP-4, beta 1 (predicted)	Ap4b1_predicted	0.941	0.401	1.578	0.015	1.148	0.108	1.192	0.295

1372628_at	AA800277	adaptor-related protein complex AP-4, sigma 1 (predicted)	Ap4s1_predicted	0.787	0.274	0.893	0.155	0.649	0.011	0.843	0.017
1396251_at	BF388318	Adaptor-related protein complex AP-4, sigma 1 (predicted)	Ap4s1_predicted	0.985	0.995	4.621	0.028	1.000	1.000	4.034	0.048
1388487_at	AI600061	adducin 1 (alpha)	Add1	0.692	0.202	0.898	0.154	0.584	0.018	0.866	0.385
1394421_at	BF282980	Adducin 1 (alpha)	Add1	1.000	0.984	1.300	0.094	1.001	0.885	1.350	0.035
1371244_at	AI412934	adenine phosphoribosyl transferase (predicted)	Aprt_predicted	0.645	0.452	1.235	0.941	0.498	0.024	1.012	0.783
1387837_at	NM_012499	adenomatosis polyposis coli	Apc	0.883	0.794	0.870	0.038	0.505	0.035	0.579	0.066
1387721_at	NM_017155	adenosine A1 receptor	Adora1	0.928	0.812	0.976	0.905	0.786	0.742	0.837	0.508
1387395_at	NM_017161	adenosine A2B receptor	Adora2b	1.027	0.584	1.564	0.271	1.057	0.051	1.149	0.326
1368973_at	NM_031006	adenosine deaminase, RNA-specific	Adar	1.018	0.046	1.078	0.242	1.022	0.242	1.436	0.138
1394528_at	BF405166	Adenosine deaminase, RNA-specific	Adar	0.805	0.178	1.000	0.298	1.312	0.097	1.002	0.973
1369630_at	BF283118	adenosine kinase	Adk	0.879	0.187	0.786	0.014	0.874	0.098	0.744	0.003
1369629_at	U90340	adenosine kinase	Adk	0.907	0.929	0.506	0.017	0.998	0.994	0.509	0.036
1398306_at	J02811	adenosine monophosphate deaminase 1 (isoform M)	Ampd1	2.094	0.071	1.082	0.087	3.013	0.049	1.069	0.209
1368342_at	NM_031544	adenosine monophosphate deaminase 3	Ampd3	13.268	0.000	5.949	0.006	10.080	0.033	1.841	0.144
1376549_at	BF394116	Adenylate cyclase 10 (soluble)	Adcy10	0.642	0.810	1.167	0.853	1.250	0.740	0.915	0.778
1367644_at	L01115	adenylate cyclase 6	Adcy6	0.475	0.020	0.549	0.011	0.363	0.128	0.635	0.177
1368892_at	NM_016989	adenylate cyclase activating polypeptide 1	Adcyap1	1.150	0.675	1.633	0.083	1.003	0.833	0.997	0.885
1386954_at	NM_030986	adenylate kinase 2	Ak2	0.880	0.646	0.997	0.547	0.509	0.036	1.045	0.684
1398349_at	AI411497	adenylate kinase 2	Ak2	0.925	0.884	1.145	0.036	0.878	0.346	1.229	0.055
1368095_at	NM_013218	adenylate kinase 3	Ak3	1.151	0.066	0.819	0.117	0.945	0.180	0.814	0.035
1371824_at	AA891949	adenylate kinase 3-like 1	Ak3l1	0.470	0.657	34.019	0.006	0.830	0.631	22.220	0.002
1376091_at	AA963616	adenylosuccinate lyase (predicted)	Adsl_predicted	0.896	0.226	1.849	0.001	0.852	0.754	1.405	0.009
1399050_at	AI232106	adenylosuccinate synthetase, non muscle (predicted)	Adss_predicted	1.077	0.420	0.936	0.133	1.040	0.583	1.029	0.150
1375587_at	AI412674	Adenylosuccinate synthetase, non muscle (predicted)	Adss_predicted	1.086	0.486	1.005	0.885	1.206	0.737	1.000	0.994
1373345_at	AW523747	adhesion molecule with Ig like domain 2	Amigo2	0.911	0.691	0.558	0.024	0.658	0.026	0.418	0.001
1367868_at	NM_031708	adhesion regulating molecule 1	Adrm1	0.699	0.482	1.359	0.005	0.648	0.034	1.346	0.019
1388373_at	BI289063	adiponectin receptor 1	Adipor1	0.937	0.879	0.821	0.254	0.862	0.323	0.662	0.013
1371598_at	BI278598	Adiponectin receptor 2	Adipor2	0.919	0.750	1.003	0.723	0.647	0.226	0.890	0.019
1390549_at	AA859796	adiponectin receptor 2	Adipor2	1.068	0.870	0.921	0.386	0.611	0.038	0.970	0.860
1390383_at	BI285616	adipose differentiation related protein	Adfp	1.401	0.122	1.610	0.033	0.757	0.261	1.227	0.090
1390850_at	AA874941	Adipose differentiation related protein	Adfp	1.520	0.221	1.598	0.002	0.814	0.039	1.233	0.068
1374958_at	AA819640	ADP-dependent glucokinase	Adpgk	0.400	0.018	1.189	0.641	0.660	0.040	0.775	0.042
1377952_at	BE102146	ADP-dependent glucokinase	Adpgk	0.515	0.054	1.703	0.901	0.408	0.067	1.176	0.910
1395163_at	BI296281	ADP-dependent glucokinase	Adpgk	2.137	0.329	1.154	0.102	2.497	0.006	0.614	0.076
1370505_at	M86341	ADP-ribosylarginine hydrolase	Adprh	0.807	0.926	0.742	0.038	0.356	0.363	0.525	0.006
1395386_at	BF411881	ADP-ribosylation factor 1	Arf1	0.825	0.256	0.788	0.769	0.822	0.224	0.974	0.823
1395241_at	BF389686	ADP-ribosylation factor 1	Arf1	0.781	0.304	1.440	0.194	1.042	0.296	1.053	0.825
1367459_at	BE329198	ADP-ribosylation factor 1	Arf1	0.760	0.642	0.992	0.453	0.691	0.285	1.013	0.568
1398817_at	NM_022518	ADP-ribosylation factor 1	Arf1	0.687	0.953	0.733	0.222	0.467	0.405	0.543	0.114
1388813_at	BE112160	ADP-ribosylation factor 2	Arf2	1.204	0.961	2.589	0.049	1.903	0.281	2.437	0.000
1388997_at	BG380819	ADP-ribosylation factor 3	Arf3	1.104	0.345	0.916	0.026	1.187	0.035	1.008	0.231
1387447_at	NM_080904	ADP-ribosylation factor 3	Arf3	1.075	0.754	1.036	0.221	1.379	0.069	0.995	0.835
1395162_at	BI301804	ADP-ribosylation factor 3	Arf3	1.000	0.961	0.930	0.751	0.994	0.308	1.177	0.806
1398758_at	NM_024151	ADP-ribosylation factor 4	Arf4	0.783	0.671	0.938	0.323	0.854	0.677	0.957	0.516
1367748_at	NM_024149	ADP-ribosylation factor 5	Arf5	0.908	0.029	0.736	0.025	0.800	0.050	0.811	0.119
1369998_at	NM_024152	ADP-ribosylation factor 6	Arf6	1.976	0.118	3.037	0.001	1.274	0.628	1.922	0.007
1376268_at	BM387435	ADP-ribosylation factor 6	Arf6	1.284	0.202	1.328	0.143	1.055	0.266	1.189	0.239
1389492_at	AA818820	ADP-ribosylation factor GTPase activating protein 1	Arfgap1	0.523	0.004	0.735	0.223	0.753	0.037	0.844	0.241
1376123_at	BM384190	ADP-ribosylation factor GTPase activating protein 1	Arfgap1	0.627	0.146	0.881	0.424	0.375	0.056	0.945	0.182
1370364_at	U35776	ADP-ribosylation factor GTPase activating protein 1	Arfgap1	0.447	0.169	0.804	0.188	0.458	0.005	0.476	0.030
1372130_at	AI408249	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited) (predicted)	Arfgef1_predicted	1.103	0.164	0.912	0.563	1.139	0.113	1.392	0.003
1373591_at	BG375435	ADP-ribosylation factor interacting protein 2	Arfip2	0.608	0.013	1.191	0.040	0.578	0.085	0.660	0.126
1370223_at	AI170798	ADP-ribosylation factor related protein 1	Arfrp1	0.812	0.706	1.816	0.006	0.859	0.198	1.594	0.046
1371690_at	AA849825	ADP-ribosylation factor-like 1	Arl1	0.682	0.384	0.872	0.034	0.682	0.012	0.725	0.008
1387358_at	NM_022385	ADP-ribosylation factor-like 1	Arl1	0.586	0.708	1.747	0.132	0.589	0.197	1.335	0.396
1368166_at	NM_031711	ADP-ribosylation factor-like 2	Arl2	1.392	0.608	0.943	0.974	1.110	0.291	1.780	0.041
1383813_at	BF567478	ADP-ribosylation factor-like 2 binding protein	Arl2bp	0.811	0.164	1.065	0.131	0.802	0.163	0.993	0.994
1389941_at	BE109130	ADP-ribosylation factor-like 2 binding protein	Arl2bp	0.789	0.179	0.900	0.714	0.683	0.047	0.848	0.166
1367747_at	NM_022700	ADP-ribosylation factor-like 3	Arl3	0.709	0.626	0.807	0.150	0.891	0.667	1.026	0.831
1367960_at	NM_019186	ADP-ribosylation factor-like 4A	Arl4a	3.236	0.001	4.429	0.000	2.037	0.001	3.247	0.013
1369729_at	NM_053979	ADP-ribosylation factor-like 5A	Arl5a	3.747	0.045	1.006	0.955	3.463	0.037	0.949	0.755

1372557_at	AI409182	ADP-ribosylation factor-like 6 (predicted)	Arl6_predicted	0.576	0.237	0.897	0.033	0.687	0.108	0.727	0.005
1389967_at	AA892386	ADP-ribosylation factor-like 6 interacting protein 1	Arl6ip1	0.743	0.705	1.268	0.136	0.753	0.458	1.420	0.050
1372085_at	AI237657	ADP-ribosylation factor-like 6 interacting protein 2	Arl6ip2	0.783	0.301	1.054	0.362	0.900	0.231	0.895	0.184
1371907_at	BE101624	ADP-ribosylation factor-like 6 interacting protein 4	Arl6ip4	0.534	0.253	1.090	0.375	0.373	0.009	0.988	0.896
1374387_at	BG662580	ADP-ribosylation factor-like 6 interacting protein 5	Arl6ip5	1.635	0.032	1.307	0.709	1.810	0.063	1.273	0.636
1369319_at	NM_023972	ADP-ribosylation factor-like 6 interacting protein 5	Arl6ip5	1.571	0.526	1.185	0.313	1.899	0.711	0.749	0.371
1372634_at	AI009334	ADP-ribosylhydrolase like 2 (predicted)	Adprhl2_predicted	0.823	0.137	2.129	0.005	0.695	0.052	2.462	0.005
1376810_at	AI103325	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)-like 1	Adprtl1	5.012	0.001	2.133	0.005	5.334	0.001	2.044	0.023
1387429_at	NM_012776	adrenergic receptor kinase, beta 1	Adrbk1	1.021	0.802	1.750	0.117	0.928	0.433	1.064	0.053
1370568_at	M58316	adrenergic receptor, alpha 2c	Adra2c	0.962	0.077	0.996	0.952	0.951	0.644	0.996	0.987
1368780_at	NM_013108	adrenergic receptor, beta 3	Adrb3	1.000	0.999	0.817	0.048	1.001	0.999	0.827	0.047
1387219_at	NM_012715	adrenomedullin	Adm	33.758	0.019	28.683	0.021	14.925	0.021	19.060	0.031
1371996_at	AI232384	AE binding protein 2 (predicted)	Aebp2_predicted	0.583	0.020	1.067	0.243	0.731	0.006	1.035	0.529
1385344_at	AW526794	AE binding protein 2 (predicted)	Aebp2_predicted	0.757	0.038	1.265	0.589	0.687	0.038	1.252	0.195
1381994_at	BM385862	AE binding protein 2 (predicted)	Aebp2_predicted	0.662	0.174	0.197	0.004	0.652	0.120	0.311	0.015
1385728_at	BE108006	AE binding protein 2 (predicted)	Aebp2_predicted	0.619	0.188	0.560	0.895	0.997	0.274	0.532	0.454
1374618_at	BI279751	AF4/FMR2 family, member 1 (predicted)	Aff1_predicted	1.538	0.044	1.322	0.001	1.418	0.171	1.363	0.015
1397154_at	BF403248	AF4/FMR2 family, member 1 (predicted)	Aff1_predicted	1.034	0.741	1.412	0.070	1.834	0.044	2.237	0.011
1381810_at	BF408753	AF4/FMR2 family, member 1 (predicted)	Aff1_predicted	1.001	0.985	0.953	0.714	1.005	0.994	0.944	0.938
1397386_at	AI715727	AF4/FMR2 family, member 4 (predicted)	Aff4_predicted	1.676	0.182	2.001	0.032	0.855	0.715	1.861	0.077
1378170_at	AI556957	AF4/FMR2 family, member 4 (predicted)	Aff4_predicted	1.058	0.252	1.371	0.325	0.965	0.554	1.645	0.039
1394682_at	BF290030	AF4/FMR2 family, member 4 (predicted)	Aff4_predicted	1.002	0.749	1.082	0.549	0.998	0.992	1.358	0.630
1387392_at	NM_013217	afadin	Af6	1.234	0.561	2.158	0.040	1.265	0.396	1.918	0.067
1371266_at	X76456	afamin	Afm	0.997	0.968	1.002	0.448	1.007	0.924	1.004	0.999
1373660_at	BI280384	AFG3(ATPase family gene 3)-like 1 (yeast) (predicted)	Afg3l1_predicted	0.630	0.030	0.725	0.506	0.928	0.046	1.004	0.370
1375022_at	AI548730	AFG3(ATPase family gene 3)-like 2 (yeast)	Afg3l2	0.963	0.818	1.249	0.094	0.693	0.057	1.138	0.072
1383395_at	AI028979	agmatine ureohydrolase (agmatinase)	Agmat	1.273	0.090	1.001	0.187	2.428	0.007	1.002	0.317
1370307_at	M64780	agrin	Agrn	13.958	0.001	8.509	0.001	20.715	0.000	7.054	0.001
1371703_at	AI407114	AHNAK nucleoprotein (desmoyokin)	Ahnak	42.936	0.011	2.690	0.086	42.606	0.009	8.250	0.001
1371982_at	AI411960	AIP1	Aip1	0.809	0.355	0.920	0.385	0.696	0.516	0.852	0.272
1373122_at	BI284400	ajuba homolog (Xenopus laevis)	Jub	1.208	0.560	1.448	0.248	1.085	0.634	1.128	0.702
1372879_at	BI283873	AKT1 substrate 1 (proline-rich) (predicted)	Akt1s1_predicted	0.621	0.017	0.999	0.628	0.693	0.000	0.993	0.950
1388394_at	BI282672	alanyl-tRNA synthetase	Aars	1.218	0.550	2.087	0.002	0.954	0.232	1.800	0.012
1378476_at	BM390047	Alanyl-tRNA synthetase like (predicted)	Aarsl_predicted	1.365	0.055	0.984	0.905	0.965	0.283	0.889	0.388
1371470_at	AI411895	Alcohol dehydrogenase 4 (class II), pi polypeptide	Adh4	0.623	0.291	0.404	0.023	0.600	0.113	0.786	0.306
1389548_at	BF288683	alcohol dehydrogenase, iron containing, 1	Adhfe1	1.012	0.809	0.272	0.031	1.001	0.892	0.273	0.031
1396383_at	BF412690	aldehyde dehydrogenase 3 family, member B1	Aldh3b1	0.711	0.040	0.997	0.743	0.822	0.083	0.997	0.726
1368003_at	NM_053896	aldehyde dehydrogenase family 1, subfamily A2	Aldh1a2	1.014	0.951	1.001	0.985	1.011	0.958	1.043	0.620
1368365_at	NM_031731	aldehyde dehydrogenase family 3, subfamily A2	Aldh3a2	0.302	0.100	0.228	0.000	0.152	0.013	0.427	0.009
1387344_at	AI407458	aldehyde dehydrogenase family 6, subfamily A1	Aldh6a1	0.399	0.051	0.506	0.007	0.700	0.064	0.446	0.003
1381411_at	AI548328	Aldehyde dehydrogenase family 6, subfamily A1	Aldh6a1	0.963	0.897	1.367	0.978	0.490	0.394	0.964	0.871
1371567_at	AI411279	aldehyde dehydrogenase family 7, member A1	Aldh7a1	0.404	0.197	0.258	0.001	0.473	0.015	0.330	0.000
1387867_at	BG672075	aldehyde dehydrogenase family 9, subfamily A1	Aldh9a1	0.458	0.004	0.605	0.034	0.484	0.000	0.784	0.094
1398753_at	NM_031000	aldo-keto reductase family 1, member A1	Akr1a1	1.039	0.421	1.350	0.012	1.008	0.221	1.308	0.053
1367734_at	NM_012498	aldo-keto reductase family 1, member B4 (aldose reductase)	Akr1b4	0.637	0.139	1.606	0.016	0.563	0.049	1.326	0.045
1370902_at	AI233740	aldo-keto reductase family 1, member B8	Akr1b8	1.111	0.462	60.374	0.000	0.583	0.251	16.152	0.001
1398612_at	BM383010	aldo-keto reductase family 1, member C12 (predicted)	Akr1c12_predicted	0.588	0.000	1.372	0.117	0.541	0.001	1.356	0.024
1371997_at	BM390833	aldo-keto reductase family 1, member E1	Akr1e1	0.324	0.023	0.326	0.019	0.404	0.053	0.242	0.023
1367843_at	NM_134407	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)	Akr7a2	0.449	0.014	0.446	0.252	0.447	0.026	0.605	0.080
1367617_at	NM_012495	aldolase A	Aldoa	0.765	0.223	1.349	0.009	0.664	0.011	1.272	0.037
1386998_at	NM_012497	aldolase C	Aldoc	1.000	0.754	1.886	0.167	3.821	0.053	3.838	0.020
1380448_at	AI112926	AlkB, alkylation repair homolog (E. coli) (predicted)	Alkbh_predicted	2.533	0.090	3.133	0.045	2.725	0.810	2.943	0.108
1371772_at	AI410425	alkB, alkylation repair homolog 3 (E. coli)	Alkbh3	0.947	0.784	2.215	0.008	0.779	0.245	1.885	0.007
1378726_at	AI556485	AlkB, alkylation repair homolog 4 (E. coli) (predicted)	Alkbh4_predicted	1.517	0.008	1.398	0.249	1.003	0.983	1.142	0.110
1375948_at	AI144919	AlkB, alkylation repair homolog 5 (E. coli) (predicted)	Alkbh5_predicted	1.260	0.449	2.583	0.056	0.693	0.715	1.827	0.037
1397525_at	AA848370	AlkB, alkylation repair homolog 5 (E. coli) (predicted)	Alkbh5_predicted	0.899	0.699	0.553	0.225	1.039	0.255	0.513	0.170
1397658_at	BF414555	AlkB, alkylation repair homolog 5 (E. coli) (predicted)	Alkbh5_predicted	0.985	0.781	1.003	0.958	0.846	0.166	0.765	0.067
1370806_at	AF465614	all-trans-13,14-dihydroretinol saturase	Retsat	0.484	0.739	0.698	0.130	0.401	0.118	0.720	0.222
1368686_at	NM_012901	alpha 1 microglobulin/bikunin	Ambp	0.777	0.346	1.031	0.841	1.037	0.783	0.964	0.571
1373366_at	BM389337	alpha glucosidase 2 alpha neutral subunit (predicted)	Ganab_predicted	0.681	0.715	0.429	0.003	0.875	0.196	0.461	0.001
1389989_at	BF397805	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	Atrx	0.791	0.322	0.879	0.468	0.900	0.412	0.968	0.600

1393798_at	BF398451	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	Atrx	0.835	0.526	0.774	0.172	0.825	0.491	0.808	0.125
1385006_at	BF393029	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	Atrx	0.967	0.860	0.593	0.048	1.205	0.548	0.644	0.026
1367794_at	NM_012488	alpha-2-macroglobulin	A2m	1.005	0.943	0.967	0.803	1.299	0.151	1.115	0.995
1372533_at	AI175790	Alpha-mannosidase-like protein mRNA, 3' UTR	---	1.347	0.017	1.437	0.005	2.060	0.006	1.514	0.034
1367775_at	NM_012816	alpha-methylacyl-CoA racemase	Amacr	0.382	0.064	0.406	0.007	0.418	0.061	0.743	0.266
1370838_s_at	BM387423	alpha-spectrin 2	Spna2	0.752	0.037	0.774	0.084	0.702	0.050	0.879	0.032
1397481_at	BE120751	Alstrom syndrome 1 (predicted)	Alms1_predicted	1.144	0.716	0.343	0.019	0.900	0.834	0.647	0.062
1369842_at	NM_022227	amiloride-sensitive cation channel 5, intestinal	Accn5	0.958	0.901	0.972	0.853	1.007	0.753	0.951	0.794
1372170_at	AI411530	aminoacylase 1	Acy1	0.923	0.581	1.652	0.090	0.896	0.596	1.212	0.123
1387223_at	NM_017193	aminoadipate aminotransferase	Aadat	0.664	0.210	0.816	0.835	0.446	0.155	1.027	0.343
1379353_at	AI233726	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase (predicted)	Aasdhppt_predicted	0.623	0.054	1.223	0.065	0.560	0.020	1.138	0.075
1377375_at	AA944898	aminoadipate-semialdehyde synthase (predicted)	Aass_predicted	0.304	0.060	0.213	0.000	0.330	0.009	0.202	0.007
1367720_at	NM_012899	aminolevulinate, delta-, dehydratase	Alad	0.230	0.001	0.966	0.586	0.107	0.028	0.831	0.094
1367982_at	NM_024484	aminolevulinic acid synthase 1	Alas1	1.173	0.753	2.485	0.001	0.758	0.932	1.857	0.018
1383920_at	BF408907	aminomethyltransferase (glycine cleavage system protein T)	Amt	0.712	0.190	0.834	0.983	0.780	0.131	0.827	0.763
1388360_at	BE110600	aminopeptidase puromycin sensitive	Npepps	1.259	0.298	1.728	0.069	1.260	0.242	1.342	0.105
1373570_at	AI411240	aminopeptidase-like 1 (predicted)	Npepl1_predicted	0.296	0.006	0.314	0.007	0.294	0.003	0.346	0.010
1387861_at	BI274118	amino-terminal enhancer of split	Aes	0.652	0.483	0.623	0.016	0.483	0.022	0.543	0.029
1369839_at	NM_022217	amphiphysin 1	Amph1	0.594	0.066	0.675	0.252	0.810	0.262	0.670	0.231
1389660_at	BE096098	amphoterin induced gene and ORF 3	Amigo3	0.552	0.141	0.948	0.797	0.760	0.475	0.832	0.520
1373442_at	AI169058	amplified in osteosarcoma	Os-9	0.893	0.626	0.783	0.303	0.941	0.804	0.810	0.028
1369502_a_at	NM_031502	amylase 1, salivary /// amylase 2, pancreatic /// similar to amylase 2, pancreatic	Amy1 /// Amy2 /// LOC499694	0.969	0.856	0.345	0.008	1.433	0.573	0.594	0.054
1369503_at	NM_031502	amylase 2, pancreatic	Amy2	1.437	0.959	0.356	0.022	1.073	0.994	0.462	0.043
1371571_at	BG671677	amyloid beta (A4) precursor protein	App	0.706	0.139	0.609	0.016	0.973	0.901	0.621	0.017
1371572_at	BM986220	amyloid beta (A4) precursor protein	App	0.786	0.744	0.583	0.014	0.772	0.242	0.684	0.033
1395120_at	BF403704	Amyloid beta (A4) precursor protein	App	0.980	0.950	1.202	0.209	1.049	0.743	0.869	0.562
1396876_at	BF393522	Amyloid beta (A4) precursor protein-binding, family A, member 1	Apba1	0.978	0.148	1.068	0.633	1.078	0.648	1.296	0.236
1376413_at	BF410366	Amyloid beta (A4) precursor protein-binding, family A, member 1	Apba1	1.032	0.699	0.963	0.875	0.988	0.873	0.947	0.870
1367842_at	NM_080478	amyloid beta (A4) precursor protein-binding, family B, member 1	Apbb1	0.934	0.400	0.820	0.120	0.818	0.405	0.961	0.130
1387185_at	NM_053957	amyloid beta (A4) precursor protein-binding, family B, member 3	Apbb3	0.370	0.409	0.819	0.419	0.645	0.354	0.887	0.334
1388121_at	M31322	amyloid beta (A4) precursor-like protein 2	Aplp2	0.742	0.095	0.391	0.000	0.826	0.254	0.446	0.009
1383096_at	AI235240	amyloid beta (A4) precursor-like protein 2	Aplp2	1.099	0.776	0.957	0.705	0.998	0.983	0.965	0.592
1380895_at	BE103215	Amyloid beta (A4) precursor-like protein 2	Aplp2	0.925	0.887	0.654	0.238	0.927	0.970	0.559	0.103
1378475_at	BF396428	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	Appbp2	0.283	0.029	0.388	0.003	0.250	0.007	0.270	0.033
1383091_at	BE113611	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	Appbp2	0.560	0.175	1.281	0.204	0.326	0.000	0.856	0.048
1387055_at	U90829	amyloid beta precursor protein binding protein 1	Appbp1	0.816	0.028	0.912	0.138	0.534	0.019	0.819	0.140
1383155_at	AA945854	Amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 13 (predicted)	Als2cr13_predicted	0.649	0.369	0.467	0.012	0.919	0.546	0.640	0.017
1377166_at	BI274184	amyotrophic lateral sclerosis 2 (juvenile) homolog (human)	Als2	0.783	0.443	1.238	0.132	0.706	0.618	1.161	0.029
1373744_at	BF548006	anaphase promoting complex subunit 1 (predicted)	Anapc1_predicted	0.673	0.071	1.397	0.077	0.758	0.052	1.003	0.947
1383101_at	BF556463	anaphase promoting complex subunit 10 (predicted)	Anapc10_predicted	0.826	0.324	0.950	0.106	0.926	0.986	1.032	0.822
1389087_at	AI599023	anaphase promoting complex subunit 2	Anapc2	1.019	0.598	1.776	0.062	0.786	0.516	1.598	0.201
1374163_at	BM389995	anaphase promoting complex subunit 4	Anapc4	0.734	0.111	0.666	0.143	0.852	0.249	0.692	0.058
1388417_at	BI281876	anaphase-promoting complex subunit 5 (predicted)	Anapc5_predicted	0.716	0.058	0.597	0.001	0.642	0.058	0.551	0.002
1370512_at	AF275151	androgen receptor-related apoptosis-associated protein CBL27	Cbl27	0.997	0.885	1.005	0.718	0.999	0.989	1.011	0.947
1397029_at	BF399100	Androgen receptor-related apoptosis-associated protein CBL27	Cbl27	0.998	0.983	0.880	0.226	1.000	0.985	0.923	0.211
1392891_at	AW535812	androgen-induced proliferation inhibitor (predicted)	Aprin_predicted	0.241	0.032	0.601	0.859	0.366	0.030	0.601	0.668
1377100_at	AI172172	androgen-induced proliferation inhibitor (predicted)	Aprin_predicted	1.210	0.668	1.929	0.010	1.082	0.573	1.061	0.421
1395053_at	BE104755	androgen-induced proliferation inhibitor (predicted)	Aprin_predicted	0.976	0.877	0.838	0.894	0.636	0.629	0.781	0.777
1393833_at	AI578461	angel homolog 1 (Drosophila) (predicted)	Angel1_predicted	0.756	0.152	0.824	0.191	0.684	0.000	0.586	0.053
1395884_at	BF414572	angel homolog 2 (Drosophila) (predicted)	Angel2_predicted	2.402	0.030	2.366	0.004	1.391	0.143	1.268	0.767
1398975_at	BI281948	angio-associated migratory protein (predicted)	Aamp_predicted	0.952	0.927	0.995	0.657	1.082	0.181	1.069	0.085
1395346_at	H33829	angio-associated migratory protein (predicted)	Aamp_predicted	1.000	0.995	0.995	0.594	1.000	0.993	0.999	0.904
1396100_at	BF563171	angiogenic factor with G patch and FHA domains 1	Aggf1	0.880	0.267	0.844	0.481	0.877	0.270	0.853	0.205
1383018_at	BF420082	angiopoietin-like 6 (predicted)	Angptl6_predicted	3.809	0.003	2.056	0.004	3.713	0.001	2.125	0.004
1398734_at	BE120772	Ankyrin 3, epithelial	Ank3	1.669	0.119	0.780	0.171	1.252	0.252	0.663	0.051
1370638_at	AF069525	ankyrin 3, epithelial	Ank3	0.761	0.673	0.583	0.014	0.858	0.138	0.333	0.022
1389493_at	AI411278	ankyrin repeat and BTB (POZ) domain containing 1	Abtb1	0.912	0.638	0.901	0.494	0.726	0.175	1.188	0.370
1368111_at	NM_134403	ankyrin repeat and BTB (POZ) domain containing 2	Abtb2	1.254	0.621	1.605	0.837	1.046	0.435	1.003	0.991
1373289_at	BI281935	ankyrin repeat and SOCS box-containing protein 8 (predicted)	Asb8_predicted	0.722	0.006	0.463	0.004	0.825	0.099	0.670	0.014
1373619_at	AA894306	ankyrin repeat domain 10	Ankrd10	0.710	0.073	0.802	0.051	0.724	0.221	0.772	0.032

1382620_at	BF523248	ankyrin repeat domain 11 (predicted)	Ankrd11_predicted	1.210	0.272	1.537	0.031	1.074	0.992	0.909	0.470
1381809_at	BE097847	ankyrin repeat domain 11 (predicted)	Ankrd11_predicted	1.160	0.320	3.123	0.013	0.502	0.171	3.372	0.173
1377811_at	AI577496	ankyrin repeat domain 12 (predicted)	Ankrd12_predicted	1.759	0.007	1.446	0.793	2.092	0.010	2.521	0.229
1386097_at	AW527230	ankyrin repeat domain 12 (predicted)	Ankrd12_predicted	2.023	0.041	1.773	0.159	2.117	0.013	1.415	0.092
1377505_at	BI296695	Ankyrin repeat domain 12 (predicted)	Ankrd12_predicted	1.065	0.361	1.010	0.904	0.826	0.181	0.945	0.853
1396195_at	BF550130	ankyrin repeat domain 13	Ankrd13	0.826	0.997	1.472	0.056	0.999	0.987	1.174	0.136
1373059_at	AA944355	ankyrin repeat domain 13	Ankrd13	0.964	0.998	1.236	0.059	0.877	0.322	1.497	0.003
1393022_at	BG380737	ankyrin repeat domain 13 family, member D (predicted)	Ankrd13d_predicted	1.004	0.581	1.027	0.974	1.009	0.975	1.001	0.128
1372069_at	BF284716	ankyrin repeat domain 15	Ankrd15	1.134	0.457	1.215	0.377	1.061	0.779	1.147	0.532
1371805_at	AI406508	ankyrin repeat domain 46	Ankrd46	0.423	0.004	0.441	0.028	0.544	0.004	0.469	0.011
1375212_at	AA964250	ankyrin repeat domain 52 (predicted)	Ankrd52_predicted	0.952	0.167	0.802	0.716	0.971	0.706	0.816	0.702
1394451_at	AI236455	annexin A1	Anxa1	1.939	0.285	1.207	0.448	1.000	0.210	1.619	0.219
1388445_at	BF287964	annexin A11	Anxa11	2.095	0.002	1.082	0.110	2.025	0.004	0.862	0.032
1367584_at	NM_019905	annexin A2	Anxa2	8.639	0.008	44.504	0.000	2.835	0.099	17.510	0.005
1367974_at	NM_012823	annexin A3	Anxa3	1.168	0.501	2.050	0.028	1.147	0.056	1.353	0.140
1395784_at	BF287979	Annexin A4	Anxa4	0.821	0.074	1.200	0.620	1.640	0.026	1.427	0.620
1389305_at	BM385237	annexin A4	Anxa4	1.498	0.084	1.004	0.045	1.516	0.037	1.101	0.533
1368908_at	NM_024155	annexin A4	Anxa4	1.289	0.297	1.742	0.122	1.183	0.625	2.012	0.005
1386862_at	NM_013132	annexin A5	Anxa5	1.620	0.161	1.623	0.001	1.609	0.076	1.223	0.008
1387673_a_at	BI285568	annexin A6	Anxa6	0.820	0.786	0.626	0.006	1.173	0.280	0.521	0.001
1368143_at	AI013902	annexin A7	Anxa7	1.590	0.036	2.032	0.001	1.035	0.836	1.614	0.008
1368142_at	NM_130416	annexin A7	Anxa7	2.598	0.059	1.443	0.140	1.107	0.771	1.340	0.598
1389441_at	BF416508	annexin V-binding protein ABP-10	Abp10	0.625	0.039	1.700	0.407	0.656	0.650	1.015	0.501
1388885_at	BI275921	anterior pharynx defective 1a homolog (C. elegans)	Aph1a	0.929	0.762	1.151	0.102	0.841	0.172	0.988	0.992
1395521_at	BI299174	Anterior pharynx defective 1b homolog (C. elegans)	Aph1b	1.050	0.800	1.368	0.131	1.153	0.462	1.291	0.168
1388440_at	AI408482	anterior pharynx defective 1b homolog (C. elegans)	Aph1b	1.045	0.811	0.996	0.984	1.058	0.572	0.669	0.685
1374775_at	AI714002	antigen identified by monoclonal antibody Ki-67 (predicted) /// similar to Mki67 protein (predicted) /// similar to Ki-67 (predicted)	Mki67_predicted /// RGD1564824_predicted /// RGD1566252_predicted	1.082	0.980	1.085	0.351	1.425	0.087	0.874	0.164
1380270_at	BF417890	Antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5 (predicted)	Mfi2_predicted	1.000	0.227	1.001	0.991	0.997	0.986	0.999	0.984
1368243_at	NM_030998	anti-Mullerian hormone type 2 receptor	Amhr2	0.687	0.076	1.281	0.141	1.009	0.084	1.015	0.775
1384675_at	AI029113	antisense paternally expressed gene 3	Apeg3	0.570	0.099	0.414	0.001	1.042	0.819	0.588	0.002
1372025_at	BI296467	Antisense paternally expressed gene 3	Apeg3	1.183	0.326	0.496	0.016	1.241	0.371	0.585	0.177
1370575_a_at	D50734	antizyme inhibitor 1	Azin1	1.049	0.372	2.233	0.024	1.088	0.810	1.930	0.020
1370191_at	AI411263	antizyme inhibitor 1	Azin1	0.651	0.597	0.818	0.159	0.766	0.154	0.915	0.228
1388450_at	BI279570	AP1 gamma subunit binding protein 1	Ap1gbp1	1.008	0.966	0.754	0.153	1.475	0.019	0.837	0.588
1367536_at	AI172106	APAF1 interacting protein (predicted)	Apip_predicted	0.623	0.460	1.605	0.003	0.619	0.021	1.093	0.114
1398805_at	NM_134394	APG3 autophagy 3-like (S. cerevisiae)	Apg3l	1.943	0.074	2.475	0.000	1.603	0.049	2.000	0.020
1367520_at	AI231050	apolipoprotein A-I binding protein (predicted)	Apoa1bp_predicted	1.001	0.943	1.434	0.785	1.051	0.150	1.162	0.323
1390879_at	BE098355	Apolipoprotein B editing complex 2 (predicted)	Apobec2_predicted	0.871	0.292	0.595	0.055	0.875	0.336	0.829	0.112
1396699_at	BF392736	Apolipoprotein B editing complex 3	Apobec3	1.190	0.646	0.963	0.755	1.292	0.515	0.926	0.534
1379604_at	BF284937	apolipoprotein L, 3 /// similar to RIKEN cDNA 2210421G13	Apol3 /// LOC500903	1.724	0.228	1.003	0.960	1.589	0.234	1.001	0.994
1368330_at	NM_053720	apoptosis antagonizing transcription factor	Aatf	1.179	0.083	10.605	0.001	1.209	0.127	6.278	0.004
1392423_at	AI602137	Apoptosis antagonizing transcription factor	Aatf	1.216	0.471	1.223	0.914	1.335	0.077	1.003	0.792
1367491_at	AI233249	apoptosis inhibitor 5 (predicted)	Api5_predicted	1.005	0.209	0.873	0.061	1.054	0.388	1.050	0.275
1379484_at	AA899459	apoptosis, caspase activation inhibitor (predicted)	Aven_predicted	0.967	0.366	1.235	0.469	0.861	0.244	1.226	0.063
1398944_at	BE116857	apoptotic chromatin condensation inducer 1	Acin1	1.055	0.205	1.079	0.872	1.299	0.037	1.010	0.168
1396098_at	BG380369	apoptotic chromatin condensation inducer 1	Acin1	0.984	0.941	0.828	0.278	1.307	0.513	0.842	0.114
1369197_at	NM_023979	apoptotic peptidase activating factor 1	Apaf1	2.157	0.061	1.398	0.020	3.754	0.001	2.477	0.010
1369198_at	AF218388	apoptotic peptidase activating factor 1	Apaf1	0.737	0.131	0.890	0.988	0.737	0.125	0.999	0.887
1376900_at	BM390531	aprataxin	Aptx	0.989	0.822	1.276	0.370	0.961	0.725	0.993	0.413
1386910_a_at	AF311054	apurinic/apyrimidinic endonuclease 1	Apex1	0.526	0.031	1.917	0.024	0.467	0.020	1.296	0.145
1371217_at	AF311054	apurinic/apyrimidinic endonuclease 1	Apex1	0.912	0.086	1.645	0.011	0.393	0.022	1.212	0.257
1380794_at	BE106342	Aquarius (predicted)	Aqr_predicted	1.599	0.078	0.940	0.187	1.206	0.125	1.318	0.295
1373704_at	BI294892	aquarius (predicted)	Aqr_predicted	0.622	0.211	0.718	0.688	0.508	0.024	1.036	0.775
1385017_at	AW533683	aquarius (predicted)	Aqr_predicted	0.844	0.884	1.322	0.161	1.190	0.375	1.629	0.141
1392689_at	AI105029	arachidonate lipoxygenase 3 (predicted)	Aloxe3_predicted	7.435	0.009	2.189	0.012	2.015	0.012	1.274	0.282
1391658_at	BF414061	archain 1	Arcn1	0.742	0.707	2.709	0.041	0.813	0.333	1.103	0.319
1398896_at	AA892567	archain 1	Arcn1	0.751	0.965	1.635	0.000	0.681	0.253	1.446	0.018
1387018_at	NM_053770	Arg/Abl-interacting protein ArgBP2	Argbp2	0.219	0.006	0.215	0.033	0.265	0.033	0.157	0.030
1368266_at	NM_017134	arginase 1	Arg1	0.645	0.017	0.145	0.005	0.763	0.158	0.276	0.023

1371265_at	X83264	arginine vasopressin receptor 2	Avpr2	1.000	0.950	0.998	0.213	1.002	0.989	0.999	0.630
1370252_at	BI282724	arginine vasopressin-induced 1	Avpi1	0.745	0.024	2.000	0.027	0.537	0.030	1.848	0.073
1370251_at	AI010260	arginine vasopressin-induced 1	Avpi1	1.069	0.235	1.003	0.975	1.004	0.946	0.988	0.906
1389009_at	BF418778	arginine/serine-rich coiled-coil 1	Rsrc1	0.920	0.084	1.930	0.111	0.764	0.391	1.576	0.169
1369049_at	NM_053885	arginine-glutamic acid dipeptide (RE) repeats	Rere	1.682	0.010	3.806	0.002	1.584	0.045	4.257	0.001
1379575_at	BF412271	Arginine-glutamic acid dipeptide (RE) repeats	Rere	1.268	0.431	1.293	0.271	1.095	0.760	1.256	0.280
1371890_at	AI172033	Arginine-glutamic acid dipeptide (RE) repeats	Rere	1.059	0.657	0.857	0.036	1.048	0.719	0.977	0.684
1396047_at	AW920332	arginine-glutamic acid dipeptide (RE) repeats	Rere	0.996	0.992	1.002	0.929	1.004	0.992	1.159	0.994
1372352_at	AI170666	arginine-rich, mutated in early stage tumors (predicted)	Armet_predicted	0.753	0.411	1.760	0.037	0.726	0.058	1.380	0.130
1377963_at	AW526938	Arginine-tRNA-protein transferase 1 (predicted)	Ate1_predicted	0.542	0.283	0.378	0.001	0.445	0.021	0.373	0.017
1394118_at	AA894340	Arginine-tRNA-protein transferase 1 (predicted)	Ate1_predicted	0.940	0.590	1.253	0.017	0.789	0.055	1.111	0.220
1377820_a_at	BI276525	Arginine-tRNA-protein transferase 1 (predicted)	Ate1_predicted	1.073	0.865	1.438	0.012	0.872	0.011	1.315	0.030
1368916_at	NM_021577	argininosuccinate lyase	Asl	0.974	0.654	0.501	0.006	0.917	0.251	0.502	0.001
1370964_at	BF283456	argininosuccinate synthetase	Ass	5.933	0.000	14.215	0.004	0.754	0.920	1.727	0.078
1367987_at	NM_031097	arginyl aminopeptidase (aminopeptidase B)	Rnpep	0.688	0.081	0.657	0.002	0.771	0.533	0.675	0.044
1372255_at	BF283284	arginyl-tRNA synthetase (predicted)	Rars_predicted	1.824	0.045	2.458	0.001	2.068	0.001	2.688	0.016
1377684_at	BE118562	arginyl-tRNA synthetase-like (predicted)	Rarsl_predicted	0.552	0.023	0.369	0.090	0.640	0.066	1.026	0.992
1379303_at	AA964811	ariadne homolog 2 (Drosophila) (predicted)	Arih2_predicted	1.025	0.472	1.078	0.071	1.060	0.471	1.044	0.792
1373141_at	AI236683	ariadne homolog 2 (Drosophila) (predicted)	Arih2_predicted	1.404	0.475	1.123	0.354	0.938	0.688	1.080	0.887
1375973_at	AI600108	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila)	Arih1	1.685	0.060	4.581	0.001	0.969	0.672	2.987	0.002
1393118_at	BI295562	armadillo repeat containing 1 (predicted)	Armc1_predicted	0.811	0.206	1.680	0.038	0.614	0.066	1.639	0.015
1392930_at	BI276980	armadillo repeat containing 1 (predicted)	Armc1_predicted	0.931	0.714	0.402	0.007	0.792	0.025	0.339	0.006
1373716_at	BM390404	armadillo repeat containing 5	Armc5	0.758	0.266	0.631	0.249	1.056	0.491	0.845	0.868
1393233_at	BG381676	Armadillo repeat containing 6 (predicted)	Armc6_predicted	1.027	0.471	0.998	0.928	1.001	0.546	0.980	0.984
1393220_at	AI502723	Armadillo repeat containing 8 (predicted)	Armc8_predicted	1.239	0.247	1.215	0.208	1.129	0.944	0.883	0.190
1385862_at	BF552350	armadillo repeat containing 9 (predicted)	Armc9_predicted	0.539	0.105	0.947	0.739	0.691	0.076	1.066	0.975
1397092_at	AI145850	armadillo repeat containing 9 (predicted)	Armc9_predicted	0.983	0.852	1.011	0.078	0.965	0.556	0.913	0.145
1373156_at	AI385330	armadillo repeat containing, X-linked 2	Armcx2	0.465	0.156	0.903	0.121	0.482	0.012	0.905	0.215
1371741_at	AI409891	ARP1 actin-related protein 1 homolog A (yeast) (predicted)	Actr1a_predicted	0.933	0.563	0.836	0.337	0.847	0.271	0.837	0.041
1373048_at	AI177051	ARP10 actin-related protein 10 homolog (S. cerevisiae)	Actr10	0.696	0.087	0.794	0.006	0.644	0.009	0.739	0.042
1398626_s_at	AW920881	ARP2 actin-related protein 2 homolog (yeast)	Actr2	1.057	0.552	1.586	0.027	0.868	0.211	1.145	0.080
1375424_at	BE107525	ARP2 actin-related protein 2 homolog (yeast)	Actr2	0.743	0.743	1.799	0.012	0.820	0.348	1.227	0.032
1370890_at	AI012420	ARP3 actin-related protein 3 homolog (yeast)	Actr3	1.285	0.086	2.278	0.004	1.042	0.363	1.789	0.036
1388128_at	BI292004	ARP3 actin-related protein 3 homolog (yeast)	Actr3	1.331	0.158	0.953	0.534	1.175	0.547	1.133	0.841
1376353_at	BI289883	ARP5 actin-related protein 5 homolog (yeast) (predicted)	Actr5_predicted	0.687	0.339	0.838	0.424	0.835	0.150	1.298	0.011
1373472_at	AI177008	ARP6 actin-related protein 6 homolog (yeast) (predicted)	Actr6_predicted	1.146	0.332	1.405	0.005	1.442	0.489	1.992	0.006
1373096_at	AI407406	ARP8 actin-related protein 8 homolog (S. cerevisiae) (predicted)	Actr8_predicted	0.624	0.274	0.820	0.091	0.543	0.082	0.999	0.181
1376297_at	BE112202	arrestin domain containing 1	Arrdc1	1.848	0.009	3.466	0.002	2.265	0.060	3.050	0.004
1370265_at	BF285345	arrestin, beta 2	Arrb2	1.064	0.473	0.786	0.052	1.164	0.102	1.345	0.156
1372142_at	AI406558	arsA arsenite transporter, ATP-binding, homolog 1 (bacterial)	Asna1	0.603	0.767	1.698	0.147	0.529	0.019	1.707	0.107
1368244_at	NM_080890	arsenic (+3 oxidation state) methyltransferase	As3mt	0.818	0.091	0.450	0.014	0.398	0.065	0.370	0.018
1389057_at	AI007774	ARV1 homolog (yeast) (predicted)	Arv1_predicted	1.430	0.129	1.595	0.010	1.561	0.043	1.414	0.059
1369244_at	NM_012780	aryl hydrocarbon receptor nuclear translocator	Arnt	0.941	0.779	2.217	0.008	0.999	0.287	0.995	0.254
1370510_a_at	AB012600	aryl hydrocarbon receptor nuclear translocator-like	Arntl	1.007	0.304	1.066	0.349	1.132	0.164	1.014	0.862
1388922_at	BM388677	aryl-hydrocarbon receptor-interacting protein	Aip	0.806	0.848	1.845	0.175	0.667	0.187	1.042	0.349
1389339_at	BF284062	Arylsulfatase A	Arsa	0.638	0.015	0.798	0.154	0.896	0.294	0.716	0.037
1375412_at	AI101331	Arylsulfatase B	Arsb	0.599	0.172	0.322	0.016	1.115	0.286	0.483	0.094
1380525_at	AA849862	arylsulfatase E (chondrodysplasia punctata 1)	Arse	0.497	0.126	0.835	0.204	1.449	0.338	0.977	0.899
1383120_at	BE107993	arylsulfatase K	Arsk	1.045	0.713	0.859	0.983	0.743	0.702	1.184	0.144
1385616_a_at	AI137136	ASF1 anti-silencing function 1 homolog A (S. cerevisiae) (predicted)	Asf1a_predicted	0.848	0.090	0.824	0.607	0.796	0.080	0.687	0.888
1379192_at	AW528096	ASF1 anti-silencing function 1 homolog A (S. cerevisiae) (predicted)	Asf1a_predicted	1.008	0.867	0.914	0.348	0.985	0.886	0.913	0.058
1382847_at	BG663056	ash1 (absent, small, or homeotic)-like (Drosophila) (predicted)	Ash1l_predicted	1.372	0.081	1.976	0.053	2.047	0.044	2.369	0.024
1380497_at	AW521174	ash1 (absent, small, or homeotic)-like (Drosophila) (predicted)	Ash1l_predicted	1.228	0.125	0.543	0.066	1.718	0.044	0.282	0.043
1382862_at	BE119506	Ash1 (absent, small, or homeotic)-like (Drosophila) (predicted)	Ash1l_predicted	1.665	0.254	1.099	0.543	1.231	0.578	1.292	0.934
1397969_at	BF401230	Ash1 (absent, small, or homeotic)-like (Drosophila) (predicted)	Ash1l_predicted	0.993	0.931	0.963	0.552	1.298	0.233	0.933	0.081
1371458_at	BF392740	Ash1 (absent, small, or homeotic)-like (Drosophila) (predicted)	Ash1l_predicted	0.944	0.943	0.974	0.981	1.026	0.489	1.164	0.993
1388871_at	BG378089	ash2 (absent, small, or homeotic)-like (Drosophila) (predicted)	Ash2l_predicted	0.821	0.472	1.048	0.379	0.685	0.024	0.779	0.161
1389719_at	BI287001	Ash2 (absent, small, or homeotic)-like (Drosophila) (predicted)	Ash2l_predicted	0.952	0.626	0.863	0.177	0.933	0.663	0.936	0.248
1393581_at	AW528001	asp (abnormal spindle)-like, microcephaly associated (Drosophila) (predicted)	Aspm_predicted	1.039	0.358	0.680	0.927	1.230	0.670	1.366	0.146
1374871_at	AI233343	asparaginase like 1	Asrgl1	0.834	0.411	0.745	0.211	0.687	0.091	0.407	0.137
1387925_at	U07202	asparagine synthetase	Asns	1.144	0.069	1.340	0.012	0.910	0.536	1.239	0.019

1373107_at	BF283792	asparagine-linked glycosylation 1 homolog (yeast, beta-1,4-mannosyltransferase) (predicted)	Alg1_predicted	0.554	0.088	0.756	0.190	0.434	0.034	0.404	0.075
1372902_at	BI289064	asparagine-linked glycosylation 12 homolog (yeast, alpha-1,6-mannosyltransferase) (predicted)	Alg12_predicted	0.622	0.268	2.863	0.016	0.782	0.042	1.452	0.135
1374459_at	AI178448	asparagine-linked glycosylation 2 homolog (yeast, alpha-1,3-mannosyltransferase)	Alg2	0.578	0.314	0.551	0.001	0.570	0.096	0.632	0.009
1379521_at	AW525817	asparagine-linked glycosylation 3 homolog (yeast, alpha-1,3-mannosyltransferase)	Alg3	0.722	0.627	1.441	0.011	0.458	0.004	1.134	0.045
1382019_at	AA998062	asparagine-linked glycosylation 5 homolog (yeast, dolichyl-phosphate beta-glucosyltransferase)	Alg5	0.457	0.001	0.478	0.000	0.585	0.006	0.554	0.001
1375042_at	BI287504	asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glucosyltransferase)	Alg8	0.860	0.872	0.759	0.280	1.644	0.208	1.030	0.901
1392422_at	AI236397	asparagine-linked glycosylation 9 homolog (yeast, alpha 1,2 mannosyltransferase) (predicted)	Alg9_predicted	0.639	0.228	1.201	0.193	0.525	0.009	1.479	0.057
1374437_at	BF419336	asparaginyl-tRNA synthetase	Nars	1.054	0.552	2.611	0.000	0.784	0.478	2.346	0.003
1393345_at	BF561145	Aspartate-beta-hydroxylase (predicted)	Asph_predicted	0.621	0.347	0.335	0.000	0.907	0.605	0.530	0.014
1398954_at	AI412298	aspartyl aminopeptidase	Dnpep	1.041	0.798	0.756	0.128	1.197	0.427	0.973	0.767
1372421_at	AA943766	aspartylglucosaminidase	Aga	0.588	0.458	0.328	0.005	0.555	0.014	0.394	0.007
1398795_at	NM_053799	aspartyl-tRNA synthetase	Dars	0.788	0.667	1.023	0.633	0.700	0.353	1.167	0.323
1376135_at	BI294730	aspartyl-tRNA synthetase 2 (mitochondrial)	Dars2	1.001	0.715	0.992	0.952	1.063	0.568	0.767	0.505
1388963_at	AI102087	astrotactin 1	Astn1	0.688	0.087	0.168	0.016	0.691	0.008	0.304	0.026
1392502_at	BI275796	AT hook containing transcription factor 1 (predicted)	Ahctf1_predicted	1.231	0.166	1.716	0.005	1.409	0.201	1.657	0.017
1381611_at	BF396355	AT hook containing transcription factor 1 (predicted)	Ahctf1_predicted	0.979	0.517	1.138	0.442	1.076	0.907	1.321	0.313
1389850_at	AA900926	AT rich interactive domain 1A (Swi1 like) (predicted)	Arid1a_predicted	1.362	0.138	0.919	0.242	0.806	0.959	0.747	0.000
1375524_at	AA956714	AT rich interactive domain 1A (Swi1 like) (predicted)	Arid1a_predicted	1.063	0.186	1.617	0.066	1.331	0.300	1.168	0.197
1382441_at	AI556402	AT rich interactive domain 1B (Swi1 like)	Arid1b	0.986	0.476	0.774	0.010	0.943	0.248	0.818	0.011
1381925_x_at	AI412401	AT rich interactive domain 1B (Swi1 like) /// hypothetical gene supported by NM_172157	Arid1b /// LOC497729	1.144	0.041	0.808	0.020	0.981	0.813	0.879	0.053
1397667_at	BG667685	AT rich interactive domain 1B (Swi1 like) /// hypothetical gene supported by NM_172157	Arid1b /// LOC497729	0.994	0.900	0.506	0.051	0.999	0.918	0.503	0.052
1379188_at	BI289741	AT rich interactive domain 2 (Arid-rfx like) (predicted)	Arid2_predicted	0.923	0.450	0.862	0.446	1.222	0.406	0.999	0.709
1379112_at	AW528085	AT rich interactive domain 4A (Rbp1 like) (predicted)	Arid4a_predicted	0.915	0.138	1.024	0.672	0.648	0.123	0.966	0.981
1376523_at	BF391127	AT rich interactive domain 4A (Rbp1 like) (predicted)	Arid4a_predicted	0.529	0.422	0.874	0.959	0.771	0.979	0.895	0.984
1368837_at	NM_053421	AT rich interactive domain 4B (Rbp1 like)	Arid4b	1.214	0.096	0.730	0.022	1.023	0.848	0.751	0.113
1381151_at	BF386697	AT rich interactive domain 4B (Rbp1 like)	Arid4b	1.103	0.174	1.565	0.465	1.696	0.173	0.876	0.334
1379311_at	AI177813	AT rich interactive domain 5A (Mrf1 like)	Arid5a	2.267	0.026	1.499	0.019	4.710	0.002	1.934	0.001
1382312_at	AW530903	AT rich interactive domain 5B (Mrf1 like) (predicted)	Arid5b_predicted	2.878	0.040	1.176	0.491	2.243	0.014	0.835	0.492
1381944_at	BF387066	Ataxia, cerebellar, Cayman type (caytaxin) (predicted)	Atcay_predicted	1.451	0.931	1.088	0.860	1.486	0.051	1.200	0.950
1369709_at	NM_012726	ataxin 1	Atxn1	1.224	0.194	1.947	0.682	1.002	0.995	0.916	0.992
1398874_at	BI274345	ataxin 10	Atxn10	0.449	0.089	0.816	0.093	0.563	0.001	0.804	0.094
1377138_at	AI709547	Ataxin 10	Atxn10	1.132	0.978	1.148	0.027	1.191	0.981	0.899	0.920
1391158_a_at	BE109041	ataxin 2 (predicted)	Atxn2_predicted	0.839	0.142	1.000	0.848	0.763	0.063	0.879	0.011
1388826_at	BE349657	ataxin 2-like (predicted)	Atxn2l_predicted	0.689	0.020	1.631	0.005	1.176	0.441	1.287	0.009
1390294_at	BE100986	Ataxin 7-like 4 (predicted)	Atxn7l4_predicted	0.277	0.042	0.813	0.796	0.278	0.007	1.070	0.662
1372375_at	BF395615	ATG16 autophagy related 16-like 1 (S. cerevisiae) (predicted)	Atg16l1_predicted	0.674	0.029	1.440	0.082	0.912	0.609	1.230	0.048
1391064_at	BI295177	ATG16 autophagy related 16-like 2 (S. cerevisiae) (predicted)	Atg16l2_predicted	1.076	0.983	0.897	0.042	1.248	0.681	0.885	0.012
1374831_at	AI172579	ATH1, acid trehalase-like 1 (yeast) (predicted)	Athl1_predicted	0.768	0.058	0.285	0.034	1.442	0.580	0.383	0.016
1374922_at	AI013096	ATP binding domain 1 family, member B (predicted)	Atpbd1b_predicted	1.077	0.783	1.845	0.037	1.110	0.261	1.526	0.004
1393604_at	BE106064	ATP binding domain 1 family, member C	Atpbd1c	0.850	0.503	0.742	0.237	0.831	0.503	0.741	0.230
1367854_at	NM_016987	ATP citrate lyase	Acly	0.609	0.001	0.609	0.000	0.665	0.001	0.714	0.030
1371892_at	BI274263	ATP synthase mitochondrial F1 complex assembly factor 2 (predicted)	Atpaf2_predicted	1.367	0.446	0.795	0.102	1.635	0.043	1.210	0.011
1398855_at	AA893531	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	Atp5f1	0.589	0.384	0.714	0.033	0.559	0.095	0.694	0.008
1367620_at	NM_053756	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3	Atp5g3	0.835	0.574	0.869	0.024	0.684	0.059	0.859	0.022
1367599_at	NM_017311	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	Atp5g1	0.618	0.346	0.745	0.042	0.560	0.006	0.681	0.108
1370207_at	AI170772	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2 /// similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2 (predicted)	Atp5g2 /// RGD1566212_predicted	0.664	0.824	1.023	0.243	0.496	0.340	0.923	0.135
1367622_at	NM_019383	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	Atp5h	0.749	0.208	0.810	0.034	0.629	0.023	0.673	0.069
1387019_at	NM_080481	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e	Atp5i	0.716	0.932	0.794	0.033	1.206	0.855	0.857	0.354
1370230_at	BG666602	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	Atp5j	0.840	0.444	0.770	0.067	0.957	0.715	0.855	0.036
1370378_at	J05266	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	Atp5a1	0.449	0.292	0.438	0.001	0.528	0.175	0.539	0.004
1370275_at	M19044	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	Atp5b	0.711	0.227	0.972	0.296	0.638	0.021	0.918	0.023
1380070_at	BG377244	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	Atp5b	0.787	0.515	0.785	0.065	0.748	0.134	0.807	0.264
1370278_at	U00926	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	Atp5d	0.603	0.430	0.828	0.302	0.479	0.001	0.857	0.291
1370284_at	AF010323	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	Atp5e	0.847	0.790	0.593	0.009	0.791	0.011	0.570	0.202
1370918_a_at	BI275939	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	Atp5c1	0.534	0.206	0.693	0.003	0.412	0.032	0.672	0.003
1370276_at	D13127	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	Atp5o	0.606	0.368	0.610	0.048	0.485	0.015	0.665	0.027
1380339_at	AW520369	ATP/GTP binding protein 1 (predicted)	Agtpbp1_predicted	1.001	0.415	1.539	0.009	1.001	0.577	0.998	0.985
1391891_at	AI711114	ATP/GTP binding protein 1 (predicted)	Agtpbp1_predicted	0.954	0.564	1.575	0.028	0.924	0.458	1.019	0.533
1373378_at	BF410522	ATP/GTP binding protein 1 (predicted)	Agtpbp1_predicted	0.858	0.610	1.528	0.014	0.822	0.272	1.484	0.046
1379561_at	AW433567	ATPase family, AAA domain containing 1	Atad1	3.045	0.011	1.431	0.030	4.072	0.001	2.128	0.007

1376599_at	AW915567	ATPase family, AAA domain containing 2 (predicted)	Atad2_predicted	0.886	0.246	0.675	0.085	0.632	0.321	0.673	0.089
1369588_a_at	NM_012915	ATPase inhibitory factor 1	Atpif1	1.135	0.442	1.136	0.903	1.031	0.645	1.086	0.901
1371229_at	M35300	ATPase inhibitory factor 1	Atpif1	1.104	0.956	1.209	0.078	0.833	0.299	1.127	0.400
1371925_at	AA893621	ATPase type 13A1 (predicted)	Atp13a1_predicted	1.746	0.005	1.613	0.002	2.438	0.021	2.101	0.025
1396884_at	BF404113	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1 (predicted)	Atp8a1_predicted	4.200	0.021	1.022	0.572	4.106	0.218	1.534	0.884
1398164_at	BF406182	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1 (predicted)	Atp8a1_predicted	1.508	0.056	1.002	0.451	0.961	0.987	0.962	0.914
1393515_at	AI145077	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1 (predicted)	Atp8a1_predicted	1.490	0.432	0.774	0.767	1.009	0.397	1.005	0.998
1370426_a_at	AI175492	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	Atp2a2	0.514	0.026	0.626	0.002	0.523	0.020	0.650	0.006
1398862_at	J04024	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	Atp2a2	0.410	0.026	0.507	0.040	0.336	0.012	0.518	0.018
1369065_a_at	NM_017290	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	Atp2a2	0.397	0.045	0.214	0.002	0.453	0.023	0.248	0.020
1397224_at	AW534277	ATPase, Ca++ transporting, plasma membrane 1	Atp2b1	0.613	0.007	0.525	0.004	0.598	0.010	0.500	0.008
1370050_at	NM_053311	ATPase, Ca++ transporting, plasma membrane 1	Atp2b1	0.571	0.070	0.778	0.063	0.734	0.191	0.764	0.029
1394714_at	BF386268	ATPase, Ca++ transporting, plasma membrane 1	Atp2b1	0.517	0.123	1.694	0.511	1.159	0.608	1.309	0.325
1386426_at	AI137869	ATPase, Ca++ transporting, plasma membrane 1	Atp2b1	0.568	0.136	1.045	0.863	0.661	0.076	0.915	0.934
1380195_at	AI145357	ATPase, Ca++ transporting, plasma membrane 1	Atp2b1	0.787	0.654	2.362	0.165	0.976	0.851	1.038	0.901
1368698_at	J03754	ATPase, Ca++ transporting, plasma membrane 2	Atp2b2	0.164	0.009	0.076	0.000	0.506	0.031	0.062	0.023
1368477_at	NM_012914	ATPase, Ca++ transporting, ubiquitous	Atp2a3	1.294	0.001	0.748	0.041	1.206	0.017	0.762	0.191
1371165_a_at	AF458230	ATPase, Ca++ transporting, ubiquitous	Atp2a3	2.119	0.115	0.360	0.091	1.536	0.997	0.285	0.061
1377386_at	AI029639	ATPase, Ca++-sequestering	Atp2c1	2.183	0.028	1.540	0.101	1.252	0.052	1.280	0.849
1387126_at	NM_131907	ATPase, Ca++-sequestering	Atp2c1	0.784	0.359	0.440	0.023	0.867	0.240	0.604	0.002
1391693_at	BM384161	ATPase, Class I, type 8B, member 1 (predicted)	Atp8b1_predicted	1.516	0.344	1.438	0.281	0.953	0.997	0.303	0.048
1398755_at	NM_130823	ATPase, H transporting, lysosomal V0 subunit c	Atp6v0c	0.995	0.805	1.480	0.095	0.635	0.093	1.276	0.484
1374431_at	BE120644	ATPase, H transporting, lysosomal V1 subunit A (predicted)	Atp6v1a1_predicted	0.867	0.072	0.630	0.002	0.792	0.195	0.886	0.054
1382048_at	BI289589	ATPase, H transporting, lysosomal V1 subunit A (predicted)	Atp6v1a1_predicted	0.816	0.934	0.653	0.132	0.840	0.464	0.799	0.463
1387664_at	NM_057213	ATPase, H transporting, lysosomal V1 subunit B2	Atp6v1b2	1.118	0.634	5.359	0.002	1.035	0.549	4.367	0.002
1371402_at	BM390600	ATPase, H transporting, lysosomal V1 subunit B2	Atp6v1b2	1.026	0.724	1.190	0.014	1.007	0.152	1.210	0.057
1398781_at	NM_053884	ATPase, H transporting, lysosomal V1 subunit F	Atp6v1f	0.975	0.968	1.572	0.029	0.707	0.039	1.396	0.198
1367873_at	NM_031785	ATPase, H+ transporting, lysosomal accessory protein 1	Atp6ap1	0.825	0.088	0.743	0.162	0.680	0.014	0.640	0.027
1379255_at	AI012226	ATPase, H+ transporting, lysosomal accessory protein 2	Atp6ap2	1.082	0.393	1.572	0.001	0.902	0.492	1.446	0.001
1396279_at	BG663051	ATPase, H+ transporting, lysosomal accessory protein 2	Atp6ap2	0.672	0.997	1.234	0.235	1.112	0.921	1.255	0.279
1380730_at	BE110564	ATPase, H+ transporting, lysosomal V0 subunit a isoform 2 (predicted)	Atp6v0a2_predicted	0.752	0.073	1.359	0.094	1.350	0.107	0.786	0.345
1382576_at	BE349645	ATPase, H+ transporting, lysosomal V0 subunit a isoform 2 (predicted)	Atp6v0a2_predicted	0.635	0.130	0.939	0.020	0.636	0.112	0.901	0.026
1372648_at	BI291338	ATPase, H+ transporting, lysosomal V0 subunit a isoform 2 (predicted)	Atp6v0a2_predicted	1.029	0.788	0.775	0.244	0.804	0.637	0.678	0.280
1387045_at	NM_031604	ATPase, H+ transporting, lysosomal V0 subunit A1	Atp6v0a1	0.725	0.040	0.682	0.044	0.948	0.286	0.898	0.160
1398930_at	BI278546	ATPase, H+ transporting, V0 subunit B (predicted)	Atp6v0b_predicted	0.983	0.602	1.741	0.003	0.866	0.022	1.621	0.015
1388365_at	BI276424	ATPase, H+ transporting, V0 subunit D isoform 1	Atp6v0d1	0.659	0.225	0.632	0.000	0.699	0.017	0.763	0.002
1367724_a_at	NM_053578	ATPase, H+ transporting, V0 subunit E isoform 1	Atp6v0e1	0.796	0.762	0.812	0.011	0.731	0.039	0.812	0.083
1372907_at	BI285242	ATPase, H+ transporting, V0 subunit E isoform 2	Atp6v0e2	0.506	0.176	0.917	0.718	0.595	0.004	0.924	0.127
1374396_at	BI293306	ATPase, H+ transporting, V1 subunit C, isoform 1	Atp6v1c1	0.864	0.175	2.195	0.001	0.657	0.071	1.691	0.026
1388325_at	BF281358	ATPase, H+ transporting, V1 subunit D	Atp6v1d	0.863	0.123	1.980	0.000	0.756	0.008	1.951	0.004
1371564_at	AI169159	ATPase, H+ transporting, V1 subunit E isoform 1	Atp6v1e1	0.615	0.212	0.870	0.081	0.626	0.031	0.935	0.440
1367585_a_at	M28647	ATPase, Na+/K+ transporting, alpha 1 polypeptide	Atp1a1	0.552	0.697	0.507	0.004	0.532	0.133	0.726	0.011
1386911_at	NM_012505	ATPase, Na+/K+ transporting, alpha 2 polypeptide	Atp1a2	0.967	0.067	1.001	0.977	0.968	0.070	0.965	0.974
1367814_at	M14137	ATPase, Na+/K+ transporting, beta 1 polypeptide	Atp1b1	0.619	0.275	0.777	0.008	0.658	0.060	0.705	0.022
1386937_at	AI232036	ATPase, Na+/K+ transporting, beta 1 polypeptide	Atp1b1	0.556	0.280	0.576	0.000	0.588	0.077	0.640	0.001
1377195_at	BF406252	ATPase, Na+/K+ transporting, beta 3 polypeptide	Atp1b3	0.532	0.013	1.367	0.153	0.916	0.448	1.529	0.068
1398300_at	BI303655	ATPase, Na+/K+ transporting, beta 3 polypeptide	Atp1b3	0.516	0.327	0.612	0.015	0.451	0.088	0.622	0.030
1394490_at	AI502114	ATP-binding cassette, sub-family A (ABC1), member 1	Abca1	1.012	0.981	0.379	0.000	0.902	0.509	0.353	0.028
1383355_at	AW918387	ATP-binding cassette, sub-family A (ABC1), member 1 /// hypothetical gene supported by NM_178095	Abca1 /// LOC497803	1.180	0.395	3.216	0.010	0.753	0.273	2.261	0.004
1384381_at	BF284523	ATP-binding cassette, sub-family A (ABC1), member 1 /// hypothetical gene supported by NM_178095	Abca1 /// LOC497803	1.843	0.882	3.309	0.220	0.711	0.602	1.310	0.494
1368081_at	NM_024396	ATP-binding cassette, sub-family A (ABC1), member 2	Abca2	0.826	0.219	0.753	0.069	0.803	0.089	0.789	0.005
1384469_at	AI502224	ATP-binding cassette, sub-family A (ABC1), member 5	Abca5	0.880	0.350	0.989	0.397	0.985	0.497	1.010	0.858
1383229_at	BE103071	ATP-binding cassette, sub-family A (ABC1), member 7	Abca7	0.945	0.809	0.719	0.325	1.128	0.618	1.047	0.276
1370583_s_at	AY082609	ATP-binding cassette, sub-family B (MDR/TAP), member 1 /// ATP-binding cassette, sub-family B (MDR/TAP), member 1A	Abcb1 /// Abcb1a	10.503	0.017	10.515	0.001	32.801	0.003	23.157	0.001
1390781_at	AA900411	ATP-binding cassette, sub-family B (MDR/TAP), member 10	Abcb10	0.660	0.185	0.590	0.968	0.680	0.991	1.155	0.763
1370465_at	AF257746	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	Abcb1a	4.832	0.021	17.261	0.001	6.314	0.006	14.199	0.005
1370464_at	AF286167	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	Abcb1a	1.375	0.027	9.620	0.001	1.913	0.009	4.538	0.003
1369161_at	NM_012690	ATP-binding cassette, sub-family B (MDR/TAP), member 4	Abcb4	2.633	0.112	1.346	0.340	2.215	0.035	1.233	0.322
1368159_at	NM_080582	ATP-binding cassette, sub-family B (MDR/TAP), member 6	Abcb6	0.255	0.033	1.082	0.182	0.324	0.075	0.943	0.166
1368484_at	NM_022238	ATP-binding cassette, sub-family B (MDR/TAP), member 9	Abcb9	0.806	0.591	0.520	0.005	0.811	0.630	0.547	0.001

1371005_at	AI059506	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	Abcc1	1.871	0.122	2.604	0.046	3.367	0.025	2.608	0.002
1381500_at	BF386748	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	Abcc1	1.077	0.382	1.465	0.136	1.498	0.154	1.158	0.523
1369698_at	AF072816	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	Abcc3	1.649	0.046	1.214	0.020	1.363	0.041	1.287	0.032
1379402_at	BE100533	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	Abcc4	0.415	0.053	0.733	0.138	0.972	0.851	1.203	0.367
1387030_at	NM_053924	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	Abcc5	1.957	0.121	1.230	0.453	3.266	0.022	1.423	0.475
1389886_at	AI406942	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	Abcc5	1.000	0.847	0.958	0.706	1.676	0.058	0.956	0.465
1391178_at	BE110066	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	Abcc8	0.797	0.492	0.796	0.509	1.673	0.325	1.275	0.439
1369632_a_at	AB052294	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	Abcc8	1.030	0.551	0.647	0.073	0.905	0.545	0.541	0.054
1368561_at	NM_033352	ATP-binding cassette, sub-family D (ALD), member 2	Abcd2	1.327	0.621	0.278	0.055	0.977	0.917	0.627	0.143
1368057_at	NM_012804	ATP-binding cassette, sub-family D (ALD), member 3	Abcd3	0.382	0.003	0.202	0.001	0.479	0.003	0.261	0.008
1392570_at	BI295850	ATP-binding cassette, sub-family D (ALD), member 4	Abcd4	0.984	0.843	1.007	0.830	1.003	0.933	1.010	0.572
1388810_at	BI278966	ATP-binding cassette, sub-family E (OABP), member 1	Abce1	0.661	0.153	0.862	0.866	0.733	0.082	0.871	0.806
1398876_at	BG380494	ATP-binding cassette, sub-family F (GCN20), member 1	Abcf1	0.684	0.147	1.314	0.040	0.898	0.110	1.363	0.323
1389608_at	AI235192	ATP-binding cassette, sub-family F (GCN20), member 2 (predicted)	Abcf2_predicted	0.900	0.682	1.240	0.114	0.762	0.541	1.217	0.015
1371456_at	BI281218	ATP-binding cassette, sub-family F (GCN20), member 3	Abcf3	0.626	0.196	1.159	0.102	0.607	0.017	0.987	0.529
1377280_at	BF390931	ATP-binding cassette, sub-family F (GCN20), member 3	Abcf3	0.997	0.689	0.970	0.416	0.999	0.885	0.967	0.446
1368103_at	NM_053502	ATP-binding cassette, sub-family G (WHITE), member 1	Abcg1	1.592	0.058	1.117	0.268	1.935	0.017	1.530	0.017
1373995_at	AW523571	ATP-binding cassette, sub-family G (WHITE), member 1	Abcg1	1.766	0.127	0.276	0.166	2.591	0.001	0.585	0.639
1380577_at	AI175616	ATP-binding cassette, sub-family G (WHITE), member 2	Abcg2	0.907	0.540	0.999	0.907	1.318	0.010	1.005	0.744
1393217_at	BF282804	ATP-binding cassette, sub-family G (WHITE), member 3	Abcg3	8.229	0.000	2.614	0.002	14.391	0.000	3.583	0.001
1386972_at	NM_017228	atrophin 1	Atn1	1.395	0.004	1.771	0.017	0.910	0.749	1.288	0.043
1387127_at	NM_031351	attractin	Atrn	0.576	0.132	0.389	0.006	0.528	0.035	0.380	0.003
1367945_at	NM_053359	ATX1 (antioxidant protein 1) homolog 1 (yeast)	Atox1	0.639	0.825	0.591	0.012	0.739	0.145	0.497	0.095
1372149_at	BM389502	AU RNA binding protein/enoyl-coenzyme A hydratase (predicted)	Auh_predicted	0.768	0.387	0.484	0.032	1.014	0.968	0.531	0.083
1398916_at	AI104388	aurora kinase A interacting protein 1	Aurkaip1	0.662	0.064	1.430	0.004	0.611	0.023	1.378	0.007
1375008_at	BF410389	aurora kinase C (predicted)	Aurkc_predicted	0.699	0.274	1.149	0.520	0.873	0.334	1.034	0.363
1371614_at	AI169001	autophagy-related 12 (yeast)	Atg12	1.013	0.706	1.966	0.001	0.729	0.071	1.734	0.003
1382735_at	BF563278	autophagy-related 12 (yeast)	Atg12	0.906	0.847	2.085	0.048	0.841	0.608	1.768	0.079
1399042_at	AI228455	autophagy-related 4B (yeast)	Atg4b	0.725	0.018	1.788	0.014	0.573	0.011	1.208	0.154
1389273_at	BG374362	autophagy-related 4B (yeast)	Atg4b	0.554	0.186	0.497	0.001	0.598	0.237	0.937	0.092
1392744_at	AI179130	autophagy-related 7 (yeast)	Atg7	1.032	0.140	0.996	0.084	1.161	0.069	1.009	0.931
1387056_at	NM_024405	axin 1	Axin1	1.136	0.433	1.790	0.021	1.098	0.879	1.389	0.071
1368291_at	NM_021752	baculoviral IAP repeat-containing 2	Birc2	2.744	0.143	3.049	0.000	3.160	0.021	2.160	0.018
1370113_at	NM_023987	baculoviral IAP repeat-containing 3	Birc3	75.086	0.002	52.503	0.000	75.272	0.001	52.961	0.000
1369248_a_at	AF304333	baculoviral IAP repeat-containing 4	Birc4	0.998	0.989	1.017	0.493	1.558	0.058	1.000	0.998
1381871_at	BM383359	BAI1-associated protein 1 (predicted)	Baiap1_predicted	2.014	0.084	1.042	0.869	0.927	0.913	1.000	0.065
1375941_at	BI292120	BAI1-associated protein 2-like 1	Baiap2l1	3.099	0.032	2.447	0.002	2.724	0.010	2.120	0.010
1368509_at	NM_053618	Bardet-Biedl syndrome 2 homolog (human)	Bbs2	0.498	0.007	0.236	0.000	0.563	0.232	0.529	0.006
1378656_at	BE105572	Bardet-Biedl syndrome 5 homolog (human) (predicted)	Bbs5_predicted	1.010	0.721	1.106	0.904	0.740	0.046	0.755	0.104
1380515_at	AI170730	Bardet-Biedl syndrome 7	Bbs7	1.146	0.714	1.198	0.139	0.737	0.533	1.226	0.939
1367820_at	NM_053631	barrier to autointegration factor 1	Banf1	1.036	0.824	1.716	0.010	0.942	0.700	2.083	0.007
1387212_at	NM_012863	basic helix-loop-helix domain containing, class B, 8	Bhlhb8	0.365	0.014	0.818	0.978	0.363	0.016	0.852	0.144
1381121_at	AW533010	Basic helix-loop-helix domain containing, class B2	Bhlhb2	2.526	0.012	7.293	0.000	1.929	0.169	2.230	0.052
1379483_at	AI548256	Basic helix-loop-helix domain containing, class B2	Bhlhb2	4.066	0.081	10.401	0.017	2.279	0.210	9.229	0.014
1369415_at	NM_053328	basic helix-loop-helix domain containing, class B2	Bhlhb2	1.177	0.681	6.317	0.016	1.060	0.396	3.691	0.004
1368511_at	NM_133303	basic helix-loop-helix domain containing, class B3	Bhlhb3	1.135	0.033	3.370	0.001	0.722	0.479	2.833	0.005
1388554_at	AI229287	basic leucine zipper and W2 domains 1	Bzw1	1.234	0.260	0.655	0.019	1.226	0.116	0.771	0.034
1371949_at	BM390332	basic leucine zipper and W2 domains 1	Bzw1	1.100	0.391	4.246	0.000	0.977	0.530	3.216	0.001
1370258_at	BI303268	basic leucine zipper and W2 domains 2	Bzw2	0.705	0.336	1.637	0.055	0.737	0.190	1.382	0.051
1377329_at	BE113460	Basic leucine zipper and W2 domains 2	Bzw2	1.007	0.991	1.004	0.936	1.009	0.995	0.999	0.983
1371384_at	BG666659	basic transcription factor 3	Btf3	0.932	0.712	1.321	0.361	0.778	0.378	1.136	0.920
1381838_at	AI548281	Basic, immunoglobulin-like variable motif containing (predicted)	Bivm_predicted	0.949	0.318	0.792	0.057	0.519	0.318	0.941	0.883
1367643_at	NM_012783	basigin	Bsg	0.822	0.689	0.625	0.020	0.886	0.398	0.639	0.004
1372588_at	AA944403	basophilic leukemia expressed protein BLES03	Bles03	1.267	0.958	1.204	0.317	2.493	0.019	1.515	0.035
1372956_at	BF420425	Bat4 gene	Bat4	1.116	0.610	1.000	0.281	0.823	0.390	0.931	0.096
1387629_at	NM_022261	B-box and SPRY domain containing	Bspry	1.217	0.547	0.965	0.590	1.036	0.278	0.966	0.526
1368118_at	NM_031328	B-cell CLL/lymphoma 10	Bcl10	1.816	0.209	1.555	0.038	1.841	0.223	1.750	0.002
1391420_at	AA964818	B-cell CLL/lymphoma 11A (zinc finger protein)	Bcl11a	1.085	0.332	1.439	0.871	0.851	0.220	1.025	0.997
1383010_at	AW531880	B-cell CLL/lymphoma 11A (zinc finger protein)	Bcl11a	0.933	0.883	0.796	0.109	1.616	0.123	1.031	0.103
1392933_a_at	BF288704	B-cell CLL/lymphoma 7A (predicted)	Bcl7a_predicted	1.099	0.265	1.079	0.562	0.434	0.116	1.141	0.343
1391855_at	AW534002	B-cell CLL/lymphoma 7A (predicted)	Bcl7a_predicted	0.991	0.904	1.476	0.012	0.812	0.042	1.274	0.136

1384335_at	BE111885	B-cell CLL/lymphoma 9-like (predicted)	Bcl9l_predicted	1.148	0.064	0.882	0.295	1.982	0.050	1.128	0.035
1384944_at	BE116855	B-cell leukemia/lymphoma 11B (predicted)	Bcl11b_predicted	1.013	0.180	1.415	0.557	1.250	0.580	1.768	0.576
1398482_at	AI411774	B-cell leukemia/lymphoma 3 (predicted)	Bcl3_predicted	26.384	0.009	15.921	0.002	51.593	0.007	15.391	0.006
1379368_at	AI237606	B-cell leukemia/lymphoma 6 (predicted)	Bcl6_predicted	1.902	0.105	9.635	0.000	2.234	0.098	10.862	0.000
1393641_at	AA925583	B-cell linker	Blnk	23.767	0.001	12.632	0.000	11.652	0.002	3.029	0.011
1372709_at	AI172204	B-cell receptor-associated protein 29	Bcap29	0.863	0.182	3.463	0.008	0.953	0.079	2.983	0.000
1367503_at	AI409930	B-cell receptor-associated protein 31	Bcap31	0.620	0.664	0.816	0.131	0.784	0.108	0.881	0.174
1367657_at	NM_017258	B-cell translocation gene 1, anti-proliferative	Btg1	1.414	0.019	1.475	0.001	1.649	0.012	1.734	0.002
1386995_at	BI288701	B-cell translocation gene 2, anti-proliferative	Btg2	1.174	0.781	2.332	0.006	0.756	0.819	1.508	0.042
1386994_at	NM_017259	B-cell translocation gene 2, anti-proliferative	Btg2	0.867	0.820	0.634	0.013	0.729	0.053	0.648	0.001
1368072_at	NM_019290	B-cell translocation gene 3	Btg3	0.642	0.074	1.100	0.136	0.532	0.015	0.919	0.845
1382993_at	AI236152	Bcl-2 binding component 3	Bbc3	2.398	0.008	2.960	0.004	2.681	0.014	1.967	0.107
1387805_at	NM_053420	BCL2/adenovirus E1B 19 kDa-interacting protein 3	Bnip3	0.533	0.220	1.656	0.016	0.377	0.044	1.682	0.012
1386978_at	NM_080888	BCL2/adenovirus E1B 19 kDa-interacting protein 3-like	Bnip3l	0.587	0.077	0.584	0.001	0.532	0.004	0.572	0.019
1367898_at	AF441118	BCL2/adenovirus E1B 19 kDa-interacting protein 3-like	Bnip3l	0.938	0.421	0.809	0.031	0.666	0.003	0.718	0.033
1380092_at	AI146096	BCL2/adenovirus E1B 19kDa-interacting protein 1	Bnip1	1.039	0.638	0.782	0.075	0.905	0.059	1.082	0.084
1367863_at	NM_080897	BCL2/adenovirus E1B 19kDa-interacting protein 1	Bnip1	0.918	0.714	0.952	0.454	0.720	0.048	1.099	0.577
1377634_at	AI715220	BCL2/adenovirus E1B 19kDa-interacting protein 1, NIP2 (predicted)	Bnip2_predicted	2.452	0.010	1.400	0.004	1.528	0.092	1.365	0.042
1390133_at	AI178277	BCL2/adenovirus E1B 19kDa-interacting protein 1, NIP2 (predicted)	Bnip2_predicted	1.212	0.168	0.652	0.092	2.181	0.029	0.826	0.113
1368066_at	NM_053812	BCL2-antagonist/killer 1	Bak1	6.454	0.079	3.832	0.000	5.766	0.000	6.807	0.011
1375550_at	BI280304	Bcl2-associated athanogene 1 (predicted)	Bag1_predicted	0.941	0.789	1.839	0.009	0.986	0.195	1.216	0.111
1390026_at	AI231792	Bcl2-associated athanogene 3	Bag3	0.943	0.705	2.654	0.099	0.697	0.525	1.546	0.251
1382376_at	BI297220	BCL2-associated athanogene 4	Bag4	1.122	0.466	1.072	0.898	0.979	0.923	1.481	0.034
1376261_at	BI282898	BCL2-associated athanogene 5	Bag5	1.034	0.052	1.500	0.021	0.482	0.009	1.165	0.036
1373868_at	AI717547	BCL2-associated transcription factor 1	Bclaf1	1.579	0.005	2.629	0.002	1.771	0.008	2.300	0.004
1391875_at	AI176106	BCL2-associated transcription factor 1	Bclaf1	1.415	0.217	2.747	0.083	1.178	0.090	1.978	0.023
1388752_at	AI408078	BCL2-associated transcription factor 1	Bclaf1	0.947	0.502	0.820	0.013	1.453	0.098	1.012	0.149
1369122_at	AF235993	Bcl2-associated X protein	Bax	1.165	0.077	2.337	0.000	1.238	0.200	2.317	0.002
1372279_at	AA892271	BCL2-like 13 (apoptosis facilitator) (predicted)	Bcl2l13_predicted	0.883	0.656	2.710	0.096	0.957	0.513	2.697	0.004
1380540_at	AI547392	BCL2-like 13 (apoptosis facilitator) (predicted)	Bcl2l13_predicted	1.364	0.735	2.326	0.686	1.016	0.625	1.069	0.852
1376115_at	AA964244	BCL2-like 13 (apoptosis facilitator) (predicted)	Bcl2l13_predicted	0.844	0.803	1.598	0.031	1.013	0.168	1.361	0.062
1393707_at	AW527957	Bcl2-like 2	Bcl2l2	0.464	0.021	0.493	0.001	0.500	0.013	0.566	0.001
1385592_at	BI289386	Bcl6 interacting corepressor (predicted)	Bcor_predicted	1.342	0.188	2.481	0.006	1.526	0.133	1.764	0.001
1374886_at	BF402630	BCS1-like (yeast)	Bcs1l	0.318	0.000	1.284	0.094	0.497	0.078	0.957	0.402
1377570_at	AI059563	Beaded filament structural protein 1	Bfsp1	1.001	0.994	0.999	0.287	1.004	0.407	1.000	0.504
1367457_at	NM_053739	beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)	Becn1	0.837	0.111	0.908	0.013	0.856	0.143	0.849	0.083
1371811_at	BI278232	Bernardinelli-Seip congenital lipodystrophy 2 homolog (human)	Bscl2	0.352	0.035	0.439	0.022	0.256	0.019	0.438	0.014
1370913_at	AI409634	Best5 protein	Best5	1019.519	0.011	107.260	0.015	1285.111	0.010	150.754	0.011
1371633_at	BI285669	beta catenin-like 1	Ctnnbl1	0.632	0.061	0.640	0.001	0.758	0.109	0.598	0.012
1370907_at	M83143	beta galactoside alpha 2,6 sialyltransferase 1	St6gal1	0.225	0.039	0.153	0.000	0.256	0.061	0.208	0.016
1385144_at	AW524749	Beta galactoside alpha 2,6 sialyltransferase 2	St6gal2	1.423	0.051	0.561	0.052	1.297	0.244	0.338	0.023
1373014_at	BE111966	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I) (predicted)	B3gat3_predicted	0.455	0.033	0.795	0.050	0.495	0.039	0.709	0.028
1371440_at	AW916647	Beta-2 microglobulin	B2m	7.040	0.000	6.195	0.001	9.634	0.000	9.111	0.002
1367595_s_at	NM_012512	beta-2 microglobulin	B2m	1.851	0.006	1.617	0.000	2.131	0.006	1.806	0.001
1373247_at	AW435407	Beta-site APP cleaving enzyme 1	Bace1	0.757	0.155	0.870	0.092	0.935	0.663	0.881	0.046
1377390_at	BG381587	beta-site APP-cleaving enzyme 2	Bace2	2.947	0.063	2.968	0.004	2.405	0.061	3.042	0.003
1374654_at	BE109603	beta-transducin repeat containing	Btrc	1.191	0.203	2.260	0.091	0.581	0.113	1.618	0.023
1392557_at	BF389151	Bicaudal C homolog 1 (Drosophila) (predicted)	Bicc1_predicted	0.748	0.291	0.727	0.087	0.965	0.867	0.795	0.068
1383822_at	AI029990	bicaudal D homolog 2 (Drosophila)	Bicd2	1.434	0.165	2.111	0.007	0.735	0.102	1.440	0.034
1388733_at	AI177631	bifunctional apoptosis regulator	Bfar	1.689	0.004	1.213	0.031	1.547	0.001	1.210	0.004
1395377_at	BE107113	bifunctional apoptosis regulator	Bfar	1.550	0.064	1.231	0.667	1.936	0.023	0.999	0.996
1368164_at	NM_053850	biliverdin reductase A	Blvra	0.560	0.021	0.802	0.901	0.705	0.096	1.001	0.906
1392539_at	AI009013	biliverdin reductase B (flavin reductase (NADPH)) (predicted)	Blvrb_predicted	1.215	0.946	0.770	0.768	0.702	0.068	0.776	0.398
1372137_at	BI279854	biogenesis of lysosome-related organelles complex-1, subunit 1 (predicted)	Bloc1s1_predicted	0.871	0.332	0.846	0.115	0.677	0.868	0.911	0.394
1398473_at	BI290651	biogenesis of lysosome-related organelles complex-1, subunit 2	Bloc1s2	0.958	0.990	1.484	0.020	0.976	0.842	1.208	0.010
1386773_at	BF524794	biotinidase	Btd	0.754	0.127	0.304	0.011	0.791	0.131	0.251	0.005
1388617_at	AW914746	biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen)	Bphl	0.392	0.007	0.367	0.001	0.387	0.001	0.315	0.000
1398317_at	BF283428	bisphosphate 3'-nucleotidase 1	Bpnt1	1.496	0.264	1.035	0.103	1.607	0.052	1.628	0.018
1372160_at	BM389738	bladder cancer associated protein homolog (human)	Blcap	0.818	0.729	0.734	0.007	0.806	0.234	0.759	0.007
1371808_at	AI012747	bleomycin hydrolase	Blmh	0.544	0.033	1.199	0.062	0.376	0.005	1.038	0.942
1392910_at	AA859968	block of proliferation 1	Bop1	0.971	0.995	1.936	0.003	0.621	0.002	1.882	0.002

1372710_at	AI175027	blocked early in transport 1 homolog (S. cerevisiae)	Bet1	0.614	0.500	0.532	0.018	0.755	0.390	0.588	0.003
1368881_at	NM_019251	blocked early in transport 1 homolog (S. cerevisiae)	Bet1	0.689	0.914	2.059	0.158	0.609	0.158	1.277	0.212
1372950_at	AI600006	blocked early in transport 1 homolog (S. cerevisiae) like	Bet1l	0.686	0.065	0.686	0.061	0.714	0.037	0.828	0.422
1370823_at	AF387513	BMP and activin membrane-bound inhibitor, homolog (Xenopus laevis)	Bambi	0.567	0.137	0.740	0.150	0.288	0.010	0.916	0.486
1379174_at	BE121123	BMP/retinoic acid-inducible neural-specific protein 2	Brinp2	1.095	0.779	0.884	0.982	1.015	0.997	0.999	0.993
1386774_at	BF551863	BMP/retinoic acid-inducible neural-specific protein 2	Brinp2	0.997	0.949	0.610	0.092	0.996	0.995	1.006	0.089
1392397_at	BF389365	BMP-2 inducible kinase	Bmp2k	0.323	0.011	0.534	0.477	0.327	0.014	0.889	0.502
1373768_at	AI406390	BMS1-like, ribosome assembly protein (yeast)	Bms1l	0.532	0.014	1.061	0.374	0.641	0.057	0.893	0.893
1383829_at	BF392234	bobby sox homolog (Drosophila) (predicted)	Bbx_predicted	1.591	0.007	1.143	0.058	2.865	0.008	1.209	0.313
1385235_at	AA818804	bol, boule-like (Drosophila) (predicted)	Boll_predicted	1.222	0.791	2.557	0.181	0.938	0.093	1.329	0.339
1372157_at	AI232807	bolA-like 1 (E. coli) (predicted)	Bola1_predicted	0.722	0.084	0.938	0.260	0.790	0.075	0.765	0.270
1390738_at	BM385476	bone marrow stromal cell antigen 2	Bst2	4.604	0.005	6.600	0.001	7.447	0.004	11.399	0.001
1371452_at	BE110662	bone marrow stromal cell-derived ubiquitin-like protein	Bmsc-UbP	0.851	0.952	0.991	0.863	0.859	0.470	1.174	0.875
1368945_at	NM_017178	bone morphogenetic protein 2	Bmp2	1.081	0.931	1.836	0.030	1.581	0.015	2.273	0.005
1369773_at	NM_017105	bone morphogenetic protein 3	Bmp3	1.008	0.994	0.699	0.058	0.861	0.278	0.959	0.042
1387232_at	NM_012827	bone morphogenetic protein 4	Bmp4	1.001	0.996	1.043	0.115	1.001	0.899	1.044	0.357
1388920_at	AI230985	bone morphogenetic protein 6	Bmp6	1.316	0.206	3.334	0.028	1.006	0.589	1.003	0.761
1368899_at	NM_030849	bone morphogenetic protein receptor, type 1A	Bmpr1a	1.058	0.666	1.172	0.022	1.155	0.379	1.149	0.047
1376843_at	BE118651	bone morphogenic protein receptor, type II (serine/threonine kinase)	Bmpr2	0.548	0.393	0.972	0.597	0.961	0.863	1.184	0.284
1382728_at	AA924018	Bone morphogenic protein receptor, type II (serine/threonine kinase)	Bmpr2	0.969	0.716	0.869	0.405	1.128	0.824	1.010	0.892
1374313_at	BI294383	BPY2 interacting protein 1 (predicted)	Bpy2ip1_predicted	1.188	0.930	1.068	0.345	1.004	0.969	1.066	0.978
1398350_at	BG380454	brain abundant, membrane attached signal protein 1	Basp1	1.714	0.008	1.668	0.007	1.655	0.010	1.743	0.020
1369310_at	NM_022300	brain abundant, membrane attached signal protein 1	Basp1	1.104	0.068	2.476	0.074	0.997	0.933	1.418	0.283
1398305_at	U30831	brain and kidney protein	Bk	0.521	0.235	0.492	0.146	0.353	0.037	1.265	0.903
1370418_s_at	U30831	brain and kidney protein /// hypothetical gene supported by NM_138849	Bk /// LOC497736	0.124	0.029	0.467	0.032	0.364	0.011	0.667	0.052
1390040_at	AA851481	brain and reproductive organ-expressed protein	Bre	0.878	0.165	0.695	0.022	0.997	0.946	0.547	0.013
1388723_at	AI171289	brain and reproductive organ-expressed protein	Bre	0.622	0.499	0.982	0.200	0.737	0.105	0.817	0.338
1388802_at	AI579422	brain expressed X-linked 1	Bex1	0.735	0.585	0.946	0.407	0.421	0.001	0.762	0.125
1373458_at	BI289546	brain expressed X-linked 4	Bex4	0.695	0.827	1.360	0.178	0.618	0.102	1.319	0.070
1388146_at	AW523578	Brain Ntab mRNA sequence	---	0.752	0.024	7.639	0.001	0.609	0.005	3.325	0.007
1376519_at	BI280846	brain protein 16	Brp16	0.744	0.215	1.008	0.987	0.529	0.048	0.932	0.208
1386867_at	NM_133561	brain protein 44-like	Brp44l	0.968	0.943	1.217	0.400	1.179	0.400	1.535	0.066
1371833_at	AI230753	brain protein I3	Bri3	1.134	0.967	2.040	0.010	0.859	0.488	1.532	0.035
1373380_at	AI169085	brain zinc finger protein	LOC362154	1.245	0.093	1.513	0.000	1.252	0.061	1.581	0.048
1385921_at	BF550329	brain zinc finger protein /// similar to brain Zn-finger protein (predicted)	LOC362154 /// RGD1562140_predicted	1.008	0.952	1.309	0.038	1.028	0.714	1.347	0.181
1373081_at	AI105000	Brain-specific angiogenesis inhibitor 1-associated protein 2	Baiap2	0.780	0.027	0.739	0.200	0.716	0.017	0.781	0.718
1374117_at	BI279562	brain-specific angiogenesis inhibitor 1-associated protein 2	Baiap2	1.021	0.287	1.002	0.913	0.732	0.091	0.990	0.845
1370869_at	AI102790	branched chain aminotransferase 1, cytosolic	Bcat1	2.439	0.190	18.575	0.000	2.166	0.386	7.129	0.002
1390726_at	BF393120	Branched chain aminotransferase 1, cytosolic	Bcat1	0.972	0.514	0.819	0.061	1.047	0.350	0.569	0.080
1369520_a_at	NM_017253	branched chain aminotransferase 1, cytosolic	Bcat1	1.070	0.860	1.567	0.101	1.244	0.046	1.200	0.138
1370906_at	BM385109	branched chain keto acid dehydrogenase E1, beta polypeptide	Bckdhb	0.703	0.266	1.175	0.074	1.264	0.448	1.399	0.008
1370897_at	J02827	branched chain ketoacid dehydrogenase E1, alpha polypeptide	Bckdha	1.004	0.751	0.986	0.898	1.003	0.023	0.997	0.987
1370842_at	BI277527	branched chain ketoacid dehydrogenase kinase	Bckdk	0.755	0.114	1.000	0.998	0.666	0.064	0.994	0.960
1374323_at	BM389139	BRCA2 and CDKN1A interacting protein (predicted)	Bccip_predicted	0.782	0.161	0.838	0.230	0.704	0.006	0.899	0.241
1381141_at	BF396613	Breast cancer 2	Brca2	1.180	0.994	1.204	0.463	1.186	0.472	1.090	0.999
1367752_at	NM_012931	breast cancer anti-estrogen resistance 1	Bcar1	1.210	0.670	1.782	0.620	1.212	0.538	1.033	0.995
1373428_at	AA851241	breast cancer metastasis-suppressor 1	Brms1	1.062	0.644	0.900	0.828	0.960	0.807	0.941	0.154
1373098_at	BF394321	breast carcinoma amplified sequence 1	Bcas1	0.997	0.601	1.227	0.939	0.970	0.472	1.229	0.177
1371868_at	AA851386	breast carcinoma amplified sequence 2 (predicted)	Bcas2_predicted	1.046	0.823	1.564	0.082	1.074	0.745	1.200	0.698
1379775_at	AI556888	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae) (predicted)	Brf1_predicted	0.702	0.079	1.251	0.189	0.778	0.333	0.934	0.384
1374891_at	BF406141	BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-like	Brf2	1.014	0.910	0.896	0.300	1.015	0.472	0.904	0.358
1379588_at	AA874805	Bridging integrator 1	Bin1	0.650	0.041	0.312	0.001	1.016	0.232	0.497	0.031
1367779_at	NM_053959	bridging integrator 1	Bin1	1.062	0.098	0.861	0.057	1.314	0.256	0.711	0.031
1396899_at	BE119227	Bridging integrator 1	Bin1	1.135	0.867	0.782	0.612	1.806	0.252	0.706	0.073
1399105_at	AA926279	bridging integrator 3	Bin3	0.705	0.637	2.090	0.013	0.968	0.928	1.684	0.151
1392514_at	BE095565	brix domain containing 1 (predicted)	Bxdc1_predicted	0.675	0.099	2.694	0.015	0.650	0.062	1.640	0.004
1389569_at	AW917092	brix domain containing 2	Bxdc2	0.844	0.081	2.449	0.006	0.765	0.007	1.696	0.006
1395479_at	BG373428	brix domain containing 2	Bxdc2	0.988	0.319	1.645	0.264	0.759	0.485	1.489	0.286
1396420_at	BF395914	Bromodomain adjacent to zinc finger domain protein 1B	Baz1b	1.194	0.583	0.907	0.811	1.321	0.209	1.038	0.678
1385853_at	BF560180	bromodomain adjacent to zinc finger domain, 1A (predicted)	Baz1a_predicted	1.651	0.099	2.226	0.007	0.962	0.622	1.024	0.112

1377727_at	BE109134	bromodomain adjacent to zinc finger domain, 1A (predicted)	Baz1a_predicted	1.421	0.178	2.347	0.044	2.049	0.051	1.854	0.029
1376533_at	BF398368	bromodomain adjacent to zinc finger domain, 2B (predicted)	Baz2b_predicted	0.559	0.004	0.852	0.502	0.823	0.185	0.912	0.342
1392421_at	AW526570	bromodomain adjacent to zinc finger domain, 2B (predicted)	Baz2b_predicted	0.975	0.389	1.173	0.774	1.000	0.204	0.834	0.470
1397486_x_at	BF404567	Bromodomain adjacent to zinc finger domain, 2B (predicted)	Baz2b_predicted	1.049	0.767	1.113	0.701	1.050	0.335	0.946	0.465
1373430_at	BG378867	bromodomain adjacent to zinc finger domain, 2B (predicted)	Baz2b_predicted	1.063	0.962	0.579	0.009	1.211	0.607	0.778	0.039
1380499_at	AI029043	Bromodomain and WD repeat domain containing 1 (predicted)	Brwd1_predicted	0.712	0.409	1.596	0.070	1.007	0.909	1.200	0.304
1398654_at	AI501129	Bromodomain and WD repeat domain containing 1 (predicted)	Brwd1_predicted	1.196	0.599	1.435	0.046	0.856	0.850	1.042	0.753
1384024_at	BI301225	bromodomain containing 1 (predicted)	Brd1_predicted	1.286	0.036	1.044	0.038	1.264	0.040	1.162	0.068
1380145_at	AW529414	Bromodomain containing 1 (predicted)	Brd1_predicted	0.921	0.862	1.056	0.914	1.046	0.467	0.767	0.046
1371719_at	AA946361	bromodomain containing 2	Brd2	1.192	0.597	1.488	0.242	0.990	0.790	1.260	0.054
1389029_at	BE108923	Bromodomain containing 3 (predicted)	Brd3_predicted	0.721	0.059	0.420	0.003	0.707	0.075	0.501	0.002
1372351_at	AI229448	bromodomain containing 4	Brd4	1.671	0.004	1.531	0.014	1.558	0.032	1.548	0.003
1375650_at	BM389207	bromodomain containing 4	Brd4	1.288	0.047	2.319	0.012	1.447	0.014	2.770	0.057
1395648_at	BF389377	Bromodomain containing 4	Brd4	1.374	0.062	0.885	0.554	1.799	0.278	0.830	0.315
1393567_at	BF389164	bromodomain containing 4	Brd4	1.000	0.632	1.186	0.200	1.004	0.933	1.004	0.993
1399055_at	BI275924	bromodomain containing 7 (predicted)	Brd7_predicted	0.622	0.419	0.972	0.147	0.859	0.220	1.019	0.839
1372207_at	AI549477	bromodomain containing 8	Brd8	1.534	0.124	0.824	0.224	1.407	0.952	1.131	0.162
1377777_at	BM391018	bromodomain containing 9 (predicted)	Brd9_predicted	1.250	0.150	0.691	0.100	1.259	0.121	0.879	0.418
1381995_at	AW530502	bruno-like 4, RNA binding protein (Drosophila) (predicted)	Brunol4_predicted	3.145	0.044	0.972	0.711	4.522	0.040	1.066	0.676
1372720_at	AA848449	BTB (POZ) domain containing 1	Btbd1	0.494	0.087	0.215	0.000	0.637	0.074	0.356	0.016
1376333_at	BI275800	BTB (POZ) domain containing 1	Btbd1	0.201	0.118	0.331	0.017	0.612	0.006	0.694	0.077
1376274_at	AI233751	BTB (POZ) domain containing 10	Btbd10	1.014	0.981	1.388	0.016	0.528	0.074	1.118	0.503
1380459_at	AI555023	BTB (POZ) domain containing 14A	Btbd14a	1.373	0.273	1.059	0.424	1.362	0.058	1.101	0.292
1379439_at	AA850609	BTB (POZ) domain containing 15	Btbd15	1.313	0.104	1.657	0.000	1.149	0.499	1.365	0.070
1382478_at	AI230481	BTB (POZ) domain containing 3 (predicted)	Btbd3_predicted	0.997	0.426	0.794	0.187	1.005	0.982	0.738	0.255
1383083_at	AI575458	Btg3 associated nuclear protein (predicted)	Banp_predicted	1.958	0.010	1.463	0.061	2.890	0.127	1.387	0.986
1372052_at	BI275918	Budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae)	Bub3	0.773	0.450	1.098	0.064	0.619	0.066	1.149	0.235
1392959_at	AA925983	Bwk1 leukemia-related gene	Bwk1	1.440	0.033	1.036	0.576	1.335	0.069	1.454	0.008
1377638_at	AI549060	Bwk1 leukemia-related gene	Bwk1	1.733	0.342	0.899	0.467	0.636	0.487	1.102	0.661
1385184_at	AI145766	Bwk1 leukemia-related gene	Bwk1	0.994	0.950	0.875	0.395	1.001	0.351	0.986	0.018
1389200_at	AA851296	bystin-like	Bysl	0.556	0.248	1.547	0.055	0.406	0.005	1.066	0.451
1388680_at	BM385686	C1GALT1-specific chaperone 1	C1galt1c1	0.652	0.277	0.279	0.005	0.575	0.084	0.378	0.006
1390754_at	BF412921	Ca2+-dependent secretion activator	Cadps	3.347	0.002	0.826	0.005	5.073	0.010	0.971	0.542
1368523_at	NM_013219	Ca2+-dependent secretion activator	Cadps	1.282	0.024	0.425	0.002	1.172	0.136	0.646	0.183
1379663_at	AI010254	Cache domain containing 1 (predicted)	Cachd1_predicted	2.500	0.011	1.019	0.193	1.354	0.181	1.152	0.341
1386947_at	NM_031334	cadherin 1	Cdh1	2.907	0.002	1.948	0.004	2.516	0.014	1.886	0.001
1393066_at	AI070787	Cadherin 1	Cdh1	0.277	0.002	0.206	0.006	0.322	0.075	0.186	0.023
1392140_at	BF419584	Cadherin 11	Cdh11	1.704	0.582	0.925	0.995	1.710	0.161	0.943	0.938
1388936_at	BI296340	cadherin 11	Cdh11	1.009	0.958	0.638	0.098	0.759	0.232	0.550	0.022
1383985_at	AW523000	cadherin 15	Cdh15	1.009	0.916	1.036	0.406	1.742	0.052	0.998	0.934
1368642_at	NM_031333	cadherin 2 /// hypothetical gene supported by NM_031333	Cdh2 /// LOC497718	1.295	0.368	0.409	0.002	0.925	0.666	0.527	0.028
1387259_at	AF097593	cadherin 2 /// hypothetical gene supported by NM_031333	Cdh2 /// LOC497718	0.755	0.394	0.879	0.853	0.912	0.645	1.018	0.828
1388045_a_at	D83348	cadherin 22	Cdh22	1.174	0.041	0.422	0.012	1.946	0.023	0.894	0.581
1378065_at	BI274450	Cadherin 22	Cdh22	1.362	0.229	0.606	0.065	1.480	0.529	0.301	0.019
1382089_at	AI070489	Cadherin 22	Cdh22	0.825	0.443	0.863	0.507	1.492	0.965	0.413	0.079
1395335_at	BF544005	Cadherin 22	Cdh22	0.904	0.521	0.566	0.018	0.907	0.597	0.553	0.083
1368887_at	NM_019161	cadherin 22	Cdh22	0.912	0.591	0.653	0.174	1.004	0.968	0.733	0.172
1392706_at	AI548870	Cadherin 23 (otocadherin)	Cdh23	0.971	0.527	0.973	0.856	0.777	0.198	0.848	0.691
1397177_at	BF409052	Cadherin 7, type 2	Cdh7	0.989	0.391	0.995	0.181	0.858	0.238	1.010	0.773
1375619_at	BF417982	Cadherin 8	Cdh8	1.440	0.486	0.923	0.980	1.783	0.476	1.200	0.754
1374910_at	BE103601	cadherin EGF LAG seven-pass G-type receptor 2	Celsr2	0.853	0.788	0.169	0.004	0.397	0.097	0.192	0.022
1368472_at	NM_031320	cadherin EGF LAG seven-pass G-type receptor 3	Celsr3	1.104	0.371	1.381	0.019	1.061	0.518	1.375	0.013
1370201_at	X04280	calbindin 1	Calb1	1.009	0.278	1.040	0.440	1.067	0.870	1.436	0.591
1370368_at	AF061947	calcineurin binding protein 1	Cabin1	1.236	0.046	0.749	0.578	1.653	0.243	0.893	0.874
1369994_at	NM_053670	calcitonin gene-related peptide-receptor component protein	Crcp	0.959	0.678	1.833	0.160	0.886	0.580	1.383	0.173
1370562_at	M11596	calcitonin-related polypeptide, beta	Calcb	13.021	0.002	5.403	0.001	7.958	0.012	6.969	0.000
1396446_at	BF522502	calcium activated nucleotidase 1	Cant1	0.487	0.505	0.622	0.847	0.332	0.091	0.663	0.126
1389588_at	H35646	calcium activated nucleotidase 1	Cant1	0.674	0.507	0.945	0.054	0.710	0.025	1.063	0.509
1367675_at	NM_031145	calcium and integrin binding 1 (calmyrin)	Cib1	1.466	0.228	3.105	0.004	1.292	0.885	1.615	0.037
1370285_at	AY078385	calcium binding and coiled coil domain 1	Calcoco1	0.575	0.211	0.679	0.049	1.013	0.616	0.758	0.184
1376715_at	AA901065	calcium binding atopy-related autoantigen 1	Cbara1	0.665	0.503	1.168	0.105	0.728	0.156	1.218	0.111

1396749_at	BF390144	calcium binding protein 1	Cabp1	0.220	0.016	4.581	0.019	0.548	0.270	3.641	0.033
1372243_at	BE112280	calcium binding protein 39 (predicted)	Cab39_predicted	0.995	0.402	1.687	0.031	0.800	0.102	1.540	0.364
1372244_at	BI285336	calcium binding protein 39 (predicted)	Cab39_predicted	0.844	0.599	1.028	0.873	0.602	0.132	0.912	0.295
1377391_at	BF390552	Calcium binding protein 39-like	Cab39l	1.022	0.379	1.025	0.951	1.013	0.868	0.954	0.728
1383341_at	BG662592	calcium binding protein 39-like	Cab39l	0.885	0.996	5.092	0.015	1.194	0.497	4.327	0.032
1371469_at	BM958511	calcium binding protein p22	Chp	0.829	0.999	0.713	0.033	0.853	0.961	0.704	0.042
1387388_at	AB070350	calcium binding protein p22 /// similar to calcium binding protein P22 (predicted) /// similar to calcium binding protein P22 (predicted)	Chp /// RGD1565588_predicted /// RGD1564956_predicted	1.030	0.898	0.913	0.724	1.000	0.975	0.886	0.774
1397151_at	BE108017	Calcium channel, voltage-dependent, alpha 2/delta 3 subunit	Cacna2d3	0.899	0.653	1.480	0.854	0.900	0.476	1.115	0.883
1397823_at	BE117531	Calcium channel, voltage-dependent, alpha2/delta subunit 1	Cacna2d1	1.990	0.040	1.365	0.134	1.296	0.542	1.213	0.222
1369649_at	AF400662	calcium channel, voltage-dependent, alpha2/delta subunit 1	Cacna2d1	0.835	0.625	0.476	0.066	0.860	0.657	0.669	0.221
1395263_at	AW529355	Calcium channel, voltage-dependent, beta 2 subunit	Cacnb2	1.256	0.056	0.779	0.093	1.144	0.903	0.783	0.283
1370178_at	BG373973	calcium channel, voltage-dependent, beta 2 subunit	Cacnb2	0.742	0.123	1.138	0.158	0.701	0.004	1.098	0.131
1374717_at	BI295624	Calcium channel, voltage-dependent, beta 2 subunit	Cacnb2	0.951	0.973	0.827	0.183	0.963	0.947	0.950	0.094
1387042_at	NM_012828	calcium channel, voltage-dependent, beta 3 subunit	Cacnb3	1.031	0.192	0.947	0.394	1.434	0.205	1.605	0.004
1368759_at	NM_053351	calcium channel, voltage-dependent, gamma subunit 2	Cacng2	0.999	0.995	0.999	0.150	1.001	0.331	1.001	0.764
1378151_at	BE114019	Calcium channel, voltage-dependent, gamma subunit 8	Cacng8	1.284	0.597	0.950	0.625	0.711	0.216	1.199	0.095
1370452_at	M59786	calcium channel, voltage-dependent, L type, alpha 1C subunit	Cacna1c	0.885	0.955	0.732	0.079	0.676	0.116	0.673	0.050
1369086_a_at	NM_017298	calcium channel, voltage-dependent, L type, alpha 1D subunit	Cacna1d	0.844	0.697	0.951	0.727	1.149	0.345	0.748	0.191
1397008_at	BF404563	Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	Cacna1a	0.914	0.151	0.718	0.348	0.764	0.203	0.725	0.519
1368398_at	NM_031601	calcium channel, voltage-dependent, T type, alpha 1H subunit	Cacna1h	2.640	0.178	0.807	0.631	2.408	0.069	0.634	0.013
1372705_at	BG376747	calcium homeostasis endoplasmic reticulum protein (predicted)	Cherp_predicted	0.792	0.098	1.371	0.330	0.779	0.031	0.943	0.870
1387086_at	NM_053334	calcium modulating ligand	Camlg	0.100	0.027	0.197	0.000	0.168	0.002	0.186	0.004
1388659_at	BI295783	calcium regulated heat stable protein 1	Carhsp1	2.108	0.013	2.479	0.003	2.410	0.006	2.617	0.007
1371536_at	AI233208	calcium regulated heat stable protein 1	Carhsp1	2.054	0.125	2.313	0.033	1.374	0.613	1.894	0.024
1367889_at	NM_134468	calcium/calmodulin-dependent protein kinase I	Camk1	0.451	0.007	0.736	0.017	0.420	0.010	0.706	0.232
1391229_at	BG381458	calcium/calmodulin-dependent protein kinase I gamma	Camk1g	0.383	0.008	0.368	0.003	0.660	0.130	0.401	0.004
1389876_at	BE111167	Calcium/calmodulin-dependent protein kinase II inhibitor 1	Camk2n1	0.961	0.789	0.639	0.040	0.790	0.130	0.489	0.043
1389824_at	BF404381	Calcium/calmodulin-dependent protein kinase II, alpha	Camk2a	1.032	0.996	1.089	0.433	1.002	0.989	1.088	0.216
1398251_a_at	NM_021739	calcium/calmodulin-dependent protein kinase II, beta	Camk2b	1.003	0.967	0.738	0.294	0.998	0.834	0.684	0.237
1368834_at	AA894330	calcium/calmodulin-dependent protein kinase II, delta	Camk2d	2.111	0.003	2.451	0.000	2.179	0.004	2.063	0.003
1391142_at	BF400657	Calcium/calmodulin-dependent protein kinase IV	Camk4	1.000	0.621	0.990	0.929	0.922	0.431	1.150	0.332
1368156_at	NM_031662	calcium/calmodulin-dependent protein kinase kinase 1, alpha	Camkk1	0.754	0.029	0.852	0.177	0.953	0.646	1.013	0.276
1368955_at	NM_022184	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	Cask	1.087	0.674	0.729	0.238	1.306	0.296	0.941	0.692
1369158_at	NM_016996	calcium-sensing receptor	Casr	0.983	0.029	0.547	0.026	0.617	0.043	0.697	0.025
1392912_at	BG664561	calcyclin binding protein	Cacybp	0.906	0.326	2.212	0.000	0.847	0.204	1.641	0.001
1392979_at	AW918443	calcyclin binding protein	Cacybp	0.845	0.901	2.098	0.031	0.756	0.408	1.289	0.340
1387772_at	NM_031969	calmodulin 1	Calm1	0.991	0.349	0.529	0.000	1.077	0.062	0.637	0.000
1369936_at	X13933	calmodulin 1	Calm1	0.878	0.752	0.484	0.001	0.946	0.990	0.676	0.011
1369937_at	BI279113	calmodulin 1	Calm1	0.944	0.825	0.720	0.136	0.901	0.169	0.755	0.282
1370246_at	AA943837	calmodulin 2	Calm2	0.707	0.579	0.965	0.361	0.634	0.174	0.752	0.031
1370873_at	AI411316	calmodulin 3	Calm3	0.770	0.181	0.322	0.014	0.676	0.127	0.250	0.003
1368101_at	NM_012518	calmodulin 3	Calm3	0.551	0.314	1.056	0.881	0.434	0.007	0.871	0.737
1373317_at	BI278721	calmodulin 4 (predicted)	Calm4_predicted	1.068	0.526	1.000	0.854	1.001	0.913	1.001	0.859
1371687_at	BI297860	calnexin	Canx	0.774	0.074	1.565	0.707	0.833	0.232	1.279	0.461
1371686_at	AA946205	calnexin	Canx	0.740	0.191	0.914	0.101	0.945	0.507	0.997	0.933
1388442_at	AA848326	calnexin	Canx	0.768	0.979	1.222	0.922	0.982	0.499	1.134	0.579
1387009_at	NM_019152	calpain 1	Capn1	0.461	0.015	0.314	0.068	0.420	0.019	0.694	0.731
1368904_at	NM_031673	calpain 10	Capn10	0.644	0.104	0.807	0.878	0.490	0.085	0.741	0.863
1376287_at	BM389585	calpain 13	Capn13	1.709	0.984	1.297	0.817	1.185	0.992	0.892	0.505
1387860_at	BF281377	calpain 2	Capn2	1.523	0.105	1.378	0.018	1.429	0.100	1.085	0.480
1373111_at	AI169441	calpain 7	Capn7	0.763	0.059	1.356	0.007	0.672	0.034	1.281	0.030
1392341_at	AW523444	Calpain, small subunit 1	Capns1	1.356	0.286	1.160	0.251	1.670	0.151	1.046	0.237
1367462_at	U10861	calpain, small subunit 1	Capns1	1.026	0.962	1.047	0.885	1.086	0.408	1.113	0.575
1373466_at	AA946474	calpastatin	Cast	0.483	0.017	0.334	0.004	0.463	0.009	0.344	0.026
1371173_a_at	Y13591	calpastatin	Cast	0.714	0.241	0.579	0.337	1.109	0.995	0.288	0.008
1369754_a_at	NM_053295	calpastatin	Cast	0.880	0.576	0.743	0.928	0.929	0.716	0.665	0.731
1391481_at	BE104424	Calpastatin	Cast	0.894	0.776	1.162	0.077	1.046	0.151	0.932	0.097
1387856_at	BI274457	calponin 3, acidic	Cnn3	1.008	0.259	1.643	0.000	1.666	0.040	1.976	0.002
1398750_at	NM_022399	calreticulin	Calr	0.879	0.800	0.881	0.290	1.106	0.453	0.824	0.469

1376732_at	BM388733	calreticulin 3	Calr3	1.131	0.326	0.789	0.580	1.129	0.326	0.996	0.992
1376225_at	BF411924	Calsenilin, presenilin binding protein, EF hand transcription factor	Csen	0.673	0.146	0.259	0.003	0.561	0.137	0.329	0.009
1388217_a_at	AJ001929	calumenin /// calumenin	Calu /// MGC124555	0.875	0.462	1.690	0.032	0.818	0.703	1.413	0.064
1368208_at	NM_133558	camello-like 1	Cml1	0.439	0.010	0.197	0.026	0.650	0.142	0.300	0.026
1369708_a_at	NM_031017	cAMP responsive element binding protein 1	Creb1	1.452	0.579	1.290	0.546	1.159	0.230	1.434	0.041
1372990_at	AI179264	cAMP responsive element binding protein 3	Creb3	0.819	0.581	1.050	0.419	0.843	0.497	0.972	0.248
1374575_at	BI304123	cAMP responsive element binding protein 3-like 1	Creb3l1	3.486	0.035	2.428	0.004	1.733	0.019	1.162	0.067
1379565_at	AA956791	cAMP responsive element binding protein 3-like 2	Creb3l2	0.716	0.115	1.907	0.078	0.586	0.114	1.544	0.047
1373429_at	BI295832	cAMP responsive element binding protein-like 1	Crebl1	0.795	0.030	0.968	0.229	0.927	0.134	1.000	0.998
1373618_at	BE113210	cAMP responsive element binding protein-like 2	Crebl2	0.744	0.678	0.595	0.021	0.689	0.322	0.747	0.017
1393550_at	BF564195	CAMP responsive element modulator	Crem	0.235	0.000	0.728	0.187	0.273	0.012	0.829	0.407
1369737_at	NM_017334	cAMP responsive element modulator	Crem	0.445	0.150	0.740	0.010	0.646	0.009	0.684	0.006
1369738_s_at	NM_017334	cAMP responsive element modulator	Crem	0.384	0.428	0.723	0.029	0.496	0.062	0.428	0.011
1387714_at	AB031423	cAMP responsive element modulator	Crem	0.871	0.946	0.813	0.354	0.932	0.408	0.903	0.711
1393008_at	BI290317	CAMP-regulated phosphoprotein 19	Arpp19	0.841	0.429	1.155	0.888	0.403	0.057	0.694	0.130
1387077_at	NM_031660	cAMP-regulated phosphoprotein 19	Arpp19	1.141	0.816	3.047	0.003	0.726	0.024	2.469	0.002
1376217_at	BM388768	cancer susceptibility candidate 1 (predicted)	Casc1_predicted	2.071	0.151	1.975	0.045	3.037	0.153	1.915	0.053
1397571_at	BF554256	Cancer susceptibility candidate 3	Casc3	1.670	0.454	0.919	0.936	0.904	0.862	0.860	0.060
1368808_at	NM_022383	CAP, adenylate cyclase-associated protein 1 (yeast)	Cap1	1.785	0.039	0.990	0.364	0.985	0.720	0.883	0.197
1368809_at	BG380723	CAP, adenylate cyclase-associated protein 1 (yeast)	Cap1	1.637	0.066	1.181	0.274	1.426	0.141	1.377	0.061
1382322_a_at	AI029769	capicua homolog (Drosophila) (predicted)	Cic_predicted	0.967	0.824	2.017	0.029	1.228	0.933	1.604	0.033
1399043_at	AI175266	capping protein (actin filament) muscle Z-line, alpha 2	Capza2	0.950	0.426	1.092	0.131	1.199	0.362	1.016	0.077
1399091_at	AI232101	capping protein (actin filament) muscle Z-line, beta	Capzb	1.123	0.558	0.927	0.443	0.927	0.842	0.961	0.360
1374481_at	AA946502	cappuccino homolog (mouse)	Cno	0.770	0.501	1.154	0.433	0.912	0.811	1.129	0.993
1371797_at	BM391890	carbamyl phosphatate synthetase 2 (mapped)	Cad_mapped	0.666	0.520	1.665	0.018	0.764	0.824	1.482	0.050
1376697_at	BI275885	carbohydrate sulfotransferase 12	Chst12	0.868	0.643	0.671	0.319	0.925	0.654	0.609	0.338
1395684_at	AW534805	Carbonic anhydrase 14 (predicted)	Car14_predicted	0.954	0.404	0.545	0.001	1.006	0.984	0.553	0.009
1373790_at	AI045400	carbonic anhydrase 14 (predicted)	Car14_predicted	1.113	0.559	0.313	0.001	1.096	0.144	0.283	0.002
1386922_at	AI408948	carbonic anhydrase 2	Ca2	1.608	0.021	1.028	0.568	1.744	0.042	1.105	0.786
1367733_at	NM_019291	carbonic anhydrase 2	Ca2	3.636	0.046	1.387	0.108	1.048	0.838	1.032	0.850
1398431_at	BI294910	carbonic anhydrase 8	Car8	1.152	0.871	1.818	0.025	1.016	0.101	1.072	0.557
1390498_at	AI230554	Carbonic anhydrase VB, mitochondrial	Ca5b	0.991	0.038	0.310	0.039	0.657	0.164	0.306	0.038
1377573_at	AI411132	carbonic anhydrase VB, mitochondrial	Ca5b	0.303	0.097	0.541	0.119	0.520	0.563	0.576	0.069
1390807_at	BG375352	carbonic anhydrase VB, mitochondrial	Ca5b	0.548	0.911	0.277	0.062	0.853	0.656	0.191	0.043
1375529_at	BF404908	carbonic reductase 4	Cbr4	0.835	0.200	0.506	0.176	0.748	0.380	0.729	0.085
1368037_at	NM_019170	carbonyl reductase 1	Cbr1	0.434	0.303	0.744	0.106	0.219	0.004	0.760	0.395
1397427_at	BI302102	Carboxylesterase 3	Ces3	1.011	0.987	1.072	0.236	1.133	0.570	1.215	0.932
1369657_at	NM_016998	carboxypeptidase A1	Cpa1	0.999	0.955	0.755	0.440	1.000	0.632	0.754	0.441
1393397_at	AI576488	carboxypeptidase A2 (pancreatic) (predicted)	Cpa2_predicted	0.353	0.024	0.248	0.003	0.467	0.073	0.168	0.035
1386921_at	NM_013128	carboxypeptidase E	Cpe	0.752	0.015	0.848	0.007	0.932	0.163	0.908	0.014
1387503_at	NM_053526	carboxypeptidase N, polypeptide 1, 50kD	Cpn1	0.266	0.000	0.405	0.008	0.364	0.003	0.497	0.032
1374672_at	BI293060	cardiac ankyrin repeat kinase	Cark	1.751	0.058	0.965	0.263	1.363	0.129	1.037	0.325
1374846_at	AI230884	cardiac lineage protein 1	Clp1	0.549	0.003	0.816	0.089	0.639	0.034	1.050	0.948
1371886_at	AI411979	carnitine acetyltransferase	Crat	0.399	0.004	0.813	0.063	0.425	0.052	1.301	0.367
1394038_at	BG371654	carnitine deficiency-associated gene expressed in ventricle 1	Cdv1	0.583	0.098	0.614	0.008	0.861	0.078	0.650	0.004
1395387_at	BI293317	carnitine deficiency-associated gene expressed in ventricle 1	Cdv1	0.585	0.436	0.938	0.055	0.964	0.435	0.982	0.933
1368426_at	NM_031987	carnitine O-octanoyltransferase	Crot	4.313	0.002	2.081	0.049	7.459	0.001	1.534	0.024
1386946_at	NM_031559	carnitine palmitoyltransferase 1a, liver	Cpt1a	2.030	0.114	0.802	0.249	1.683	0.342	0.650	0.078
1367742_at	NM_013200	carnitine palmitoyltransferase 1b, muscle	Cpt1b	0.818	0.723	0.762	0.159	1.296	0.162	0.727	0.077
1386927_at	NM_012930	carnitine palmitoyltransferase 2	Cpt2	0.295	0.042	0.167	0.001	0.307	0.000	0.209	0.022
1390569_at	AI231438	carnosine dipeptidase 1 (metallopeptidase M20 family)	Cndp1	0.936	0.551	1.005	0.928	0.958	0.557	1.001	0.941
1377044_at	AW143175	Cartilage acidic protein 1	Crtac1	0.905	0.600	1.332	0.196	1.914	0.025	1.000	0.920
1374646_at	BM387173	Casein kinase 1, alpha 1	Csnk1a1	0.825	0.226	0.748	0.025	0.933	0.383	0.922	0.167
1369312_a_at	U77583	casein kinase 1, alpha 1	Csnk1a1	0.715	0.364	0.950	0.778	0.648	0.316	0.931	0.938
1394689_at	BE117217	Casein kinase 1, alpha 1	Csnk1a1	1.152	0.674	1.125	0.964	1.154	0.639	0.858	0.198
1389859_at	AI235291	Casein kinase 1, alpha 1	Csnk1a1	1.006	0.953	0.670	0.131	1.119	0.473	0.723	0.211
1370819_at	AB063114	casein kinase 1, delta	Csnk1d	1.295	0.179	3.344	0.004	1.003	0.748	2.098	0.019
1373332_at	AA946432	Casein kinase 1, delta	Csnk1d	0.898	0.204	0.694	0.001	1.076	0.551	0.663	0.055
1370527_a_at	L07578	casein kinase 1, delta	Csnk1d	1.136	0.737	7.928	0.031	1.386	0.096	3.664	0.002
1387108_at	BF281311	casein kinase 2, beta subunit	Csnk2b	0.689	0.884	1.323	0.141	0.541	0.144	1.238	0.204
1375636_at	AI600042	Casein kinase II, alpha 1 polypeptide	Csnk2a1	0.567	0.019	0.936	0.276	0.620	0.001	0.933	0.071

1376616_at	BF551036	Casein kinase II, alpha 1 polypeptide	Csnk2a1	0.365	0.041	0.465	0.001	0.408	0.038	0.576	0.015
1384339_s_at	BF288177	casein kinase II, alpha 1 polypeptide	Csnk2a1	0.956	0.578	0.389	0.171	0.948	0.681	0.769	0.095
1382160_at	AI236331	Casein kinase II, alpha 2, polypeptide (predicted)	Csnk2a2_predicted	1.773	0.021	3.051	0.004	1.815	0.023	2.537	0.015
1371326_at	BI276957	casein kinase II, alpha 2, polypeptide (predicted)	Csnk2a2_predicted	1.310	0.101	1.575	0.001	1.699	0.005	1.696	0.024
1378282_at	BI290750	casein kinase II, alpha 2, polypeptide (predicted)	Csnk2a2_predicted	0.956	0.900	1.762	0.020	0.805	0.890	2.470	0.013
1377192_a_at	BM384629	caseinolytic peptidase X (E.coli)	Clpx	1.370	0.199	2.435	0.000	1.010	0.905	1.669	0.044
1398698_at	BG371721	Caseinolytic peptidase X (E.coli)	Clpx	2.001	0.440	1.917	0.121	1.339	0.523	1.947	1.000
1371027_at	BF556820	Casitas B-lineage lymphoma b	Cblb	1.000	0.115	1.423	0.106	1.069	0.699	1.107	0.297
1392847_at	BE118227	Casitas B-lineage lymphoma-like 1 (predicted)	Cbll1_predicted	0.844	0.156	2.251	0.004	1.211	0.394	1.710	0.011
1372434_at	BE098114	CASK-interacting protein CIP98	Cip98	1.797	0.004	4.242	0.001	1.117	0.682	2.903	0.001
1368545_at	NM_057138	CASP8 and FADD-like apoptosis regulator	Cflar	7.503	0.001	4.484	0.000	1.724	0.581	2.697	0.002
1392386_at	AI578435	CASP8 and FADD-like apoptosis regulator	Cflar	2.269	0.007	1.146	0.797	1.624	0.046	1.409	0.096
1391811_at	AI556437	CASP8 and FADD-like apoptosis regulator	Cflar	1.393	0.285	0.822	0.395	1.734	0.094	0.445	0.474
1379919_at	AI575276	CASP8 and FADD-like apoptosis regulator	Cflar	0.929	0.332	0.652	0.136	1.015	0.727	0.931	0.473
1387605_at	NM_130422	caspase 12	Casp12	1.501	0.110	1.028	0.426	3.641	0.025	1.092	0.115
1367890_at	NM_022522	caspase 2	Casp2	1.281	0.428	0.957	0.415	0.879	0.663	0.878	0.005
1390386_at	BM387008	caspase 3, apoptosis related cysteine protease	Casp3	2.508	0.072	0.688	0.090	3.127	0.073	1.735	0.311
1381173_at	BG375010	Caspase 4, apoptosis-related cysteine peptidase	Casp4	17.972	0.004	5.704	0.001	15.891	0.004	17.306	0.009
1387818_at	NM_053736	caspase 4, apoptosis-related cysteine peptidase	Casp4	18.891	0.007	41.240	0.005	26.132	0.005	65.607	0.001
1389170_at	BF283754	caspase 7	Casp7	0.396	0.454	0.571	0.007	0.306	0.170	0.721	0.061
1369557_at	NM_022260	caspase 7	Casp7	0.922	0.781	0.640	0.152	1.005	0.745	0.639	0.148
1369262_at	NM_022277	caspase 8	Casp8	1.084	0.827	1.002	0.978	1.090	0.078	1.014	0.880
1373194_at	BF282281	caspase 8 associated protein 2 (predicted)	Casp8ap2_predicted	0.438	0.057	0.352	0.031	0.535	0.011	0.723	0.113
1382586_at	AW919926	Caspase 8 associated protein 2 (predicted)	Casp8ap2_predicted	1.024	0.558	0.718	0.101	1.101	0.559	1.028	0.751
1373440_at	AI175525	caspase 8 associated protein 2 (predicted)	Casp8ap2_predicted	0.518	0.618	1.073	0.609	0.713	0.541	1.580	0.050
1370962_at	AI136555	castration induced prostatic apoptosis-related protein 1	Cipar1	0.998	0.875	0.947	0.198	1.001	0.988	0.975	0.291
1367995_at	NM_012520	catalase	Cat	0.793	0.526	1.957	0.001	0.722	0.493	2.116	0.004
1376228_at	BF419434	Catalytic/ protein phosphatase type 2C	---	1.005	0.901	1.002	0.961	5.313	0.077	1.055	0.759
1368826_at	NM_012531	catechol-O-methyltransferase	Comt	1.183	0.215	2.799	0.003	1.921	0.039	2.914	0.001
1373150_at	AW251225	catechol-O-methyltransferase domain containing 1 (predicted)	Comtd1_predicted	1.001	0.990	1.292	0.141	0.999	0.996	2.004	0.035
1398354_at	AI555457	catenin (cadherin associated protein), alpha-like 1 (predicted)	Ctnnal1_predicted	0.451	0.007	0.416	0.006	0.286	0.022	0.369	0.005
1369733_at	NM_053357	catenin (cadherin associated protein), beta 1	Ctnnb1	2.447	0.335	1.567	0.035	0.927	0.977	0.860	0.520
1373067_at	AI102738	Catenin (cadherin associated protein), beta 1	Ctnnb1	1.149	0.426	0.952	0.554	0.952	0.563	0.903	0.437
1388415_at	BE109560	catenin (cadherin associated protein), delta 1 (predicted)	Ctnnd1_predicted	1.522	0.015	0.902	0.926	1.489	0.048	1.069	0.277
1371921_at	BM986272	catenin (cadherin-associated protein), alpha 1	Catna1	1.391	0.001	1.666	0.000	1.291	0.054	1.488	0.018
1390723_at	BF386742	Catenin (cadherin-associated protein), alpha 1	Catna1	1.631	0.039	0.977	0.371	1.773	0.025	1.100	0.593
1367646_at	NM_022597	cathepsin B	Ctsb	1.048	0.606	1.049	0.141	0.927	0.646	0.940	0.151
1367651_at	NM_134334	cathepsin D	Ctsd	0.738	0.757	0.835	0.237	0.798	0.373	0.950	0.349
1373258_at	AI169359	cathepsin F	Ctsf	0.563	0.304	0.441	0.025	0.535	0.001	0.368	0.025
1370244_at	AI176595	cathepsin L	Ctsl	0.637	0.488	1.274	0.051	0.497	0.130	1.160	0.219
1370245_at	AI232474	cathepsin L	Ctsl	0.782	0.944	2.807	0.003	0.427	0.150	2.624	0.007
1370885_at	AA849399	cathepsin Z	Ctsz	1.033	0.815	0.857	0.047	0.976	0.869	0.805	0.790
1394735_at	BF409552	cation channel, sperm associated 2	Catsper2	0.996	0.835	0.950	0.095	1.803	0.075	0.907	0.557
1387726_at	NM_023963	caudal type homeo box 2	Cdx2	0.965	0.843	0.996	0.797	0.951	0.402	1.072	0.350
1385519_at	BE105678	CBFA2T1 identified gene homolog (human) (predicted)	Cbfa2t1_predicted	1.199	0.294	0.810	0.404	0.385	0.062	1.302	0.697
1395076_at	BE117804	CBFA2T1 identified gene homolog (human) (predicted)	Cbfa2t1_predicted	1.438	0.762	0.620	0.175	0.907	0.947	0.761	0.367
1385215_at	BF388857	CBFA2T1 identified gene homolog (human) (predicted)	Cbfa2t1_predicted	0.856	0.862	0.792	0.570	0.978	0.872	1.040	0.727
1367602_at	AI013390	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	Cited2	0.074	0.114	0.695	0.391	0.464	0.237	0.835	0.578
1367601_at	NM_053698	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	Cited2	0.235	0.234	2.667	0.079	1.286	0.952	1.201	0.331
1384126_a_at	AW917217	CCAAT/enhancer binding protein (C/EBP), alpha	Cebpa	1.440	0.141	0.653	0.122	0.895	0.586	1.036	0.898
1398959_at	AA850070	CCAAT/enhancer binding protein (C/EBP), delta	Cebpd	0.722	0.010	0.942	0.580	0.734	0.145	0.819	0.023
1387343_at	NM_013154	CCAAT/enhancer binding protein (C/EBP), delta	Cebpd	2.342	0.017	10.822	0.006	1.112	0.045	5.419	0.005
1374842_at	BF287009	CCAAT/enhancer binding protein zeta (predicted)	Cebpz_predicted	0.742	0.002	1.442	0.028	0.723	0.027	1.369	0.026
1370337_at	AF133731	CCCTC-binding factor	Ctcf	0.986	0.945	1.483	0.049	0.867	0.155	1.242	0.152
1372988_at	BF397012	CCR4-NOT transcription complex, subunit 10	Cnot10	0.615	0.051	0.972	0.391	0.722	0.084	1.147	0.066
1376067_at	AA800637	CCR4-NOT transcription complex, subunit 2	Cnot2	0.896	0.087	0.510	0.016	0.879	0.092	0.554	0.014
1373190_at	AI101401	CCR4-NOT transcription complex, subunit 4	Cnot4	1.314	0.302	1.401	0.661	1.468	0.151	1.060	0.697
1393619_at	AI045762	CCR4-NOT transcription complex, subunit 6-like (predicted)	Cnot6l_predicted	1.076	0.409	0.672	0.025	1.436	0.022	1.107	0.512
1367515_at	BE111850	CCR4-NOT transcription complex, subunit 7 (predicted)	Cnot7_predicted	2.450	0.003	1.478	0.027	2.040	0.036	1.596	0.004
1379624_at	AA964442	CCR4-NOT transcription complex, subunit 8	Cnot8	0.989	0.232	0.999	0.995	0.993	0.968	1.006	0.869
1372253_at	AI408162	CCR4-NOT transcription complex, subunit 8	Cnot8	1.004	0.986	0.712	0.049	1.005	0.978	0.921	0.868

1398827_at	NM_013087	CD 81 antigen	Cd81	1.023	0.966	0.969	0.323	1.027	0.346	1.110	0.176
1368490_at	NM_021744	CD14 antigen	Cd14	0.872	0.925	1.001	0.483	1.001	0.993	1.302	0.390
1367681_at	NM_022523	CD151 antigen	Cd151	0.745	0.101	0.703	0.049	0.620	0.089	0.422	0.027
1379716_at	AA956555	CD163 antigen (predicted)	Cd163_predicted	1.166	0.806	0.867	0.640	1.066	0.620	0.858	0.274
1386886_at	NM_031812	CD164 antigen	Cd164	0.720	0.064	0.742	0.006	0.759	0.003	0.796	0.024
1393863_at	AA999005	CD180 antigen (predicted)	Cd180_predicted	1.763	0.272	1.355	0.372	1.022	0.371	1.044	0.086
1368593_at	NM_017079	CD1d1 antigen	Cd1d1	0.497	0.889	1.505	0.311	0.700	0.548	1.574	0.012
1372036_at	BG378032	CD2 antigen (cytoplasmic tail) binding protein 2 (predicted)	Cd2bp2_predicted	1.047	0.123	0.765	0.032	1.253	0.081	0.791	0.085
1385676_at	BG379822	CD2 antigen (cytoplasmic tail) binding protein 2 (predicted)	Cd2bp2_predicted	0.664	0.330	1.394	0.015	1.017	0.706	1.006	0.165
1395530_at	AI555739	CD2 antigen (cytoplasmic tail) binding protein 2 (predicted)	Cd2bp2_predicted	1.135	0.413	0.827	0.166	1.020	0.898	0.741	0.013
1380908_at	AA924563	Cd200 antigen	Cd200	1.570	0.126	0.726	0.766	1.306	0.445	0.998	0.984
1369670_at	NM_031518	Cd200 antigen	Cd200	1.001	0.989	1.042	0.564	0.689	0.031	0.806	0.031
1369953_a_at	BI285141	CD24 antigen	Cd24	0.255	0.062	0.334	0.041	0.237	0.032	0.245	0.011
1383962_at	BI275530	Cd27 binding protein (Hindu God of destruction) (predicted)	Siva_predicted	0.443	0.101	0.935	0.477	0.333	0.014	0.942	0.679
1374198_at	BF398424	CD276 antigen	Cd276	1.782	0.134	1.220	0.094	1.327	0.111	1.091	0.427
1372071_at	AI102320	CD320 antigen	Cd320	0.640	0.297	0.833	0.074	0.680	0.005	0.569	0.011
1368975_at	NM_013127	CD38 antigen	Cd38	1.464	0.176	1.714	0.765	1.697	0.282	2.339	0.278
1390325_at	BI289418	CD38 antigen	Cd38	1.199	0.853	0.901	0.514	1.191	0.297	0.992	0.740
1387952_a_at	AF065147	CD44 antigen	Cd44	9.394	0.001	8.059	0.004	4.654	0.064	4.774	0.014
1368921_a_at	NM_012924	CD44 antigen	Cd44	13.454	0.009	11.345	0.001	9.246	0.016	8.394	0.002
1369559_a_at	NM_019195	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	Cd47	3.430	0.093	3.614	0.003	3.314	0.008	4.111	0.004
1367929_at	NM_012925	CD59 antigen	Cd59	0.690	0.002	0.223	0.000	0.807	0.004	0.345	0.001
1367709_at	NM_017125	CD63 antigen	Cd63	0.926	0.897	1.179	0.010	0.841	0.004	1.138	0.031
1384837_at	AI137672	CD69 antigen	Cd69	191.709	0.000	120.693	0.000	92.214	0.001	87.158	0.000
1367679_at	NM_013069	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	Cd74	13.211	0.020	17.999	0.001	49.917	0.001	73.895	0.000
1386976_at	NM_031797	CD82 antigen	Cd82	3.404	0.001	10.516	0.000	5.886	0.001	11.892	0.000
1390529_at	AI412355	CD83 antigen (predicted)	Cd83_predicted	4.692	0.000	1.561	0.190	12.975	0.004	2.058	0.009
1381206_at	BE121026	CD96 antigen	Cd96	1.030	0.072	1.766	0.020	1.129	0.021	2.445	0.006
1382527_at	AI764706	CD96 antigen	Cd96	0.431	0.224	1.153	0.108	0.909	0.453	0.995	0.661
1399141_at	BF404428	CDC like kinase 4	Clk4	1.087	0.579	1.224	0.056	1.163	0.844	0.992	0.438
1376544_at	BF414624	CDC14 cell division cycle 14 homolog A (S. cerevisiae) (predicted)	Cdc14a_predicted	2.090	0.210	1.298	0.374	0.896	0.232	1.183	0.899
1399074_at	BI279569	CDC16 cell division cycle 16 homolog (S. cerevisiae)	Cdc16	0.667	0.202	0.862	0.065	0.604	0.080	0.753	0.034
1389646_at	BE100584	CDC23 (cell division cycle 23, yeast, homolog)	Cdc23	0.593	0.078	0.572	0.003	0.544	0.120	0.691	0.216
1373246_at	BF397920	CDC23 (cell division cycle 23, yeast, homolog)	Cdc23	0.929	0.633	0.586	0.004	0.891	0.383	0.621	0.010
1396320_at	BF396773	Cdc2-related kinase, arginine/serine-rich	Crkrs	1.118	0.304	0.938	0.453	1.049	0.647	1.159	0.788
1387546_at	NM_138916	Cdc2-related kinase, arginine/serine-rich	Crkrs	1.288	0.387	1.448	0.065	1.395	0.369	1.016	0.868
1394887_x_at	AI407383	Cdc2-related kinase, arginine/serine-rich	Crkrs	1.297	0.817	0.784	0.232	0.932	0.334	0.907	0.233
1375910_at	AA874943	CDC42 effector protein (Rho GTPase binding) 3 (predicted)	Cdc42ep3_predicted	1.248	0.085	1.359	0.058	1.110	0.030	1.184	0.230
1388730_at	AI407903	CDC42 effector protein (Rho GTPase binding) 4 (predicted)	Cdc42ep4_predicted	1.136	0.764	1.605	0.065	0.891	0.694	1.161	0.534
1397853_s_at	BG672534	Cdc42 guanine nucleotide exchange factor (GEF) 9	Arhgef9	2.621	0.021	0.999	0.997	1.172	0.604	0.972	0.998
1388468_at	BI284508	CDC42 small effector 1	Cdc42se1	0.557	0.072	1.283	0.041	0.618	0.055	1.021	0.433
1388530_at	BM389459	CDC42 small effector 1	Cdc42se1	1.504	0.369	5.415	0.015	1.313	0.547	3.350	0.012
1374357_at	AI713763	CDC91 cell division cycle 91-like 1 (S. cerevisiae)	Cdc91l1	1.259	0.135	0.909	0.438	1.012	0.987	0.890	0.366
1399022_at	AI177513	CDC-like kinase 1	Clk1	1.331	0.024	0.941	0.500	1.812	0.006	0.979	0.558
1368235_at	NM_134340	CDC-like kinase 3	Clk3	0.702	0.011	1.516	0.016	1.019	0.553	1.594	0.058
1398801_at	NM_134415	CDK105 protein	Cdk105	0.854	0.579	1.267	0.289	0.864	0.305	1.089	0.607
1388443_at	AI177871	CDK2 (cyclin-dependent kinase 2)-associated protein 1 (predicted)	Cdk2ap1_predicted	0.542	0.251	0.654	0.004	0.324	0.002	0.610	0.018
1367879_at	NM_024488	CDK5 regulatory subunit associated protein 3	Cdk5rap3	0.961	0.804	1.113	0.061	1.025	0.742	0.999	0.965
1390214_a_at	BI284812	CDKN1A interacting zinc finger protein 1 (predicted)	Ciz1_predicted	1.147	0.115	2.570	0.028	0.863	0.365	1.711	0.038
1392991_at	AA859535	CDNA clone IMAGE:7130415	---	0.740	0.029	1.144	0.812	0.697	0.038	0.985	0.440
1385965_at	AI045533	CDNA clone IMAGE:7131734	---	0.810	0.258	1.054	0.053	0.716	0.023	1.062	0.336
1394041_at	BI293870	CDNA clone IMAGE:7131734	---	0.776	0.277	1.174	0.009	0.793	0.141	1.046	0.090
1389287_at	BI279573	CDNA clone IMAGE:7193711	---	2.479	0.003	2.022	0.011	2.021	0.004	1.847	0.002
1373808_at	BF417211	CDNA clone IMAGE:7193711	---	1.737	0.469	2.395	0.000	1.270	0.728	2.434	0.009
1390227_at	AI101017	CDNA clone IMAGE:7300848	---	0.991	0.651	0.744	0.491	0.960	0.802	0.952	0.803
1390912_at	BE101168	CDNA clone IMAGE:7300848	---	0.999	0.733	0.660	0.037	1.002	0.994	0.659	0.039
1396091_at	BI296193	CDNA clone IMAGE:7301487	---	0.624	0.132	1.748	0.012	0.473	0.302	1.521	0.034
1375895_at	BI275908	CDNA clone IMAGE:7302535, with apparent retained intron	---	0.910	0.139	1.938	0.000	1.039	0.459	1.833	0.000
1393109_at	BI274436	CDNA clone IMAGE:7302574	---	0.223	0.101	0.093	0.000	0.184	0.011	0.130	0.006
1384453_at	AI045824	CDNA clone IMAGE:7303447	---	1.170	0.188	1.000	0.802	0.873	0.285	0.794	0.704
1371448_at	AI599295	CDNA clone IMAGE:7303896	---	0.615	0.159	0.598	0.036	0.621	0.029	0.972	0.354

1383349_at	BE115594	CDNA clone IMAGE:7304849	---	2.719	0.003	1.113	0.234	5.913	0.000	1.816	0.006
1389545_at	BF281994	CDNA clone IMAGE:7307013	---	1.686	0.101	1.662	0.002	1.181	0.309	1.810	0.005
1389601_at	BI293610	CDNA clone IMAGE:7308494	---	1.260	0.774	1.451	0.726	1.628	0.145	1.220	0.161
1390449_at	BI289132	CDNA clone IMAGE:7309127	---	1.085	0.028	1.233	0.311	2.614	0.013	2.214	0.026
1377922_at	BE111094	CDNA clone IMAGE:7312313	---	1.259	0.220	0.808	0.021	1.130	0.404	0.945	0.844
1389331_at	AI104371	CDNA clone IMAGE:7313169	---	1.128	0.208	1.427	0.008	1.552	0.013	1.673	0.002
1391639_at	AI170084	CDNA clone IMAGE:7313169	---	0.844	0.585	0.924	0.810	1.883	0.193	1.391	0.200
1376892_at	AI102061	CDNA clone IMAGE:7313785	---	0.624	0.154	0.148	0.005	0.771	0.389	0.200	0.002
1374161_at	AI104686	CDNA clone IMAGE:7316678	---	0.450	0.052	0.683	0.015	0.620	0.081	0.742	0.009
1383705_at	BG670702	CDNA clone IMAGE:7317308	---	0.561	0.690	1.886	0.270	0.596	0.190	1.121	0.618
1399062_at	BI301008	CDNA clone IMAGE:7317308	---	0.962	0.933	1.480	0.182	0.636	0.573	1.336	0.117
1388700_at	AW253004	CDNA clone IMAGE:7317367	---	1.239	0.007	1.074	0.812	0.953	0.316	0.964	0.486
1376764_at	AI406412	CDNA clone IMAGE:7319904	---	0.672	0.224	0.153	0.000	0.719	0.015	0.120	0.016
1383127_at	BI295823	CDNA clone IMAGE:7320912	---	0.744	0.049	0.436	0.003	0.695	0.006	0.656	0.029
1372760_at	AI176579	CDNA clone IMAGE:7321089	---	1.020	0.815	1.428	0.048	0.961	0.744	1.199	0.083
1389986_at	AI008409	CDNA clone IMAGE:7321089	---	1.178	0.875	1.131	0.125	1.156	0.146	1.067	0.103
1392904_at	BF544602	CDNA clone IMAGE:7321811	---	1.162	0.467	1.181	0.149	1.060	0.763	1.171	0.176
1379341_at	BG378132	CDNA clone IMAGE:7322363	---	1.220	0.298	2.833	0.024	1.272	0.116	2.340	0.001
1383400_at	BI293535	CDNA clone IMAGE:7324288	---	1.152	0.088	1.037	0.170	0.709	0.052	0.993	0.408
1374509_at	BI275722	CDNA clone IMAGE:7324860	---	0.570	0.017	0.493	0.002	0.499	0.061	0.569	0.005
1388710_at	BI281986	CDNA clone IMAGE:7365357	---	1.036	0.960	1.481	0.001	0.643	0.023	1.159	0.493
1373943_at	AI237047	CDNA clone IMAGE:7365681	---	0.789	0.036	0.583	0.001	0.748	0.035	0.690	0.000
1372308_at	BM386869	CDNA clone IMAGE:7366335	---	0.812	0.386	0.747	0.244	0.364	0.033	0.610	0.018
1373520_at	BI285960	CDNA clone IMAGE:7367270	---	1.633	0.047	1.410	0.039	1.200	0.085	0.781	0.528
1399028_at	AI171954	CDNA clone IMAGE:7367808	---	1.330	0.094	1.116	0.224	1.289	0.004	1.123	0.077
1395584_at	C06826	CDNA clone IMAGE:7367808	---	1.398	0.154	1.024	0.889	1.306	0.127	1.012	0.682
1390621_at	BG376889	CDNA clone IMAGE:7367808	---	1.294	0.392	0.777	0.506	0.756	0.274	0.774	0.150
1373405_at	AI410762	CDNA clone IMAGE:7373898	---	2.148	0.130	1.088	0.276	2.586	0.077	1.468	0.035
1379597_at	AI011037	CDNA clone IMAGE:7375470	---	0.358	0.004	0.833	0.361	0.849	0.071	0.624	0.759
1372624_at	BF551377	CDNA clone IMAGE:7375734	---	1.360	0.017	0.597	0.009	1.152	0.042	0.830	0.137
1385667_x_at	AI029796	CDNA clone IMAGE:7379585	---	0.726	0.000	0.476	0.004	0.737	0.038	0.528	0.009
1383194_a_at	AI030349	CDNA clone IMAGE:7379585	---	0.558	0.018	0.490	0.001	0.580	0.002	0.539	0.059
1385540_at	AI044916	CDNA clone IMAGE:7379764	---	1.604	0.046	0.463	0.005	1.204	0.303	0.484	0.020
1386258_at	AA945099	CDNA clone IMAGE:7386859	---	0.683	0.067	0.970	0.298	0.947	0.817	1.141	0.758
1383629_a_at	BI289966	CDNA clone IMAGE:7386859	---	0.735	0.075	0.977	0.037	0.767	0.424	1.099	0.747
1374368_at	BI291066	CDNA clone IMAGE:7389555	---	0.886	0.119	1.438	0.021	0.711	0.097	1.471	0.005
1393704_at	AI136988	CDNA clone IMAGE:7442534	---	1.123	0.339	1.379	0.043	1.018	0.973	1.637	0.190
1376014_at	AI045725	CDNA clone IMAGE:7453109	---	1.009	0.990	0.908	0.250	1.022	0.921	0.680	0.187
1389142_at	AI013361	CDNA clone IMAGE:7455024	---	0.680	0.588	0.425	0.002	0.612	0.173	0.442	0.003
1378446_at	BI283723	CDNA clone IMAGE:7457557	---	0.928	0.837	0.653	0.090	1.051	0.964	0.886	0.074
1379558_at	AA957033	CDNA clone IMAGE:7930522	---	1.286	0.119	0.346	0.001	6.189	0.000	1.150	0.922
1371721_at	BI281103	CDNA clone IMAGE:7932112	---	0.839	0.280	1.324	0.260	1.448	0.292	1.648	0.064
1374635_at	AW527151	CDNA clone IMAGE:7932607	---	1.285	0.785	0.640	0.242	1.002	0.989	1.002	0.998
1383896_at	BM387943	CDNA clone MGC:105591 IMAGE:7313723	---	0.685	0.078	1.702	0.004	0.999	0.463	1.579	0.104
1371460_at	AA859261	CDNA clone MGC:105597 IMAGE:7314502	---	0.682	0.582	0.895	0.774	0.510	0.052	1.083	0.734
1394388_at	AA858844	CDNA clone MGC:105701 IMAGE:7309421	---	0.635	0.191	1.016	0.637	0.650	0.019	1.083	0.169
1383912_at	BM390524	CDNA clone MGC:109201 IMAGE:7306744	---	1.823	0.035	2.294	0.006	2.058	0.007	2.493	0.001
1371401_at	BI278836	CDNA clone MGC:109637 IMAGE:7367801	---	0.592	0.984	0.670	0.091	0.660	0.904	0.766	0.107
1399007_at	BF557930	CDNA clone MGC:109642 IMAGE:7368024	---	0.645	0.362	0.745	0.624	0.693	0.021	0.900	0.311
1371434_at	AI172362	CDNA clone MGC:112638 IMAGE:7376647	---	1.402	0.104	1.838	0.003	1.399	0.007	2.159	0.000
1388572_at	BM389961	CDNA clone MGC:112923 IMAGE:7380411	---	0.726	0.008	0.701	0.408	0.769	0.290	1.128	0.257
1391997_at	AW523656	CDNA clone MGC:112923 IMAGE:7380411	---	1.004	0.952	1.001	0.189	0.991	0.989	0.939	0.067
1398006_at	AI454795	CDNA clone MGC:116179 IMAGE:7455942	---	0.999	0.993	1.020	0.174	1.519	0.209	1.003	0.941
1375296_at	AI407178	CDNA clone MGC:125029 IMAGE:7458016	---	0.694	0.004	1.433	0.005	0.786	0.004	1.256	0.025
1371956_at	BG372686	CDNA clone MGC:93760 IMAGE:7108525	---	0.509	0.152	0.427	0.001	0.463	0.011	0.489	0.002
1398360_at	AI009805	CDNA clone MGC:93791 IMAGE:7109632	---	0.908	0.885	1.491	0.039	0.702	0.014	1.379	0.005
1371856_at	AI408941	CDNA clone MGC:93828 IMAGE:7110880	---	1.095	0.128	1.084	0.747	1.361	0.008	1.033	0.334
1397313_at	AI716841	CDNA clone MGC:93828 IMAGE:7110880	---	1.019	0.997	0.879	0.589	1.064	0.992	0.397	0.091
1389387_at	BF561377	CDNA clone MGC:93913 IMAGE:7112877	---	2.314	0.116	2.189	0.026	3.205	0.002	3.653	0.007
1367490_at	AI102046	CDNA clone MGC:94668 IMAGE:7192222	---	0.594	0.022	0.601	0.036	0.496	0.025	0.801	0.318
1372340_at	BM386355	CDNA clone MGC:94725 IMAGE:7193416	---	0.778	0.656	1.128	0.252	0.810	0.492	1.063	0.103

1398942_at	BI278885	CDNA clone MGC:95041 IMAGE:7123253	---	0.554	0.078	0.556	0.000	0.697	0.007	0.789	0.008
1384256_at	BI293599	CDNA clone MGC:95252 IMAGE:7133376	---	0.664	0.050	0.938	0.991	0.592	0.007	0.941	0.906
1368248_at	NM_031242	CDP-diacylglycerol synthase 1	Cds1	0.848	0.745	1.862	0.002	1.733	0.031	2.019	0.001
1387900_at	D82928	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	Cdipt	0.805	0.335	0.940	0.174	0.810	0.039	0.930	0.327
1368480_at	NM_053492	CDW92 antigen	Cdw92	2.753	0.001	1.151	0.250	2.399	0.002	1.261	0.156
1379130_at	BF396303	CDW92 antigen	Cdw92	1.155	0.070	1.064	0.086	1.129	0.495	0.978	0.675
1372651_at	AI144726	CDW92 antigen	Cdw92	1.189	0.370	0.194	0.000	1.688	0.212	0.298	0.082
1370935_at	AI105205	CDW92 antigen	Cdw92	1.263	0.384	0.640	0.111	1.268	0.333	0.568	0.093
1381870_at	BG377539	CDW92 antigen	Cdw92	0.931	0.677	0.753	0.258	1.095	0.082	0.734	0.178
1373054_at	AA801076	CDW92 antigen	Cdw92	0.902	0.723	0.585	0.064	1.084	0.895	0.659	0.168
1374620_at	BM392373	CEA-related cell adhesion molecule 1	Ceacam1	1.033	0.771	0.543	0.013	1.391	0.218	0.623	0.010
1385767_at	BF411017	cell adhesion molecule JCAM	LOC304000	0.777	0.166	0.677	0.035	1.389	0.471	0.829	0.700
1396317_at	AI764350	cell cycle progression 1 (predicted)	Ccpg1_predicted	0.536	0.083	0.214	0.000	0.778	0.024	0.358	0.006
1375027_at	AI407365	Cell cycle progression 1 (predicted)	Ccpg1_predicted	0.577	0.370	0.679	0.010	0.620	0.063	0.660	0.006
1376199_at	BF419187	cell cycle related kinase	Ccrk	0.802	0.306	0.966	0.803	0.767	0.240	0.686	0.715
1387371_at	NM_133571	cell division cycle 25 homolog A (S. cerevisiae)	Cdc25a	1.101	0.202	1.531	0.002	0.959	0.502	1.461	0.003
1377558_at	BF393165	Cell division cycle 25 homolog A (S. cerevisiae)	Cdc25a	1.258	0.787	1.507	0.620	1.094	0.280	1.051	0.240
1370034_at	NM_133572	cell division cycle 25 homolog B (S. cerevisiae)	Cdc25b	0.986	0.618	0.257	0.005	0.996	0.958	0.219	0.002
1388727_at	BM387151	cell division cycle 26	Cdc26	0.609	0.070	0.339	0.003	0.348	0.011	0.437	0.021
1372339_at	AA866438	cell division cycle 26	Cdc26	1.138	0.141	1.038	0.464	0.799	0.122	0.732	0.106
1388534_at	AA851369	Cell division cycle 26	Cdc26	0.471	0.635	1.267	0.038	0.425	0.100	0.936	0.072
1382664_at	AW525662	cell division cycle 27 homolog (S. cerevisiae)	Cdc27	1.377	0.112	2.107	0.001	0.987	0.361	1.354	0.007
1393534_at	AI059500	Cell division cycle 2-like 5 (cholinesterase-related cell division controller)	Cdc2l5	1.687	0.074	1.055	0.823	1.008	0.436	0.851	0.922
1386164_at	AI170800	Cell division cycle 2-like 5 (cholinesterase-related cell division controller)	Cdc2l5	1.000	0.734	1.490	0.018	0.999	0.109	0.828	0.837
1398574_a_at	AI170800	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	Cdc2l5	0.986	0.761	1.135	0.805	0.797	0.133	1.054	0.343
1388286_a_at	L38482	cell division cycle 34 homolog (S. cerevisiae) (predicted)	Cdc34_predicted	0.789	0.425	2.568	0.009	0.969	0.439	2.393	0.001
1388400_at	BG375350	cell division cycle 34 homolog (S. cerevisiae) (predicted)	Cdc34_predicted	1.199	0.799	1.929	0.002	0.965	0.867	2.314	0.008
1367453_at	NM_053743	cell division cycle 37 homolog (S. cerevisiae)	Cdc37	0.932	0.971	1.819	0.017	0.792	0.073	1.460	0.034
1374074_at	BF285292	cell division cycle 37 homolog (S. cerevisiae)-like 1	Cdc37l1	0.629	0.137	0.611	0.026	0.701	0.074	0.647	0.016
1392673_at	BF552510	cell division cycle 37 homolog (S. cerevisiae)-like 1	Cdc37l1	1.045	0.615	1.853	0.265	0.881	0.769	2.138	0.168
1388724_at	BF284434	cell division cycle 40 homolog (yeast) (predicted)	Cdc40_predicted	0.909	0.896	1.420	0.095	0.715	0.129	1.527	0.106
1370825_a_at	AA925473	cell division cycle 42 homolog (S. cerevisiae)	Cdc42	0.913	0.939	1.387	0.006	0.837	0.248	1.284	0.031
1398793_at	NM_053527	cell division cycle 5-like (S. pombe)	Cdc5l	0.697	0.412	0.933	0.765	0.653	0.362	1.051	0.366
1379346_at	BI290578	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	Cdc73	0.828	0.578	1.454	0.063	0.924	0.750	1.176	0.130
1383940_at	BG375704	cell division cycle associated 1	Cdca1	1.003	0.987	0.635	0.101	1.344	0.219	0.637	0.095
1374739_at	AI236771	cell division cycle associated 4	Cdca4	0.927	0.629	1.355	0.624	1.206	0.851	1.253	0.315
1387244_at	NM_053899	cell growth regulator with ring finger domain 1	Cgrrf1	1.381	0.233	1.915	0.011	1.225	0.260	2.233	0.000
1368141_at	AF242550	cellular nucleic acid binding protein 1	Cnbp1	0.957	0.824	1.189	0.069	0.838	0.380	1.288	0.001
1381968_at	AI029175	cellular repressor of E1A-stimulated genes (predicted)	Creg_predicted	0.833	0.295	7.041	0.001	0.774	0.188	4.657	0.001
1375428_at	BE099979	cellular repressor of E1A-stimulated genes (predicted)	Creg_predicted	0.955	0.452	2.810	0.007	1.034	0.829	1.360	0.100
1369725_at	NM_020101	centaurin, alpha 2	Centa2	1.475	0.797	0.889	0.506	1.264	0.279	0.879	0.299
1392815_at	BE114489	Centaurin, delta 1 (predicted)	Centd1_predicted	3.366	0.002	1.332	0.005	1.985	0.022	1.113	0.057
1388511_at	AI412079	centaurin, delta 2	Centd2	1.890	0.000	1.358	0.936	1.760	0.042	1.173	0.639
1377926_at	AA924061	Centaurin, gamma 2 (predicted)	Centg2_predicted	1.166	0.629	1.028	0.063	0.728	0.273	1.534	0.811
1383834_at	BI285391	centaurin, gamma 3 (predicted)	Centg3_predicted	0.856	0.380	0.907	0.306	0.672	0.126	0.762	0.131
1375977_at	AA958015	centrin 2	Cetn2	0.608	0.508	0.482	0.000	0.700	0.070	0.795	0.021
1388141_at	BI293883	centrin 3	Cetn3	0.975	0.325	1.512	0.065	0.604	0.043	1.249	0.343
1385349_at	BF389818	centrin 4 (predicted)	Cetn4_predicted	1.561	0.063	0.606	0.162	1.439	0.176	0.747	0.168
1372883_at	BE109061	centromere autoantigen B (predicted)	Cenpb_predicted	0.744	0.007	0.910	0.739	0.650	0.010	1.000	0.894
1379538_at	BE104961	centromere protein J (predicted)	Cenpj_predicted	5.322	0.009	2.700	0.042	11.664	0.017	2.727	0.002
1382613_at	AW144049	Centrosomal protein 152 (predicted)	Cep152_predicted	1.766	0.221	4.401	0.000	0.836	0.415	3.785	0.040
1382765_at	AA996645	centrosomal protein 27 (predicted)	Cep27_predicted	0.652	0.125	1.589	0.063	0.640	0.202	1.588	0.058
1377829_at	BI291153	centrosomal protein 57	Cep57	0.577	0.027	0.624	0.018	0.482	0.030	0.639	0.011
1378274_at	BF389658	Centrosomal protein 76	Cep76	0.665	0.184	1.222	0.023	0.935	0.753	1.151	0.147
1385824_at	BF388819	centrosome-associated protein 350	Cap350	1.252	0.409	2.262	0.076	2.184	0.035	3.107	0.135
1375987_at	AW525194	ceramide kinase (predicted)	Cerk_predicted	0.794	0.192	0.444	0.003	0.662	0.004	0.542	0.015
1374139_at	BG671589	cerebellar degeneration-related 2	Cdr2	0.659	0.888	2.466	0.001	0.957	0.912	2.250	0.003
1381972_at	BG673626	cereblon	Crbn	0.689	0.115	0.837	0.127	0.831	0.143	0.957	0.279
1377047_at	AI710879	Cereblon	Crbn	0.789	0.555	0.312	0.003	0.757	0.059	0.401	0.006
1383177_at	AI232085	Cereblon	Crbn	0.666	0.644	0.648	0.081	0.729	0.270	0.635	0.032
1378479_at	BI285912	ceroid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	Cln3	1.138	0.385	1.781	0.159	6.791	0.015	1.434	0.310

1389598_at	BI280367	ceroid-lipofuscinosis, neuronal 6 (predicted)	Cln6_predicted	0.357	0.001	0.977	0.623	0.352	0.007	0.917	0.047
1375026_at	AI105369	ceroid-lipofuscinosis, neuronal 6 (predicted)	Cln6_predicted	0.771	0.294	1.018	0.987	0.579	0.024	0.569	0.365
1389791_at	AI179775	ceroid-lipofuscinosis, neuronal 8	Cln8	0.198	0.119	0.388	0.000	0.302	0.000	0.483	0.001
1368419_at	AF202115	ceruloplasmin	Cp	65.875	0.000	38.543	0.000	145.013	0.000	41.980	0.000
1368418_a_at	AF202115	ceruloplasmin	Cp	38.320	0.002	41.974	0.000	52.472	0.000	60.254	0.002
1368420_at	NM_012532	ceruloplasmin	Cp	57.870	0.002	40.226	0.002	121.710	0.000	55.033	0.005
1374557_at	BF394235	CG6210-like	LOC362065	0.498	0.376	0.999	0.990	0.508	0.316	1.109	0.799
1382427_at	BG373237	CGG triplet repeat binding protein 1 (predicted)	Cggbp1_predicted	2.508	0.080	10.231	0.016	1.413	0.021	4.339	0.074
1375280_at	AW913871	CGI-146 protein	PNAS-4	0.664	0.669	1.772	0.055	0.774	0.292	1.729	0.331
1376312_a_at	BI284236	CGI-146 protein	PNAS-4	0.989	0.964	1.276	0.972	1.202	0.898	1.589	0.090
1380665_at	BF418059	CGI-58-like protein	LOC316122	1.401	0.028	1.350	0.046	1.112	0.088	1.228	0.063
1389573_at	AI170665	ChaC, cation transport regulator-like 1 (E. coli) (predicted)	Chac1_predicted	2.182	0.085	1.485	0.063	1.237	0.900	1.054	0.061
1372536_at	AI105042	chaperone, ABC1 activity of bc1 complex like (S. pombe)	Cabc1	0.314	0.003	0.084	0.001	0.316	0.001	0.120	0.017
1371418_at	BG665035	chaperonin containing TCP1, subunit 2 (beta)	Cct2	0.499	0.120	1.032	0.496	0.477	0.056	0.889	0.337
1371403_at	AA799545	chaperonin subunit 3 (gamma)	Cct3	0.787	0.120	1.684	0.001	0.588	0.003	1.407	0.002
1390261_at	AI059850	Chaperonin subunit 3 (gamma)	Cct3	1.381	0.164	1.904	0.003	1.208	0.882	1.482	0.009
1371656_at	BI283657	chaperonin subunit 4 (delta)	Cct4	0.830	0.277	1.747	0.000	0.722	0.014	1.538	0.006
1376570_at	BF417274	chaperonin subunit 5 (epsilon)	Cct5	0.839	0.535	1.813	0.006	0.668	0.014	1.793	0.005
1395508_at	BG665309	chaperonin subunit 5 (epsilon)	Cct5	0.545	0.904	0.998	0.995	0.787	0.146	1.430	0.352
1398960_at	AI172328	chaperonin subunit 6a (zeta)	Cct6a	0.895	0.149	1.108	0.294	0.765	0.012	1.126	0.282
1377006_at	AA875047	Chaperonin subunit 6a (zeta)	Cct6a	0.998	0.990	1.116	0.321	0.791	0.489	0.899	0.138
1371641_at	BM388827	chaperonin subunit 7 (eta) (predicted)	Cct7_predicted	0.793	0.326	1.731	0.003	0.817	0.061	1.592	0.003
1392918_at	BE115650	chaperonin subunit 8 (theta) (predicted)	Cct8_predicted	0.737	0.257	1.343	0.000	0.626	0.049	1.188	0.001
1373784_at	BF409759	chaperonin subunit 8 (theta) (predicted)	Cct8_predicted	0.991	0.979	0.771	0.592	1.065	0.203	1.072	0.798
1372787_at	BE106508	charged amino acid rich leucine zipper 1	Crlz1	0.994	0.888	2.184	0.006	0.969	0.993	1.877	0.008
1387062_a_at	NM_080400	checkpoint kinase 1 homolog (S. pombe)	Chek1	1.459	0.061	2.029	0.064	1.977	0.002	0.989	0.234
1384728_at	BE112826	checkpoint suppressor 1 (predicted)	Ches1_predicted	1.125	0.296	1.003	0.981	1.085	0.324	1.154	0.164
1377713_at	AI639381	checkpoint suppressor 1 (predicted)	Ches1_predicted	1.403	0.406	0.870	0.509	0.760	0.557	0.852	0.081
1383313_at	BE120149	checkpoint with forkhead and ring finger domains	Chfr	0.911	0.583	0.559	0.001	0.876	0.155	0.597	0.005
1367973_at	NM_031530	chemokine (C-C motif) ligand 2	Ccl2	962.723	0.005	511.882	0.004	987.110	0.004	124.055	0.002
1369814_at	AF053312	chemokine (C-C motif) ligand 20	Ccl20	168.860	0.000	139.685	0.000	62.205	0.006	14.863	0.004
1376850_a_at	AI058901	chemokine (C-C motif) ligand 27 (predicted)	Ccl27_predicted	1.012	0.096	0.976	0.602	1.002	0.558	1.000	0.996
1369983_at	NM_031116	chemokine (C-C motif) ligand 5	Ccl5	0.597	0.317	4.418	0.009	77.432	0.000	182.099	0.000
1379935_at	BF419899	chemokine (C-C motif) ligand 7	Ccl7	131.265	0.001	59.296	0.000	128.020	0.001	7.414	0.001
1392737_at	AI044644	Chemokine (C-C motif) receptor 5	Ccr5	0.741	0.396	0.994	0.782	0.913	0.218	1.049	0.323
1398591_at	AI707080	chemokine (C-C motif) receptor-like 2 (predicted)	Ccrl2_predicted	1.006	0.988	1.002	0.977	2.962	0.037	0.997	0.983
1368200_at	NM_134455	chemokine (C-X3-C motif) ligand 1	Cx3cl1	13.041	0.013	1.005	0.826	13.329	0.007	1.003	0.321
1387316_at	NM_030845	chemokine (C-X-C motif) ligand 1	Cxcl1	392.450	0.000	189.826	0.001	36.359	0.024	6.641	0.002
1387969_at	U22520	chemokine (C-X-C motif) ligand 10	Cxcl10	262.954	0.015	80.668	0.019	332.406	0.014	188.777	0.012
1379365_at	BF281987	chemokine (C-X-C motif) ligand 11	Cxcl11	79.732	0.005	128.180	0.010	93.689	0.005	151.358	0.009
1369633_at	AI171777	chemokine (C-X-C motif) ligand 12	Cxcl12	1.500	0.032	1.181	0.196	1.486	0.169	1.064	0.083
1368760_at	NM_053647	chemokine (C-X-C motif) ligand 2	Cxcl2	282.144	0.001	47.336	0.001	15.910	0.056	1.535	0.332
1382454_at	AI044222	chemokine (C-X-C motif) ligand 9	Cxcl9	290.483	0.000	197.180	0.005	913.843	0.001	334.675	0.004
1373544_at	AI170387	chemokine (C-X-C motif) ligand 9	Cxcl9	238.152	0.001	199.846	0.003	587.954	0.002	287.997	0.002
1387984_at	AF253065	chemokine-like factor	Cklf	6.669	0.039	2.309	0.123	4.576	0.028	2.638	0.039
1387956_s_at	AF253064	chemokine-like factor	Cklf	2.138	0.336	1.920	0.126	3.283	0.294	2.760	0.062
1381009_at	BF403637	Chemokine-like receptor 1	Cmklr1	1.049	0.911	0.997	0.249	0.996	0.983	0.999	0.544
1368287_at	NM_032083	chimerin (chimaerin) 1	Chn1	1.072	0.208	0.754	0.025	1.461	0.250	1.091	0.551
1391386_at	AI412693	Chimerin (chimaerin) 1	Chn1	1.000	0.630	1.189	0.896	0.883	0.592	0.950	0.562
1368331_at	NM_031023	chitobiase, di-N-acetyl-	Ctbs	0.955	0.377	1.080	0.521	1.104	0.779	1.222	0.405
1369010_at	NM_053677	CHK2 checkpoint homolog (S. pombe)	Chek2	1.191	0.613	0.622	0.168	0.960	0.698	0.673	0.167
1392453_at	AI763523	chloride channel 3	Clcn3	0.767	0.254	0.853	0.119	0.550	0.068	1.017	0.135
1380547_at	BI288519	chloride channel 3	Clcn3	0.578	0.277	0.649	0.171	0.399	0.222	0.644	0.152
1367893_a_at	NM_133414	chloride channel CLIC-like 1	Clcc1	0.825	0.629	1.363	0.125	0.733	0.105	0.850	0.185
1367772_at	NM_031719	chloride channel, nucleotide-sensitive, 1A	Clns1a	0.807	0.064	0.928	0.186	0.872	0.087	1.171	0.159
1375633_at	AI012221	chloride intracellular channel 1	Clic1	1.658	0.036	1.416	0.057	1.316	0.040	1.136	0.004
1381993_at	BI293548	chloride intracellular channel 2	Clic2	2.540	0.782	1.012	0.810	2.748	0.231	0.985	0.922
1377765_at	AA848723	chloride intracellular channel 4	Clic4	5.623	0.071	6.054	0.025	7.158	0.001	6.352	0.002
1387420_at	NM_031818	chloride intracellular channel 4	Clic4	1.396	0.117	1.375	0.164	1.729	0.196	1.377	0.053
1387032_at	NM_012829	cholecystokinin	Cck	0.987	0.925	1.105	0.803	0.989	0.896	1.109	0.926
1369787_at	NM_012688	cholecystokinin A receptor	Cckar	0.229	0.003	0.055	0.001	0.253	0.017	0.106	0.036

1380063_at	AI169398	cholesterol 25-hydroxylase	Ch25h	2.241	0.163	0.983	0.734	4.340	0.050	0.989	0.777
1368692_a_at	AW140851	choline kinase alpha	Chka	1.369	0.299	2.113	0.001	1.037	0.699	1.450	0.005
1367718_at	NM_017177	choline kinase beta	Chkb	0.948	0.803	0.992	0.246	0.935	0.386	0.784	0.027
1379770_at	BF282951	choline phosphotransferase 1	Chpt1	0.724	0.121	0.840	0.205	0.725	0.120	0.846	0.250
1388977_at	BM390401	choline/ethanolamine phosphotransferase 1	Cept1	1.282	0.379	1.909	0.003	1.884	0.051	2.155	0.006
1387462_at	NM_012527	cholinergic receptor, muscarinic 3	Chrm3	0.935	0.940	1.058	0.830	0.917	0.675	0.766	0.798
1395429_at	BF281401	Cholinergic receptor, nicotinic, alpha polypeptide 7	Chrna7	1.428	0.259	1.597	0.308	1.864	0.134	1.932	0.124
1369091_at	NM_012528	cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)	Chrnb1	0.976	0.318	0.678	0.367	1.021	0.113	0.907	0.431
1373561_at	AI012498	chondroitin polymerizing factor	D1bwg1363e	0.560	0.113	0.517	0.003	0.556	0.030	0.410	0.010
1390072_at	BF401531	Chondroitin sulfate proteoglycan 4	Cspg4	0.999	0.831	1.094	0.512	0.998	0.995	1.007	0.509
1387080_at	NM_031583	chondroitin sulfate proteoglycan 6	Cspg6	0.757	0.330	1.017	0.541	0.693	0.003	0.900	0.308
1390668_at	BG378312	chondroitin sulfate proteoglycan 6	Cspg6	0.891	0.771	1.571	0.727	1.268	0.503	2.371	0.295
1388943_at	BI279670	chromatin accessibility complex 1 (predicted)	Chrac1_predicted	0.914	0.498	0.654	0.078	0.977	0.884	0.826	0.199
1367512_at	AA998435	chromatin modifying protein 5	Chmp5	1.141	0.128	1.175	0.027	1.454	0.009	1.323	0.018
1388510_at	BI289511	chromatin modifying protein 6 (predicted)	Chmp6_predicted	0.685	0.216	1.394	0.022	0.487	0.049	1.069	0.020
1374695_at	BF564593	Chromobox homolog 1 (Drosophila HP1 beta) (predicted)	Cbx1_predicted	1.610	0.013	1.777	0.004	2.003	0.000	1.658	0.003
1385157_at	BF389675	chromobox homolog 1 (Drosophila HP1 beta) (predicted)	Cbx1_predicted	1.327	0.116	2.648	0.016	2.953	0.002	1.630	0.025
1371395_at	AA851329	chromobox homolog 3 (HP1 gamma homolog, Drosophila)	Cbx3	0.651	0.002	0.804	0.015	0.515	0.014	0.803	0.002
1373885_at	BF398015	chromobox homolog 5 (Drosophila HP1a) (predicted)	Cbx5_predicted	0.972	0.575	1.544	0.110	1.412	0.396	1.377	0.215
1375307_at	BI275772	chromobox homolog 6	Cbx6	0.646	0.135	0.491	0.053	0.546	0.219	0.624	0.030
1371672_at	AI406275	chromobox homolog 7	Cbx7	0.257	0.020	0.347	0.008	0.577	0.064	0.465	0.022
1376008_at	BI275819	chromobox homolog 8 (Drosophila, Pc class)	Cbx8	0.909	0.575	0.910	0.087	0.892	0.309	0.501	0.077
1389469_at	AA858645	chromodomain helicase DNA binding protein 1-like (predicted)	Chd1l_predicted	1.585	0.060	0.771	0.417	1.245	0.364	0.727	0.062
1379830_at	BF396633	Chromodomain helicase DNA binding protein 2 (predicted)	Chd2_predicted	1.533	0.023	1.345	0.013	1.403	0.077	1.426	0.001
1397779_at	BF562254	Chromodomain helicase DNA binding protein 2 (predicted)	Chd2_predicted	0.976	0.063	0.984	0.123	1.049	0.734	1.459	0.054
1381683_at	BE118824	chromodomain helicase DNA binding protein 2 (predicted)	Chd2_predicted	1.101	0.966	1.324	0.386	1.003	0.471	1.579	0.568
1397200_at	BF412612	chromodomain helicase DNA binding protein 4	Chd4	0.768	0.091	0.744	0.293	0.667	0.028	0.704	0.120
1385779_at	BF413917	chromodomain helicase DNA binding protein 4	Chd4	0.873	0.107	0.996	0.348	0.874	0.425	0.987	0.801
1372441_at	BE107091	chromodomain helicase DNA binding protein 4	Chd4	0.684	0.420	0.889	0.988	0.979	0.466	1.115	0.292
1379580_at	BF398050	chromodomain helicase DNA binding protein 6 (predicted)	Chd6_predicted	0.536	0.042	0.405	0.002	0.711	0.323	0.675	0.145
1378361_at	BF523068	chromodomain helicase DNA binding protein 7 (predicted)	Chd7_predicted	1.012	0.088	1.390	0.107	0.789	0.991	1.219	0.299
1382504_at	AI599104	chromodomain helicase DNA binding protein 7 (predicted)	Chd7_predicted	0.980	0.999	1.001	0.992	0.981	0.696	0.999	0.993
1375527_at	BF282681	chromodomain helicase DNA binding protein 8	Chd8	0.581	0.312	1.149	0.284	1.039	0.806	1.125	0.558
1387235_at	NM_021655	chromogranin A	Chga	0.639	0.425	0.299	0.001	0.649	0.013	0.266	0.007
1368034_at	NM_012526	chromogranin B	Chgb	0.793	0.267	0.298	0.000	0.664	0.003	0.346	0.004
1398974_at	AI171615	chromosome segregation 1-like (S. cerevisiae) (predicted)	Cse1l_predicted	0.677	0.468	1.216	0.008	0.705	0.015	1.004	0.204
1399094_at	AA859919	churchill domain containing 1 (predicted)	Churc1_predicted	0.800	0.461	0.932	0.451	0.892	0.599	0.759	0.845
1370107_at	NM_054009	chymotrypsin-like	Ctrl	1.001	0.998	1.255	0.328	5.248	0.100	2.721	0.029
1369951_at	NM_012536	Chymotrypsinogen B	Ctrb	0.920	0.122	0.226	0.111	1.400	0.085	0.256	0.029
1389577_at	AI101160	cirrhosis, autosomal recessive 1A (human)	Cirh1a	0.364	0.012	1.050	0.582	0.364	0.005	1.377	0.089
1386942_at	NM_022596	cis-Golgi matrix protein GM130	Golga2	0.821	0.965	1.182	0.023	0.705	0.402	0.861	0.519
1374190_at	BG380750	citrate lyase beta like	Clybl	0.662	0.227	0.117	0.000	0.643	0.214	0.112	0.016
1369967_at	NM_130755	citrate synthase	Cs	0.755	0.293	3.233	0.012	0.582	0.281	2.756	0.003
1375295_at	AI009657	Citrate synthase	Cs	0.732	0.451	1.421	0.006	0.602	0.004	1.311	0.023
1389137_at	AA957183	Citron	Cit	0.802	0.281	1.088	0.565	0.675	0.120	0.800	0.226
1372056_at	AI406687	CKLF-like MARVEL transmembrane domain containing 6	Cmtm6	2.346	0.004	1.068	0.370	4.077	0.001	1.898	0.026
1398842_at	BM386513	clathrin, heavy polypeptide (Hc)	Cltc	0.601	0.001	0.636	0.004	0.730	0.001	0.751	0.044
1386875_a_at	M19261	clathrin, light polypeptide (Lca)	Clta	1.164	0.589	2.035	0.003	0.985	0.936	1.866	0.007
1375324_at	BE095893	Clathrin, light polypeptide (Lcb)	Cltb	0.402	0.485	0.901	0.730	0.468	0.084	0.782	0.218
1367907_a_at	M19262	clathrin, light polypeptide (Lcb)	Cltb	0.687	0.548	1.208	0.914	0.538	0.004	0.851	0.255
1376711_at	BG673439	claudin 11	Cldn11	0.652	0.019	1.581	0.097	1.785	0.002	1.507	0.211
1369184_at	NM_131905	claudin 16	Cldn16	1.013	0.972	0.998	0.956	1.006	0.939	1.000	0.983
1388547_at	BE328951	claudin 4	Cldn4	9.737	0.001	4.206	0.004	3.533	0.154	2.279	0.016
1370894_at	AJ011811	claudin 7	Cldn7	1.236	0.473	1.336	0.941	0.859	0.276	1.000	0.999
1390407_at	AA955196	claudin domain containing 1	Cldnd1	0.713	0.361	1.006	0.091	0.663	0.013	0.889	0.165
1377935_at	AI231223	Claudin domain containing 1	Cldnd1	0.640	0.423	0.963	0.058	0.796	0.228	0.686	0.081
1377670_at	AW915580	cleavage and polyadenylation factor subunit homolog (S. cerevisiae) (predicted)	Pcf11_predicted	1.150	0.054	0.765	0.032	1.246	0.014	0.867	0.067
1374666_at	BI298206	Cleavage and polyadenylation factor subunit homolog (S. cerevisiae) (predicted)	Pcf11_predicted	0.658	0.058	0.953	0.798	0.924	0.073	0.905	0.590
1393692_at	AA965160	cleavage and polyadenylation factor subunit homolog (S. cerevisiae) (predicted)	Pcf11_predicted	0.799	0.466	1.277	0.686	0.749	0.354	0.652	0.241
1376004_at	BF285297	Cleavage and polyadenylation specific factor 5	Cpsf5	0.807	0.269	0.722	0.114	0.689	0.187	0.664	0.010
1397288_at	BM390376	Cleavage and polyadenylation specific factor 5	Cpsf5	3.156	0.358	0.456	0.041	0.582	0.395	0.331	0.020

1398356_at	BF420718	cleavage and polyadenylation specific factor 5	Cpsf5	1.117	0.728	1.725	0.045	0.667	0.323	1.550	0.033
1376811_a_at	BE108383	cleavage and polyadenylation specific factor 6, 68kDa (predicted)	Cpsf6_predicted	0.678	0.086	2.640	0.001	0.891	0.390	2.140	0.008
1379729_at	AI071906	Cleavage and polyadenylation specific factor 6, 68kDa (predicted)	Cpsf6_predicted	0.801	0.920	1.307	0.295	0.635	0.268	1.124	0.132
1374711_at	BF283512	cleavage and polyadenylation specificity factor 3	Cpsf3	0.642	0.484	0.589	0.128	0.406	0.019	1.002	0.913
1383115_at	AW522557	Cleavage stimulation factor, 3' pre-RNA subunit 2, tau (predicted)	Cstf2t_predicted	1.053	0.709	0.738	0.225	1.257	0.047	1.118	0.050
1389348_at	BF282442	cleavage stimulation factor, 3' pre-RNA, subunit 1	Cstf1	0.899	0.032	2.003	0.060	0.926	0.086	0.999	0.998
1384935_at	AI070621	Cleavage stimulation factor, 3' pre-RNA, subunit 3 (predicted)	Cstf3_predicted	1.299	0.080	1.546	0.046	1.490	0.013	1.123	0.132
1396900_at	BE106436	Cleavage stimulation factor, 3' pre-RNA, subunit 3 (predicted)	Cstf3_predicted	1.202	0.211	1.065	0.797	0.999	0.987	0.998	0.762
1371473_at	BI284472	cleft lip and palate associated transmembrane protein 1 (predicted)	Clptm1_predicted	0.587	0.849	0.731	0.194	0.687	0.618	0.851	0.118
1368099_at	NM_053722	CLIP associating protein 2	Clasp2	0.765	0.552	0.589	0.009	1.721	0.107	0.712	0.029
1392560_at	BG153281	Clone UI-R-FJ0-cpu-i-10-0-UI unknown mRNA	---	1.316	0.125	1.061	0.814	1.230	0.451	0.880	0.149
1371579_at	AI012456	Clone UI-R-FJ0-cpu-m-15-0-UI unknown mRNA	---	0.648	0.021	0.614	0.013	0.749	0.024	0.753	0.037
1367997_at	NM_022947	ClpB caseinolytic peptidase B homolog (E. coli)	Clpb	0.708	0.096	1.239	0.032	0.494	0.293	1.030	0.781
1367784_a_at	AF314657	clusterin	Clu	0.947	0.687	0.873	0.093	0.905	0.741	1.324	0.118
1388246_at	AF314657	clusterin	Clu	0.892	0.785	0.862	0.030	0.940	0.539	1.358	0.237
1379829_at	BF418799	c-myc binding protein (predicted)	Mycbp_predicted	0.790	0.341	0.449	0.035	1.080	0.864	0.618	0.029
1372132_at	BI279729	CNDP dipeptidase 2 (metallopeptidase M20 family)	Cndp2	0.855	0.095	1.052	0.150	1.508	0.022	1.709	0.031
1389368_at	AW253242	Cnksr family member 3	Cnksr3	21.848	0.006	17.039	0.009	21.041	0.004	14.097	0.002
1388596_at	AI411057	coactosin-like 1 (Dictyostelium) (predicted)	Cotl1_predicted	0.870	0.093	0.730	0.029	0.661	0.037	0.517	0.026
1369182_at	NM_013057	coagulation factor III	F3	8.658	0.005	5.663	0.000	1.017	0.916	2.923	0.001
1388377_at	AW142717	coatomer protein complex subunit alpha	Copa	0.792	0.350	0.955	0.262	0.823	0.348	0.897	0.067
1367461_at	NM_080781	coatomer protein complex, subunit beta 1	Copb1	0.779	0.241	0.914	0.787	0.800	0.099	0.923	0.969
1367454_at	NM_021765	coatomer protein complex, subunit beta 2 (beta prime)	Copb2	0.797	0.470	1.003	0.204	0.823	0.147	0.961	0.406
1371802_at	AA891472	coatomer protein complex, subunit epsilon (predicted)	Cope_predicted	0.598	0.137	0.725	0.065	0.622	0.031	0.652	0.069
1372464_at	BE109050	coatomer protein complex, subunit gamma	Copg	0.631	0.316	0.859	0.135	0.731	0.129	0.785	0.020
1380430_at	BF386177	Coatomer protein complex, subunit gamma	Copg	0.793	0.443	1.184	0.973	1.236	0.270	0.941	0.531
1371810_at	BF284093	Coatomer protein complex, subunit gamma	Copg	0.685	0.940	0.386	0.000	0.700	0.309	0.405	0.008
1396754_at	BF403379	Coatomer protein complex, subunit zeta 1 (predicted)	Copz1_predicted	1.533	0.010	0.994	0.324	2.204	0.002	1.932	0.145
1375520_at	AI007763	Coatomer protein complex, subunit zeta 1 (predicted)	Copz1_predicted	0.699	0.097	0.783	0.066	0.728	0.185	0.831	0.102
1394565_at	BF406339	coatomer protein complex, subunit zeta 1 (predicted)	Copz1_predicted	0.451	0.534	0.865	0.411	0.310	0.092	0.553	0.017
1372305_at	AA893634	coatomer protein complex, subunit zeta 2 (predicted)	Copz2_predicted	0.552	0.002	0.954	0.999	0.618	0.021	0.921	0.798
1368585_at	NM_017110	cocaine and amphetamine regulated transcript	Cart	0.593	0.550	0.149	0.008	0.650	0.107	0.120	0.005
1373304_at	BM392002	Coenzyme A synthase	Coasy	0.459	0.033	0.394	0.007	0.413	0.001	0.559	0.007
1390281_a_at	AI407062	coenzyme Q10 homolog A (yeast) (predicted)	Coq10a_predicted	0.389	0.020	0.519	0.001	0.589	0.097	0.479	0.019
1372753_at	BI285643	coenzyme Q6 homolog (yeast)	Coq6	0.689	0.395	2.154	0.003	0.318	0.027	1.321	0.089
1371909_at	AA850406	cofactor required for Sp1 transcriptional activation, subunit 3	Crsp3	1.181	0.103	0.836	0.066	1.184	0.101	1.170	0.664
1398344_at	BI287962	cofactor required for Sp1 transcriptional activation, subunit 6	Crsp6	2.999	0.006	1.562	0.049	3.771	0.000	1.084	0.339
1377263_at	BF399036	cofactor required for Sp1 transcriptional activation, subunit 9 (predicted)	Crsp9_predicted	0.771	0.299	0.935	0.974	1.284	0.021	1.201	0.236
1370184_at	BG666614	cofilin 1, non-muscle	Cfl1	1.016	0.416	1.558	0.028	0.813	0.268	1.171	0.073
1387871_at	BM389673	cofilin 1, non-muscle	Cfl1	1.089	0.472	1.130	0.062	0.853	0.222	1.098	0.005
1388928_at	BF399310	cofilin 2, muscle (predicted)	Cfl2_predicted	0.877	0.320	0.989	0.833	0.640	0.210	0.819	0.386
1388483_at	BI296011	cofilin 2, muscle (predicted)	Cfl2_predicted	1.048	0.861	2.050	0.007	0.977	0.329	1.832	0.017
1377254_a_at	BI295640	Cohen syndrome homolog 1 (predicted)	Cohh1_predicted	0.967	0.379	0.780	0.003	1.041	0.755	0.796	0.048
1375864_at	BI274151	coiled-coil and C2 domain containing 1B	Cc2d1b	0.856	0.525	1.334	0.959	1.629	0.055	1.011	0.699
1375938_at	BF411424	coiled-coil domain containing 12 (predicted)	Ccdc12_predicted	1.368	0.664	0.780	0.669	0.756	0.507	1.153	0.516
1373171_at	BI294854	coiled-coil domain containing 21	Ccdc21	0.982	0.727	1.443	0.034	0.873	0.122	1.233	0.160
1372361_at	AW529931	coiled-coil domain containing 22 (predicted)	Ccdc22_predicted	0.643	0.094	1.406	0.011	0.756	0.966	1.280	0.086
1378406_at	BF394636	Coiled-coil domain containing 39 (predicted)	Ccdc39_predicted	0.692	0.713	0.916	0.975	0.865	0.820	1.158	0.534
1397358_at	AI105407	coiled-coil domain containing 39 (predicted)	Ccdc39_predicted	1.007	0.974	0.998	0.674	0.999	0.314	1.001	0.093
1388736_at	AI175383	coiled-coil domain containing 43	Ccdc43	0.776	0.719	1.311	0.042	0.988	0.488	1.325	0.055
1387944_at	AF092207	coiled-coil domain containing 5	Ccdc5	1.150	0.592	0.743	0.025	1.891	0.082	0.535	0.014
1374005_at	AI233232	coiled-coil domain containing 51	Ccdc51	0.949	0.147	0.882	0.131	0.997	0.659	0.903	0.161
1375634_at	AA799472	coiled-coil domain containing 53 (predicted)	Ccdc53_predicted	0.518	0.374	0.372	0.005	0.345	0.004	0.406	0.015
1373475_at	BM390469	coiled-coil domain containing 58 (predicted)	Ccdc58_predicted	0.705	0.345	2.678	0.007	0.992	0.932	2.100	0.025
1383271_at	BM391624	coiled-coil domain containing 59 (predicted)	Ccdc59_predicted	1.004	0.987	1.190	0.149	1.010	0.960	1.270	0.653
1389126_at	BG373580	coiled-coil-helix-coiled-coil-helix domain containing 1 (predicted)	Chchd1_predicted	0.631	0.170	1.574	0.016	0.829	0.174	1.307	0.042
1371312_at	AA799736	coiled-coil-helix-coiled-coil-helix domain containing 2	Chchd2	0.881	0.441	1.369	0.008	0.894	0.482	1.022	0.907
1389291_at	AA850511	coiled-coil-helix-coiled-coil-helix domain containing 3 (predicted)	Chchd3_predicted	0.844	0.701	1.375	0.047	0.740	0.276	1.385	0.023
1373001_at	AA817990	coiled-coil-helix-coiled-coil-helix domain containing 4	Chchd4	1.198	0.546	3.988	0.003	0.895	0.455	2.643	0.003
1389625_at	BI299402	coiled-coil-helix-coiled-coil-helix domain containing 4	Chchd4	0.999	0.925	1.504	0.439	1.001	0.985	3.245	0.055
1372134_at	AW918650	coiled-coil-helix-coiled-coil-helix domain containing 6 (predicted)	Chchd6_predicted	0.583	0.912	1.661	0.009	0.441	0.050	1.653	0.063

1374731_at	BI275929	Coilin	Coil	3.699	0.003	0.919	0.704	4.911	0.000	1.504	0.030
1376302_at	AA955175	Coilin	Coil	0.447	0.027	0.316	0.007	0.904	0.064	0.325	0.020
1393523_at	AI059075	Coilin	Coil	1.702	0.144	1.158	0.709	0.511	0.433	1.802	0.358
1393623_at	AI502247	Coilin	Coil	0.926	0.575	0.416	0.000	0.718	0.425	0.438	0.000
1385904_at	BG153342	cold inducible RNA binding protein	Cirbp	0.379	0.001	0.223	0.005	0.423	0.004	0.197	0.024
1369083_at	NM_031147	cold inducible RNA binding protein	Cirbp	1.002	0.976	1.003	0.462	1.081	0.546	0.995	0.996
1370376_a_at	AA866458	cold shock domain protein A	Csda	0.595	0.022	2.444	0.009	0.513	0.005	1.966	0.051
1387899_at	U52102	collapsin response mediator protein 1	Crmp1	1.363	0.134	0.892	0.242	0.952	0.383	0.616	0.049
1379631_at	AI071665	colony stimulating factor 1 (macrophage)	Csf1	12.692	0.003	3.316	0.087	4.153	0.063	1.328	0.224
1380582_at	AW535553	colony stimulating factor 1 (macrophage)	Csf1	1.004	0.893	0.999	0.997	1.002	0.979	1.001	0.999
1372801_at	AI171256	COMM domain containing 10	Commd10	0.554	0.293	1.312	0.062	0.493	0.064	1.358	0.077
1372148_at	BI281210	COMM domain containing 2 (predicted)	Commd2_predicted	0.584	0.131	1.122	0.017	0.516	0.060	1.082	0.141
1398894_at	AI178763	COMM domain containing 3	Commd3	0.937	0.791	1.460	0.015	1.237	0.297	1.509	0.003
1372304_at	BG378042	COMM domain containing 4 (predicted)	Commd4_predicted	0.489	0.042	1.120	0.604	0.813	0.193	0.931	0.322
1370327_at	AF290194	COMM domain containing 5	Commd5	0.924	0.814	1.200	0.112	0.794	0.322	1.075	0.738
1376493_at	AI408996	COMM domain containing 7	Commd7	0.835	0.509	1.229	0.629	0.748	0.039	0.962	0.224
1373294_at	AI234292	COMM domain containing 8 (predicted)	Commd8_predicted	1.274	0.488	1.390	0.010	1.200	0.605	1.231	0.028
1398334_a_at	BF417278	COMM domain containing 9	Commd9	0.828	0.957	1.431	0.013	0.696	0.028	1.287	0.241
1367968_at	NM_133622	common salivary protein 1	LOC171161	1.007	0.993	0.897	0.496	1.071	0.864	1.007	0.516
1398784_at	NM_019259	complement component 1, q subcomponent binding protein	C1qbp	0.702	0.724	2.549	0.002	0.614	0.022	2.060	0.003
1376652_at	BF418957	complement component 1, q subcomponent, alpha polypeptide	C1qa	0.670	0.034	0.561	0.052	0.545	0.074	0.798	0.383
1383241_at	BI292425	complement component 1, r subcomponent	C1r	126.901	0.000	146.089	0.000	129.915	0.000	153.914	0.000
1387893_at	D88250	complement component 1, s subcomponent /// similar to complement component 1, s subcomponent (predicted)	C1s /// RGD1561715_predicted	35.793	0.006	34.474	0.000	51.490	0.006	59.153	0.001
1383391_a_at	AI716125	complement component 2	C2	2.561	0.188	1.044	0.059	3.794	0.120	4.228	0.045
1368000_at	NM_016994	complement component 3	C3	46.869	0.001	96.778	0.000	11.805	0.008	15.836	0.004
1369764_at	NM_012516	complement component 4 binding protein, alpha	C4bpa	9.632	0.002	43.178	0.000	6.120	0.007	7.866	0.021
1368695_at	NM_016995	complement component 4 binding protein, beta	C4bpb	17.716	0.015	15.080	0.001	10.190	0.002	1.325	0.243
1393123_at	BM392153	complement component 8, gamma polypeptide (predicted)	C8g_predicted	0.704	0.263	0.398	0.013	1.108	0.657	0.606	0.083
1368741_at	NM_057146	complement component 9	C9	1.966	0.060	3.894	0.028	1.215	0.305	1.008	0.971
1389470_at	AI639117	complement factor B	Cfb	6.621	0.064	25.852	0.000	28.534	0.000	58.358	0.002
1387798_a_at	D42115	complement receptor related protein	Crry	1.969	0.123	0.873	0.227	1.808	0.099	1.100	0.127
1394096_at	AI555027	complement receptor related protein	Crry	2.618	0.860	1.307	0.016	2.335	0.201	1.576	0.052
1385238_at	AA926087	Complexin 4 (predicted)	Cplx4_predicted	0.600	0.159	0.621	0.014	0.671	0.171	0.618	0.015
1374301_at	BI294695	component of oligomeric golgi complex 1 (predicted)	Cog1_predicted	0.536	0.411	0.664	0.011	0.668	0.022	0.696	0.159
1383206_at	AA955098	component of oligomeric golgi complex 3	Cog3	0.983	0.684	1.171	0.001	1.165	0.288	1.027	0.239
1396663_at	BI300284	Component of oligomeric golgi complex 4 (predicted)	Cog4_predicted	1.413	0.231	1.623	0.229	1.151	0.862	0.944	0.798
1372819_at	BM382870	component of oligomeric golgi complex 4 (predicted)	Cog4_predicted	0.903	0.818	1.002	0.768	0.920	0.354	0.893	0.709
1398471_at	BF288063	component of oligomeric golgi complex 6	Cog6	0.464	0.041	0.610	0.002	0.508	0.132	0.737	0.019
1379876_at	AI407943	component of oligomeric golgi complex 7	Cog7	0.590	0.522	0.601	0.002	0.563	0.069	0.494	0.128
1374045_at	AI598851	Component of oligomeric golgi complex 8 (predicted)	Cog8_predicted	0.445	0.009	0.299	0.018	0.655	0.239	0.454	0.010
1390794_at	BI289098	component of oligomeric golgi complex 8 (predicted)	Cog8_predicted	0.352	0.122	0.426	0.002	0.280	0.011	0.431	0.020
1395117_at	BE106475	congenital dyserythropoietic anemia, type I (predicted)	Cdan1_predicted	1.000	0.939	0.994	0.972	0.983	0.878	1.000	0.998
1393740_at	BI294230	connector enhancer of kinase suppressor of Ras 1	Cnksr1	3.104	0.007	3.704	0.002	7.163	0.001	7.416	0.001
1391455_at	AI228280	conserved nuclear protein Nhn1	Nhn1	0.996	0.302	0.947	0.256	0.783	0.267	0.502	0.071
1369351_at	NM_019329	contactin 3	Cntn3	0.918	0.792	1.276	0.206	0.931	0.467	1.359	0.587
1373029_at	AI169377	COP9 (constitutive photomorphogenic) homolog, subunit 2 (Arabidopsis thaliana)	Cops2	0.977	0.928	1.683	0.003	0.820	0.033	1.593	0.063
1398972_at	AW916366	COP9 (constitutive photomorphogenic) homolog, subunit 3 (Arabidopsis thaliana)	Cops3	0.612	0.068	0.615	0.004	0.649	0.010	0.727	0.012
1395352_at	BF282468	COP9 (constitutive photomorphogenic) homolog, subunit 3 (Arabidopsis thaliana)	Cops3	0.913	0.993	0.557	0.073	0.762	0.089	0.741	0.051
1371476_at	AI411531	COP9 (constitutive photomorphogenic) homolog, subunit 4 (Arabidopsis thaliana)	Cops4	0.932	0.123	1.448	0.025	0.926	0.301	1.323	0.027
1395565_at	BG669198	COP9 (constitutive photomorphogenic) homolog, subunit 4 (Arabidopsis thaliana)	Cops4	0.655	0.830	1.392	0.146	0.900	0.768	0.898	0.331
1395618_at	BG673431	COP9 (constitutive photomorphogenic) homolog, subunit 4 (Arabidopsis thaliana)	Cops4	0.791	0.883	1.365	0.109	0.711	0.269	1.022	0.938
1372209_at	AI105072	COP9 (constitutive photomorphogenic) homolog, subunit 5 (Arabidopsis thaliana)	Cops5	0.706	0.582	1.350	0.067	0.522	0.023	1.098	0.164
1399011_at	AI409481	COP9 (constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana) (predicted)	Cops6_predicted	0.855	0.621	0.966	0.369	0.961	0.209	0.874	0.584
1374460_at	BM386508	COP9 (constitutive photomorphogenic) homolog, subunit 7a (Arabidopsis thaliana) (predicted)	Cops7a_predicted	0.751	0.310	2.722	0.101	0.581	0.038	2.843	0.147
1389897_at	BE110772	COP9 (constitutive photomorphogenic) homolog, subunit 7a (Arabidopsis thaliana) (predicted)	Cops7a_predicted	0.998	0.983	1.645	0.134	0.998	0.965	0.999	0.994
1398955_at	BG378922	COP9 (constitutive photomorphogenic) homolog, subunit 8 (Arabidopsis thaliana)	Cops8	0.834	0.406	1.800	0.007	0.842	0.091	1.367	0.005
1378519_at	BF398120	Copine I (predicted)	Cpne1_predicted	0.657	0.599	0.993	0.971	0.526	0.201	0.999	0.992
1392984_at	BG671686	copine III (predicted)	Cpne3_predicted	1.180	0.238	2.147	0.384	2.633	0.101	1.897	0.638
1371993_at	AI237636	Copine III (predicted)	Cpne3_predicted	1.782	0.247	0.695	0.004	2.600	0.004	0.991	0.573
1387038_at	NM_053425	copper chaperone for superoxide dismutase	Ccs	0.348	0.080	0.756	0.051	0.254	0.003	0.718	0.065

1377998_at	BI288705	coproporphyrinogen oxidase	Cpox	0.775	0.301	0.826	0.183	0.712	0.030	1.186	0.113
1387446_at	NM_022950	core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase	C1galt1	1.288	0.048	5.447	0.000	1.293	0.004	2.137	0.001
1399033_at	AA945869	core binding factor beta	Cbfb	0.587	0.450	0.387	0.012	0.889	0.460	0.475	0.000
1395821_at	BF524120	core binding factor beta	Cbfb	1.033	0.994	0.946	0.200	0.704	0.555	0.758	0.026
1390762_at	BE103006	core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (predicted)	Cbfa2t2_predicted	1.024	0.434	2.110	0.064	1.022	0.653	1.374	0.110
1379674_at	BE115481	core-binding factor, runt domain, alpha subunit 2; translocated to, 3 (predicted)	Cbfa2t3_predicted	0.740	0.034	0.574	0.004	0.553	0.035	0.507	0.023
1388682_at	AI598397	cornichon homolog (Drosophila) (predicted)	Cnih_predicted	0.511	0.116	0.584	0.002	0.521	0.006	0.620	0.025
1373747_at	BG381691	cornichon homolog 2 (Drosophila)	Cnih2	1.124	0.692	1.451	0.157	3.232	0.034	2.664	0.019
1388151_at	AI008369	coronin 7	Coro7	1.004	0.999	0.944	0.992	0.878	0.345	1.002	0.993
1379656_a_at	AW529016	coronin, actin binding protein 2A	Coro2a	1.311	0.962	1.920	0.057	0.912	0.579	1.188	0.298
1370390_at	AF140359	coronin, actin binding protein 6	Coro6	0.997	0.877	0.851	0.351	1.100	0.193	0.638	0.369
1398769_at	NM_019222	coronin, actin-binding protein, 1B	Coro1b	1.204	0.500	1.434	0.026	0.932	0.342	1.272	0.083
1370123_a_at	AF054618	cortactin	Cttn	1.196	0.334	2.250	0.023	1.232	0.103	1.868	0.076
1371465_at	BM390681	cortactin	Cttn	0.712	0.548	0.501	0.006	0.664	0.036	0.584	0.008
1397902_at	BF548780	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	Cox15	1.350	0.510	0.678	0.078	1.225	0.222	0.670	0.212
1375922_at	BI296988	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	Cox15	0.941	0.919	0.720	0.008	0.920	0.614	0.793	0.015
1371658_at	BM389065	COX4 neighbor	Cox4nb	0.700	0.902	1.215	0.015	0.399	0.063	1.025	0.536
1374273_at	BG665433	Coxsackie virus and adenovirus receptor	Cxadr	0.471	0.006	0.360	0.002	0.639	0.059	0.448	0.018
1384816_at	AI137518	coxsackie virus and adenovirus receptor	Cxadr	0.729	0.360	0.739	0.049	1.028	0.725	0.906	0.293
1370264_at	BI288556	CPG2 protein	CPG2	0.689	0.156	0.262	0.007	0.872	0.484	0.485	0.007
1378886_x_at	BE102928	CPG2 protein	CPG2	0.971	0.865	0.744	0.054	1.022	0.983	0.801	0.053
1398263_at	NM_019355	CPG2 protein	CPG2	1.313	0.988	1.542	0.452	1.006	0.925	1.644	0.173
1384718_at	AI030198	Craniofacial development protein 1	Cfdp1	1.716	0.008	1.949	0.026	1.731	0.181	1.295	0.047
1373824_at	AW433973	craniofacial development protein 1	Cfdp1	1.489	0.333	1.851	0.016	2.126	0.025	1.617	0.076
1395825_at	BF284859	Craniofacial development protein 1	Cfdp1	0.843	0.969	1.905	0.736	0.817	0.489	1.234	0.835
1387830_at	NM_017096	C-reactive protein, pentraxin-related	Crp	1.001	0.545	0.456	0.046	1.003	0.643	0.457	0.046
1367740_at	M14400	creatine kinase, brain	Ckb	0.195	0.045	0.123	0.001	0.146	0.013	0.090	0.006
1390566_a_at	BI301453	creatine kinase, mitochondrial 1, ubiquitous	Ckmt1	6.595	0.001	6.072	0.002	5.459	0.005	3.816	0.003
1373828_at	AI412614	CREB regulated transcription coactivator 2	Crtc2	2.333	0.020	2.122	0.005	2.217	0.030	1.489	0.156
1387300_at	NM_053797	Crn, crooked neck-like 1 (Drosophila)	Crnkl1	1.496	0.121	0.812	0.152	1.527	0.195	0.999	0.992
1383648_x_at	BI283883	crumbs homolog 3 (Drosophila)	Crb3	2.252	0.001	1.847	0.006	1.959	0.004	1.636	0.002
1383647_a_at	BI283883	crumbs homolog 3 (Drosophila)	Crb3	1.830	0.038	2.031	0.016	1.944	0.003	1.611	0.001
1384397_x_at	AI072527	crumbs homolog 3 (Drosophila)	Crb3	1.731	0.085	1.619	0.132	1.007	0.533	1.631	0.154
1392640_at	AI412155	cryptochrome 1 (photolyase-like)	Cry1	1.830	0.117	2.383	0.016	1.265	0.783	2.411	0.038
1388385_at	BG371710	crystallin, beta A2	Cryba2	0.358	0.012	0.209	0.001	0.345	0.002	0.283	0.008
1382349_at	AI408238	crystallin, gamma S	Crygs	0.573	0.174	0.749	0.765	0.855	0.427	0.774	0.686
1376051_at	BI293393	crystallin, lamda 1	Cryl1	0.758	0.062	0.610	0.011	0.740	0.061	0.528	0.014
1374628_at	AI232098	crystallin, zeta	Cryz	1.090	0.729	0.994	0.970	1.002	0.963	1.025	0.808
1392506_at	AI575645	crystallin, zeta (quinone reductase)-like 1	Cryzl1	0.546	0.003	0.788	0.171	0.823	0.258	0.854	0.052
1371592_at	AI600236	c-src tyrosine kinase	Csk	1.170	0.091	1.026	0.906	0.728	0.044	0.764	0.128
1390535_at	BE098745	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1 (predicted)	Ctdp1_predicted	1.620	0.094	2.553	0.001	1.220	0.841	1.674	0.043
1388533_at	BM390302	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1	Ctdsp1	0.616	0.446	0.607	0.005	0.497	0.010	0.515	0.004
1391635_at	AI044500	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like (predicted)	Ctdspl_predicted	0.972	0.937	0.623	0.045	0.659	0.345	0.764	0.281
1387978_at	U49057	CTD-binding SR-like protein rA9	LOC245925	0.675	0.021	0.763	0.086	0.698	0.167	0.998	0.993
1397102_at	AI502196	CTD-binding SR-like protein rA9	LOC245925	1.109	0.424	1.230	0.057	1.479	0.380	0.954	0.089
1367984_at	NM_019384	CTD-binding SR-like rA1	LOC56081	0.847	0.112	0.731	0.600	0.737	0.009	1.036	0.704
1370029_at	NM_019201	C-terminal binding protein 1	Ctbp1	0.949	0.517	1.123	0.412	0.865	0.426	1.008	0.927
1387113_at	NM_053335	C-terminal binding protein 2	Ctbp2	2.370	0.007	1.540	0.066	2.398	0.006	1.343	0.612
1392299_at	BE113875	C-terminal PDZ domain ligand of neuronal nitric oxide synthase	Capon	2.152	0.162	0.861	0.035	1.152	0.882	0.908	0.054
1379450_at	BM383195	CTTNBP2 N-terminal like (predicted)	Cttnbp2nl_predicted	7.381	0.007	1.940	0.045	13.920	0.000	5.801	0.022
1382873_at	BF414250	CTTNBP2 N-terminal like (predicted)	Cttnbp2nl_predicted	1.191	0.521	1.641	0.118	2.131	0.104	2.953	0.061
1390782_at	BI295930	C-type lectin domain family 14, member a	Clec14a	1.016	0.362	0.965	0.297	0.940	0.792	1.009	0.978
1376368_at	BE095878	CUE domain containing 2 (predicted)	Cuedc2_predicted	0.569	0.048	0.996	0.760	0.564	0.032	0.975	0.959
1393029_at	BF410771	CUG triplet repeat, RNA binding protein 1	Cugbp1	1.151	0.111	0.951	0.904	0.978	0.618	0.960	0.338
1393568_at	BF404793	CUG triplet repeat, RNA binding protein 1	Cugbp1	1.086	0.383	1.372	0.029	1.250	0.146	1.063	0.333
1388704_at	AA892394	CUG triplet repeat, RNA binding protein 1	Cugbp1	1.024	0.604	0.516	0.013	0.858	0.310	0.682	0.151
1393257_at	BI293905	CUG triplet repeat, RNA binding protein 1	Cugbp1	0.934	0.825	1.125	0.158	0.887	0.416	1.171	0.338
1371900_at	BF408840	CUG triplet repeat, RNA binding protein 1	Cugbp1	1.138	0.963	0.571	0.049	0.968	0.402	0.666	0.111
1397217_at	BF408757	CUG triplet repeat, RNA binding protein 2	Cugbp2	1.564	0.151	1.289	0.256	1.647	0.144	1.298	0.246
1397673_at	AW523660	CUG triplet repeat, RNA binding protein 2	Cugbp2	1.014	0.566	0.797	0.080	1.725	0.050	1.099	0.459
1396654_at	BF403645	CUG triplet repeat, RNA binding protein 2	Cugbp2	0.599	0.630	1.746	1.000	0.375	0.438	1.147	0.979

1380670_at	BE095613	CUG triplet repeat, RNA binding protein 2	Cugbp2	1.089	0.848	0.608	0.148	2.846	0.004	0.954	0.831
1388195_at	AW140475	CUG triplet repeat, RNA binding protein 2	Cugbp2	1.122	0.851	0.743	0.061	1.017	0.890	0.860	0.087
1388855_at	BI284428	cullin 1 (predicted)	Cul1_predicted	1.190	0.185	1.571	0.012	1.351	0.014	1.601	0.007
1383106_at	BI295890	cullin 2 (predicted)	Cul2_predicted	1.452	0.076	1.333	0.108	1.665	0.015	1.328	0.121
1378127_at	BF420355	cullin 2 (predicted)	Cul2_predicted	1.647	0.210	1.283	0.965	1.366	0.074	0.854	0.363
1393343_at	BE115856	cullin 3 (predicted)	Cul3_predicted	0.501	0.002	0.599	0.107	0.413	0.039	0.814	0.130
1399132_at	BI285751	cullin 3 (predicted)	Cul3_predicted	0.652	0.121	0.809	0.011	0.705	0.068	0.904	0.028
1369068_at	NM_022683	cullin 5	Cul5	1.165	0.044	1.983	0.084	1.002	0.520	1.005	0.990
1393306_at	BF551475	Cullin 5	Cul5	1.036	0.425	0.766	0.143	0.884	0.755	0.756	0.137
1367972_at	NM_054004	cullin associated and neddylation disassociated 1	Cand1	0.691	0.152	1.178	0.062	0.635	0.008	1.190	0.078
1370421_a_at	AB029342	cullin-associated and neddylation-dissociated 2 (putative)	Cand2	0.550	0.014	0.566	0.015	0.507	0.050	0.641	0.108
1377406_at	BI275251	Cullin-associated and neddylation-dissociated 2 (putative)	Cand2	0.874	0.586	0.660	0.011	0.740	0.061	0.661	0.022
1385024_at	AW535558	cutC copper transporter homolog (E.coli) (predicted)	Cutc_predicted	0.395	0.014	0.798	0.132	0.429	0.010	0.730	0.093
1385888_at	AA963272	Cut-like 1 (Drosophila)	Cutl1	1.005	0.371	0.620	0.032	1.561	0.068	0.753	0.006
1385887_at	BE107316	Cut-like 1 (Drosophila)	Cutl1	0.940	0.634	0.814	0.299	1.359	0.116	0.777	0.011
1371024_at	AW527515	cut-like 1 (Drosophila)	Cutl1	1.028	0.869	1.002	0.789	1.004	0.981	0.973	0.215
1391079_at	BI295875	Cut-like 1 (Drosophila)	Cutl1	0.995	0.909	0.956	0.602	1.005	0.969	0.954	0.614
1372138_at	BM390477	Cut-like 1 (Drosophila)	Cutl1	0.911	0.930	0.720	0.635	1.552	0.265	0.848	0.533
1395105_at	AW527267	CWF19-like 2, cell cycle control (S. pombe) (predicted)	Cwf19l2_predicted	1.222	0.140	1.239	0.033	1.075	0.233	1.038	0.652
1388875_at	AI410353	CXXC finger 1 (PHD domain)	Cxxc1	1.230	0.986	2.292	0.013	0.939	0.798	2.233	0.001
1368801_at	NM_053342	CXXC finger 4	Cxxc4	0.416	0.008	0.193	0.001	0.485	0.011	0.226	0.011
1394284_at	AW143904	CXXC finger 4	Cxxc4	0.254	0.057	0.371	0.106	0.950	0.545	1.089	0.509
1371629_at	AI105444	CXXC finger 5	Cxxc5	1.284	0.178	1.367	0.168	1.362	0.196	1.134	0.140
1375231_a_at	BI281838	CXXC finger 5	Cxxc5	1.004	0.375	1.537	0.006	1.385	0.158	1.409	0.084
1387897_at	L16532	cyclic nucleotide phosphodiesterase 1	Cnp1	3.562	0.076	1.838	0.014	3.600	0.003	2.496	0.008
1370693_a_at	M18630	cyclic nucleotide phosphodiesterase 1	Cnp1	2.529	0.091	1.629	0.173	4.332	0.054	1.934	0.012
1389566_at	AW253821	cyclin B2	Ccnb2	0.640	0.394	0.658	0.246	0.605	0.170	0.673	0.203
1390343_at	AA998893	Cyclin C	Ccnc	0.611	0.295	0.476	0.001	0.591	0.043	0.678	0.000
1375666_at	BE098802	cyclin D binding myb-like transcription factor 1	Dmtf1	1.252	0.067	1.381	0.002	1.281	0.222	1.168	0.036
1383075_at	BI295861	cyclin D1	Ccnd1	0.665	0.108	0.541	0.052	0.757	0.116	0.650	0.017
1371643_at	AW143798	cyclin D1	Ccnd1	0.478	0.118	0.428	0.005	0.689	0.163	0.548	0.012
1371150_at	X75207	cyclin D1	Ccnd1	0.858	0.983	1.048	0.833	0.831	0.866	0.999	0.782
1370810_at	L09752	cyclin D2	Ccnd2	1.151	0.640	0.638	0.069	1.223	0.280	0.534	0.067
1369935_at	NM_012766	cyclin D3	Ccnd3	0.381	0.088	0.619	0.019	0.516	0.000	0.616	0.021
1398340_at	AI317832	cyclin D-type binding-protein 1	Ccndbp1	0.588	0.092	0.320	0.000	0.667	0.024	0.375	0.000
1391681_at	AI409729	Cyclin E2 (predicted)	Ccne2_predicted	1.354	0.600	0.947	0.959	1.170	0.305	0.689	0.722
1367875_at	NM_031030	cyclin G associated kinase	Gak	0.999	0.983	1.342	0.006	0.858	0.136	1.365	0.055
1367764_at	NM_012923	cyclin G1	Ccng1	0.822	0.881	1.370	0.012	0.782	0.861	1.611	0.025
1371953_at	AI408309	Cyclin G2 (predicted)	Ccng2_predicted	4.589	0.012	2.448	0.003	4.508	0.007	2.539	0.004
1368083_at	NM_052981	cyclin H	Ccnh	0.922	0.752	1.480	0.089	1.036	0.323	1.289	0.119
1388370_at	AA945706	cyclin I (predicted)	Ccni_predicted	0.932	0.146	0.741	0.000	1.049	0.917	0.877	0.015
1392937_at	BF557327	cyclin I (predicted)	Ccni_predicted	0.911	0.870	0.628	0.358	0.908	0.564	0.816	0.430
1368050_at	NM_053662	cyclin L1	Ccnl1	1.611	0.029	2.757	0.004	1.955	0.005	1.798	0.011
1382164_at	AI236548	Cyclin L2	Ccnl2	1.041	0.652	1.850	0.122	1.030	0.179	1.463	0.092
1381294_at	BF409260	Cyclin M1 (predicted)	Cnnm1_predicted	1.269	0.082	0.971	0.908	0.835	0.253	0.749	0.617
1376142_at	BE120410	Cyclin M1 (predicted)	Cnnm1_predicted	1.001	0.988	0.849	0.103	1.062	0.556	0.855	0.108
1382269_at	BM388183	cyclin M2	Cnnm2	0.520	0.003	1.586	0.087	0.779	0.321	1.378	0.033
1380970_at	BI281399	Cyclin M2	Cnnm2	1.003	0.520	1.166	0.339	1.000	0.996	0.992	0.989
1391270_at	BE112177	Cyclin M3 (predicted)	Cnnm3_predicted	0.372	0.012	0.192	0.004	0.335	0.000	0.374	0.006
1382124_at	BE105042	Cyclin M3 (predicted)	Cnnm3_predicted	0.797	0.117	0.707	0.362	0.617	0.018	0.861	0.434
1369950_at	NM_053593	cyclin-dependent kinase 4	Cdk4	0.712	0.204	1.056	0.554	0.486	0.005	0.807	0.054
1368088_at	NM_080885	cyclin-dependent kinase 5	Cdk5	0.534	0.080	0.167	0.025	0.263	0.010	0.419	0.004
1397324_at	BE117105	Cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	Cdk7	1.848	0.108	1.043	0.907	1.709	0.381	0.759	0.330
1388171_at	AW916118	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	Cdk7	0.484	0.117	0.930	0.567	0.606	0.010	1.171	0.580
1372759_at	H31766	cyclin-dependent kinase 9 (CDC2-related kinase)	Cdk9	0.922	0.694	1.627	0.006	0.875	0.553	1.254	0.045
1388674_at	AI010427	cyclin-dependent kinase inhibitor 1A	Cdkn1a	2.989	0.037	20.309	0.002	3.698	0.004	21.063	0.001
1373812_at	BE110915	cyclin-dependent kinase inhibitor 1B	Cdkn1b	1.144	0.103	0.797	0.007	1.298	0.239	0.765	0.030
1369192_at	NM_031762	cyclin-dependent kinase inhibitor 1B	Cdkn1b	0.891	0.553	0.879	0.293	0.846	0.597	0.661	0.187
1372299_at	AI013919	cyclin-dependent kinase inhibitor 1C (P57)	Cdkn1c	1.129	0.631	1.569	0.104	1.036	0.884	1.069	0.771
1370054_at	NM_131902	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	Cdkn2c	0.578	0.028	0.325	0.003	0.491	0.010	0.449	0.018
1370226_at	AI409867	cystatin B	Cstb	1.160	0.332	1.790	0.040	0.739	0.514	1.930	0.003

1370855_at	BG666933	cystatin C	Cst3	0.876	0.921	0.627	0.017	0.858	0.377	0.712	0.008
1368162_at	NM_133566	cystatin E/M	Cst6	0.796	0.870	0.805	0.073	0.644	0.103	0.567	0.249
1370057_at	NM_017148	cysteine and glycine-rich protein 1	Csrp1	1.829	0.494	4.103	0.022	1.499	0.261	2.371	0.044
1370282_at	U44948	cysteine and glycine-rich protein 2	Csrp2	0.178	0.047	0.094	0.004	0.124	0.001	0.121	0.023
1376797_at	AA997458	cysteine and glycine-rich protein 2 binding protein (predicted)	Csrp2bp_predicted	0.675	0.237	1.832	0.039	0.776	0.900	1.805	0.028
1377738_a_at	AI176855	cysteine and histidine rich 1	Cyhr1	0.651	0.131	0.305	0.013	0.720	0.187	0.465	0.048
1383160_at	AA892238	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1 (predicted)	Chordc1_predicted	1.070	0.670	1.866	0.024	1.033	0.306	1.836	0.023
1367755_at	NM_052809	cysteine dioxygenase 1, cytosolic	Cdo1	0.126	0.003	0.338	0.002	0.120	0.013	0.313	0.001
1368290_at	NM_031327	cysteine rich protein 61	Cyr61	1.004	0.996	0.987	0.970	1.005	0.996	0.995	0.989
1398286_at	M64755	cysteine sulfinic acid decarboxylase	Csad	1.774	0.967	0.877	0.991	1.000	1.000	0.811	0.892
1382037_at	AI600057	cysteine-rich motor neuron 1 (predicted)	Crim1_predicted	1.037	0.551	1.531	0.045	1.204	0.220	1.290	0.142
1368633_at	NM_022859	cysteine-rich secretory protein 1	Crisp1	1.844	0.028	1.010	0.965	1.090	0.662	0.970	0.949
1388594_at	BG371453	cysteine-rich with EGF-like domains 1	Creld1	0.430	0.008	0.940	0.197	0.541	0.020	0.807	0.030
1377016_at	BE106888	cysteine-rich with EGF-like domains 2	Creld2	0.874	0.927	2.140	0.049	1.306	0.112	1.989	0.050
1374034_at	BG379410	cysteinyl-tRNA synthetase (predicted)	Cars_predicted	1.192	0.123	1.104	0.885	1.356	0.178	0.741	0.878
1376754_at	AI176610	cysteinyl-tRNA synthetase (predicted)	Cars_predicted	1.392	0.485	1.350	0.053	1.464	0.301	1.284	0.554
1394970_at	BI279660	cysteinyl-tRNA synthetase (predicted)	Cars_predicted	1.104	0.638	1.005	0.727	1.124	0.197	0.956	0.772
1391572_at	BE109168	cysteinyl-tRNA synthetase (predicted)	Cars_predicted	1.006	0.968	0.878	0.818	0.999	0.232	0.861	0.626
1390692_at	BE105721	cytidine 5'-triphosphate synthase (predicted)	Ctps_predicted	0.700	0.201	1.458	0.036	0.430	0.004	1.295	0.055
1394431_at	AI704014	cytidine and dCMP deaminase domain containing 1	Cdadc1	1.008	0.243	0.589	0.004	0.851	0.875	0.661	0.004
1385329_at	BF401322	cytidine and dCMP deaminase domain containing 1	Cdadc1	1.010	0.727	0.601	0.052	1.318	0.054	1.108	0.422
1371804_at	AI172266	cytidine and dCMP deaminase domain containing 1	Cdadc1	0.897	0.954	1.970	0.012	1.091	0.759	1.995	0.027
1373650_at	AI172078	cytidine monophospho-N-acetylneuraminic acid synthetase	Cmas	0.518	0.081	0.754	0.001	0.411	0.011	0.643	0.022
1389135_at	AW140637	cytidine triphosphate synthase II	Ctps2	1.185	0.752	1.615	0.008	1.071	0.337	2.320	0.011
1373365_at	AI100861	cytidylate kinase	Cmpk	1.087	0.474	0.805	0.117	1.210	0.922	0.830	0.034
1372846_at	AI179227	cytochrome b, ascorbate dependent 3	Cybasc3	0.857	0.490	0.971	0.741	1.617	0.634	1.078	0.126
1379344_at	AI176057	Cytochrome b-245, beta polypeptide	Cybb	1.822	0.023	5.080	0.004	1.588	0.027	2.529	0.009
1386904_a_at	AF007107	cytochrome b-5	Cyb5	0.374	0.236	0.405	0.019	0.466	0.031	0.575	0.039
1370808_at	J03867	cytochrome b5 reductase 3	Cyb5r3	0.228	0.007	0.105	0.002	0.181	0.013	0.058	0.016
1370827_at	AF307840	cytochrome b5 reductase 4	Cyb5r4	1.130	0.184	1.617	0.001	1.105	0.224	1.551	0.018
1370005_at	NM_030586	cytochrome b5 type B	Cyb5b	0.870	0.037	2.378	0.124	0.919	0.111	1.527	0.110
1398383_at	BI282164	cytochrome b-561 (predicted)	Cyb561_predicted	0.652	0.298	0.507	0.028	0.491	0.011	0.536	0.047
1399111_at	AI102191	cytochrome b-561 domain containing 2	Cyb561d2	0.409	0.112	0.892	0.234	0.458	0.016	0.625	0.345
1367607_at	NM_017202	cytochrome c oxidase subunit IV isoform 1	Cox4i1	0.977	0.887	1.070	0.087	0.802	0.018	0.834	0.798
1386887_at	NM_053586	cytochrome c oxidase subunit Vb	Cox5b	0.798	0.701	0.968	0.344	0.648	0.025	1.017	0.429
1371337_at	BG378939	cytochrome c oxidase subunit VIIa polypeptide 2 like (predicted)	Cox7a2l_predicted	0.986	0.931	1.615	0.010	0.804	0.013	1.185	0.119
1371387_at	AA866477	cytochrome c oxidase subunit VIIb	Cox7b	0.740	0.715	0.849	0.177	0.961	0.256	0.927	0.247
1370888_at	X15030	cytochrome c oxidase, subunit Va	Cox5a	0.895	0.893	1.371	0.061	0.807	0.380	1.310	0.034
1370861_at	BI282326	cytochrome c oxidase, subunit VIa, polypeptide 1	Cox6a1	0.886	0.984	0.999	0.800	0.651	0.053	0.987	0.963
1367757_at	NM_019360	cytochrome c oxidase, subunit VIc	Cox6c	0.768	0.840	0.905	0.189	0.575	0.064	0.781	0.190
1367629_at	NM_022503	cytochrome c oxidase, subunit VIIa 2	Cox7a2	0.970	0.882	0.783	0.119	0.926	0.444	0.826	0.181
1388113_at	BG673321	cytochrome c oxidase, subunit VIIIa	Cox8a	0.854	0.684	0.834	0.062	0.786	0.144	0.990	0.145
1394658_at	AI176811	Cytochrome c oxidase, subunit XVII assembly protein homolog (yeast)	Cox17	0.884	0.343	1.209	0.881	1.005	0.673	1.016	0.880
1369984_at	NM_053540	cytochrome c oxidase, subunit XVII assembly protein homolog (yeast)	Cox17	0.685	0.617	1.535	0.051	0.695	0.274	0.760	0.394
1387773_at	NM_012839	cytochrome c, somatic	Cycs	0.851	0.315	1.502	0.088	0.989	0.466	1.416	0.026
1369939_at	AI104240	cytochrome c, somatic	Cycs	0.901	0.922	1.069	0.026	0.947	0.339	1.216	0.021
1369321_s_at	NM_012840	cytochrome c, testis /// phosphodiesterase 11A	Cyct /// Pde11a	0.654	0.725	1.963	0.290	1.923	0.975	1.862	0.858
1371342_at	BI277021	cytochrome c-1 (predicted)	Cyc1_predicted	0.450	0.105	1.223	0.850	0.640	0.021	1.062	0.556
1387916_at	U39208	cytochrome P450 4F6	Cyp4f6	0.958	0.563	0.938	0.074	0.775	0.369	0.837	0.110
1368990_at	NM_012940	cytochrome P450, family 1, subfamily b, polypeptide 1	Cyp1b1	1.000	0.994	0.600	0.078	0.997	0.957	0.729	0.102
1378551_at	BE118606	cytochrome P450, family 20, subfamily A, polypeptide 1	Cyp20a1	0.982	0.278	1.368	0.007	0.883	0.473	1.262	0.018
1387583_at	NM_130408	cytochrome P450, family 26, subfamily A, polypeptide 1	Cyp26a1	1.003	0.995	0.892	0.149	1.884	0.070	0.892	0.589
1387914_at	M73231	cytochrome P450, family 27, subfamily a, polypeptide 1	Cyp27a1	4.779	0.021	6.504	0.000	36.640	0.001	31.496	0.006
1368636_at	NM_053763	cytochrome P450, family 27, subfamily b, polypeptide 1	Cyp27b1	1.271	0.314	0.965	0.798	1.631	0.116	0.861	0.499
1367979_s_at	NM_012941	cytochrome P450, subfamily 51	Cyp51	0.554	0.086	1.037	0.526	0.479	0.107	0.866	0.053
1387020_at	BG664123	cytochrome P450, subfamily 51	Cyp51	0.486	0.134	0.954	0.636	0.413	0.029	0.872	0.070
1370475_at	M20406	cytochrome P450IIB3	Cyp2b3	0.996	0.984	1.002	0.917	1.004	0.180	1.005	0.874
1385334_at	AA818166	Cytochrome P450-like protein	Loc266761	0.650	0.002	0.371	0.000	0.576	0.036	0.640	0.090
1388127_at	AI170346	cytochrome P450-like protein	Loc266761	0.773	0.658	1.120	0.708	0.726	0.225	1.741	0.103
1372498_at	BF285068	cytokine induced apoptosis inhibitor 1	Ciapin1	0.477	0.043	1.393	0.040	0.346	0.020	1.653	0.002
1378586_at	BI291842	Cytokine inducible SH2-containing protein	Cish	2.029	0.154	0.971	0.747	2.089	0.140	1.001	0.989

1389294_at	AI103084	cytoplasmic FMR1 interacting protein 1 (predicted)	Cyfip1_predicted	1.555	0.043	1.055	0.963	1.368	0.057	0.908	0.051
1379150_at	BF404462	Cytoplasmic FMR1 interacting protein 2 (predicted)	Cyfip2_predicted	0.763	0.229	0.958	0.712	1.542	0.181	1.549	0.164
1398533_at	BE105837	cytoplasmic FMR1 interacting protein 2 (predicted)	Cyfip2_predicted	1.031	0.537	1.345	0.320	0.813	0.990	1.375	1.000
1368571_at	NM_021997	cytoplasmic linker 2	Cyln2	2.463	0.020	2.614	0.000	3.041	0.004	2.149	0.001
1377589_at	BF386215	Cytoplasmic linker 2	Cyln2	1.614	0.984	1.580	0.039	1.589	0.282	1.281	0.492
1375685_at	BI282257	cytoplasmic linker associated protein 1	Clasp1	2.751	0.000	1.030	0.458	3.030	0.001	1.091	0.391
1384015_at	AI044920	cytoplasmic linker associated protein 1	Clasp1	1.426	0.209	2.581	0.063	1.362	0.041	1.213	0.390
1392996_at	BG668435	cytoplasmic polyadenylation element binding protein 1 (predicted)	Cpeb1_predicted	1.372	0.388	1.638	0.011	1.116	0.431	1.819	0.012
1390628_at	AI010275	cytoplasmic polyadenylation element binding protein 2 (predicted)	Cpeb2_predicted	1.498	0.005	1.426	0.052	1.419	0.005	1.219	0.023
1396225_at	BG666316	cytoplasmic polyadenylation element binding protein 2 (predicted)	Cpeb2_predicted	1.168	0.337	1.872	0.020	0.970	0.765	2.272	0.113
1372223_at	BG374299	cytoplasmic polyadenylation element binding protein 4 (predicted)	Cpeb4_predicted	1.474	0.007	0.731	0.036	1.216	0.442	0.745	0.035
1393294_at	BG671389	cytoplasmic polyadenylation element binding protein 4 (predicted)	Cpeb4_predicted	1.803	0.047	2.029	0.013	1.295	0.538	1.460	0.021
1388405_at	BI294780	cytoskeleton associated protein 5	Ckap5	1.117	0.980	1.112	0.123	0.953	0.829	1.152	0.244
1371885_at	BI282366	cytoskeleton-associated protein 1 (predicted)	Ckap1_predicted	0.927	0.952	2.757	0.002	0.671	0.519	2.105	0.008
1375654_at	BI278813	cytoskeleton-associated protein 4 (predicted)	Ckap4_predicted	1.515	0.022	1.114	0.772	0.810	0.195	1.588	0.829
1375643_at	BM384259	cytoskeleton-associated protein 4 (predicted)	Ckap4_predicted	0.829	0.453	0.697	0.036	0.732	0.712	0.796	0.006
1384198_at	BF288648	cytosolic ovarian carcinoma antigen 1 (predicted)	Cova1_predicted	0.771	0.323	0.712	0.098	1.118	0.180	0.778	0.212
1397692_at	BE104820	cytotoxic granule-associated RNA binding protein 1	Tia1	1.251	0.024	0.947	0.657	1.478	0.045	0.854	0.543
1374786_at	BI298817	Cytotoxic granule-associated RNA binding protein 1	Tia1	1.191	0.740	0.454	0.016	0.784	0.224	0.768	0.134
1387874_at	AI230048	D site albumin promoter binding protein	Dbp	1.160	0.435	5.773	0.010	1.006	0.921	7.062	0.015
1388105_at	BE113021	D123 gene product	D123	0.443	0.199	0.653	0.016	0.547	0.022	0.814	0.018
1372166_at	AI169146	D4, zinc and double PHD fingers family 2 (predicted)	Dpf2_predicted	1.290	0.124	1.522	0.032	1.646	0.003	1.617	0.012
1399162_a_at	AJ277077	damage-specific DNA binding protein 1	Ddb1	0.334	0.351	0.409	0.006	0.535	0.010	0.596	0.083
1383205_at	BI288833	dapper homolog 2, antagonist of beta-catenin (xenopus) (predicted)	Dact2_predicted	1.058	0.802	2.213	0.013	0.957	0.388	1.160	0.566
1373046_at	AW918273	DAZ associated protein 1	Dazap1	1.462	0.256	2.822	0.003	1.677	0.156	2.409	0.009
1372511_at	AI102612	DAZ associated protein 2	Dazap2	0.844	0.247	1.656	0.105	1.123	0.074	1.484	0.155
1382281_at	BI296136	DAZ associated protein 2	Dazap2	1.002	0.284	0.994	0.660	0.940	0.830	0.745	0.638
1367532_at	AA893186	DAZ associated protein 2	Dazap2	0.962	0.340	0.924	0.541	0.787	0.831	1.024	0.772
1385369_at	BI290883	DAZ interacting protein 1-like	Dzip1l	3.521	0.009	5.073	0.023	3.320	0.009	4.074	0.069
1372999_at	AI171216	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	Dcun1d5	1.029	0.676	0.965	0.837	1.052	0.932	1.074	0.180
1375432_at	AI171599	DD6A4-12(7)-2 mRNA, partial sequence	---	0.981	0.228	1.106	0.906	1.357	0.171	1.125	0.241
1394597_at	AI101356	DDHD domain containing 1	Ddhd1	0.783	0.558	1.593	0.613	1.138	0.741	1.076	0.087
1392072_at	BE108176	D-dopachrome tautomerase	Ddt	0.788	0.004	0.939	0.324	0.815	0.347	0.800	0.098
1367793_at	NM_024131	D-dopachrome tautomerase	Ddt	0.485	0.514	1.845	0.112	0.304	0.001	1.332	0.060
1371837_at	AA851926	ddx5 gene	Ddx5	0.576	0.010	0.335	0.000	0.703	0.023	0.428	0.002
1373319_at	BF419628	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	Ddx1	0.722	0.209	1.246	0.014	0.687	0.010	1.230	0.392
1397529_at	BI296754	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	Ddx17	0.814	0.532	0.382	0.003	0.728	0.348	0.395	0.005
1397405_at	BM385221	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	Ddx17	0.927	0.857	0.231	0.003	0.883	0.868	0.238	0.002
1377945_at	AI111512	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	Ddx18	0.769	0.003	1.513	0.026	0.965	0.699	1.251	0.065
1397508_at	BE106682	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	Ddx18	0.731	0.015	1.341	0.132	0.761	0.428	1.029	0.209
1383559_at	AI144819	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19	Ddx19	1.112	0.213	1.575	0.072	0.999	0.443	1.029	0.085
1380012_at	BF399592	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19	Ddx19	1.096	0.599	1.006	0.452	1.001	0.536	0.847	0.351
1388814_at	AI408110	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19	Ddx19	0.789	0.626	0.821	0.247	0.420	0.046	0.743	0.008
1388843_at	BI296771	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19	Ddx19	0.782	0.691	0.917	0.682	0.999	0.683	1.040	0.502
1375901_at	AI178527	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21a	Ddx21a	0.955	0.030	1.603	0.026	0.850	0.116	1.610	0.015
1396187_at	AI136551	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21a	Ddx21a	1.019	0.740	1.023	0.924	0.556	0.045	1.095	0.104
1373809_at	BI296325	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21b /// hypothetical protein LOC606294	Ddx21b /// LOC606294	0.643	0.143	0.375	0.013	0.487	0.039	0.263	0.006
1376739_at	AW252511	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	Ddx24	0.800	0.038	1.722	0.011	0.719	0.289	1.538	0.019
1376116_at	BM389678	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	Ddx24	0.888	0.550	1.007	0.594	0.808	0.100	1.104	0.455
1368619_at	NM_031630	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25	Ddx25	0.702	0.087	0.412	0.008	0.902	0.265	0.311	0.011
1397551_at	BG373974	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	Ddx27	0.978	0.447	1.591	0.067	0.899	0.790	1.143	0.486
1384377_at	BI284877	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28 (predicted)	Ddx28_predicted	0.648	0.058	1.059	0.047	0.484	0.030	1.112	0.403
1387048_at	NM_053563	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	Ddx39	0.912	0.649	2.962	0.000	0.921	0.814	2.394	0.001
1372377_at	BM389310	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41 (predicted)	Ddx41_predicted	0.872	0.200	0.686	0.028	0.694	0.123	0.776	0.035
1376596_at	BI295847	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42 (predicted)	Ddx42_predicted	1.123	0.289	1.047	0.451	1.023	0.790	1.073	0.623
1379896_at	BM390256	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42 (predicted)	Ddx42_predicted	1.250	0.396	2.230	0.007	1.218	0.114	1.466	0.050
1387912_at	U25746	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	Ddx46	0.419	0.057	0.341	0.000	0.508	0.022	0.312	0.028
1375554_at	BM390927	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	Ddx47	0.972	0.718	1.444	0.008	0.722	0.172	1.196	0.421
1374332_at	AI171365	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49 (predicted)	Ddx49_predicted	0.673	0.353	2.139	0.027	0.493	0.026	2.401	0.039
1390688_at	AA799576	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	Ddx50	0.930	0.374	2.122	0.000	1.268	0.269	1.539	0.014
1373682_at	BI290764	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51 (predicted)	Ddx51_predicted	0.775	0.287	1.299	0.471	0.555	0.056	1.164	0.940

1368588_at	NM_053525	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	Ddx52	1.337	0.349	2.258	0.055	3.419	0.059	2.251	0.040
1391889_at	BG671963	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	Ddx52	1.049	0.501	1.401	0.111	1.022	0.932	1.050	0.038
1378497_at	BF400776	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55 (predicted)	Ddx55_predicted	0.822	0.058	1.087	0.088	0.620	0.034	0.876	0.203
1383635_at	BM385099	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59	Ddx59	0.472	0.009	0.710	0.944	0.579	0.003	1.424	0.249
1376468_at	AI411501	dead end homolog 1 (zebrafish)	Dnd1	0.788	0.618	1.163	0.264	0.611	0.061	1.001	0.295
1395533_at	BF552813	dead end homolog 1 (zebrafish)	Dnd1	0.544	0.991	0.710	0.052	0.333	0.072	0.205	0.000
1391118_at	BI280337	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae) (predicted)	Ddx11_predicted	0.906	0.992	0.999	0.309	1.004	0.986	1.010	0.468
1370979_at	BF282783	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 20, 103kD	Ddx20	1.088	0.698	1.187	0.054	1.214	0.111	1.364	0.024
1399123_at	BI302415	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26	Ddx26	1.310	0.135	0.611	0.002	0.889	0.435	0.555	0.005
1380464_at	AI145031	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26	Ddx26	0.926	0.596	0.992	0.984	1.761	0.514	0.958	0.897
1385482_at	BI293434	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26	Ddx26	1.133	0.743	0.618	0.277	1.296	0.746	1.557	0.456
1372242_at	AI169598	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	Ddx3x	1.045	0.492	0.746	0.003	1.010	0.192	0.946	0.411
1386535_at	BG667163	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	Ddx3x	1.070	0.716	0.895	0.031	1.477	0.229	0.683	0.061
1385214_at	BF391513	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	Ddx3x	0.880	0.888	2.351	0.013	1.663	0.807	1.417	0.133
1374506_at	BI296403	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 31 (predicted)	Ddx31_predicted	0.694	0.031	0.552	0.051	0.479	0.023	0.513	0.035
1374470_at	AI102264	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57	Dhx57	1.043	0.982	0.567	0.031	1.178	0.417	0.721	0.093
1398937_at	BI279381	DEAH (Asp-Glu-Ala-His) box polypeptide 15 (predicted)	Dhx15_predicted	0.852	0.434	1.269	0.011	0.851	0.104	0.999	0.240
1399084_at	BF405883	DEAH (Asp-Glu-Ala-His) box polypeptide 16	Dhx16	0.962	0.537	0.969	0.659	1.115	0.402	0.969	0.167
1374858_at	BF420262	DEAH (Asp-Glu-Ala-His) box polypeptide 29 (predicted)	Dhx29_predicted	0.762	0.008	1.057	0.581	0.804	0.389	1.205	0.075
1388595_at	AI102995	DEAH (Asp-Glu-Ala-His) box polypeptide 30	Dhx30	0.627	0.053	1.027	0.718	0.735	0.048	1.051	0.617
1395579_at	BG666347	DEAH (Asp-Glu-Ala-His) box polypeptide 32 (predicted)	Dhx32_predicted	0.491	0.305	0.583	0.167	0.218	0.064	0.590	0.153
1377763_at	BF283765	DEAH (Asp-Glu-Ala-His) box polypeptide 33 (predicted)	Dhx33_predicted	0.867	0.874	0.447	0.063	1.126	0.726	0.551	0.016
1376437_at	BM383834	DEAH (Asp-Glu-Ala-His) box polypeptide 33 (predicted)	Dhx33_predicted	0.726	0.902	1.259	0.482	0.870	0.529	0.998	0.415
1385871_at	AA859982	DEAH (Asp-Glu-Ala-His) box polypeptide 36 (predicted)	Dhx36_predicted	1.490	0.062	1.296	0.106	0.774	0.109	1.146	0.064
1385872_at	AI237532	DEAH (Asp-Glu-Ala-His) box polypeptide 36 (predicted)	Dhx36_predicted	1.293	0.069	1.430	0.010	0.793	0.158	1.184	0.128
1377906_at	BF404389	DEAH (Asp-Glu-Ala-His) box polypeptide 36 (predicted)	Dhx36_predicted	0.987	0.952	0.994	0.938	0.538	0.980	0.997	0.984
1377785_at	BI275330	DEAH (Asp-Glu-Ala-His) box polypeptide 40	Dhx40	0.566	0.885	2.011	0.001	0.703	0.475	1.602	0.029
1374299_at	BF398414	DEAH (Asp-Glu-Ala-His) box polypeptide 9 (predicted)	Dhx9_predicted	0.704	0.051	0.610	0.020	0.777	0.855	0.575	0.006
1389535_at	BI285645	death associated protein 3	Dap3	0.989	0.400	1.006	0.957	1.109	0.306	0.971	0.684
1376788_at	AA818353	death associated protein kinase 1 (predicted)	Dapk1_predicted	1.427	0.163	1.588	0.001	1.585	0.088	1.906	0.001
1379911_at	BI281823	death associated protein kinase 1 (predicted)	Dapk1_predicted	1.003	0.965	1.002	0.787	0.959	0.612	1.408	0.694
1398434_at	BE107465	Death associated transcription factor 1 (predicted)	Datf1_predicted	1.457	0.124	0.860	0.109	1.471	0.098	0.992	0.491
1393698_at	BE106785	Death associated transcription factor 1 (predicted)	Datf1_predicted	1.165	0.632	0.995	0.982	1.001	0.314	1.003	0.623
1382326_at	AI555347	Death effector domain-containing	Dedd	1.323	0.033	1.050	0.981	1.447	0.087	1.034	0.310
1369941_at	NM_022526	death-associated protein	Dap	1.380	0.218	1.604	0.021	0.967	0.364	1.286	0.808
1392216_at	BF403731	Death-associated protein kinase 3	Dapk3	1.716	0.235	5.896	0.031	1.472	0.339	3.196	0.009
1367621_at	NM_022546	death-associated protein kinase 3	Dapk3	0.999	0.936	1.242	0.326	1.001	0.701	0.999	0.873
1390185_at	BE109709	decapping enzyme, scavenger	Dcps	0.793	0.548	2.047	0.223	1.469	0.218	1.437	0.490
1387951_at	AB032395	decay accelarating factor 1	Daf1	2.377	0.109	2.846	0.010	1.793	0.691	2.570	0.017
1380352_at	AA956439	Dedicator of cyto-kinesis 1 (predicted)	Dock1_predicted	1.244	0.715	1.149	0.774	0.965	0.091	1.003	0.636
1384525_at	AI549335	dedicator of cytokinesis 11	Dock11	1.741	0.059	0.717	0.046	1.416	0.627	0.911	0.969
1370905_at	BI291229	dedicator of cytokinesis 9	Dock9	0.752	0.356	0.972	0.822	1.171	0.248	1.317	0.022
1367465_at	AI013627	defender against cell death 1	Dad1	0.732	0.243	0.870	0.112	0.705	0.014	0.819	0.026
1369660_at	AF068860	defensin beta 1	Defb1	3.204	0.043	1.914	0.049	1.752	0.115	1.101	0.951
1386988_at	NM_031801	deformed epidermal autoregulatory factor 1 (Drosophila)	Deaf1	0.647	0.014	0.275	0.012	0.653	0.536	0.474	0.004
1367770_at	NM_053323	degenerative spermatocyte homolog 1 (Drosophila)	Degs1	0.605	0.994	0.796	0.134	0.682	0.097	0.975	0.442
1388687_at	BI274588	dehydrodolichyl diphosphate synthase	Dhdds	0.420	0.225	0.743	0.182	0.329	0.015	0.626	0.183
1390172_at	AI409946	dehydrogenase E1 and transketolase domain containing 1	Dhtkd1	0.383	0.029	0.446	0.004	0.713	0.691	0.538	0.016
1389407_at	BE099453	dehydrogenase/reductase (SDR family) member 1	Dhrs1	0.295	0.000	0.251	0.003	0.393	0.016	0.299	0.027
1391259_at	BE104618	Dehydrogenase/reductase (SDR family) member 1	Dhrs1	0.340	0.006	0.462	0.004	0.271	0.003	0.322	0.013
1373240_at	BI276935	dehydrogenase/reductase (SDR family) member 3	Dhrs3	0.862	0.321	0.482	0.009	0.998	0.987	0.345	0.003
1370814_at	AB062758	dehydrogenase/reductase (SDR family) member 4	Dhrs4	0.305	0.004	0.069	0.003	0.442	0.039	0.110	0.013
1374617_at	AI408791	dehydrogenase/reductase (SDR family) member 7B	Dhrs7b	0.781	0.268	1.133	0.708	1.019	0.867	1.083	0.599
1374440_at	BE098506	dehydrogenase/reductase (SDR family) member 8	Dhrs8	1.142	0.407	1.948	0.131	1.191	0.348	1.536	0.061
1388832_at	AI104245	dehydrogenase/reductase (SDR family) X chromosome (predicted)	Dhrsx_predicted	0.750	0.692	1.091	0.065	1.132	0.707	0.999	0.983
1387103_s_at	NM_031720	deiodinase, iodothyronine, type II /// solute carrier family 25 (mitochondrial carrier, brain), member 14	Dio2 /// Slc25a14	0.468	0.130	0.690	0.010	0.591	0.323	0.619	0.015
1372259_at	BI295054	DEK oncogene (DNA binding)	Dek	1.115	0.613	0.847	0.030	2.172	0.012	0.935	0.102
1374564_at	BE099401	deltex 2 homolog (Drosophila)	Dtx2	1.336	0.001	0.672	0.090	2.534	0.007	0.928	0.460
1370506_at	U46149	demethyl-Q 7	Coq7	0.547	0.097	1.004	0.998	0.283	0.104	0.508	0.134
1380021_at	AI059486	DENN/MADD domain containing 2D (predicted)	Dennd2d_predicted	8.539	0.007	13.240	0.001	13.389	0.000	13.476	0.000
1387626_at	NM_024158	deoxycytidine kinase	Dck	0.784	0.883	1.004	0.999	1.008	0.915	1.748	0.443

1372799_at	BF285179	deoxyguanosine kinase (predicted)	Dguok_predicted	1.136	0.809	0.374	0.021	0.922	0.536	0.458	0.001
1379435_at	AI599463	deoxyguanosine kinase (predicted)	Dguok_predicted	1.435	0.994	0.355	0.041	0.613	0.384	0.397	0.166
1388803_at	AA892493	deoxyhypusine synthase	Dhps	0.530	0.755	0.710	0.683	0.692	0.269	1.041	0.820
1370914_at	BM384112	deoxynucleotidyltransferase, terminal, interacting protein 1	Dnttip1	0.715	0.168	0.898	0.700	0.480	0.269	0.883	0.437
1370915_s_at	BM384112	deoxynucleotidyltransferase, terminal, interacting protein 1	Dnttip1	0.551	0.214	0.865	0.541	0.582	0.067	0.576	0.593
1383256_at	BF410997	deoxynucleotidyltransferase, terminal, interacting protein 2 (predicted)	Dnttip2_predicted	0.627	0.028	1.133	0.111	0.648	0.004	1.072	0.827
1382119_at	BI303937	deoxynucleotidyltransferase, terminal, interacting protein 2 (predicted)	Dnttip2_predicted	0.982	0.795	0.953	0.098	0.894	0.851	0.964	0.033
1379676_a_at	AW527320	deoxyribonuclease 1-like 1	Dnase1l1	1.354	0.008	0.984	0.463	1.820	0.084	2.485	0.026
1368294_at	NM_053907	deoxyribonuclease I-like 3	Dnase1l3	1.212	0.208	0.829	0.986	2.446	0.012	1.092	0.356
1383067_a_at	AW141143	deoxythymidylate kinase (predicted)	Dtymk_predicted	0.990	0.619	1.436	0.167	1.496	0.127	1.154	0.347
1383068_at	BI290898	deoxythymidylate kinase (predicted)	Dtymk_predicted	0.907	0.819	1.174	0.038	1.148	0.330	1.079	0.356
1387865_at	AI411157	deoxyuridine triphosphatase	Dut	0.279	0.002	0.303	0.023	0.271	0.003	0.384	0.000
1376914_at	AW253690	DEP domain containing 1a (predicted)	Depdc1a_predicted	1.798	0.244	0.739	0.056	1.364	0.148	0.797	0.289
1380817_at	BF394055	DEP domain containing 2 (predicted)	Depdc2_predicted	1.179	0.667	0.891	0.172	0.880	0.998	1.033	0.600
1373752_at	BE108494	DEP domain containing 5 (predicted)	Depdc5_predicted	1.047	0.085	0.521	0.046	1.727	0.958	0.916	0.218
1395562_at	AW524172	Dephospho-CoA kinase domain containing	Dcakd	0.791	0.772	0.997	0.923	1.025	0.286	0.995	0.680
1373461_at	AI412649	dermal papilla derived protein 6	DERP6	1.109	0.547	1.431	0.024	1.450	0.024	1.376	0.118
1373947_at	BI278545	dermatopontin (predicted)	Dpt_predicted	1.000	0.731	0.609	0.059	0.998	0.307	0.598	0.038
1375936_at	BI279663	desmocollin 2	Dsc2	0.498	0.132	1.038	0.764	0.520	0.056	0.842	0.300
1388506_at	AW144509	desmoplakin	Dsp	1.516	0.005	1.855	0.075	1.292	0.035	2.483	0.210
1371375_at	BI285599	destrin	Dstn	1.354	0.107	1.537	0.010	0.878	0.602	1.057	0.352
1375881_at	AI170442	destrin	Dstn	1.815	0.132	1.259	0.228	0.868	0.897	0.906	0.154
1380545_at	BF419027	development and differentiation enhancing (predicted)	Ddef1_predicted	0.427	0.007	1.081	0.360	0.948	0.244	0.782	0.905
1390441_at	AW527409	Development and differentiation enhancing (predicted)	Ddef1_predicted	0.768	0.260	0.389	0.003	0.616	0.026	0.617	0.021
1385228_x_at	AI059117	development and differentiation enhancing (predicted)	Ddef1_predicted	0.893	0.362	1.590	0.010	1.096	0.738	1.593	0.013
1384717_at	AA894199	Development and differentiation enhancing (predicted)	Ddef1_predicted	0.882	0.618	0.886	0.872	1.228	0.126	0.903	0.122
1381018_a_at	BG378709	development and differentiation enhancing (predicted)	Ddef1_predicted	1.032	0.925	1.240	0.025	0.846	0.026	1.144	0.166
1381019_x_at	BG378709	development and differentiation enhancing (predicted)	Ddef1_predicted	1.019	0.937	1.347	0.313	1.020	0.094	1.217	0.151
1391602_at	AW527113	developmentally regulated GTP binding protein 1	Drg1	3.140	0.091	0.740	0.514	0.571	0.413	0.923	0.146
1386979_at	NM_133395	developmentally regulated protein TPO1	Tpo1	1.387	0.197	1.046	0.926	2.186	0.064	1.182	0.103
1376307_a_at	BI289591	developmentally regulated RNA-binding protein 1	Drb1	0.585	0.007	0.635	0.003	0.675	0.086	0.886	0.758
1372017_at	BE110572	diablo homolog (Drosophila)	Diablo	0.584	0.012	0.797	0.008	0.531	0.061	0.763	0.090
1367745_at	NM_031143	diacylglycerol kinase zeta	Dgkz	0.828	0.075	1.964	0.242	0.673	0.102	1.735	0.233
1387190_at	NM_080787	diacylglycerol kinase, alpha	Dgka	0.988	0.896	1.226	0.041	2.171	0.034	1.116	0.186
1397303_at	AI178467	Diacylglycerol kinase, alpha	Dgka	1.035	0.916	1.010	0.967	0.790	0.249	1.096	0.997
1381486_at	BF386108	Diacylglycerol kinase, beta	Dgkb	1.211	0.927	0.763	0.479	0.917	0.824	1.026	0.104
1374109_at	AI230466	diacylglycerol kinase, theta (predicted)	Dgkq_predicted	0.808	0.141	0.646	0.114	0.864	0.288	0.987	0.278
1367915_at	NM_053437	diacylglycerol O-acyltransferase 1	Dgat1	0.754	0.495	0.902	0.690	0.635	0.027	0.737	0.085
1389371_at	AI104077	Diaphanous homolog 2 (Drosophila) (predicted)	Diap2_predicted	1.821	0.514	1.833	0.010	1.147	0.534	1.503	0.004
1370235_at	AI175009	diazepam binding inhibitor	Dbi	0.888	0.671	0.689	0.188	0.907	0.453	0.784	0.055
1367909_at	NM_134387	dicarbonyl L-xylulose reductase	Dcxr	0.240	0.008	0.888	0.719	0.264	0.008	0.570	0.251
1398643_at	BF388566	Dicer1, Dcr-1 homolog (Drosophila)	Dicer1	1.635	0.486	0.717	0.671	0.604	0.023	0.896	0.801
1388685_at	AI011749	DiGeorge syndrome critical region gene 2	Dgcr2	0.709	0.023	0.696	0.019	0.582	0.050	0.575	0.014
1373424_at	BF284776	DiGeorge syndrome critical region gene 6 (predicted)	Dgcr6_predicted	0.934	0.692	0.863	0.574	1.004	0.978	0.622	0.186
1370075_at	NM_130400	dihydrofolate reductase	Dhfr	1.025	0.150	1.182	0.506	1.199	0.249	1.447	0.016
1373201_at	AI412898	Dihydrolipoamide branched chain transacylase E2	Dbt	0.363	0.052	0.606	0.016	0.487	0.001	0.533	0.006
1373016_at	AI410493	dihydrolipoamide dehydrogenase	Dld	0.350	0.483	0.942	0.318	0.750	0.667	0.793	0.020
1388194_at	BI295900	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	Dlat	0.580	0.091	0.583	0.150	0.572	0.033	0.722	0.431
1370879_at	D90401	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	Dlst	0.895	0.658	0.831	0.117	1.189	0.809	0.898	0.132
1382348_at	AI230216	dihydroorotate dehydrogenase	Dhodh	0.532	0.019	1.634	0.021	0.545	0.010	1.454	0.069
1380728_at	BE118404	Dihydropyrimidinase-like 2	Dpysl2	0.983	0.972	0.602	0.449	0.915	0.772	0.584	0.613
1388479_at	BI294841	Dihydropyrimidinase-like 3	Dpysl3	4.091	0.002	1.912	0.105	5.804	0.000	1.664	0.073
1387141_at	NM_023023	dihydropyrimidinase-like 5	Dpysl5	0.602	0.962	0.450	0.001	1.302	0.227	0.516	0.009
1389595_at	BM386615	dihydrouridine synthase 2-like, SMM1 homolog (S. cerevisiae) (predicted)	Dus2l_predicted	1.800	0.111	1.277	0.074	0.680	0.559	2.096	0.027
1374979_at	AI102764	dihydrouridine synthase 3-like (S. cerevisiae)	Dus3l	1.116	0.698	2.254	0.017	1.079	0.715	2.364	0.047
1367966_at	NM_053748	dipeptidylpeptidase 3	Dpp3	1.069	0.866	1.173	0.018	1.110	0.659	0.980	0.755
1367722_at	NM_031973	dipeptidylpeptidase 7	Dpp7	1.105	0.339	2.310	0.005	0.835	0.108	1.821	0.006
1382213_at	AI535527	dipeptidylpeptidase 8 (predicted)	Dpp8_predicted	1.524	0.053	1.371	0.019	1.519	0.104	1.329	0.093
1374964_at	AI175505	dipeptidylpeptidase 8 (predicted)	Dpp8_predicted	1.326	0.282	0.973	0.814	1.245	0.279	0.911	0.363
1370053_at	BE116953	Discs, large (Drosophila) homolog-associated protein 1	Dlgap1	0.679	0.203	1.249	0.679	1.650	0.784	1.110	0.854
1394485_at	AW532781	Discs, large (Drosophila) homolog-associated protein 1	Dlgap1	1.176	0.244	1.000	0.998	1.006	0.934	1.003	0.983

1384197_at	AW521536	Discs, large (Drosophila) homolog-associated protein 1	Dlgap1	1.495	0.576	1.564	0.110	1.776	0.038	0.899	0.917
1380807_at	AW529655	Discs, large homolog 1 (Drosophila)	Dlgh1	0.662	0.503	0.465	0.189	1.836	0.328	0.643	0.135
1388816_at	AI413060	Discs, large homolog 1 (Drosophila)	Dlgh1	1.079	0.530	0.796	0.101	1.152	0.969	0.907	0.467
1398276_at	NM_022282	discs, large homolog 2 (Drosophila)	Dlgh2	0.509	0.054	1.970	0.034	0.165	0.002	1.043	0.269
1387210_at	NM_019621	discs, large homolog 4 (Drosophila) /// hypothetical gene supported by NM_019621	Dlgh4 /// LOC497670	1.014	0.864	0.980	0.754	1.397	0.106	0.917	0.218
1377121_at	AW520410	Discs, large homolog 5 (Drosophila) (predicted)	Dlg5_predicted	0.821	0.783	0.878	0.183	0.741	0.034	0.907	0.069
1367618_a_at	NM_130734	discs, large homolog 5 (Drosophila) (predicted)	Dlg5_predicted	0.973	0.982	1.194	0.016	0.750	0.067	1.144	0.085
1376684_at	AA874827	discs, large homolog 7 (Drosophila) (predicted)	Dlg7_predicted	1.001	0.996	0.993	0.993	1.339	0.456	0.995	0.985
1370507_at	U67140	discs, large homolog-associated protein 4 (Drosophila)	Dlgap4	1.474	0.078	2.389	0.028	1.661	0.076	2.176	0.016
1398184_at	BI294805	Dishevelled associated activator of morphogenesis 1 (predicted)	Daam1_predicted	1.338	0.055	1.171	0.511	1.287	0.971	1.051	0.307
1369997_at	NM_031820	dishevelled, dsh homolog 1 (Drosophila)	Dvl1	1.021	0.418	2.239	0.005	0.512	0.018	1.676	0.015
1375433_at	AI412473	Dispatched homolog 2 (Drosophila) (predicted)	Disp2_predicted	0.875	0.142	0.383	0.001	0.686	0.070	0.436	0.005
1390102_at	AI168996	disrupted in renal carcinoma 2 homolog (human)	Dirc2	1.170	0.138	0.752	0.330	1.010	0.991	0.800	0.037
1380558_at	BM391243	distal-less homeobox 3 (predicted)	Dlx3_predicted	1.100	0.736	1.187	0.917	1.268	0.245	1.152	0.673
1367516_at	BG375549	distrobrevin binding protein 1	Dtnbp1	1.896	0.034	3.959	0.000	1.516	0.020	3.489	0.014
1397473_at	AI029288	distrobrevin binding protein 1	Dtnbp1	1.722	0.154	1.565	0.014	1.595	0.601	1.844	0.085
1398928_at	BG378296	divalent cation tolerant protein CUTA	Cuta	0.551	0.164	1.549	0.006	0.569	0.000	1.289	0.017
1396056_at	AW527531	Dmx-like 1 (predicted)	Dmxl1_predicted	1.296	0.055	0.802	0.769	0.999	0.788	0.968	0.910
1373772_at	AI179516	DNA (cytosine-5-)-methyltransferase 1	Dnmt1	0.828	0.134	0.870	0.519	0.999	0.451	0.998	0.987
1369438_at	NM_022857	DNA binding protein N5	N5	1.195	0.813	1.084	0.382	1.469	0.526	1.004	0.842
1383495_at	AI556858	DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae) (predicted)	Dclre1a_predicted	1.713	0.119	0.787	0.305	0.935	0.963	0.566	0.013
1388591_at	BM383669	DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae)	Dclre1b	0.843	0.202	0.817	0.234	1.008	0.684	1.092	0.165
1389195_at	AI236726	DNA fragmentation factor, alpha subunit	Dffa	0.903	0.838	0.877	0.168	1.247	0.341	1.288	0.036
1387604_at	NM_053362	DNA fragmentation factor, beta subunit	Dffb	0.999	0.894	0.827	0.234	0.999	0.958	0.736	0.239
1392678_a_at	AA956455	DNA methyltransferase 3A	Dnmt3a	2.815	0.016	1.457	0.012	1.713	0.008	1.471	0.031
1384804_at	AI029751	DNA methyltransferase 3A	Dnmt3a	1.481	0.821	1.386	0.102	0.814	0.205	1.445	0.056
1388182_at	BE108911	DNA primase, p49 subunit	Prim1	0.563	0.084	0.791	0.785	0.522	0.039	0.843	0.321
1384368_at	AA900084	DNA2 DNA replication helicase 2-like (yeast) (predicted)	Dna2l_predicted	0.483	0.094	0.539	0.060	0.534	0.010	0.540	0.001
1375758_at	BF404935	DNA2 DNA replication helicase 2-like (yeast) (predicted)	Dna2l_predicted	1.030	0.235	0.940	0.931	1.003	0.971	1.235	0.451
1376178_at	BF403703	DNA-damage inducible transcript 3	Ddit3	1.810	0.023	1.954	0.081	1.417	0.082	1.671	0.017
1369590_a_at	NM_024134	DNA-damage inducible transcript 3	Ddit3	1.658	0.052	7.860	0.001	1.189	0.131	7.104	0.000
1368025_at	NM_080906	DNA-damage-inducible transcript 4	Ddit4	1.568	0.210	3.356	0.000	1.632	0.065	3.060	0.006
1398819_at	NM_022934	DnaJ (Hsp40) homolog, subfamily A, member 1	Dnaja1	0.977	0.893	1.361	0.004	1.057	0.368	1.119	0.122
1387780_at	NM_032079	DnaJ (Hsp40) homolog, subfamily A, member 2	Dnaja2	0.789	0.456	1.712	0.008	0.795	0.335	1.674	0.004
1378392_at	BG377107	DnaJ (Hsp40) homolog, subfamily A, member 3	Dnaja3	0.749	0.347	1.411	0.040	0.717	0.071	1.378	0.083
1389845_at	BI282224	DnaJ (Hsp40) homolog, subfamily A, member 3	Dnaja3	0.761	0.492	1.401	0.003	0.621	0.016	1.232	0.016
1372103_at	BM386931	DnaJ (Hsp40) homolog, subfamily A, member 4	Dnaja4	0.526	0.061	0.255	0.005	0.520	0.023	0.296	0.002
1398343_at	AI104324	DnaJ (Hsp40) homolog, subfamily A, member 4	Dnaja4	0.873	0.274	1.019	0.871	0.884	0.474	0.919	0.484
1395572_at	BF565278	DnaJ (Hsp40) homolog, subfamily A, member 4	Dnaja4	1.042	0.643	1.017	0.924	1.017	0.656	0.669	0.039
1388722_at	AA945704	DnaJ (Hsp40) homolog, subfamily B, member 1 (predicted)	Dnajb1_predicted	0.614	0.075	2.580	0.017	0.682	0.106	1.706	0.119
1383302_at	BM384926	DnaJ (Hsp40) homolog, subfamily B, member 1 (predicted)	Dnajb1_predicted	0.745	0.092	19.688	0.001	0.886	0.176	2.911	0.055
1389308_at	BI295873	DnaJ (Hsp40) homolog, subfamily B, member 11	Dnajb11	0.603	0.145	1.353	0.032	0.834	0.483	1.293	0.056
1372722_at	AI175031	DnaJ (Hsp40) homolog, subfamily B, member 4	Dnajb4	0.389	0.055	0.545	0.010	0.429	0.001	0.650	0.033
1378843_at	AW528827	DnaJ (Hsp40) homolog, subfamily B, member 6	Dnajb6	1.386	0.162	1.215	0.534	1.053	0.567	1.546	0.096
1391422_at	BE100486	DnaJ (Hsp40) homolog, subfamily B, member 6	Dnajb6	1.230	0.412	2.034	0.058	1.339	0.008	1.820	0.174
1382024_at	BM383877	DnaJ (Hsp40) homolog, subfamily B, member 6 /// similar to mDj4 (predicted) /// similar to DnaJ homolog subfamily B member 6 (Heat shock protein J2) (predicted)	Dnajb6 /// RGD1562684_predicted /// RGD1565241_predicted	1.023	0.620	1.159	0.247	1.064	0.372	1.004	0.956
1387116_at	NM_012699	DnaJ (Hsp40) homolog, subfamily B, member 9	Dnajb9	1.054	0.632	1.256	0.083	0.830	0.645	1.168	0.022
1392388_at	BE112281	DnaJ (Hsp40) homolog, subfamily C, member 1 (predicted)	Dnajc1_predicted	1.055	0.088	0.825	0.085	0.576	0.012	0.962	0.403
1376079_at	BI295806	DnaJ (Hsp40) homolog, subfamily C, member 1 (predicted)	Dnajc1_predicted	0.606	0.330	0.621	0.004	0.477	0.035	0.600	0.017
1389290_at	AI172034	DnaJ (Hsp40) homolog, subfamily C, member 10	Dnajc10	0.801	0.035	0.562	0.028	0.948	0.517	0.700	0.045
1373813_at	BM388610	DnaJ (Hsp40) homolog, subfamily C, member 10	Dnajc10	0.776	0.929	0.488	0.001	1.084	0.672	0.993	0.777
1372189_at	AI411144	DnaJ (Hsp40) homolog, subfamily C, member 13 (predicted)	Dnajc13_predicted	1.250	0.039	0.850	0.031	1.527	0.147	1.004	0.957
1369714_at	NM_053690	DnaJ (Hsp40) homolog, subfamily C, member 14	Dnajc14	1.755	0.053	1.700	0.805	1.730	0.108	1.482	0.511
1373064_at	BM390416	DnaJ (Hsp40) homolog, subfamily C, member 15 (predicted)	Dnajc15_predicted	0.586	0.219	1.170	0.372	0.432	0.008	1.228	0.169
1373004_at	AA964764	DnaJ (Hsp40) homolog, subfamily C, member 2	Dnajc2	0.993	0.983	1.567	0.104	0.693	0.059	1.024	0.880
1370073_at	NM_022232	DnaJ (Hsp40) homolog, subfamily C, member 3	Dnajc3	0.844	0.248	0.882	0.214	0.778	0.111	0.878	0.196
1372428_at	BG380252	DnaJ (Hsp40) homolog, subfamily C, member 4	Dnajc4	1.029	0.552	1.859	0.093	0.985	0.757	1.035	0.294
1369813_at	U39320	DnaJ (Hsp40) homolog, subfamily C, member 5	Dnajc5	0.876	0.791	24.502	0.001	0.265	0.036	15.709	0.002
1377125_at	AW523481	DnaJ (Hsp40) homolog, subfamily C, member 6 (predicted)	Dnajc6_predicted	0.587	0.001	0.456	0.001	0.587	0.001	0.591	0.004

1386648_at	AW914996	DnaJ (Hsp40) homolog, subfamily C, member 6 (predicted)	Dnajc6_predicted	0.624	0.008	0.356	0.004	0.638	0.004	0.485	0.002
1374744_at	BF392285	DnaJ (Hsp40) homolog, subfamily C, member 7	Dnajc7	0.938	0.129	1.055	0.351	0.523	0.152	0.916	0.386
1371784_at	BI285682	DnaJ (Hsp40) homolog, subfamily C, member 7	Dnajc7	1.007	0.543	1.016	0.500	1.406	0.006	0.813	0.555
1378781_at	AI712400	DnaJ (Hsp40) homolog, subfamily C, member 8	Dnajc8	1.655	0.105	1.091	0.047	1.132	0.423	1.073	0.814
1367492_at	AI227785	DnaJ (Hsp40) homolog, subfamily C, member 8	Dnajc8	0.967	0.477	1.259	0.031	1.163	0.381	1.306	0.071
1383181_at	AI704947	DnaJ (Hsp40) homolog, subfamily C, member 9 (predicted)	Dnajc9_predicted	0.458	0.013	0.783	0.061	0.279	0.010	0.920	0.054
1368664_at	AI138041	dnaj-like protein	LOC56764	1.549	0.416	0.988	0.971	1.060	0.996	0.950	0.989
1383630_at	BG377464	docking protein 3 (predicted)	Dok3_predicted	1.002	0.283	1.005	0.933	0.767	0.206	1.060	0.771
1372300_at	BI288838	docking protein 4 (predicted)	Dok4_predicted	0.906	0.392	0.987	0.900	0.970	0.331	0.989	0.893
1380004_at	BG373440	Dodecenoyl-coenzyme A delta isomerase	Dci	1.228	0.250	0.506	0.128	1.301	0.243	1.189	0.747
1367659_s_at	NM_017306	dodecenoyl-coenzyme A delta isomerase	Dci	1.266	0.942	0.858	0.262	1.581	0.084	0.940	0.878
1377593_at	BI284172	dolichol-phosphate (beta-D) mannosyltransferase 1 (predicted)	Dpm1_predicted	0.511	0.128	0.648	0.005	0.510	0.007	0.681	0.018
1391372_at	BF405555	Dolichol-phosphate (beta-D) mannosyltransferase 1 (predicted)	Dpm1_predicted	0.798	0.355	1.475	0.122	1.087	0.741	1.060	0.223
1367751_at	NM_019252	dolichol-phosphate (beta-D) mannosyltransferase 2	Dpm2	0.531	0.333	0.671	0.013	0.458	0.045	0.890	0.201
1372247_at	BF282907	dolichyl-di-phosphooligosaccharide-protein glycotransferase (predicted)	Ddost_predicted	0.749	0.477	0.719	0.004	0.786	0.269	0.693	0.007
1372270_at	BM391270	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)	H2afx	1.069	0.530	1.200	0.025	1.307	0.484	1.198	0.011
1368064_a_at	U31884	dopa decarboxylase	Ddc	0.836	0.142	0.166	0.001	0.652	0.050	0.139	0.008
1368479_at	M35077	dopamine receptor D1A	Drd1a	1.033	0.928	1.101	0.170	1.720	0.070	1.140	0.067
1374651_at	BM386987	dopey family member 2 (predicted)	Dopey2_predicted	0.755	0.186	0.402	0.001	0.585	0.015	0.312	0.012
1388589_at	BG381046	DOT1-like, histone H3 methyltransferase (S. cerevisiae) (predicted)	Dot1l_predicted	1.289	0.076	1.672	0.167	1.041	0.684	1.457	0.194
1369686_at	U78857	double cortin and calcium/calmodulin-dependent protein kinase-like 1	Dcamkl1	0.310	0.005	0.212	0.001	0.361	0.021	0.148	0.000
1374966_at	BE109057	doublecortin	Dcx	0.688	0.532	0.115	0.000	0.980	0.346	0.112	0.016
1389066_at	BI274408	Down syndrome critical region gene 1-like 1	Dscr1l1	0.084	0.001	0.092	0.020	0.157	0.037	0.143	0.002
1396528_at	BF404786	Down syndrome critical region gene 1-like 1	Dscr1l1	0.726	0.214	0.148	0.003	0.523	0.064	0.242	0.007
1374235_at	AI138048	Down syndrome critical region gene 1-like 1	Dscr1l1	0.766	0.261	0.676	0.077	0.454	0.017	0.658	0.000
1398560_at	AW530670	Down syndrome critical region gene 1-like 1	Dscr1l1	0.996	0.912	0.553	0.066	1.324	0.213	0.572	0.102
1396706_at	BF398967	Down syndrome critical region gene 1-like 1	Dscr1l1	1.030	0.963	0.590	0.154	1.061	0.562	0.877	0.417
1388686_at	AI170193	Down syndrome critical region homolog 1 (human)	Dscr1	0.999	0.991	1.141	0.695	1.016	0.362	1.675	0.003
1371385_at	BF407158	Down syndrome critical region homolog 2 (human) (predicted)	Dscr2_predicted	0.710	0.157	0.923	0.014	0.555	0.021	0.924	0.072
1391648_at	BF545697	Down syndrome critical region homolog 6 (human) (predicted)	Dscr6_predicted	0.174	0.005	0.089	0.010	0.241	0.095	0.190	0.056
1372453_at	AI012637	down-regulator of transcription 1	Dr1	0.655	0.009	0.602	0.009	0.726	0.053	0.605	0.043
1384005_at	BG662895	down-regulator of transcription 1	Dr1	0.897	0.202	0.990	0.131	0.999	0.969	0.858	0.342
1376026_at	AI178243	downstream neighbor of SON	Donson	7.996	0.007	3.972	0.005	33.425	0.000	14.901	0.004
1390272_at	BM386608	DPH5 homolog (S. cerevisiae)	Dph5	0.861	0.603	2.219	0.015	0.862	0.349	2.218	0.029
1389483_at	AI408686	Dpy-19-like 1 (C. elegans) (predicted)	Dpy19l1_predicted	0.519	0.000	0.617	0.002	0.587	0.004	0.666	0.088
1375174_at	BI296653	Dpy-19-like 1 (C. elegans) (predicted)	Dpy19l1_predicted	0.728	0.974	0.971	0.860	0.990	0.973	0.908	0.402
1371383_at	BI296428	Dr1 associated protein 1 (negative cofactor 2 alpha) (predicted)	Drap1_predicted	1.031	0.906	1.250	0.401	1.249	0.018	1.173	0.067
1368274_at	NM_031352	drebrin-like	Dbnl	3.249	0.006	1.646	0.099	4.082	0.000	1.985	0.029
1373460_at	AI178790	D-serine modulator-1	Dsm-1	1.271	0.452	0.717	0.124	1.332	0.328	0.338	0.068
1378377_at	BF552453	dual adaptor for phosphotyrosine and 3-phosphoinositides 1 (predicted)	Dapp1_predicted	1.001	0.954	2.497	0.032	1.333	0.165	1.366	0.448
1387414_at	NM_024141	dual oxidase 2	Duox2	1.350	0.190	2.101	0.186	1.002	0.974	0.997	0.978
1368146_at	U02553	dual specificity phosphatase 1	Dusp1	4.539	0.001	7.228	0.000	2.852	0.027	4.757	0.000
1394028_at	AW916472	dual specificity phosphatase 10 (predicted)	Dusp10_predicted	2.275	0.057	0.459	0.003	1.237	0.421	0.441	0.043
1376576_at	BM387750	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	Dusp11	1.053	0.713	1.803	0.042	1.369	0.033	1.384	0.034
1387457_at	NM_022248	dual specificity phosphatase 12	Dusp12	1.002	0.949	1.218	0.253	1.053	0.703	0.998	0.778
1375967_a_at	AI172067	dual specificity phosphatase 22 (predicted)	Dusp22_predicted	0.767	0.159	0.934	0.439	0.980	0.389	0.964	0.670
1374379_at	BF396810	Dual specificity phosphatase 23 (predicted)	Dusp23_predicted	0.319	0.255	0.492	0.008	0.342	0.123	0.533	0.087
1375475_at	BE111304	Dual specificity phosphatase 5	Dusp5	0.216	0.041	0.980	0.878	0.159	0.035	0.979	0.891
1368124_at	NM_133578	dual specificity phosphatase 5	Dusp5	0.462	0.136	0.285	0.001	0.225	0.004	0.327	0.032
1382778_at	AI231350	Dual specificity phosphatase 6	Dusp6	0.736	0.289	1.081	0.595	1.416	0.643	1.074	0.523
1377064_at	AI602811	dual specificity phosphatase 6	Dusp6	0.688	0.566	1.001	0.678	1.265	0.553	0.998	0.441
1377992_at	AI111775	Dual specificity phosphatase 7	Dusp7	0.446	0.285	0.913	0.869	0.402	0.035	0.578	0.027
1386396_at	AW528387	dual specificity phosphatase 8 (predicted)	Dusp8_predicted	1.576	0.001	1.485	0.055	1.650	0.009	1.408	0.458
1373340_at	AI179321	dual specificity phosphatase 9	Dusp9	0.999	0.966	1.370	0.058	0.999	0.998	1.239	0.054
1370183_at	BI303285	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	Dyrk1a	1.284	0.375	2.160	0.005	1.141	0.576	2.013	0.048
1383601_at	BI295614	DUF729 domain containing 1 (predicted)	Dufd1_predicted	1.561	0.179	1.901	0.072	2.259	0.060	1.017	0.823
1381555_at	BI288686	DUF729 domain containing 1 (predicted)	Dufd1_predicted	1.716	0.283	1.435	0.260	2.342	0.051	1.035	0.925
1375299_at	AI103331	Dullard homolog (Xenopus laevis)	Dullard	0.903	0.514	0.978	0.258	0.922	0.075	0.973	0.456
1373502_at	BM389188	Dymeclin (predicted)	Dym_predicted	0.327	0.164	1.048	0.622	0.203	0.010	0.844	0.195
1380042_at	AA964012	Dynactin 1	Dctn1	0.318	0.008	0.980	0.789	0.706	0.105	0.739	0.604

1367848_at	NM_024130	dynactin 1	Dctn1	0.459	0.033	0.714	0.025	0.356	0.023	0.779	0.038
1371834_at	BF283695	dynactin 2	Dctn2	0.781	0.031	1.071	0.223	0.931	0.826	0.897	0.220
1398900_at	AA893211	dynactin 3 (predicted)	Dctn3_predicted	0.814	0.363	0.780	0.084	0.542	0.010	0.761	0.357
1387236_at	NM_053404	dynactin 4	Dctn4	2.110	0.007	2.467	0.002	1.384	0.067	2.125	0.051
1368537_at	AI045623	dynactin 4	Dctn4	1.518	0.236	1.321	0.645	1.156	0.995	0.602	0.077
1373441_at	BI296970	dynactin 5	Dctn5	1.268	0.042	0.866	0.808	1.110	0.154	1.062	0.333
1371533_at	BI282273	dynactin 6 (predicted)	Dctn6_predicted	0.677	0.089	1.130	0.213	0.659	0.016	1.159	0.139
1368292_at	NM_080689	dynamin 1	Dnm1	0.996	0.976	0.946	0.746	1.000	0.999	0.802	0.723
1386460_x_at	AI237251	dynamin 1-like	Dnm1l	0.845	0.136	0.873	0.038	0.912	0.228	0.855	0.040
1394227_at	AI237251	dynamin 1-like	Dnm1l	0.846	0.282	0.920	0.760	0.839	0.279	0.939	0.485
1369220_at	NM_053655	dynamin 1-like	Dnm1l	1.163	0.315	0.711	0.021	0.837	0.305	0.459	0.038
1388022_a_at	AF132727	dynamin 1-like	Dnm1l	0.464	0.322	1.154	0.846	0.458	0.925	0.853	0.196
1383183_at	AI072458	dynamin 1-like	Dnm1l	0.563	0.408	0.365	0.187	0.375	0.126	0.527	0.067
1396562_at	BF409832	Dynamin 2	Dnm2	0.914	0.547	1.731	0.152	0.904	0.781	1.114	0.316
1398803_at	NM_019226	dynein cytoplasmic 1 heavy chain 1	Dync1h1	1.391	0.086	1.353	0.011	1.433	0.083	1.628	0.012
1387025_at	NM_019234	dynein cytoplasmic 1 intermediate chain 1	Dync1i1	0.684	0.344	0.978	0.771	0.393	0.017	1.100	0.655
1399147_at	AI111975	Dynein cytoplasmic 1 light intermediate chain 1	Dync1li1	2.294	0.714	1.016	0.731	1.604	0.287	0.999	0.896
1370576_at	AF181992	dynein cytoplasmic 1 light intermediate chain 1	Dync1li1	1.118	0.994	0.904	0.325	1.029	0.995	0.872	0.062
1374573_at	BE113181	dynein cytoplasmic 2 light intermediate chain 1	Dync2li1	0.983	0.985	1.317	0.759	1.003	0.090	0.975	0.994
1369976_at	NM_053319	dynein light chain LC8-type 1	Dynll1	0.540	0.297	0.509	0.024	0.479	0.003	0.715	0.150
1372612_at	BG372973	dynein light chain LC8-type 2	Dynll2	0.739	0.013	0.816	0.003	0.822	0.006	0.821	0.002
1387782_at	NM_080697	dynein light chain LC8-type 2	Dynll2	0.689	0.140	1.614	0.060	0.436	0.164	1.283	0.110
1372514_s_at	AA892303	dynein, axonemal, light chain 4	Dnalc4	0.618	0.052	0.845	0.350	0.628	0.057	0.588	0.190
1388785_at	AA892303	dynein, axonemal, light chain 4	Dnalc4	1.082	0.759	1.254	0.660	0.900	0.782	1.353	0.015
1368676_at	NM_023024	dynein, cytoplasmic, heavy polypeptide 2 /// hypothetical gene supported by NM_023024	Dnch2 /// LOC497827	1.137	0.881	0.477	0.041	1.641	0.952	0.513	0.046
1386952_a_at	NM_053880	dynein, cytoplasmic, intermediate chain 2	Dncic2	1.196	0.324	1.420	0.034	1.124	0.413	1.273	0.003
1370179_at	AI102949	dynein, cytoplasmic, light chain 2A	Dncl2a	0.817	0.449	0.865	0.322	0.747	0.040	0.947	0.701
1368402_at	NM_031026	dynein, cytoplasmic, light intermediate polypeptide 2	Dncli2	0.979	0.527	0.592	0.004	0.845	0.063	0.666	0.002
1373256_at	BM391119	Dynein-like protein 2	DLP2	0.871	0.381	0.757	0.067	0.874	0.673	0.645	0.033
1385559_at	BF562977	Dynein-like protein 2	DLP2	0.997	0.550	1.736	0.023	1.063	0.832	0.999	0.999
1368649_at	NM_133419	dyskeratosis congenita 1, dyskerin	Dkc1	0.789	0.677	2.092	0.061	2.105	0.280	1.831	0.170
1375357_at	BE112237	dystonia 1	Dyt1	0.521	0.270	0.574	0.027	0.533	0.082	0.718	0.010
1398000_at	BF394082	Dystonin (predicted)	Dst_predicted	1.920	0.014	2.017	0.666	1.910	0.026	2.148	0.384
1376130_a_at	BM390663	dystrobrevin, beta	Dtnb	1.083	0.254	1.042	0.398	1.405	0.057	1.511	0.348
1371430_at	AW251326	dystroglycan 1	Dag1	0.767	0.033	0.516	0.015	0.633	0.057	0.530	0.021
1371429_at	BF281192	dystroglycan 1	Dag1	0.569	0.456	0.434	0.004	0.336	0.002	0.564	0.002
1395970_at	BI297496	Dystrophia myotonica-containing WD repeat motif	Dmwd	1.112	0.139	1.072	0.968	0.962	0.784	1.183	0.864
1373915_at	AI044427	dystrophia myotonica-protein kinase (predicted)	Dmpk_predicted	1.164	0.313	0.485	0.019	1.035	0.714	0.594	0.111
1373916_at	AI237356	E1A binding protein p300	Ep300	1.339	0.051	0.883	0.005	1.307	0.042	1.025	0.302
1378682_at	BF390772	E1A binding protein p300	Ep300	0.834	0.590	0.965	0.554	0.918	0.176	0.996	0.903
1369307_at	NM_133403	E1A binding protein p300	Ep300	1.004	0.984	0.922	0.268	1.005	0.933	0.808	0.500
1388992_at	AI169305	E1A binding protein p400	Ep400	1.890	0.039	1.577	0.001	1.883	0.010	1.623	0.003
1388154_at	U31668	E2F transcription factor 5	E2f5	0.973	0.826	0.677	0.080	1.258	0.223	1.333	0.066
1374137_at	AA818055	E74-like factor 1	Elf1	4.713	0.020	1.663	0.198	4.535	0.019	1.783	0.031
1382637_at	AI137223	E74-like factor 2	Elf2	0.997	0.979	1.546	0.211	1.009	0.986	1.000	0.999
1389130_at	AW525131	E74-like factor 2	Elf2	1.105	0.994	1.017	0.282	0.915	0.361	1.094	0.492
1374119_at	BI279615	E74-like factor 3	Elf3	2.821	0.007	4.960	0.009	1.523	0.347	3.626	0.000
1394709_at	AI406967	Early B-cell factor 1	Ebf1	1.238	0.996	1.978	0.320	0.971	0.939	1.087	0.909
1394985_at	BI294752	early endosome antigen 1 (predicted)	Eea1_predicted	1.273	0.037	1.031	0.145	1.360	0.239	1.113	0.496
1368321_at	NM_012551	early growth response 1	Egr1	5.955	0.005	0.221	0.004	2.809	0.012	0.278	0.010
1387306_a_at	NM_053633	early growth response 2	Egr2	1.425	0.177	0.906	0.779	1.053	0.473	0.848	0.807
1392791_at	AA964492	Early growth response 3	Egr3	1.001	0.402	1.692	0.969	1.043	0.778	1.013	0.945
1388397_at	BI281160	EBNA1 binding protein 2	Ebna1bp2	0.574	0.297	2.044	0.004	0.333	0.028	1.866	0.006
1370544_at	AF335571	echinoderm microtubule associated protein like 2	Eml2	1.324	0.036	0.829	0.195	1.945	0.011	1.034	0.496
1373527_at	BI275677	echinoderm microtubule associated protein like 3 (predicted)	Eml3_predicted	1.081	0.512	0.763	0.061	1.465	0.073	0.490	0.038
1376082_at	BE107033	ecotropic viral integration site 1 (predicted)	Evi1_predicted	1.148	0.533	1.061	0.452	1.198	0.458	0.854	0.313
1388666_at	AI179988	ectodermal-neural cortex 1	Enc1	5.162	0.004	7.619	0.001	3.104	0.012	4.947	0.003
1382710_at	AA997271	Ectodermal-neural cortex 1	Enc1	2.570	0.007	5.514	0.010	1.065	0.891	2.338	0.053
1384687_at	AI071307	ectodermal-neural cortex 1	Enc1	2.128	0.078	18.570	0.001	2.418	0.091	13.859	0.001
1370845_at	BI288690	ectonucleoside triphosphate diphosphohydrolase 2	Entpd2	1.192	0.266	4.093	0.000	1.786	0.066	2.656	0.001
1384866_at	AI070096	ectonucleoside triphosphate diphosphohydrolase 3	Entpd3	1.143	0.087	0.682	0.011	1.118	0.067	0.771	0.001

1375728_at	AI511102	Ectonucleoside triphosphate diphosphohydrolase 4 (predicted)	Entpd4_predicted	0.895	0.966	1.283	0.042	0.832	0.665	0.999	0.989
1382434_at	AI059015	ectonucleoside triphosphate diphosphohydrolase 5	Entpd5	0.665	0.015	1.482	0.163	0.482	0.207	1.133	0.467
1368536_at	NM_057104	ectonucleotide pyrophosphatase/phosphodiesterase 2	Enpp2	0.792	0.099	0.409	0.006	2.954	0.053	0.513	0.080
1373912_at	AI170859	Ectonucleotide pyrophosphatase/phosphodiesterase 4 (predicted)	Enpp4_predicted	3.341	0.005	1.530	0.354	10.765	0.002	2.785	0.019
1388926_at	AI409048	Ectonucleotide pyrophosphatase/phosphodiesterase 5	Enpp5	1.163	0.482	0.788	0.466	1.178	0.104	1.197	0.150
1374388_at	AI408294	EF hand domain containing 2	Efhd2	1.011	0.811	0.995	0.963	0.987	0.726	1.044	0.409
1373196_at	BF404514	EF hand domain family, member A2	Efha2	0.544	0.005	0.325	0.009	0.811	0.271	0.391	0.046
1393240_at	AI112299	EGF-containing fibulin-like extracellular matrix protein 2	Efemp2	0.999	0.671	0.984	0.984	1.000	0.919	1.023	0.995
1371023_at	AW524873	EGF-like-domain, multiple 4	Egfl4	0.750	0.708	0.557	0.006	0.979	0.926	0.641	0.032
1393335_at	BF418373	EGF-like-domain, multiple 6	Egfl6	1.007	0.783	0.985	0.250	0.993	0.987	1.102	0.252
1389207_at	BI282122	EGL nine homolog 1 (C. elegans)	Egln1	0.869	0.066	2.700	0.001	0.682	0.917	2.948	0.000
1373794_at	BE329050	EGL nine homolog 2 (C. elegans)	Egln2	1.203	0.247	0.802	0.152	1.207	0.411	0.822	0.076
1377665_at	AA998979	EH-domain containing 1	Ehd1	1.537	0.002	1.002	0.602	1.816	0.049	1.155	0.466
1372317_at	AI177867	EH-domain containing 1	Ehd1	1.006	0.965	1.493	0.183	0.999	0.859	1.063	0.632
1374399_at	AA801107	EH-domain containing 4	Ehd4	4.559	0.006	6.630	0.000	5.430	0.001	5.911	0.007
1372106_at	BI284307	EH-domain containing 4	Ehd4	7.197	0.011	2.537	0.116	10.089	0.000	1.800	0.061
1375739_at	BF395171	EH-domain containing 4	Ehd4	3.113	0.124	6.175	0.006	3.516	0.002	4.715	0.007
1374107_at	AI229668	elaC homolog 2 (E. coli)	Elac2	0.630	0.072	0.977	0.306	0.569	0.066	1.128	0.800
1387471_at	NM_012553	elastase 2	Ela2	1.110	0.954	0.707	0.496	1.076	0.964	0.702	0.401
1372325_at	BI303596	elastin microfibril interfacer 1 (predicted)	Emilin1_predicted	0.953	0.434	1.053	0.974	1.150	0.334	1.056	0.999
1391006_at	AI235353	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (predicted)	Elavl1_predicted	1.178	0.042	1.719	0.061	1.056	0.169	1.425	0.113
1382952_at	C06972	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (predicted)	Elavl1_predicted	0.682	0.088	1.113	0.107	0.598	0.036	1.083	0.191
1375892_at	BF559812	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (predicted)	Elavl1_predicted	1.344	0.475	1.180	0.513	1.227	0.831	1.001	0.525
1391743_at	BE104552	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (predicted)	Elavl1_predicted	0.921	0.550	1.028	0.379	0.810	0.217	0.971	0.099
1393188_at	BF548232	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (predicted)	Elavl1_predicted	1.027	0.883	1.169	0.706	0.704	0.078	0.971	0.104
1383736_at	AI145457	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) /// hypothetical gene supported by NM_173309	Elavl2 /// LOC497806	0.935	0.962	1.306	0.053	1.374	0.050	1.484	0.018
1397319_at	BF542311	Electron transferring flavoprotein, alpha polypeptide	Etfa	1.105	0.327	1.088	0.305	1.281	0.412	1.111	0.354
1371253_at	AA942749	electron transferring flavoprotein, alpha polypeptide	Etfa	0.962	0.364	1.149	0.964	0.922	0.642	1.208	0.270
1388358_at	AW252650	electron-transfer-flavoprotein, beta polypeptide	Etfb	0.548	0.257	0.591	0.058	0.497	0.004	0.423	0.134
1371519_at	AA851258	electron-transferring-flavoprotein dehydrogenase	Etfdh	0.542	0.196	0.751	0.005	0.489	0.029	0.705	0.027
1385063_at	BG377323	ELK1, member of ETS oncogene family	Elk1	1.611	0.098	0.503	0.041	0.977	0.983	0.715	0.425
1374797_at	BM391920	ELL associated factor 1 (predicted)	Eaf1_predicted	1.065	0.596	2.453	0.000	1.049	0.595	2.464	0.008
1371515_at	AI100773	Elongation factor 1 homolog (ELF1, S. cerevisiae) (predicted)	Elof1_predicted	0.857	0.798	1.145	0.725	0.713	0.037	1.074	0.087
1388714_at	AI008458	elongation factor RNA polymerase II (predicted)	Ell_predicted	0.932	0.421	2.480	0.002	1.388	0.160	1.903	0.012
1389680_at	BI291626	elongation factor RNA polymerase II 2	Ell2	0.759	0.903	1.010	0.860	0.658	0.042	0.882	0.115
1392920_at	BE109672	Elongation factor RNA polymerase II-like 3	Ell3	1.032	0.155	1.195	0.936	1.364	0.074	1.049	0.230
1371698_at	BF282614	elongation factor Tu GTP binding domain containing 2	Eftud2	0.831	0.981	0.646	0.950	0.509	0.124	1.599	0.159
1391534_at	BG666735	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2 (predicted)	Elovl2_predicted	0.380	0.018	0.337	0.000	0.362	0.012	0.394	0.027
1377729_at	BG668988	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4 (predicted)	Elovl4_predicted	1.271	0.078	0.621	0.056	0.662	0.463	0.618	0.013
1388108_at	BE116152	ELOVL family member 6, elongation of long chain fatty acids (yeast)	Elovl6	0.432	0.091	0.358	0.003	0.378	0.007	0.355	0.003
1394401_at	BF396857	ELOVL family member 6, elongation of long chain fatty acids (yeast)	Elovl6	0.404	0.103	0.324	0.027	0.360	0.113	0.484	0.049
1368541_at	NM_053719	embigin	Emb	0.763	0.534	0.545	0.000	0.762	0.082	0.499	0.001
1373462_at	AI170325	embryonic ectoderm development (predicted)	Eed_predicted	1.161	0.191	2.070	0.018	1.622	0.193	1.513	0.035
1370017_at	NM_012948	emerin	Emd	0.496	0.006	0.812	0.030	0.559	0.030	0.861	0.023
1377797_at	AI071470	EMG1 nucleolar protein homolog (S. cerevisiae) (predicted)	Emg1_predicted	0.832	0.835	2.263	0.065	0.644	0.220	1.462	0.665
1391462_at	AI179635	emopamil binding protein-like (predicted)	Ebpl_predicted	0.494	0.000	0.773	0.371	0.524	0.001	0.862	0.311
1396450_at	AW918724	enabled homolog (Drosophila)	Enah	0.863	0.052	1.202	0.618	0.950	0.396	1.099	0.097
1373535_at	BF397848	enabled homolog (Drosophila)	Enah	1.061	0.058	1.630	0.009	1.536	0.036	1.831	0.002
1397449_at	AI059353	Enabled homolog (Drosophila)	Enah	0.782	0.258	0.448	0.030	1.126	0.467	0.670	0.193
1367861_at	NM_024147	Ena-vasodilator stimulated phosphoprotein	Evl	0.264	0.001	0.358	0.004	0.326	0.144	0.165	0.066
1389816_at	AA926357	endonuclease G	Endog	0.997	0.225	0.999	0.999	0.999	0.360	1.001	0.985
1376431_at	BM387357	endoplasmic reticulum chaperone SIL1 homolog (S. cerevisiae)	Sil1	0.871	0.355	0.496	0.000	0.761	0.043	0.503	0.030
1387031_at	U36482	endoplasmic reticulum protein 29	Erp29	0.487	0.160	0.452	0.008	0.514	0.438	0.401	0.018
1398898_at	BI278623	Endosulfine alpha	Ensa	1.085	0.128	1.406	0.037	1.096	0.391	1.371	0.053
1369702_at	NM_021842	endosulfine alpha	Ensa	1.059	0.502	0.858	0.639	0.999	0.773	0.898	0.079
1395713_at	AI136510	Endosulfine alpha	Ensa	1.320	0.724	1.100	0.207	1.629	0.106	1.164	0.028
1389912_at	BI289922	endosulfine alpha	Ensa	0.957	0.916	1.096	0.138	1.044	0.264	1.077	0.340
1370048_at	NM_053936	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	Edg2	1.624	0.171	2.980	0.015	1.166	0.257	2.323	0.361
1386989_at	NM_017192	endothelial differentiation, sphingolipid G-protein-coupled receptor, 5	Edg5	1.010	0.701	1.001	0.941	1.641	0.190	1.475	0.134
1375189_at	BI285635	endothelial differentiation-related factor 1 (predicted)	Edf1_predicted	0.948	0.879	1.093	0.771	0.813	0.473	1.110	0.570

1367801_at	NM_053596	endothelin converting enzyme 1	Ece1	1.072	0.784	0.419	0.010	0.988	0.484	0.518	0.003
1379396_at	AI101913	engulfment and cell motility 1, ced-12 homolog (C. elegans) (predicted)	Elmo1_predicted	0.728	0.958	0.200	0.000	1.001	0.986	0.218	0.000
1371613_at	BM386781	engulfment and cell motility 2, ced-12 homolog (C. elegans)	Elmo2	0.693	0.063	0.539	0.065	0.841	0.191	0.645	0.118
1374995_at	BI291645	engulfment and cell motility 3, ced-12 homolog (C. elegans)	Elmo3	0.828	0.258	1.000	0.997	0.931	0.401	0.917	0.111
1377834_at	AW434262	enhancer of polycomb homolog 1 (Drosophila) (predicted)	Epc1_predicted	1.683	0.039	1.396	0.033	1.966	0.028	1.221	0.070
1383467_at	AW918173	enhancer of polycomb homolog 2 (Drosophila) (predicted)	Epc2_predicted	1.313	0.105	2.055	0.034	0.688	0.033	2.172	0.069
1382120_at	AI535147	enhancer of polycomb homolog 2 (Drosophila) (predicted)	Epc2_predicted	0.944	0.749	1.255	0.129	1.072	0.678	1.191	0.196
1384890_at	AA998678	enhancer of zeste homolog 1 (Drosophila) (predicted)	Ezh1_predicted	1.379	0.076	3.617	0.066	1.002	0.986	1.452	0.647
1367575_at	NM_012554	enolase 1, alpha /// similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (predicted)	Eno1 /// RGD1563294_predicted	0.703	0.141	1.705	0.009	0.617	0.047	1.620	0.011
1370341_at	AF019973	enolase 2, gamma	Eno2	0.631	0.082	1.204	0.129	0.521	0.012	1.154	0.271
1386885_at	NM_022594	enoyl coenzyme A hydratase 1, peroxisomal	Ech1	0.425	0.123	0.707	0.030	0.314	0.003	0.612	0.009
1374585_at	AW915152	enoyl Coenzyme A hydratase domain containing 1	Echdc1	0.552	0.013	0.489	0.002	0.643	0.028	0.588	0.010
1394971_at	BE119142	Enoyl Coenzyme A hydratase domain containing 1	Echdc1	1.072	0.947	0.620	0.069	1.188	0.411	0.618	0.170
1367829_at	NM_078623	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	Echs1	0.659	0.301	0.926	0.514	0.719	0.104	0.850	0.654
1375855_at	AI171799	ependymin related protein 2 (zebrafish)	Epdr2	0.353	0.042	0.601	0.013	0.269	0.013	0.700	0.114
1374143_at	AI602491	Eph receptor A2 (predicted)	Epha2_predicted	2.528	0.009	1.802	0.019	2.798	0.071	1.526	0.025
1380658_at	BF402406	Eph receptor A3	Epha3	1.084	0.843	0.923	0.623	1.723	0.144	0.893	0.991
1395262_at	BF402135	EphA5	Epha5	1.432	0.393	1.231	0.899	1.572	0.200	1.274	0.591
1374403_at	BF412072	ephrin B1	Efnb1	0.819	0.200	0.649	0.026	0.806	0.117	0.977	0.489
1368325_at	NM_012842	epidermal growth factor	Egf	1.730	0.011	0.755	0.211	1.243	0.071	0.643	0.054
1370830_at	M37394	epidermal growth factor receptor	Egfr	1.300	0.049	2.011	0.098	0.986	0.064	1.689	0.059
1370699_a_at	AF187818	epidermal growth factor receptor /// peptidase D (mapped)	Egfr /// Pepd_mapped	0.511	0.006	1.258	0.007	0.532	0.011	0.981	0.915
1399152_at	BF559107	epidermal growth factor receptor pathway substrate 15	Eps15	0.684	0.528	1.441	0.127	1.525	0.412	2.663	0.035
1383213_at	BF393611	epidermal growth factor receptor pathway substrate 8 (predicted) /// similar to Eps8	Eps8_predicted /// LOC365516	1.184	0.058	1.772	0.057	0.999	0.994	1.531	0.024
1370835_at	AF267197	epidermal Langerhans cell protein LCP1	RGD708449	0.665	0.635	0.957	0.170	0.655	0.684	0.851	0.095
1371681_at	AI145556	epidermal Langerhans cell protein LCP1	RGD708449	0.978	0.831	1.023	0.507	0.875	0.106	1.011	0.798
1369587_at	NM_021689	epiregulin	Ereg	3.114	0.021	1.038	0.606	2.129	0.308	1.004	0.984
1371527_at	BI275741	epithelial membrane protein 1	Emp1	3.246	0.041	1.374	0.111	4.140	0.030	1.146	0.795
1377752_at	BE112998	epithelial membrane protein 2	Emp2	1.017	0.217	13.291	0.032	1.111	0.037	5.607	0.032
1375908_at	BI282616	epithelial V-like antigen 1 (predicted)	Eva1_predicted	3.567	0.009	1.020	0.745	1.052	0.988	0.998	0.740
1372568_at	AI411270	EPM2A (laforin) interacting protein 1 (predicted)	Epm2aip1_predicted	0.705	0.423	0.503	0.004	0.807	0.078	0.550	0.004
1381179_at	BF415421	EPM2A (laforin) interacting protein 1 (predicted)	Epm2aip1_predicted	0.965	0.943	0.999	0.935	1.001	0.950	0.999	0.988
1387669_a_at	NM_012844	epoxide hydrolase 1, microsomal	Ephx1	1.077	0.062	1.104	0.308	1.031	0.995	2.331	0.012
1369663_at	NM_022936	epoxide hydrolase 2, cytoplasmic	Ephx2	0.922	0.992	0.683	0.140	0.860	0.532	0.845	0.153
1372654_at	BI285918	EPS8-like 2 (predicted)	Eps8l2_predicted	1.961	0.002	1.615	0.010	1.740	0.055	1.295	0.016
1369453_at	NM_057136	Epsin 1	Epn1	0.763	0.160	0.970	0.737	0.790	0.052	0.832	0.845
1392223_at	AW521110	epsin 2	Epn2	1.543	0.007	1.715	0.004	1.095	0.148	1.282	0.023
1371562_at	BI296640	epsin 2	Epn2	1.110	0.133	0.977	0.704	1.079	0.885	0.924	0.192
1373093_at	AI169756	ERBB receptor feedback inhibitor 1	Errfi1	2.441	0.078	3.192	0.004	1.028	0.852	2.339	0.011
1372233_at	AI228649	ERGIC and golgi 3 (predicted)	Ergic3_predicted	0.775	0.727	0.549	0.002	0.686	0.104	0.812	0.050
1387964_a_at	AY071924	ERO1-like (S. cerevisiae)	Ero1l	0.736	0.383	1.603	0.056	0.480	0.167	1.556	0.071
1387910_at	AB019256	erythrocyte protein band 4.1-like 1	Epb4.1l1	0.499	0.067	0.553	0.003	0.546	0.029	0.432	0.033
1370503_s_at	AB032828	erythrocyte protein band 4.1-like 3	Epb4.1l3	0.479	0.044	0.949	0.157	0.647	0.014	1.102	0.262
1368515_at	NM_053927	erythrocyte protein band 4.1-like 3	Epb4.1l3	0.702	0.471	0.447	0.003	1.147	0.427	0.534	0.076
1385033_at	AI548918	Erythrocyte protein band 4.1-like 4b (predicted)	Epb4.1l4b_predicted	2.243	0.016	1.406	0.018	1.449	0.055	1.784	0.010
1379788_at	AI231019	Erythrocyte protein band 4.1-like 4b (predicted)	Epb4.1l4b_predicted	4.458	0.020	1.498	0.220	3.692	0.018	1.315	0.468
1374984_at	AA858925	erythrocyte protein band 4.1-like 5	Epb4.1l5	0.583	0.137	0.929	0.513	1.059	0.652	1.117	0.808
1394101_at	BE109260	Erythrocyte protein band 4.1-like 5	Epb4.1l5	0.831	0.769	1.075	0.261	1.162	0.442	1.162	0.364
1369988_at	NM_017002	erythropoietin receptor	Epor	0.999	0.990	1.033	0.637	1.001	0.989	1.000	0.998
1398903_at	AI411425	esterase D/formylglutathione hydrolase (mapped)	Esd_mapped	0.614	0.472	1.385	0.059	0.540	0.008	1.253	0.256
1391510_at	BF398331	estrogen receptor-binding fragment-associated gene 9	Ebag9	0.522	0.771	0.437	0.016	0.894	0.714	0.539	0.042
1390439_at	BG372835	estrogen receptor-binding fragment-associated gene 9	Ebag9	0.866	0.987	0.626	0.004	0.934	0.095	0.804	0.551
1374741_at	AI171726	Estrogen related receptor, alpha	Esrra	0.958	0.398	1.318	0.010	0.981	0.282	1.356	0.011
1381445_at	AA996810	Estrogen-related receptor gamma	Esrrg	1.150	0.537	0.672	0.705	1.685	0.029	0.743	0.752
1398875_at	AI105044	estrous-specific protein, 250 kDa /// similar to RIKEN cDNA 1500004O14	LOC246270 /// LOC366277	0.915	0.702	0.665	0.014	0.917	0.147	0.854	0.048
1371710_at	BM391283	Ethanolamine kinase 1 (predicted)	Etnk1_predicted	0.841	0.045	0.416	0.001	1.199	0.440	0.512	0.003
1388642_at	AI412114	etoposide induced 2.4 mRNA	Ei24	1.028	0.733	1.239	0.056	1.207	0.409	1.263	0.037
1382593_at	AA963276	Ets variant gene 1 (predicted)	Etv1_predicted	1.737	0.073	0.564	0.139	2.351	0.778	0.527	0.126
1392555_at	AI112936	Ets variant gene 1 (predicted)	Etv1_predicted	1.569	0.312	0.317	0.013	1.404	0.243	0.389	0.081

1392477_at	AI059914	ets variant gene 1 (predicted)	Etv1_predicted	1.438	0.656	0.483	0.015	1.597	0.304	0.522	0.098
1383447_at	AI101323	ets variant gene 5 (ets-related molecule) (predicted)	Etv5_predicted	1.168	0.260	6.516	0.013	0.827	0.061	8.322	0.002
1382122_at	BE113124	Ets variant gene 5 (ets-related molecule) (predicted)	Etv5_predicted	0.971	0.669	2.173	0.306	0.966	0.793	2.136	0.023
1374055_at	BF285169	Ets2 repressor factor (predicted)	Erf_predicted	0.913	0.116	3.226	0.004	1.063	0.850	2.198	0.072
1388716_at	BE109525	euchromatic histone lysine N-methyltransferase 2	Ehmt2	0.913	0.867	1.085	0.815	0.688	0.274	0.945	0.079
1376578_at	BM389055	euchromatic histone methyltransferase 1 (predicted)	Ehmt1_predicted	1.640	0.025	1.215	0.142	1.604	0.039	1.241	0.154
1379979_at	AI548961	Eukaryotic elongation factor-2 kinase	Eef2k	0.638	0.225	0.922	0.090	0.667	0.258	0.383	0.058
1370109_s_at	NM_033539	eukaryotic translation elongation factor 1 alpha 1	Eef1a1	1.035	0.683	1.039	0.366	0.871	0.596	0.982	0.145
1388110_at	X61043	eukaryotic translation elongation factor 1 alpha 1 /// similar to eukaryotic translation elongation factor 1 alpha 1 (predicted)	Eef1a1 /// RGD1566344_predicted	0.900	0.062	0.996	0.663	0.881	0.475	0.907	0.190
1388449_at	AI175551	eukaryotic translation elongation factor 1 beta 2 (predicted)	Eef1b2_predicted	0.861	0.740	0.992	0.798	0.651	0.165	0.974	0.806
1388134_at	BG380216	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	Eef1d	0.694	0.246	1.149	0.022	0.583	0.005	0.869	0.290
1373200_at	AI600237	eukaryotic translation elongation factor 1 epsilon 1 (predicted)	Eef1e1_predicted	0.596	0.354	1.274	0.282	0.567	0.096	1.142	0.039
1388297_at	BM391203	eukaryotic translation elongation factor 1 gamma	Eef1g	0.927	0.490	0.982	0.482	0.768	0.121	0.927	0.900
1394744_at	AI556327	Eukaryotic translation elongation factor 1 gamma	Eef1g	1.145	0.671	2.075	0.323	1.364	0.343	1.028	0.609
1370003_at	NM_017245	eukaryotic translation elongation factor 2	Eef2	0.777	0.986	0.929	0.364	0.715	0.134	0.972	0.085
1384147_at	AA955540	eukaryotic translation initiation factor 1A	Eif1a	1.045	0.389	2.891	0.007	1.183	0.107	2.751	0.005
1397892_at	BI301150	eukaryotic translation initiation factor 1A	Eif1a	1.221	0.736	2.497	0.108	1.033	0.929	2.084	0.075
1395840_at	AW520679	eukaryotic translation initiation factor 1A	Eif1a	0.627	0.950	3.249	0.108	0.679	0.542	2.120	0.074
1373411_at	BE109655	eukaryotic translation initiation factor 1B (predicted)	Eif1b_predicted	0.682	0.574	1.013	0.587	0.532	0.053	0.963	0.302
1380593_at	AI008189	Eukaryotic translation initiation factor 2 alpha kinase 1	Eif2ak1	1.455	0.574	0.999	0.660	1.259	0.036	0.556	0.430
1387272_at	NM_013223	eukaryotic translation initiation factor 2 alpha kinase 1	Eif2ak1	0.985	0.997	1.023	0.691	0.903	0.338	1.245	0.118
1368326_at	NM_031599	eukaryotic translation initiation factor 2 alpha kinase 3	Eif2ak3	2.213	0.009	2.132	0.007	2.743	0.013	1.883	0.026
1374224_at	AI169164	eukaryotic translation initiation factor 2 alpha kinase 4 (predicted)	Eif2ak4_predicted	0.880	0.245	0.891	0.084	1.002	0.819	0.867	0.051
1385118_at	BI292531	eukaryotic translation initiation factor 2, subunit 1 alpha	Eif2s1	0.498	0.018	0.545	0.003	0.697	0.152	0.758	0.135
1367713_at	NM_019356	eukaryotic translation initiation factor 2, subunit 1 alpha	Eif2s1	0.560	0.127	1.215	0.913	0.394	0.010	1.074	0.524
1374397_at	BE107498	eukaryotic translation initiation factor 2, subunit 2 (beta)	Eif2s2	0.864	0.382	1.481	0.003	0.641	0.131	1.347	0.001
1398936_at	AI598546	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	Eif2s3x	1.047	0.815	1.079	0.510	0.987	0.454	0.982	0.324
1397693_at	BG662620	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	Eif2s3x	1.356	0.941	1.115	0.440	0.547	0.104	0.940	0.188
1370311_at	U05821	eukaryotic translation initiation factor 2B, subunit 1 alpha	Eif2b1	0.335	0.117	1.065	0.440	0.626	0.016	1.071	0.592
1367714_at	NM_032058	eukaryotic translation initiation factor 2B, subunit 2 beta	Eif2b2	1.192	0.017	1.180	0.892	0.934	0.998	1.170	0.864
1368967_at	NM_133609	eukaryotic translation initiation factor 2B, subunit 3 gamma	Eif2b3	1.249	0.279	2.212	0.003	0.707	0.079	1.424	0.029
1386970_at	NM_053950	eukaryotic translation initiation factor 2B, subunit 4 delta	Eif2b4	0.350	0.025	0.925	0.745	0.638	0.016	1.093	0.598
1387940_at	U19516	eukaryotic translation initiation factor 2B, subunit 5 epsilon	Eif2b5	0.967	0.837	0.864	0.644	0.479	0.066	0.790	0.209
1375249_at	BE109033	eukaryotic translation initiation factor 2C, 1 (predicted)	Eif2c1_predicted	0.891	0.261	0.939	0.075	1.037	0.753	0.834	0.367
1368867_at	BF281131	eukaryotic translation initiation factor 2C, 2	Eif2c2	1.967	0.008	10.317	0.003	2.202	0.004	5.129	0.001
1368866_at	NM_021597	eukaryotic translation initiation factor 2C, 2	Eif2c2	1.069	0.886	3.029	0.047	1.167	0.987	5.097	0.014
1390703_at	AW251303	Eukaryotic translation initiation factor 3, subunit 1 alpha (predicted)	Eif3s1_predicted	1.187	0.122	1.002	0.860	0.991	0.864	1.000	0.966
1388424_at	AI407015	eukaryotic translation initiation factor 3, subunit 1 alpha (predicted)	Eif3s1_predicted	0.665	0.251	1.652	0.008	0.509	0.070	1.216	0.062
1395199_at	AA998946	eukaryotic translation initiation factor 3, subunit 1 alpha (predicted)	Eif3s1_predicted	0.730	0.438	1.668	0.323	0.571	0.063	1.268	0.590
1389968_at	BG376953	eukaryotic translation initiation factor 3, subunit 10 (theta)	Eif3s10	0.705	0.619	0.948	0.280	0.816	0.673	0.973	0.315
1379485_at	BF389640	eukaryotic translation initiation factor 3, subunit 10 (theta)	Eif3s10	0.849	0.813	1.399	0.027	1.077	0.624	1.398	0.810
1381339_at	AI113218	eukaryotic translation initiation factor 3, subunit 12 (predicted)	Eif3s12_predicted	0.673	0.123	0.998	0.999	0.654	0.099	1.029	0.519
1372735_at	BI283109	eukaryotic translation initiation factor 3, subunit 12 (predicted)	Eif3s12_predicted	0.771	0.535	1.037	0.753	0.609	0.004	0.852	0.839
1388390_at	AI231784	eukaryotic translation initiation factor 3, subunit 3 gamma	Eif3s3	0.965	0.859	1.505	0.006	0.782	0.002	1.264	0.057
1388381_at	AI411198	eukaryotic translation initiation factor 3, subunit 4 (delta)	Eif3s4	0.802	0.774	1.311	0.078	0.859	0.032	0.948	0.568
1373040_at	BI281752	eukaryotic translation initiation factor 3, subunit 5 (epsilon) (predicted)	Eif3s5_predicted	0.888	0.498	1.507	0.042	0.829	0.014	1.473	0.058
1371973_at	AI237620	eukaryotic translation initiation factor 3, subunit 6	Eif3s6	1.185	0.400	1.252	0.117	1.070	0.281	1.227	0.059
1398929_at	AW525691	eukaryotic translation initiation factor 3, subunit 6 interacting protein	Eif3s6ip	0.651	0.225	0.861	0.110	0.553	0.002	0.936	0.128
1390880_at	BF420467	eukaryotic translation initiation factor 3, subunit 6 interacting protein	Eif3s6ip	0.751	0.542	0.375	0.074	0.587	0.203	0.382	0.039
1388568_at	AA891553	eukaryotic translation initiation factor 3, subunit 7 (zeta)	Eif3s7	0.800	0.116	1.788	0.003	0.678	0.002	1.452	0.016
1388378_at	AI412236	eukaryotic translation initiation factor 3, subunit 8, 110kDa	Eif3s8	0.739	0.471	1.279	0.006	0.639	0.117	1.137	0.076
1397674_at	AI502930	eukaryotic translation initiation factor 3, subunit 8, 110kDa	Eif3s8	0.623	0.505	0.918	0.954	0.548	0.019	0.724	0.179
1388576_at	BF281368	eukaryotic translation initiation factor 3, subunit 9 (eta)	Eif3s9	0.798	0.359	1.811	0.010	0.683	0.019	1.483	0.029
1388322_at	AI170773	eukaryotic translation initiation factor 4 gamma, 1	Eif4g1	0.909	0.633	1.521	0.033	0.849	0.132	1.284	0.128
1395702_at	AW522392	eukaryotic translation initiation factor 4 gamma, 1 /// similar to Eif4g1 protein (predicted)	Eif4g1 /// RGD1563212_predicted	1.237	0.676	2.160	0.064	1.001	0.154	1.465	0.227
1390340_a_at	AA899256	eukaryotic translation initiation factor 4 gamma, 1 /// similar to Eif4g1 protein (predicted)	Eif4g1 /// RGD1563212_predicted	0.749	0.975	1.272	0.273	0.798	0.346	0.795	0.286
1367469_at	BG667162	Eukaryotic translation initiation factor 4 gamma, 2	Eif4g2	0.836	0.694	1.223	0.005	0.791	0.391	1.104	0.087
1388359_at	AI599478	Eukaryotic translation initiation factor 4 gamma, 2	Eif4g2	0.727	0.881	0.492	0.024	0.615	0.604	0.530	0.010

1373364_at	BI294767	eukaryotic translation initiation factor 4 gamma, 3 (predicted)	Eif4g3_predicted	1.169	0.373	0.518	0.009	1.181	0.826	0.613	0.025
1397520_at	BG672378	eukaryotic translation initiation factor 4, gamma 2 (predicted)	Eif4g2_predicted	0.948	0.755	0.724	0.642	0.372	0.064	0.813	0.496
1371936_at	BI284436	eukaryotic translation initiation factor 4A1	Eif4a1	0.669	0.281	1.105	0.632	0.709	0.329	0.888	0.510
1397697_at	BF558764	Eukaryotic translation initiation factor 4A2	Eif4a2	0.710	0.079	0.397	0.008	0.553	0.252	0.603	0.001
1371642_at	AI169170	eukaryotic translation initiation factor 4A2	Eif4a2	0.982	0.735	1.015	0.806	0.923	0.348	0.848	0.158
1372124_at	BI278814	eukaryotic translation initiation factor 4B	Eif4b	1.206	0.250	3.459	0.001	0.958	0.493	2.161	0.015
1371404_at	AI172206	eukaryotic translation initiation factor 4B	Eif4b	1.023	0.926	1.303	0.167	0.851	0.428	1.092	0.785
1398799_at	NM_053974	eukaryotic translation initiation factor 4E	Eif4e	0.925	0.037	1.083	0.198	0.892	0.076	1.093	0.097
1386888_at	NM_053857	eukaryotic translation initiation factor 4E binding protein 1	Eif4ebp1	1.128	0.561	4.301	0.012	0.650	0.235	2.243	0.087
1398846_at	BE107346	eukaryotic translation initiation factor 5	Eif5	1.079	0.267	1.501	0.033	0.908	0.719	1.506	0.106
1388206_a_at	K01677	eukaryotic translation initiation factor 5	Eif5	1.365	0.425	2.790	0.004	1.067	0.719	2.044	0.015
1398845_at	BF282186	eukaryotic translation initiation factor 5	Eif5	1.031	0.603	1.345	0.002	0.878	0.061	1.468	0.006
1371329_at	BI283681	eukaryotic translation initiation factor 5A	Eif5a	0.824	0.743	1.385	0.032	0.863	0.817	1.464	0.117
1383867_at	BE102803	Eukaryotic translation initiation factor 5A2 (predicted)	Eif5a2_predicted	0.936	0.484	1.935	0.030	1.442	0.243	1.828	0.029
1388947_at	BI291654	eukaryotic translation initiation factor 5B	Eif5b	1.291	0.147	1.346	0.003	0.833	0.556	1.104	0.194
1395237_at	BE117773	eukaryotic translation initiation factor 5B	Eif5b	0.843	0.988	1.227	0.020	1.004	0.993	1.032	0.871
1389038_at	BF285301	eukaryotic translation termination factor 1	Etf1	0.820	0.561	1.682	0.002	0.676	0.002	1.517	0.002
1373917_at	BE100459	Eukaryotic translation termination factor 1	Etf1	0.791	0.688	1.046	0.692	0.760	0.558	0.860	0.219
1373420_at	AI175479	evolutionarily conserved signaling intermediate in Toll pathway	MGC94704	0.449	0.003	1.041	0.075	0.415	0.002	1.203	0.214
1389289_at	AW534728	Ewing sarcoma breakpoint region 1	Ewsr1	0.953	0.513	1.812	0.067	1.019	0.158	1.373	0.053
1374011_at	BM388758	excision repair cross-complementing rodent repair deficiency, complementation group 3	Ercc3	0.748	0.722	0.679	0.072	0.824	0.462	0.826	0.052
1383953_at	BM384968	excision repair cross-complementing rodent repair deficiency, complementation group 5 (mapped)	Ercc5_mapped	0.953	0.338	0.605	0.129	4.041	0.053	1.086	0.349
1379299_at	BE106364	excision repair cross-complementing rodent repair deficiency, complementation group 8 (predicted)	Ercc8_predicted	0.742	0.158	1.018	0.897	0.570	0.379	1.001	0.805
1368225_at	NM_134414	exocyst complex component 2	Exoc2	1.122	0.430	0.427	0.027	1.484	0.004	0.895	0.579
1374656_at	AA851443	exocyst complex component 3	Exoc3	0.710	0.021	1.077	0.292	0.846	0.034	1.103	0.289
1370686_at	U32575	exocyst complex component 3	Exoc3	0.853	0.221	0.898	0.932	0.585	0.061	1.048	0.846
1389624_s_at	AA851443	exocyst complex component 3	Exoc3	0.602	0.466	1.289	0.797	0.614	0.079	0.731	0.088
1376774_at	BG380482	Exocyst complex component 4	Exoc4	1.037	0.877	0.689	0.112	1.159	0.134	0.959	0.324
1395155_at	BF386083	exocyst complex component 5	Exoc5	1.291	0.024	1.211	0.241	1.302	0.454	1.572	0.038
1387841_at	NM_022204	exocyst complex component 5	Exoc5	1.138	0.687	4.080	0.011	0.720	0.209	2.353	0.038
1387369_at	NM_019277	exocyst complex component 6	Exoc6	5.539	0.006	3.076	0.021	6.941	0.006	3.851	0.010
1387237_at	BM388722	exocyst complex component 7	Exoc7	0.656	0.005	0.582	0.044	0.668	0.045	0.700	0.064
1368538_at	NM_022691	exocyst complex component 7	Exoc7	0.247	0.092	0.263	0.030	0.245	0.020	0.521	0.380
1378780_at	BF410325	Exophilin 5 (predicted)	Exph5_predicted	1.110	0.666	0.840	0.816	2.251	0.156	0.713	0.209
1379348_at	BF420491	exosome component 2 (predicted)	Exosc2_predicted	0.291	0.075	0.842	0.608	0.548	0.055	1.251	0.870
1392111_at	AW435086	exosome component 3 (predicted)	Exosc3_predicted	0.931	0.233	1.213	0.206	0.701	0.005	1.005	0.910
1371670_at	BF407149	exosome component 4 (predicted)	Exosc4_predicted	0.367	0.182	1.366	0.025	0.422	0.031	1.266	0.222
1372688_at	BI296190	exosome component 7	Exosc7	0.528	0.122	0.846	0.581	0.570	0.202	0.904	0.220
1372343_at	BM384065	exosome component 8 (predicted)	Exosc8_predicted	0.930	0.501	1.846	0.505	0.773	0.038	1.543	0.314
1398384_at	BI298225	exosome component 9	Exosc9	0.709	0.018	0.707	0.240	1.035	0.595	0.823	0.091
1371611_at	BM387363	exostoses (multiple) 2 (predicted)	Ext2_predicted	0.516	0.260	0.600	0.001	0.434	0.006	0.621	0.001
1379354_at	AA851239	exostoses (multiple)-like 2	Extl2	0.840	0.133	0.695	0.125	0.624	0.115	0.747	0.110
1388150_at	AW533924	exportin 1, CRM1 homolog (yeast)	Xpo1	0.930	0.101	3.184	0.001	0.756	0.034	3.338	0.014
1385864_at	BF542299	exportin 4 (predicted)	Xpo4_predicted	1.082	0.142	1.322	0.015	1.012	0.987	1.076	0.106
1385428_at	AI072630	exportin 4 (predicted)	Xpo4_predicted	0.615	0.849	1.911	0.019	0.584	0.039	1.716	0.007
1389063_at	BG378160	exportin 6	Xpo6	2.538	0.021	2.492	0.004	2.666	0.000	2.932	0.012
1371516_at	BM391834	exportin 7	Xpo7	0.759	0.007	1.123	0.155	0.904	0.258	1.149	0.270
1397312_at	AI574904	exportin 7	Xpo7	0.938	0.069	1.018	0.643	0.970	0.970	1.020	0.471
1393983_at	AA998204	exportin, tRNA (nuclear export receptor for tRNAs) (predicted)	Xpot_predicted	0.872	0.593	3.205	0.000	0.772	0.400	2.996	0.007
1370295_at	D13374	expressed in non-metastatic cells 1	Nme1	0.652	0.448	1.130	0.559	0.707	0.005	0.947	0.330
1367766_at	NM_031833	expressed in non-metastatic cells 2	Nme2	0.872	0.693	1.345	0.074	0.796	0.720	1.247	0.138
1382732_at	BE116084	extracellular link domain-containing 1 (predicted)	Xlkd1_predicted	1.707	0.417	0.983	0.918	0.871	0.813	1.374	0.199
1387279_at	NM_053796	F11 receptor	F11r	2.265	0.020	2.027	0.019	1.721	0.202	2.074	0.000
1376921_at	BG381722	FAD-dependent oxidoreductase domain containing 1 (predicted)	Foxred1_predicted	0.968	0.929	0.913	0.132	0.989	0.151	1.845	0.170
1393412_at	AW920562	family with sequence similarity 3, member C	Fam3c	0.627	0.132	1.250	0.002	0.595	0.058	1.014	0.999
1379398_at	BM385853	Family with sequence similarity 31, member B (predicted)	Fam31b_predicted	1.047	0.753	1.190	0.557	1.306	0.842	1.090	0.685
1381193_at	BE115518	family with sequence similarity 34, member A (predicted)	Fam34a_predicted	1.185	0.858	2.769	0.006	0.561	0.067	2.844	0.010
1390697_at	BI278125	family with sequence similarity 51, member A1 homolog (human)	Fam51a1	0.987	0.980	0.766	0.174	1.552	0.553	1.160	0.343
1383287_at	BE329232	far upstream element (FUSE) binding protein 1	Fubp1	0.840	0.563	0.548	0.267	0.957	0.669	1.069	0.819
1381483_at	BE118096	Far upstream element (FUSE) binding protein 3	Fubp3	1.328	0.468	0.874	0.015	1.198	0.434	0.648	0.114
1382390_at	AI177572	Far upstream element (FUSE) binding protein 3	Fubp3	0.936	0.894	0.648	0.002	1.135	0.642	0.783	0.086

1367667_at	NM_031840	farensyl diphosphate synthase	Fdps	0.686	0.080	1.060	0.474	0.761	0.319	1.078	0.925
1367839_at	NM_019238	farnesyl diphosphate farnesyl transferase 1	Fdft1	0.844	0.039	1.423	0.019	0.629	0.080	1.038	0.656
1389906_at	AW530769	farnesyl diphosphate farnesyl transferase 1	Fdft1	0.414	0.189	1.194	0.127	0.623	0.401	0.730	0.253
1367824_at	NM_012847	farnesyltransferase, CAAX box, alpha	Fnta	0.597	0.078	1.352	0.013	0.733	0.004	1.292	0.040
1389991_at	BI278555	Fas (TNFRSF6) binding factor 1 (predicted)	Fbf1_predicted	0.567	0.053	0.969	0.754	1.164	0.298	1.002	0.986
1370044_at	NM_080895	Fas apoptotic inhibitory molecule	Faim	0.643	0.033	0.455	0.005	0.543	0.034	0.409	0.002
1387800_at	NM_080891	Fas death domain-associated protein	Daxx	2.964	0.036	2.228	0.006	9.100	0.005	4.061	0.012
1387587_at	NM_012908	Fas ligand (TNF superfamily, member 6)	Faslg	1.293	0.262	1.021	0.534	1.166	0.722	1.005	0.997
1372551_at	AI227743	Fas-activated serine/threonine kinase	Fastk	0.501	0.027	0.516	0.111	0.475	0.162	0.613	0.207
1369995_at	NM_130406	Fas-associated factor 1	Faf1	0.697	0.136	1.867	0.009	0.495	0.005	1.349	0.096
1367918_at	NM_031066	fasciculation and elongation protein zeta 1 (zygin I)	Fez1	1.342	0.392	1.020	0.050	2.545	0.002	1.018	0.606
1388137_a_at	AA955230	fasciculation and elongation protein zeta 2 (zygin II)	Fez2	1.252	0.253	1.431	0.004	1.239	0.333	1.538	0.018
1370033_at	NM_020104	fast myosin alkali light chain	Mlc3	1.001	0.998	0.992	0.983	1.002	0.984	1.009	0.856
1369909_s_at	NM_139107	fasting-inducible integral membrane protein TM6P1	Tm6p1	0.615	0.175	0.618	0.397	0.599	0.246	0.645	0.261
1367654_at	NM_031819	fat tumor suppressor homolog (Drosophila)	Fath	0.733	0.042	0.625	0.055	0.607	0.001	0.745	0.112
1381620_at	BF389656	Fat tumor suppressor homolog (Drosophila)	Fath	1.011	0.567	1.183	0.105	0.853	0.570	2.568	0.027
1368717_at	NM_024132	fatty acid amide hydrolase	Faah	0.544	0.002	0.249	0.013	0.430	0.029	0.537	0.137
1384341_at	AI136853	fatty acid amide hydrolase	Faah	0.430	0.022	0.464	0.017	0.407	0.047	0.186	0.071
1370281_at	U13253	fatty acid binding protein 5, epidermal	Fabp5	1.885	0.310	19.415	0.000	0.880	0.662	7.715	0.000
1367857_at	NM_053445	fatty acid desaturase 1	Fads1	0.213	0.007	0.280	0.000	0.253	0.045	0.274	0.022
1375782_at	BF412915	Fatty acid desaturase 1	Fads1	0.963	0.327	0.985	0.454	0.948	0.360	0.938	0.255
1368453_at	NM_031344	fatty acid desaturase 2	Fads2	0.863	0.044	0.241	0.020	0.758	0.061	0.351	0.045
1372476_at	AW533321	fatty acid desaturase 3	Fads3	0.784	0.084	0.956	0.347	0.776	0.084	0.827	0.845
1367708_a_at	AI179334	fatty acid synthase	Fasn	0.317	0.042	0.935	0.656	0.456	0.056	0.769	0.170
1367707_at	NM_017332	fatty acid synthase	Fasn	0.327	0.145	0.495	0.001	0.121	0.037	0.499	0.098
1375043_at	BF415939	FBJ murine osteosarcoma viral oncogene homolog	Fos	0.334	0.049	0.699	0.048	0.330	0.013	0.295	0.105
1393101_at	BM385838	F-box and leucine-rich repeat protein 10	Fbxl10	0.669	0.090	0.944	0.418	0.486	0.016	0.989	0.997
1399154_at	BF389273	F-box and leucine-rich repeat protein 11 (predicted)	Fbxl11_predicted	1.135	0.310	0.839	0.017	1.237	0.016	1.044	0.582
1384489_at	BM387189	F-box and leucine-rich repeat protein 11 (predicted)	Fbxl11_predicted	0.999	0.663	0.777	0.236	1.344	0.092	0.944	0.607
1378294_at	BF282402	F-box and leucine-rich repeat protein 12	Fbxl12	1.864	0.054	1.929	0.012	2.172	0.037	2.019	0.011
1383465_at	AI058747	F-box and leucine-rich repeat protein 14 (predicted)	Fbxl14_predicted	1.079	0.802	0.955	0.634	1.479	0.225	1.076	0.402
1373147_at	AI145387	F-box and leucine-rich repeat protein 3	Fbxl3	1.469	0.044	0.748	0.013	1.558	0.178	0.652	0.002
1372969_at	BI289651	F-box and leucine-rich repeat protein 3	Fbxl3	2.187	0.068	1.991	0.002	1.407	0.057	1.672	0.016
1377484_at	BE096747	F-box and leucine-rich repeat protein 3	Fbxl3	1.000	0.738	0.998	0.979	0.992	0.641	0.999	0.974
1391005_at	AA997732	F-box and leucine-rich repeat protein 4 (predicted)	Fbxl4_predicted	0.722	0.052	0.968	0.829	0.652	0.622	0.839	0.592
1372776_at	BM392017	F-box and leucine-rich repeat protein 5 (predicted)	Fbxl5_predicted	1.365	0.038	1.068	0.798	1.283	0.015	0.911	0.062
1389078_at	BF282132	F-box and leucine-rich repeat protein 6	Fbxl6	0.995	0.969	2.135	0.096	0.984	0.932	2.521	0.027
1381753_at	BF416214	F-box and leucine-rich repeat protein 7 (predicted)	Fbxl7_predicted	1.488	0.550	2.470	0.062	5.926	0.061	1.095	0.763
1395138_at	AW534201	F-box and leucine-rich repeat protein 7 (predicted)	Fbxl7_predicted	1.600	0.823	1.320	0.618	0.787	0.390	0.936	0.467
1393407_at	AW915859	F-box and WD-40 domain protein 2 (predicted)	Fbxw2_predicted	0.719	0.364	1.088	0.704	0.694	0.033	0.926	0.298
1385772_at	BF416058	F-box and WD-40 domain protein 2 (predicted)	Fbxw2_predicted	1.556	0.468	0.943	0.620	1.484	0.375	1.028	0.952
1392469_at	AI102773	F-box and WD-40 domain protein 2 (predicted)	Fbxw2_predicted	0.826	0.636	1.665	0.022	0.770	0.118	1.674	0.013
1373211_at	BF283421	F-box and WD-40 domain protein 4 (predicted)	Fbxw4_predicted	0.902	0.419	1.859	0.341	1.130	0.595	1.200	0.109
1388518_at	AA799654	F-box and WD-40 domain protein 5	Fbxw5	0.743	0.027	0.891	0.035	0.856	0.270	1.140	0.562
1389106_at	AI407555	F-box and WD-40 domain protein 9	Fbxw9	0.720	0.009	1.160	0.112	0.978	0.060	1.061	0.076
1389518_at	AI009763	F-box only protein 10 (predicted)	Fbxo10_predicted	0.859	0.321	1.753	0.007	1.044	0.834	1.392	0.025
1376587_at	AA818128	F-box only protein 11	Fbxo11	1.279	0.378	0.689	0.007	1.471	0.004	0.839	0.088
1372393_at	AI409506	F-box only protein 18 (predicted)	Fbxo18_predicted	1.079	0.683	0.690	0.096	1.104	0.537	0.713	0.001
1392649_at	AI030616	F-box only protein 21 (predicted)	Fbxo21_predicted	0.673	0.361	0.655	0.991	1.090	0.750	1.001	0.995
1376602_a_at	AI030899	F-box only protein 22	Fbxo22	0.866	0.071	1.091	0.612	1.204	0.054	1.190	0.156
1379401_a_at	AW918372	F-box only protein 33 (predicted)	Fbxo33_predicted	0.463	0.096	0.701	0.180	0.551	0.053	0.599	0.164
1383354_a_at	BF566664	F-box only protein 33 (predicted)	Fbxo33_predicted	0.686	0.170	0.585	0.061	0.644	0.208	0.512	0.022
1381903_at	AW533341	F-box only protein 33 (predicted)	Fbxo33_predicted	0.735	0.276	0.796	0.053	0.684	0.301	0.690	0.080
1372662_at	AI176698	F-box only protein 34 (predicted)	Fbxo34_predicted	0.582	0.050	0.917	0.582	0.671	0.003	0.900	0.405
1384364_at	AW521356	F-box only protein 4 (predicted)	Fbxo4_predicted	1.036	0.592	1.406	0.037	1.113	0.528	1.276	0.069
1384988_at	BM385403	F-box only protein 5 (predicted)	Fbxo5_predicted	1.006	0.996	1.353	0.708	1.002	0.489	1.002	0.962
1370820_at	AF393484	F-box only protein 6b	Fbxo6b	1.303	0.700	2.475	0.018	1.339	0.044	3.197	0.011
1399133_at	AW520767	F-box only protein 7	Fbxo7	1.523	0.073	2.837	0.001	1.636	0.019	2.426	0.001
1373835_at	AI009785	F-box only protein 8	Fbxo8	0.758	0.642	0.497	0.073	0.637	0.061	0.624	0.002
1388470_at	AA892772	F-box only protein 9	Fbxo9	0.509	0.018	0.399	0.003	0.412	0.091	0.511	0.012
1376561_at	AW523739	F-box protein 16	Fbxo16	0.151	0.039	0.563	0.274	0.143	0.023	0.449	0.002

1382059_at	BI289529	F-box protein 30	Fbxo30	1.324	0.063	2.910	0.000	1.381	0.156	2.315	0.001
1392747_at	AI030920	F-box protein 30	Fbxo30	0.911	0.691	2.797	0.000	0.823	0.090	1.704	0.027
1372873_at	BM385705	F-box protein 38 (predicted)	Fbxo38_predicted	0.725	0.007	0.537	0.002	0.782	0.009	0.653	0.003
1381228_at	AI073001	F-box protein 39	Fbxo39	8.031	0.018	2.234	0.032	21.814	0.001	5.556	0.000
1384502_at	BI290539	F-box protein 42 (predicted)	Fbxo42_predicted	1.859	0.139	2.325	0.015	0.516	0.251	0.795	0.972
1383544_at	AI385372	FCH and double SH3 domains 1 (predicted)	Fchsd1_predicted	1.453	0.522	2.383	0.017	0.999	0.620	1.288	0.187
1389074_at	AI232737	FCH and double SH3 domains 2 (predicted)	Fchsd2_predicted	1.145	0.382	1.357	0.016	0.987	0.920	1.083	0.281
1384067_at	BF288361	FCH domain only 2 (predicted)	Fcho2_predicted	1.689	0.138	1.714	0.557	1.006	0.998	1.815	0.677
1395222_at	BF287049	FCH domain only 2 (predicted)	Fcho2_predicted	1.631	0.201	1.024	0.388	1.886	0.040	1.137	0.272
1398098_at	AW522192	FCH domain only 2 (predicted)	Fcho2_predicted	1.439	0.478	1.797	0.006	2.085	0.589	1.273	0.593
1393722_at	BE108945	fem-1 homolog c (C.elegans) (predicted)	Fem1c_predicted	1.155	0.815	1.823	0.135	0.710	0.581	1.182	0.120
1398417_at	BE104341	feminization 1 homolog a (C. elegans)	Fem1a	0.661	0.700	0.895	0.944	0.787	0.341	0.740	0.067
1372054_at	BG380399	Feminization 1 homolog a (C. elegans)	Fem1a	0.665	0.880	0.460	0.460	0.494	0.032	0.490	0.133
1393843_at	AI071911	feminization 1 homolog b (C. elegans) (predicted)	Fem1b_predicted	0.319	0.015	3.152	0.031	0.130	0.002	1.567	0.023
1386643_at	BF552914	feminization 1 homolog b (C. elegans) (predicted)	Fem1b_predicted	1.021	0.698	2.334	0.044	0.888	0.159	0.666	0.013
1375402_at	BF391604	FERM domain containing 4A (predicted)	Frmd4a_predicted	1.500	0.994	1.607	0.741	1.666	0.954	1.029	0.623
1390464_at	BI291381	FERM domain containing 4B	Frmd4b	4.398	0.052	3.094	0.050	3.065	0.085	4.809	0.038
1378492_at	BF396209	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derived) (predicted)	Farp1_predicted	1.322	0.025	1.345	0.015	1.222	0.302	1.484	0.044
1391017_at	AI058490	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derived) (predicted)	Farp1_predicted	1.022	0.803	1.003	0.915	1.329	0.286	1.000	0.854
1374239_at	BI282835	FERM, RhoGEF and pleckstrin domain protein 2 (predicted)	Farp2_predicted	0.821	0.336	0.578	0.015	1.063	0.551	0.556	0.001
1391798_at	BF564518	FERM, RhoGEF and pleckstrin domain protein 2 (predicted)	Farp2_predicted	1.275	0.404	1.330	0.738	0.927	0.811	0.929	0.131
1389827_at	AI408556	Ferredoxin 1	Fdx1	0.632	0.033	1.021	0.983	0.553	0.006	1.199	0.023
1368336_at	NM_017126	ferredoxin 1	Fdx1	0.471	0.267	1.378	0.274	0.524	0.002	1.112	0.437
1367559_at	L01122	ferritin light chain 1	Ftl1	0.904	0.933	2.412	0.002	0.673	0.019	2.089	0.002
1367565_a_at	NM_012848	ferritin, heavy polypeptide 1	Fth1	0.903	0.571	1.055	0.373	0.831	0.074	1.028	0.829
1390388_at	BF283951	ferrochelatase (predicted)	Fech_predicted	0.595	0.206	0.708	0.044	0.772	0.060	1.174	0.392
1375347_at	BE107103	Fetal Alzheimer antigen (predicted)	Falz_predicted	1.049	0.032	0.871	0.159	0.928	0.609	0.815	0.282
1390616_at	BI296731	Fetal Alzheimer antigen (predicted)	Falz_predicted	1.002	0.607	1.001	0.993	0.880	0.844	0.998	0.977
1376182_at	BM383074	Fetal Alzheimer antigen (predicted)	Falz_predicted	1.102	0.643	0.759	0.072	0.701	0.331	0.796	0.009
1370203_at	AI408972	FGF receptor activating protein 1	Frag1	1.415	0.196	1.787	0.119	1.610	0.175	1.188	0.392
1370204_at	BG373817	FGF receptor activating protein 1	Frag1	0.996	0.947	1.452	0.070	0.943	0.830	0.999	0.981
1385727_at	BE107623	FGFR1 oncogene partner 2	Fgfr1op2	1.576	0.033	3.591	0.012	1.693	0.083	2.064	0.067
1393829_at	AI639475	FGFR1 oncogene partner 2	Fgfr1op2	1.535	0.246	1.473	0.161	1.217	0.251	1.188	0.056
1388528_at	AW433875	fibrillarin	Fbl	0.628	0.770	2.656	0.005	0.597	0.011	2.101	0.039
1370511_at	U05675	fibrinogen, B beta polypeptide	Fgb	4.230	0.042	10.327	0.018	1.487	0.278	3.095	0.177
1370086_at	NM_012559	fibrinogen, gamma polypeptide	Fgg	1.544	0.242	4.916	0.059	5.977	0.081	5.878	0.039
1383516_at	BG663284	fibrinogen-like 2	Fgl2	1.856	0.084	0.824	0.118	0.869	0.027	0.976	0.311
1392894_at	AI716194	fibrinogen-like 2	Fgl2	1.355	0.441	0.168	0.003	0.906	0.202	0.232	0.017
1399072_at	BI283002	fibroblast growth factor (acidic) intracellular binding protein	Fibp	0.498	0.079	0.417	0.003	0.570	0.026	0.673	0.111
1387606_at	NM_019305	fibroblast growth factor 2	Fgf2	1.056	0.942	0.883	0.121	0.913	0.246	0.715	0.057
1370747_at	D14839	fibroblast growth factor 9	Fgf9	0.999	0.375	1.002	0.995	0.816	0.174	1.000	0.990
1384056_at	BF410980	Fibroblast growth factor receptor 3	Fgfr3	0.974	0.875	0.713	0.024	1.027	0.329	0.731	0.008
1389801_at	BF391339	fibroblast growth factor receptor 4	Fgfr4	0.308	0.088	0.438	0.194	0.741	0.102	0.644	0.234
1370234_at	AA893484	fibronectin 1	Fn1	0.361	0.178	0.061	0.000	0.440	0.029	0.051	0.000
1378057_at	BE103354	fibronectin leucine rich transmembrane protein 3 (predicted)	Flrt3_predicted	1.002	0.998	0.997	0.975	1.008	0.840	0.695	0.938
1383396_at	AA894079	fibronectin type III domain containing 3a (predicted)	Fndc3a_predicted	1.359	0.005	0.833	0.009	1.800	0.002	1.150	0.216
1376823_at	AI599269	Fibronectin type III domain containing 3a (predicted)	Fndc3a_predicted	0.989	0.477	0.670	0.010	0.649	0.842	0.783	0.144
1373206_at	BI289093	fibronectin type III domain containing 3B (predicted)	Fndc3b_predicted	1.114	0.578	1.680	0.019	0.898	0.859	1.255	0.095
1373416_at	AI176320	fibronectin type III domain containing 3B (predicted)	Fndc3b_predicted	1.420	0.739	1.570	0.048	0.996	0.755	1.290	0.983
1391085_at	BE118077	Fibronigen-like protein 1	Fgl1	0.710	0.261	0.349	0.014	0.726	0.678	0.488	0.016
1389533_at	AA944398	fibulin 2	Fbln2	1.153	0.413	1.545	0.135	1.016	0.957	1.108	0.379
1378804_at	BE098265	Fidgetin (predicted)	Fign_predicted	1.641	0.060	1.354	0.427	1.855	0.086	1.137	0.149
1379463_at	AW525176	filamin A interacting protein 1	Filip1	0.223	0.001	0.178	0.000	0.056	0.010	0.210	0.051
1375089_at	BF411781	filamin A interacting protein 1	Filip1	0.402	0.059	0.157	0.026	0.405	0.059	0.156	0.025
1373286_at	AA875261	filamin binding LIM protein 1	Fblim1	3.157	0.001	3.510	0.044	1.559	0.028	1.341	0.377
1391827_at	AI013675	filamin, beta (predicted)	Flnb_predicted	1.490	0.014	1.076	0.707	0.731	0.952	1.350	0.886
1371316_at	AI177362	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived) protein /// similar to Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived)	Fau /// LOC499305	0.806	0.272	1.169	0.148	0.787	0.006	0.928	0.657
1389621_at	BE113454	FIP1 like 1 (S. cerevisiae)	Fip1l1	0.795	0.253	1.744	0.014	0.654	0.093	1.692	0.003
1371594_at	AA892378	fission 1 (mitochondrial outer membrane) homolog (yeast)	Fis1	0.723	0.542	0.834	0.507	0.621	0.048	0.990	0.338
1375546_at	AI009616	fizzy/cell division cycle 20 related 1 (Drosophila) (predicted)	Fzr1_predicted	1.024	0.851	1.500	0.217	1.463	0.105	1.247	0.405

1372653_at	BI276210	FK506 binding protein 11	Fkbp11	0.482	0.219	0.738	0.045	0.656	0.067	0.648	0.080
1368019_at	NM_019906	FK506 binding protein 12-rapamycin associated protein 1	Frap1	0.589	0.135	0.961	0.711	0.640	0.183	0.875	0.941
1383976_at	AW527549	FK506 binding protein 14	Fkbp14	1.151	0.371	0.629	0.050	2.790	0.162	0.886	0.154
1372525_at	AI227721	FK506 binding protein 14	Fkbp14	1.119	0.842	0.645	0.043	0.632	0.781	1.042	0.713
1369621_s_at	NM_053308	FK506 binding protein 1a	Fkbp1a	1.138	0.585	1.577	0.401	0.739	0.296	0.993	0.399
1398829_at	AI598372	FK506 binding protein 1a	Fkbp1a	0.944	0.598	1.042	0.045	0.786	0.667	1.042	0.118
1398828_at	U09386	FK506 binding protein 1a	Fkbp1a	1.187	0.644	1.682	0.005	0.846	0.957	1.535	0.009
1392479_at	AA925694	FK506 binding protein 1a	Fkbp1a	1.176	0.719	1.131	0.439	1.278	0.806	0.779	0.020
1380500_s_at	BF561706	FK506 binding protein 2 (predicted)	Fkbp2_predicted	0.922	0.363	0.829	0.189	0.848	0.258	0.754	0.183
1375669_at	BI285619	FK506 binding protein 2 (predicted)	Fkbp2_predicted	0.759	0.547	0.733	0.013	0.705	0.077	0.713	0.076
1380501_x_at	BF561706	FK506 binding protein 2 (predicted)	Fkbp2_predicted	1.030	0.916	1.229	0.125	0.973	1.000	1.076	0.282
1378291_at	BF549558	FK506 binding protein 3 (predicted)	Fkbp3_predicted	0.686	0.077	0.590	0.090	1.008	0.302	0.359	0.046
1388882_at	AA891798	FK506 binding protein 3 (predicted)	Fkbp3_predicted	0.712	0.091	0.774	0.253	0.878	0.170	0.905	0.101
1392567_at	AI556652	FK506 binding protein 3 (predicted)	Fkbp3_predicted	1.216	0.463	1.002	0.989	1.285	0.394	1.338	0.369
1389844_at	BE113154	FK506 binding protein 4	Fkbp4	0.352	0.077	2.537	0.007	0.219	0.003	1.757	0.029
1388901_at	AW534837	FK506 binding protein 5	Fkbp5	1.003	0.994	1.262	0.101	1.076	0.278	1.232	0.086
1380611_at	BI284255	FK506 binding protein 5	Fkbp5	1.002	0.996	4.470	0.035	0.529	0.037	3.392	0.194
1384344_at	AI060231	FK506 binding protein 7 (predicted)	Fkbp7_predicted	0.378	0.002	0.250	0.006	0.237	0.025	0.480	0.009
1371528_at	BI274519	FK506 binding protein 8	Fkbp8	0.873	0.281	1.221	0.796	1.282	0.012	1.046	0.666
1390995_at	BF389385	FK506 binding protein-like	Fkbpl	1.176	0.125	1.555	0.628	0.537	0.025	1.585	0.711
1392320_s_at	AI763657	FKBP-associated protein	Glmn	0.372	0.011	1.243	0.481	1.046	0.312	1.373	0.026
1381564_at	AI763657	FKBP-associated protein	Glmn	0.602	0.145	1.253	0.191	1.399	0.306	1.305	0.116
1379885_at	BF282998	flavin containing monooxygenase 4	Fmo4	0.997	0.327	0.993	0.955	1.080	0.639	1.043	0.365
1395026_at	BI293319	flavin containing monooxygenase 4	Fmo4	1.015	0.777	1.002	0.975	1.016	0.941	1.283	0.185
1383248_at	AI454611	flavin containing monooxygenase 5	Fmo5	0.900	0.239	0.537	0.132	0.847	0.242	0.534	0.132
1372113_at	AA850662	flightless I homolog (Drosophila)	Fliih	0.992	0.962	0.900	0.092	0.899	0.531	0.933	0.193
1373757_at	AW529298	FLN29 gene product	Fln29	3.128	0.006	0.989	0.181	4.934	0.007	1.580	0.005
1368241_a_at	NM_022701	flotillin 1	Flot1	0.915	0.602	0.980	0.741	1.144	0.691	1.437	0.120
1367746_a_at	NM_031830	flotillin 2	Flot2	1.638	0.037	1.857	0.001	1.797	0.002	1.870	0.010
1374878_at	H35236	Fms interacting protein	Fmip	0.637	0.076	1.489	0.069	0.749	0.095	1.657	0.064
1393145_at	AA899892	follicular lymphoma variant translocation 1 (predicted)	Fvt1_predicted	1.140	0.063	1.009	0.955	0.931	0.588	1.013	0.925
1396826_at	AW522542	Follicular lymphoma variant translocation 1 (predicted)	Fvt1_predicted	0.878	0.622	1.551	0.740	1.126	0.788	0.760	0.494
1372526_at	BI278582	folliculin	Flcn	1.336	0.012	2.202	0.000	1.209	0.013	1.850	0.005
1368821_at	NM_024369	follistatin-like 1	Fstl1	0.862	0.148	0.999	0.147	0.854	0.383	0.999	0.976
1368822_at	BI290885	follistatin-like 1	Fstl1	1.393	0.743	1.143	0.937	1.893	0.193	1.090	0.780
1396896_at	AW524895	follistatin-like 4 (predicted)	Fstl4_predicted	2.088	0.631	1.177	0.525	1.943	0.145	0.933	0.457
1395882_at	AW527138	Follistatin-like 4 (predicted)	Fstl4_predicted	1.667	0.739	1.052	0.941	1.580	0.076	1.881	0.997
1381272_at	BE120246	Follistatin-like 4 (predicted)	Fstl4_predicted	0.898	0.814	1.106	0.199	0.935	0.626	1.316	0.478
1368711_at	NM_012743	forkhead box A2	Foxa2	1.283	0.300	1.068	0.215	0.743	0.012	1.241	0.072
1374969_at	AA799832	forkhead box D4	Foxd4	0.657	0.244	0.455	0.005	0.612	0.008	0.542	0.026
1377347_at	AW531892	Forkhead box J3 (predicted)	Foxj3_predicted	0.610	0.335	2.464	0.005	0.798	0.172	2.148	0.004
1396965_at	BF406350	Forkhead box O1A	Foxo1a	0.846	0.443	0.690	0.095	1.281	0.013	0.912	0.276
1394691_at	AA924778	forkhead box P1	Foxp1	0.732	0.043	0.996	0.297	1.434	0.932	1.006	0.983
1373804_at	AI230954	forkhead box P1	Foxp1	0.759	0.581	1.056	0.192	1.655	0.523	1.305	0.381
1378495_at	BF414427	Forkhead box P1	Foxp1	1.143	0.604	0.997	0.997	0.958	0.890	1.005	0.985
1393676_at	BE106495	Forkhead box P1	Foxp1	1.057	0.749	0.636	0.051	1.134	0.451	0.628	0.129
1398075_at	BF418304	Forkhead box P1	Foxp1	1.006	0.985	1.000	0.994	1.010	0.976	1.009	0.628
1378793_at	BE121233	Forkhead box P4 (predicted)	Foxp4_predicted	1.173	0.030	1.754	0.640	1.393	0.165	1.262	0.471
1398402_at	AW144081	forkhead box P4 (predicted)	Foxp4_predicted	2.302	0.107	1.253	0.216	2.481	0.043	1.053	0.077
1385464_at	AI070944	Forkhead box Q1	Foxq1	2.987	0.003	3.259	0.001	2.844	0.040	3.141	0.003
1368550_at	NM_022858	forkhead box Q1 /// hypothetical gene supported by NM_022858	Foxq1 /// LOC497713	2.054	0.007	1.813	0.006	2.261	0.028	2.243	0.002
1376589_at	BG380345	forkhead box R1 (predicted)	Foxr1_predicted	0.685	0.321	1.378	0.001	0.657	0.012	1.288	0.025
1376992_a_at	AI058900	forkhead box R1 (predicted)	Foxr1_predicted	0.785	0.483	0.728	0.022	1.077	0.983	0.745	0.015
1377258_at	BE107204	Forkhead box R1 (predicted)	Foxr1_predicted	1.130	0.970	0.648	0.273	1.048	0.840	0.917	0.846
1373537_at	BE113175	Formin binding protein 1	Fnbp1	1.592	0.072	0.986	0.868	2.173	0.068	1.101	0.998
1388684_at	BI274480	formin binding protein 4	Fnbp4	2.294	0.009	2.708	0.002	2.460	0.014	2.577	0.001
1376470_at	BG372703	formin binding protein 4	Fnbp4	1.269	0.311	0.847	0.093	2.511	0.067	1.034	0.962
1397517_at	BF404640	formin binding protein 4	Fnbp4	0.737	0.398	1.044	0.713	0.506	0.990	1.661	0.061
1384945_at	AI501447	forty-two-three domain containing 1	Fyttd1	0.767	0.334	1.167	0.312	0.674	0.816	0.808	0.175
1383098_at	BG667845	forty-two-three domain containing 1	Fyttd1	0.979	0.804	0.641	0.005	0.958	0.816	0.446	0.002
1368489_at	NM_012953	fos-like antigen 1	Fosl1	2.168	0.001	1.380	0.200	1.156	0.294	1.249	0.244

1372107_at	BG673187	four and a half LIM domains 1	Fhl1	1.043	0.672	0.944	0.157	1.047	0.377	0.859	0.164
1369313_at	NM_031677	four and a half LIM domains 2	Fhl2	15.199	0.047	19.798	0.005	1.677	0.228	1.458	0.085
1382267_at	BF390450	four jointed box 1 (Drosophila) (predicted)	Fjx1_predicted	1.201	0.165	1.001	0.981	1.218	0.425	1.148	0.175
1368977_a_at	AF061242	fractured callus expressed transcript 1	Fxc1	0.664	0.000	0.500	0.037	0.701	0.002	0.691	0.056
1393734_at	AA997025	Fractured callus expressed transcript 1	Fxc1	0.412	0.018	0.780	0.057	0.431	0.034	0.999	0.735
1383236_at	BE118678	fragile X mental retardation gene 1, autosomal homolog	Fxr1h	0.966	0.929	1.899	0.011	0.922	0.784	2.229	0.054
1378054_at	BE108397	fragile X mental retardation gene 1, autosomal homolog	Fxr1h	0.901	0.953	1.758	0.089	0.725	0.073	1.397	0.015
1373435_at	BG373419	fragile X mental retardation gene 2, autosomal homolog (predicted)	Fxr2h_predicted	1.097	0.411	2.068	0.011	0.851	0.726	1.670	0.023
1394707_at	AW533764	Fragile X mental retardation gene 2, autosomal homolog (predicted)	Fxr2h_predicted	1.015	0.971	0.960	0.966	1.176	0.517	0.979	0.914
1393459_at	AI705393	fragile X mental retardation syndrome 1 homolog	Fmr1	1.233	0.315	1.078	0.470	1.478	0.014	1.461	0.135
1387685_at	NM_024366	frequenin homolog (Drosophila)	Freq	1.409	0.983	1.069	0.680	1.029	0.963	1.099	0.276
1390914_at	AI071474	Friend leukemia integration 1	Fli1	0.966	0.899	0.997	0.954	0.971	0.928	0.992	0.053
1388994_at	AW917849	Frizzled homolog 6 (Drosophila)	Fzd6	0.937	0.399	0.471	0.001	0.905	0.278	0.638	0.009
1375961_at	AI072892	frizzled-related protein	Frzb	0.446	0.001	0.199	0.001	0.555	0.002	0.201	0.042
1373615_at	BM391538	frizzled-related protein	Frzb	0.669	0.373	0.219	0.101	0.423	0.030	0.180	0.063
1368077_at	NM_012558	fructose-1,6- biphosphatase 1	Fbp1	1.096	0.953	1.000	0.970	4.089	0.003	1.061	0.749
1385601_at	BE115019	FSHD region gene 1 (predicted)	Frg1_predicted	0.732	0.563	0.791	0.241	0.674	0.064	1.039	0.621
1393914_at	AI709526	Ftsj homolog 1 (E. coli) (predicted)	Ftsj1_predicted	1.004	0.842	0.652	0.038	1.001	0.968	0.662	0.141
1376512_at	BI290160	FtsJ homolog 2 (E. coli) (predicted)	Ftsj2_predicted	0.353	0.020	0.993	0.928	0.480	0.012	1.000	0.993
1374288_at	BG374267	FtsJ homolog 3 (E. coli)	Ftsj3	0.511	0.028	1.303	0.182	0.761	0.103	1.316	0.270
1376753_at	BE105571	Fucose-1-phosphate guanylyltransferase	Fpgt	0.777	0.420	0.600	0.012	0.880	0.037	0.689	0.078
1392351_at	BI288242	fucose-1-phosphate guanylyltransferase	Fpgt	0.903	0.628	1.652	0.029	1.374	0.759	0.999	0.897
1367737_at	NM_012562	fucosidase, alpha-L- 1, tissue	Fuca	0.570	0.344	0.277	0.000	0.656	0.013	0.388	0.010
1376249_at	BM389993	fucosidase, alpha-L- 2, plasma	Fuca2	0.452	0.043	0.345	0.012	0.447	0.019	0.343	0.001
1368709_at	NM_031236	fucosyltransferase 1	Fut1	0.597	0.663	0.405	0.019	0.285	0.019	0.492	0.027
1387097_at	NM_031635	fucosyltransferase 2 (secretor status included)	Fut2	0.772	0.117	0.835	0.076	0.978	0.253	1.072	0.986
1388643_at	AI177839	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	Fut8	0.972	0.550	0.991	0.927	0.967	0.265	0.793	0.312
1379263_at	AW251362	fukutin related protein	Fkrp	0.314	0.039	0.448	0.007	0.715	0.014	0.453	0.079
1375872_at	AI144944	Fukuyama type congenital muscular dystrophy homolog (human) (predicted)	Fcmd_predicted	0.592	0.069	0.690	0.010	0.486	0.013	0.691	0.046
1375785_at	AI101490	Fukuyama type congenital muscular dystrophy homolog (human) (predicted)	Fcmd_predicted	0.658	0.403	0.676	0.180	0.502	0.027	0.619	0.292
1367670_at	NM_017005	fumarate hydratase 1	Fh1	0.341	0.010	0.639	0.010	0.578	0.017	0.768	0.004
1368092_at	NM_017181	fumarylacetoacetate hydrolase	Fah	0.256	0.033	0.407	0.121	0.607	0.128	0.684	0.100
1372676_at	BI275774	fumarylacetoacetate hydrolase domain containing 1	Fahd1	0.352	0.003	0.551	0.001	0.301	0.035	1.091	0.768
1373134_at	BE329450	fumarylacetoacetate hydrolase domain containing 2A (predicted)	Fahd2a_predicted	0.391	0.025	0.312	0.002	0.269	0.017	0.484	0.027
1373956_at	BF284313	FUN14 domain containing 1	Fundc1	0.875	0.946	0.396	0.016	0.936	0.672	0.846	0.043
1380269_at	AA859619	FUS interacting protein (serine-arginine rich) 1	Fusip1	0.627	0.071	1.154	0.373	0.649	0.244	0.961	0.442
1383703_at	BE109151	FUS interacting protein (serine-arginine rich) 1	Fusip1	0.700	0.194	0.809	0.100	0.800	0.088	0.666	0.049
1393946_at	BG377118	FUS interacting protein (serine-arginine rich) 1	Fusip1	0.748	0.484	1.591	0.742	0.686	0.020	1.369	0.848
1382052_at	BF284373	FUS interacting protein (serine-arginine rich) 1	Fusip1	0.684	0.915	1.126	0.109	1.025	0.907	1.126	0.061
1385103_at	BF390999	fused toes	Fts	0.523	0.051	0.770	0.902	0.467	0.135	0.946	0.797
1373837_at	BI296633	fused toes	Fts	0.692	0.076	0.884	0.470	0.632	0.104	0.935	0.466
1375689_at	BI300470	Fusion, derived from t(12;16) malignant liposarcoma (human)	Fus	1.698	0.030	1.180	0.117	1.526	0.108	1.070	0.539
1373195_at	AW532485	fusion, derived from t(12;16) malignant liposarcoma (human)	Fus	1.072	0.634	1.260	0.132	1.069	0.996	1.212	0.102
1370248_at	AA851939	FXYD domain-containing ion transport regulator 6	Fxyd6	0.524	0.171	0.073	0.000	0.521	0.067	0.092	0.026
1373683_at	AI230396	fyn proto-oncogene	Fyn	0.841	0.299	1.603	0.707	0.860	0.642	1.929	0.037
1369156_at	NM_024368	fyn-related kinase	Frk	4.715	0.022	1.388	0.047	1.337	0.366	1.007	0.239
1379434_at	BE100206	FYVE, RhoGEF and PH domain containing 1	Fgd1	0.848	0.122	1.933	0.012	0.776	0.088	1.651	0.020
1376042_at	BF284673	FYVE, RhoGEF and PH domain containing 1	Fgd1	0.699	0.128	0.276	0.002	0.574	0.069	0.522	0.001
1367756_at	NM_053625	G elongation factor	Gfm	0.433	0.085	0.663	0.046	0.461	0.025	0.636	0.109
1379909_at	AA963315	G kinase anchoring protein 1	Gkap1	1.114	0.887	1.043	0.919	0.989	0.872	0.987	0.574
1397234_at	AI598507	G patch domain containing 1 (predicted)	Gpatc1_predicted	1.078	0.010	1.141	0.979	1.945	0.117	0.989	0.698
1377436_at	BE108338	G patch domain containing 1 (predicted)	Gpatc1_predicted	1.157	0.584	1.048	0.589	1.350	0.756	1.431	0.141
1390930_at	BF406924	G patch domain containing 2	Gpatc2	2.485	0.032	2.891	0.006	3.073	0.043	2.481	0.001
1367963_at	NM_022404	G protein beta subunit-like	Gbl	0.318	0.075	1.014	0.886	1.139	0.113	0.906	0.620
1398783_at	NM_053969	G protein pathway suppressor 1	Gps1	0.501	0.176	0.728	0.085	0.529	0.000	0.836	0.303
1373170_at	BI294756	G protein pathway suppressor 2 (predicted)	Gps2_predicted	0.930	0.362	2.098	0.043	0.771	0.710	1.184	0.172
1379956_at	AI013395	G protein-coupled receptor 107 (predicted)	Gpr107_predicted	0.985	0.812	0.768	0.105	1.056	0.315	1.005	0.996
1389188_at	BE111778	G protein-coupled receptor 108	Gpr108	0.900	0.061	0.989	0.451	1.082	0.423	1.041	0.201
1388109_at	BI290677	G protein-coupled receptor 116	Gpr116	1.005	0.998	0.703	0.105	1.105	0.069	0.766	0.124
1393148_at	BF542593	G protein-coupled receptor 137B (predicted)	Gpr137b_predicted	0.461	0.158	1.789	0.084	0.183	0.046	2.527	0.155
1384747_at	BF404188	G protein-coupled receptor 137B (predicted)	Gpr137b_predicted	0.890	0.491	0.872	0.417	1.008	0.578	0.815	0.983

1397460_at	BE119491	G protein-coupled receptor 158 (predicted)	Gpr158_predicted	0.966	0.894	1.100	0.226	1.054	0.743	1.048	0.320
1382739_at	AI045718	G protein-coupled receptor 19	Gpr19	4.260	0.019	8.113	0.000	6.004	0.000	8.436	0.000
1397425_at	AI172341	G protein-coupled receptor 21 (predicted)	Gpr21_predicted	1.233	0.338	1.222	0.539	1.354	0.763	0.931	0.312
1388004_at	AF087947	G protein-coupled receptor 37-like 1	Gpr37l1	1.183	0.288	2.009	0.103	1.037	0.981	1.026	0.203
1374934_at	BF405151	G protein-coupled receptor 39	Gpr39	0.502	0.320	1.010	0.545	0.727	0.161	0.966	0.927
1371696_at	AI412938	G protein-coupled receptor 56	Gpr56	1.093	0.387	2.299	0.006	0.651	0.121	1.640	0.016
1369792_at	U12006	G protein-coupled receptor 6	Gpr6	0.135	0.002	0.087	0.000	0.122	0.001	0.059	0.014
1387666_at	AF203907	G protein-coupled receptor 85	Gpr85	1.075	0.147	1.076	0.805	0.597	0.130	0.984	0.609
1372313_at	BI275972	G protein-coupled receptor 89 (predicted)	Gpr89_predicted	0.383	0.222	0.479	0.009	0.466	0.012	0.430	0.008
1387148_at	NM_134386	G protein-coupled receptor associated sorting protein 1	Gprasp1	0.426	0.027	0.569	0.043	0.447	0.062	0.574	0.009
1368408_at	NM_030829	G protein-coupled receptor kinase 5	Gprk5	1.995	0.030	1.510	0.094	2.569	0.015	1.039	0.884
1393987_s_at	BI274742	G protein-coupled receptor kinase 6	Gprk6	1.392	0.057	1.708	0.139	1.932	0.032	1.474	0.037
1368647_at	NM_031657	G protein-coupled receptor kinase 6	Gprk6	1.756	0.120	1.957	0.275	1.139	0.674	1.137	0.835
1370015_at	NM_031814	G protein-coupled receptor kinase interactor 1	Git1	1.412	0.190	1.523	0.081	0.865	0.433	1.476	0.045
1396596_at	BF402645	G protein-coupled receptor kinase-interactor 2	Git2	1.574	0.046	1.196	0.557	1.231	0.619	0.634	0.108
1389315_at	AI408598	G protein-coupled receptor kinase-interactor 2	Git2	1.024	0.495	1.598	0.048	1.721	0.829	1.128	0.113
1371671_at	AI228513	G protein-coupled receptor, family C, group 5, member B (predicted)	Gprc5b_predicted	0.700	0.256	1.718	0.016	0.759	0.227	1.595	0.029
1373693_at	BF414143	G protein-coupled receptor, family C, group 5, member C	Gprc5c	1.016	0.850	1.001	0.288	0.832	0.029	0.999	0.963
1388395_at	AI406939	G0/G1 switch gene 2	G0s2	6.744	0.008	5.911	0.013	1.976	0.375	2.705	0.039
1371585_at	BE108192	G1 to S phase transition 1	Gspt1	1.198	0.025	1.185	0.444	1.006	0.407	1.224	0.239
1394732_at	BF289237	G1 to S phase transition 1	Gspt1	1.342	0.618	1.323	0.174	1.112	0.349	1.116	0.120
1376890_at	BE117326	G4 protein	G4	1.004	0.873	0.969	0.566	0.913	0.936	1.000	0.423
1380170_at	BI303388	GABA(A) receptor-associated protein like 2	Gabarapl2	1.563	0.250	0.470	0.006	1.114	0.360	0.365	0.016
1367783_at	NM_022706	GABA(A) receptor-associated protein like 2	Gabarapl2	1.055	0.333	0.979	0.248	1.176	0.014	1.015	0.567
1368074_at	NM_080783	galactose-4-epimerase, UDP	Gale	0.994	0.997	0.999	0.694	0.998	0.988	1.002	0.261
1382063_at	BM385090	galactosidase, alpha (mapped)	Gla_mapped	0.689	0.269	0.795	0.080	0.909	0.099	0.791	0.151
1376781_at	BI286116	Galactosidase, beta 1 (mapped)	Glb1_mapped	0.463	0.037	0.679	0.034	0.651	0.305	0.947	0.208
1387088_at	NM_033237	galanin	Gal	1.124	0.284	1.010	0.997	1.390	0.126	0.889	0.997
1387702_at	U30290	galanin receptor 1	Galr1	0.414	0.000	0.769	0.042	0.417	0.001	0.475	0.041
1378772_at	BF403919	Gamma-aminobutyric acid (GABA) A receptor, subunit gamma 3	Gabrg3	1.000	0.989	0.998	0.977	1.002	0.947	1.001	0.966
1388039_a_at	AF283276	gamma-aminobutyric acid (GABA) B receptor 1	Gabbr1	0.816	0.508	0.517	0.065	1.040	0.806	0.554	0.011
1375720_at	AI171785	Gamma-aminobutyric acid (GABA) B receptor 1	Gabbr1	0.776	0.997	0.566	0.004	0.734	0.209	0.646	0.006
1387383_at	NM_031802	gamma-aminobutyric acid (GABA) B receptor 2	Gabbr2	0.335	0.028	0.303	0.002	0.500	0.018	0.414	0.031
1369904_at	NM_012956	gamma-aminobutyric acid (GABA-A) receptor, subunit beta 1	Gabrb1	0.851	0.528	0.520	0.004	0.870	0.656	0.518	0.010
1380828_at	AI145413	gamma-aminobutyric acid A receptor, alpha 1	Gabra1	0.961	0.325	1.052	0.853	0.646	0.777	1.047	0.601
1370804_at	AF161588	gamma-aminobutyric acid receptor associated protein	Gabarap	0.660	0.522	1.094	0.521	0.543	0.111	0.962	0.288
1368314_at	NM_031756	gamma-glutamyl carboxylase	Ggcx	0.637	0.080	0.459	0.006	0.631	0.040	0.524	0.007
1368470_at	NM_012960	gamma-glutamyl hydrolase	Ggh	0.663	0.411	0.403	0.001	0.637	0.018	0.388	0.001
1368307_at	NM_130423	gamma-glutamyltransferase-like 3	Ggtl3	0.687	0.191	0.460	0.021	0.798	0.711	0.551	0.005
1382498_x_at	BF408710	ganglioside-induced differentiation-associated protein 1-like 1 (predicted)	Gdap1l1_predicted	2.317	0.041	1.042	0.484	1.344	0.515	0.956	0.471
1379377_at	BG371655	ganglioside-induced differentiation-associated-protein 2	Gdap2	1.794	0.051	1.614	0.022	1.941	0.013	1.252	0.021
1372002_at	AI411352	gap junction membrane channel protein alpha 1	Gja1	0.934	0.700	0.866	0.335	0.568	0.615	1.157	0.986
1368473_at	NM_019280	gap junction membrane channel protein alpha 5	Gja5	0.850	0.320	1.142	0.868	0.985	0.578	0.986	0.973
1369796_at	NM_019281	gap junction membrane channel protein alpha 9	Gja9	1.583	0.360	0.498	0.080	1.188	0.583	0.553	0.060
1373386_at	AI179953	gap junction membrane channel protein beta 2	Gjb2	5.658	0.041	3.228	0.073	4.585	0.051	2.273	0.186
1368481_at	NM_012714	gastric inhibitory polypeptide receptor	Gipr	0.554	0.005	0.138	0.001	0.637	0.046	0.124	0.015
1382163_at	BE118901	GATA binding protein 3	Gata3	1.004	0.985	1.082	0.735	1.207	0.334	1.069	0.689
1375613_at	AW525075	GATA binding protein 6	Gata6	1.179	0.529	1.003	0.985	1.077	0.028	1.001	0.903
1372073_at	AI008814	GATA zinc finger domain containing 2A	Gatad2a	1.185	0.010	2.108	0.010	0.900	0.395	1.506	0.048
1392552_at	BE109744	GATA zinc finger domain containing 2B	Gatad2b	1.862	0.045	2.478	0.003	0.848	0.009	1.621	0.028
1374945_at	BI281827	GCD14/PCMT domain containing protein RGD1359191	RGD1359191	0.463	0.003	1.391	0.086	0.423	0.000	2.402	0.058
1375288_at	BI299737	GCN1 general control of amino-acid synthesis 1-like 1 (yeast) (predicted)	Gcn1l1_predicted	0.996	0.945	0.718	0.152	0.994	0.963	0.720	0.153
1367460_at	BM387347	GDP dissociation inhibitor 2	Gdi2	0.822	0.159	0.952	0.014	0.814	0.001	0.974	0.120
1398822_at	NM_017276	GDP dissociation inhibitor 2	Gdi2	0.497	0.880	0.627	0.144	0.426	0.597	0.523	0.007
1393713_at	BM389780	GDP-mannose 4, 6-dehydratase	Gmds	0.673	0.716	0.730	0.381	0.560	0.135	0.723	0.057
1372859_at	AI598958	GDP-mannose pyrophosphorylase A	Gmppa	0.878	0.429	0.581	0.020	1.054	0.547	0.586	0.006
1392701_at	BI285572	GDP-mannose pyrophosphorylase B (predicted)	Gmppb_predicted	0.503	0.030	1.420	0.030	0.552	0.045	0.998	0.987
1371414_at	BI285576	gelsolin	Gsn	1.042	0.941	0.919	0.895	1.041	0.970	0.978	0.709
1382216_at	BF283004	gem (nuclear organelle) associated protein 6	Gemin6	0.801	0.027	2.332	0.023	0.750	0.022	1.053	0.170
1392700_at	AA900604	Geminin (predicted)	Gmnn_predicted	0.665	0.090	1.319	0.116	0.797	0.004	0.996	0.987
1384070_at	BF544982	Gem-interacting protein (predicted)	Gmip_predicted	0.728	0.718	0.852	0.061	0.775	0.839	0.918	0.106

1388032_a_at	D87927	gene model 1960, (NCBI)	Gm1960	3.312	0.005	2.958	0.008	1.034	0.999	0.999	0.823
1370633_at	D87927	gene model 1960, (NCBI)	Gm1960	7.260	0.049	4.231	0.006	1.105	0.998	1.027	0.947
1371524_at	AI009608	gene trap locus 3	Gtl3	0.623	0.720	0.807	0.090	0.609	0.027	1.000	0.241
1369548_at	NM_022208	general transcription factor 2a, 1	Gtf2a1	0.791	0.311	0.742	0.554	0.778	0.271	0.603	0.341
1399114_at	AA996974	general transcription factor II E, polypeptide 2 (beta subunit) (predicted)	Gtf2e2_predicted	0.849	0.583	1.437	0.076	1.114	0.167	1.116	0.092
1373094_at	AW917124	general transcription factor II H, polypeptide 1 (predicted)	Gtf2h1_predicted	1.112	0.812	2.875	0.001	0.829	0.246	1.694	0.001
1382030_at	BF398500	general transcription factor II H, polypeptide 2 (predicted)	Gtf2h2_predicted	1.047	0.740	0.819	0.508	1.331	0.141	0.725	0.070
1385803_at	BM388555	general transcription factor II H, polypeptide 2 (predicted)	Gtf2h2_predicted	1.001	0.763	1.151	0.353	1.003	0.965	0.967	0.854
1395837_at	BE119517	General transcription factor II H, polypeptide 2 (predicted)	Gtf2h2_predicted	0.998	0.998	1.173	0.913	1.175	0.243	0.942	0.348
1385517_at	AI715835	general transcription factor II I	Gtf2i	0.914	0.040	0.688	0.010	0.903	0.288	0.689	0.044
1371931_at	BI274753	general transcription factor II I	Gtf2i	0.390	0.085	0.333	0.000	0.391	0.040	0.461	0.022
1379550_a_at	BF290483	general transcription factor II I repeat domain-containing 1	Gtf2ird1	1.380	0.082	1.692	0.013	1.208	0.375	1.404	0.000
1387775_at	NM_053345	general transcription factor IIa 2	Gtf2a2	0.837	0.315	0.993	0.941	0.863	0.096	0.992	0.427
1368220_at	NM_031041	general transcription factor IIB	Gtf2b	0.562	0.552	0.413	0.021	0.794	0.189	0.509	0.013
1393106_x_at	BF420770	general transcription factor IIF, polypeptide 1	Gtf2f1	0.522	0.037	0.678	0.004	0.321	0.007	0.376	0.057
1383627_a_at	BF420770	general transcription factor IIF, polypeptide 1	Gtf2f1	0.659	0.132	0.813	0.058	0.373	0.074	0.600	0.011
1368233_at	NM_031042	general transcription factor IIF, polypeptide 2	Gtf2f2	0.566	0.230	1.395	0.229	0.681	0.277	1.465	0.119
1372415_at	BM385649	general transcription factor IIH, polypeptide 3	Gtf2h3	0.652	0.010	0.455	0.010	0.830	0.392	0.498	0.004
1371035_at	BE098763	general transcription factor III A	Gtf3a	0.872	0.045	1.815	0.006	0.712	0.092	1.190	0.073
1370231_at	AI234022	general transcription factor III C 1	Gtf3c1	0.556	0.287	0.516	0.013	0.636	0.093	0.289	0.050
1395486_at	BF413851	general transcription factor III C 1	Gtf3c1	1.106	0.862	3.768	0.000	0.908	0.184	1.379	0.030
1389574_at	AI014004	general transcription factor IIIC, polypeptide 2, beta 110kDa	Gtf3c2	0.837	0.296	0.796	0.300	0.814	0.456	0.880	0.138
1368117_at	NM_022865	gephyrin	Gphn	1.428	0.143	0.956	0.317	1.301	0.141	1.063	0.553
1379556_a_at	AI105210	geranylgeranyl diphosphate synthase 1	Ggps1	1.536	0.001	1.097	0.099	0.968	0.551	1.120	0.056
1386215_at	AI101566	geranylgeranyl diphosphate synthase 1	Ggps1	0.952	0.629	0.447	0.009	1.715	0.002	1.104	0.428
1375960_at	BF281879	germ cell-less homolog 1 (Drosophila)	Gmcl1	0.462	0.003	0.452	0.014	0.562	0.008	0.617	0.050
1372726_at	AI176792	germinal histone H4 gene	Hist1h4b	0.849	0.302	0.911	0.078	0.847	0.061	1.028	0.455
1374600_at	BM986536	germinal histone H4 gene	Hist1h4b	1.185	0.399	1.008	0.982	1.091	0.449	1.002	0.888
1379654_at	AA946433	GIY-YIG domain containing 2	Giyd2	0.931	0.988	1.188	0.739	1.020	0.991	1.089	0.046
1393357_at	AW253109	GLE1 RNA export mediator-like (yeast)	Gle1l	1.315	0.109	1.251	0.009	2.074	0.059	1.570	0.005
1373504_at	BF287967	GLI pathogenesis-related 1 (glioma)	Glipr1	0.996	0.913	0.982	0.750	0.986	0.380	1.004	0.984
1387663_at	NM_031032	glia maturation factor, beta	Gmfb	2.211	0.108	9.924	0.001	1.409	0.513	9.605	0.001
1373490_at	BG666787	glia maturation factor, gamma	Gmfg	1.628	0.158	2.172	0.081	0.725	0.251	1.907	0.122
1382077_at	BF388974	GLI-Kruppel family member GLI3	Gli3	1.443	0.760	0.900	0.259	0.855	0.762	0.729	0.128
1374234_at	AI073183	GLI-Kruppel family member HKR3	Hkr3	0.940	0.762	0.999	0.199	0.943	0.891	1.000	0.503
1371471_at	BF281741	glioma tumor suppressor candidate region gene 2	Gltscr2	0.827	0.491	1.425	0.010	1.028	0.116	1.183	0.303
1369888_at	NM_012707	glucagon	Gcg	0.711	0.086	0.095	0.000	0.767	0.011	0.165	0.005
1370522_at	L04796	glucagon receptor	Gcgr	2.690	0.016	2.105	0.081	2.060	0.046	0.887	0.244
1369699_at	NM_012728	glucagon-like peptide 1 receptor	Glp1r	0.472	0.131	0.315	0.007	0.964	0.186	0.392	0.019
1389265_at	BI284270	glucan (1,4-alpha-), branching enzyme 1	Gbe1	0.584	0.255	1.749	0.034	0.907	0.669	1.666	0.004
1388067_a_at	AF205779	glucocorticoid modulatory element binding protein 2	Gmeb2	1.404	0.025	2.606	0.004	1.700	0.002	1.896	0.000
1387312_a_at	NM_012565	glucokinase	Gck	0.196	0.001	0.222	0.007	0.322	0.082	0.236	0.017
1371894_at	AI409037	glucosamine (N-acetyl)-6-sulfatase	Gns	1.105	0.022	1.389	0.001	1.314	0.028	1.690	0.006
1394614_at	BI290687	glucosamine (N-acetyl)-6-sulfatase	Gns	1.959	0.065	2.658	0.156	0.646	0.062	1.775	0.320
1395265_at	BF419323	glucosamine (N-acetyl)-6-sulfatase	Gns	1.201	0.608	1.122	0.259	1.015	0.487	1.497	0.020
1373669_at	BG374650	glucosamine-6-phosphate deaminase 2 (predicted)	Gnpda2_predicted	3.529	0.000	1.890	0.001	4.136	0.000	2.406	0.002
1368770_at	NM_022276	glucosaminyl (N-acetyl) transferase 1, core 2	Gcnt1	1.298	0.852	1.274	0.576	1.196	0.690	0.820	0.379
1374903_at	AI234819	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme /// hypothetical gene supported by NM_001001511	Gcnt2 /// LOC497712	6.625	0.002	0.562	0.005	5.039	0.007	0.606	0.022
1371561_at	AA849522	glucose 6 phosphatase, catalytic, 3	G6pc3	1.087	0.601	1.278	0.051	1.156	0.034	1.235	0.015
1371392_at	BI283882	glucose phosphate isomerase	Gpi	0.427	0.211	1.045	0.035	0.515	0.003	1.037	0.832
1367856_at	NM_017006	glucose-6-phosphate dehydrogenase X-linked	G6pdx	0.638	0.010	1.322	0.143	0.699	0.016	1.102	0.031
1367991_at	NM_031749	glucosidase 1	Gcs1	0.561	0.097	0.783	0.045	0.316	0.006	0.895	0.088
1399040_at	AI178644	glucosidase beta 2	Gba2	0.668	0.912	0.404	0.330	0.904	0.604	0.194	0.037
1371799_at	AI175438	glucosidase, alpha, acid	Gaa	0.757	0.476	0.728	0.052	0.549	0.021	0.737	0.066
1378239_at	BF404337	glucosidase, alpha, acid	Gaa	0.999	0.966	0.821	0.949	0.728	0.087	0.845	0.384
1367901_at	NM_017015	glucuronidase, beta	Gusb	0.370	0.002	0.257	0.004	0.574	0.035	0.488	0.014
1380590_at	BE115496	Glucuronidase, beta	Gusb	1.341	0.030	2.173	0.009	1.336	0.050	1.581	0.051
1373139_at	AI012608	Glucuronidase, beta	Gusb	0.682	0.273	0.833	0.089	0.710	0.031	0.699	0.132
1370030_at	NM_017305	glutamate cysteine ligase, modifier subunit	Gclm	0.795	0.947	2.298	0.006	0.825	0.345	2.215	0.005
1370200_at	BI284411	glutamate dehydrogenase 1	Glud1	0.318	0.033	0.256	0.000	0.238	0.001	0.313	0.007
1387878_at	AW916644	glutamate dehydrogenase 1	Glud1	0.380	0.058	0.451	0.000	0.264	0.005	0.427	0.001

1368272_at	D00252	glutamate oxaloacetate transaminase 1	Got1	0.523	0.153	0.912	0.521	0.818	0.180	1.091	0.638
1389871_at	BI296539	glutamate oxaloacetate transaminase 2, mitochondrial	Got2	1.011	0.532	1.077	0.791	1.698	0.111	1.071	0.874
1367819_at	NM_013177	glutamate oxaloacetate transaminase 2, mitochondrial	Got2	0.833	0.973	1.138	0.145	0.771	0.272	1.318	0.089
1380327_at	AI408747	Glutamate receptor interacting protein 1	Grip1	1.146	0.085	0.586	0.370	1.981	0.002	0.785	0.118
1369343_at	NM_032069	glutamate receptor interacting protein 1	Grip1	1.018	0.942	0.818	0.049	0.996	0.932	0.825	0.060
1377546_at	BF397279	Glutamate receptor, ionotropic, 4	Gria4	1.460	0.583	1.913	0.863	0.962	0.108	1.314	0.422
1387171_at	NM_017261	glutamate receptor, ionotropic, AMPA2	Gria2	0.368	0.007	0.060	0.007	0.343	0.012	0.146	0.028
1394578_at	BI299761	Glutamate receptor, ionotropic, AMPA2	Gria2	0.459	0.064	0.272	0.005	0.660	0.284	0.439	0.006
1368401_at	M85035	glutamate receptor, ionotropic, AMPA2	Gria2	0.477	0.065	0.201	0.001	0.551	0.001	0.385	0.019
1393995_at	AW534561	Glutamate receptor, ionotropic, AMPA2	Gria2	0.932	0.406	0.298	0.031	0.632	0.067	0.524	0.020
1392248_at	AI145008	Glutamate receptor, ionotropic, delta 1	Grid1	0.518	0.024	0.971	0.788	1.358	0.361	0.987	1.000
1375783_at	BF404569	Glutamate receptor, ionotropic, kainate 5	Grik5	1.034	0.737	1.038	0.872	1.381	0.246	1.033	0.894
1368306_at	U08259	glutamate receptor, ionotropic, NMDA2C	Grin2c	0.816	0.245	1.249	0.211	0.591	0.174	0.801	0.314
1372724_at	BI284904	glutamate receptor, ionotropic, N-methyl D-asparate-associated protein 1 (glutamate binding)	Grina	2.152	0.229	2.205	0.005	2.398	0.003	2.773	0.001
1374267_at	BG378154	Glutamate receptor, ionotropic, N-methyl D-asparate-associated protein 1 (glutamate binding)	Grina	1.283	0.518	1.037	0.917	1.297	0.712	0.996	0.931
1398889_at	BE113383	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	Grinl1a	0.720	0.111	1.212	0.028	0.695	0.022	1.183	0.042
1371051_at	BG664035	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	Grinl1a	0.899	0.705	1.326	0.180	0.518	0.932	1.083	0.923
1387286_at	NM_017011	glutamate receptor, metabotropic 1	Grm1	1.106	0.909	1.001	0.841	0.996	0.949	1.114	0.205
1367633_at	BI296610	glutamate-ammonia ligase (glutamine synthase)	Glul	2.445	0.008	1.299	0.589	0.798	0.845	0.852	0.255
1367632_at	NM_017073	glutamate-ammonia ligase (glutamine synthase)	Glul	1.247	0.102	0.464	0.003	1.202	0.139	0.509	0.002
1386870_at	BI275294	glutamate-ammonia ligase (glutamine synthase)	Glul	1.706	0.125	1.601	0.088	1.198	0.815	0.805	0.289
1375569_at	BM386267	glutamate-ammonia ligase (glutamine synthase)	Glul	0.907	0.193	0.949	0.588	1.091	0.737	0.975	0.276
1389426_at	AW528806	glutamate-ammonia ligase (glutamine synthase)	Glul	0.812	0.927	0.744	0.040	0.695	0.236	0.716	0.078
1372523_at	AA892770	glutamate-cysteine ligase, catalytic subunit	Gclc	0.974	0.938	3.399	0.001	0.840	0.398	2.332	0.003
1374569_at	BF419158	glutamate-rich WD repeat containing 1	Grwd1	0.858	0.558	3.995	0.051	0.859	0.256	2.400	0.138
1368344_at	NM_017007	glutamic acid decarboxylase 1	Gad1	0.466	0.002	0.610	0.003	0.678	0.016	0.671	0.075
1370760_a_at	M38350	glutamic acid decarboxylase 1	Gad1	0.471	0.170	1.667	0.803	0.456	0.157	1.295	0.423
1369462_at	NM_012563	glutamic acid decarboxylase 2	Gad2	0.489	0.339	0.122	0.016	0.435	0.022	0.190	0.010
1382232_at	AI454322	Glutamic pyruvate transaminase (alanine aminotransferase) 2 (predicted)	Gpt2_predicted	0.792	0.378	0.715	0.102	0.419	0.044	0.544	0.015
1384903_at	AI535168	glutamic pyruvate transaminase (alanine aminotransferase) 2 (predicted)	Gpt2_predicted	1.005	0.994	1.021	0.977	1.012	0.636	0.997	0.827
1382521_at	AA925755	glutaminase	Gls	1.289	0.139	0.706	0.047	1.840	0.111	0.743	0.029
1367805_at	NM_012569	glutaminase	Gls	0.756	0.362	0.373	0.003	0.998	0.991	0.293	0.001
1370375_at	J05499	glutaminase 2 (liver, mitochondrial)	Gls2	0.281	0.099	0.336	0.012	0.282	0.101	0.357	0.011
1393735_at	AI712582	Glutamine and serine rich 1 (predicted)	Qser1_predicted	1.721	0.017	1.178	0.299	2.934	0.008	2.251	0.059
1380179_at	AI548649	Glutamine and serine rich 1 (predicted)	Qser1_predicted	1.199	0.493	2.012	0.091	0.774	0.071	1.007	0.916
1389254_at	AA800519	Glutamine and serine rich 1 (predicted)	Qser1_predicted	0.956	0.710	0.520	0.005	0.936	0.525	0.668	0.008
1396831_at	AI501417	Glutamine repeat protein 1 (predicted)	Glrp1_predicted	1.040	0.408	0.822	0.486	0.793	0.162	1.025	0.939
1377761_at	BI296057	glutamine-fructose-6-phosphate transaminase 2	Gfpt2	6.511	0.001	1.422	0.113	6.027	0.002	1.505	0.002
1383831_at	BI280298	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	Qrsl1	0.994	0.982	1.016	0.907	0.998	0.967	1.001	0.738
1371930_at	BG380882	glutaminyl-tRNA synthetase /// similar to glutaminyl-tRNA synthetase (predicted)	Qars /// RGD1562301_predicted	1.053	0.314	0.899	0.068	1.205	0.072	1.198	0.106
1368513_at	AW144216	glutamyl aminopeptidase	Enpep	0.980	0.779	0.941	0.811	0.654	0.032	0.831	0.401
1373418_at	BM388143	glutamyl-prolyl-tRNA synthetase	Eprs	0.802	0.009	1.501	0.002	0.705	0.005	1.254	0.044
1383455_at	BF553211	glutamyl-prolyl-tRNA synthetase	Eprs	0.677	0.010	1.222	0.064	0.706	0.072	1.183	0.683
1382040_at	AI234919	glutamyl-prolyl-tRNA synthetase	Eprs	0.586	0.398	0.814	0.653	0.748	0.451	0.709	0.088
1367705_at	AF319950	glutaredoxin 1 (thioltransferase)	Glrx1	0.233	0.008	0.064	0.002	0.477	0.355	0.095	0.019
1386908_at	NM_022278	glutaredoxin 1 (thioltransferase)	Glrx1	0.348	0.026	0.088	0.000	0.680	0.102	0.220	0.012
1374340_at	AA848536	Glutaredoxin 2 (thioltransferase)	Glrx2	0.652	0.098	0.750	0.011	0.705	0.018	0.715	0.013
1386594_at	BF558518	Glutaredoxin 2 (thioltransferase)	Glrx2	1.580	0.125	1.067	0.746	1.153	0.344	0.950	0.571
1383062_at	BE105102	Glutaredoxin 2 (thioltransferase)	Glrx2	1.200	0.434	0.655	0.006	1.226	0.175	0.787	0.083
1373675_at	AW525635	glutaredoxin 2 (thioltransferase)	Glrx2	0.736	0.449	1.153	0.079	0.698	0.253	1.021	0.315
1393159_at	BG671304	Glutaredoxin 2 (thioltransferase)	Glrx2	0.901	0.676	1.598	0.012	1.580	0.881	1.203	0.927
1389286_at	AI232948	glutaredoxin 5 homolog (S. cerevisiae) (predicted)	Glrx5_predicted	1.098	0.648	0.846	0.539	0.751	0.112	0.782	0.064
1388788_at	BG664131	glutaryl-Coenzyme A dehydrogenase (predicted)	Gcdh_predicted	0.788	0.053	0.792	0.082	0.639	0.035	0.674	0.041
1384638_at	AI030545	Glutaryl-Coenzyme A dehydrogenase (predicted)	Gcdh_predicted	0.706	0.404	0.355	0.002	0.652	0.200	0.303	0.008
1367576_at	S41066	glutathione peroxidase 1	Gpx1	1.001	0.649	2.403	0.011	0.792	0.598	1.460	0.101
1374070_at	AA800587	glutathione peroxidase 2	Gpx2	3.566	0.076	14.737	0.000	2.248	0.065	10.684	0.001
1369926_at	NM_022525	glutathione peroxidase 3	Gpx3	0.690	0.542	0.163	0.019	0.695	0.569	0.125	0.059
1386871_at	NM_017165	glutathione peroxidase 4	Gpx4	0.718	0.595	1.644	0.102	0.558	0.001	1.056	0.310
1372125_at	BF408445	glutathione peroxidase 7 (predicted)	Gpx7_predicted	1.025	0.874	1.602	0.254	0.774	0.029	0.847	0.398
1381703_at	AW525915	Glutathione reductase	Gsr	1.453	0.003	3.386	0.019	1.095	0.810	3.079	0.006

1367774_at	NM_031509	glutathione S-transferase A3	Gsta3	0.580	0.017	6.336	0.005	0.453	0.069	1.778	0.026
1398378_at	AI231779	glutathione S-transferase kappa 1	Gstk1	0.818	0.890	1.096	0.106	0.733	0.842	0.816	0.043
1389832_at	BE113459	glutathione S-transferase omega 1	Gsto1	0.618	0.224	1.535	0.008	0.658	0.027	1.593	0.008
1368354_at	NM_053293	glutathione S-transferase theta 1	Gstt1	1.008	0.198	0.678	0.011	0.929	0.301	0.755	0.229
1372297_at	AI234527	glutathione S-transferase, alpha 4	Gsta4	1.002	0.360	0.726	0.452	0.500	0.323	0.542	0.819
1370813_at	U86635	glutathione S-transferase, mu 5	Gstm5	1.084	0.911	0.932	0.976	1.099	0.080	0.999	0.998
1387023_at	NM_031154	glutathione S-transferase, mu type 3	Gstm3	0.375	0.002	0.136	0.001	0.384	0.003	0.120	0.005
1370365_at	L38615	glutathione synthetase	Gss	0.459	0.006	1.473	0.019	0.502	0.236	1.626	0.213
1388122_at	X02904	glutathione-S-transferase, pi 1 /// glutathione S-transferase, pi 2	Gstp1 /// Gstp2	0.829	0.586	4.614	0.009	0.519	0.044	6.305	0.015
AFFX_Rat_GAPI	AFFX_Rat_GAPI	glyceraldehyde-3-phosphate dehydrogenase	Gapdh	0.824	0.103	1.005	0.445	0.815	0.010	0.994	0.901
AFFX_Rat_GAPI	AFFX_Rat_GAPI	glyceraldehyde-3-phosphate dehydrogenase	Gapdh	0.728	0.260	0.967	0.444	0.674	0.069	0.873	0.102
AFFX_Rat_GAPI	AFFX_Rat_GAPI	glyceraldehyde-3-phosphate dehydrogenase	Gapdh	0.825	0.274	1.049	0.233	0.706	0.093	0.880	0.038
1367557_s_at	NM_017008	glyceraldehyde-3-phosphate dehydrogenase /// similar to glyceraldehyde-3-phosphate dehydrogenase (predicted) /// similar to glyceraldehyde-3-phosphate dehydrogenase (predicted) /// similar to glyceraldehyde-3-phosphate dehydrogenase (predicted) /// similar to glyceraldehyde-3-phosphate dehydrogenase (predicted)	Gapdh /// RGD1564688_predicted /// RGD1564351_predicted /// RGD1561683_predicted /// RGD1565368_predicted	0.812	0.196	0.976	0.943	0.772	0.039	0.938	0.265
1369510_at	NM_023964	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	Gapdhs	0.919	0.079	1.001	0.835	0.921	0.491	0.998	0.873
1369666_at	BG378763	Glycerol-3-phosphate dehydrate dehydrogenase (mtGPDH) mRNA, 3'UTR, mRNA sequence	---	0.621	0.380	0.541	0.203	0.590	0.589	0.782	0.051
1387670_at	U08027	glycerol-3-phosphate dehydrogenase 2, mitochondrial	Gpd2	1.334	0.264	1.119	0.674	1.063	0.203	1.003	0.476
1368890_at	NM_053410	glyceronephosphate O-acyltransferase	Gnpat	0.578	0.004	1.246	0.393	0.734	0.439	0.994	0.438
1368891_at	AI014001	Glyceronephosphate O-acyltransferase	Gnpat	0.971	0.241	0.848	0.379	1.645	0.043	1.061	0.614
1378235_at	AI549590	glycerophosphodiester phosphodiesterase domain containing 1 (predicted)	Gdpd1_predicted	0.689	0.031	0.876	0.418	0.628	0.014	1.184	0.597
1382325_at	AW525471	glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	Gcat	0.595	0.409	0.915	0.126	0.458	0.038	0.770	0.319
1367908_at	NM_133598	glycine cleavage system protein H (aminomethyl carrier)	Gcsh	0.429	0.079	1.107	0.059	0.340	0.006	0.817	0.056
1384128_at	BF393261	glycine-, glutamate-, thienylcyclohexylpiperidine-binding protein	LOC246295	0.472	0.009	0.828	0.116	0.694	0.099	0.681	0.255
1389714_at	AI103146	Glycogen synthase kinase 3 alpha	Gsk3a	1.332	0.132	5.738	0.002	1.167	0.563	2.418	0.004
1386883_at	NM_017344	glycogen synthase kinase 3 alpha	Gsk3a	1.001	0.262	1.071	0.682	0.999	0.286	1.002	0.998
1370267_at	BF287444	glycogen synthase kinase 3 beta	Gsk3b	0.997	0.993	2.002	0.101	1.003	0.997	2.186	0.127
1367900_at	NM_031043	glycogenin 1	Gyg1	0.875	0.821	1.704	0.039	0.658	0.117	1.503	0.085
1388480_at	AI412863	glycolipid transfer protein (predicted)	Gltp_predicted	0.959	0.513	0.814	0.235	1.087	0.130	0.963	0.596
1368187_at	NM_133298	glycoprotein (transmembrane) nmb	Gpnmb	1.123	0.344	12.599	0.000	0.790	0.557	7.309	0.004
1367852_s_at	NM_053931	glycoprotein Ib, beta polypeptide /// septin 5	Gp1bb /// Sept5	1.000	0.995	0.999	0.992	0.612	0.998	0.997	0.983
1373773_at	BF394166	glycoprotein m6a	Gpm6a	0.608	0.067	0.408	0.629	0.781	0.160	0.727	0.910
1371358_at	BI282960	glycoprotein, synaptic 2	Gpsn2	0.517	0.123	0.330	0.000	0.464	0.012	0.320	0.008
1380833_at	AI045802	glycosylphosphatidylinositol specific phospholipase D1	Gpld1	0.225	0.048	0.414	0.011	0.799	0.067	0.515	0.016
1372050_at	BI279577	Glycosyltransferase 25 domain containing 1 (predicted)	Glt25d1_predicted	0.723	0.238	1.187	0.544	0.704	0.083	1.196	0.728
1388893_at	AI411616	glycosyltransferase 8 domain containing 1	Glt8d1	1.117	0.250	0.965	0.603	1.036	0.183	0.949	0.395
1395652_at	BI296264	glycosyltransferase-like 1B	Gyltl1b	0.592	0.037	0.464	0.032	0.609	0.130	0.464	0.045
1376132_at	BI289512	glycosyltransferase-like protein	LOC362129	1.372	0.176	1.989	0.007	0.915	0.668	2.254	0.145
1388715_at	AA818089	glycyl-tRNA synthetase	Gars	0.449	0.004	0.760	0.014	0.426	0.001	0.783	0.047
1395730_at	AW507352	glycyl-tRNA synthetase /// similar to Glycyl-tRNA synthetase (predicted)	Gars /// RGD1559871_predicted	1.003	0.798	0.642	0.044	0.534	0.779	0.343	0.082
1399098_at	AI103970	glyoxylase 1	Glo1	0.633	0.135	0.690	0.089	0.700	0.009	0.565	0.120
1373337_at	AI412065	glyoxylate reductase/hydroxypyruvate reductase (predicted)	Grhpr_predicted	0.279	0.001	1.098	0.442	0.276	0.006	0.430	0.022
1387039_at	NM_030828	glypican 1	Gpc1	0.455	0.007	0.893	0.262	0.265	0.002	0.569	0.016
1392888_at	AI071251	glypican 4	Gpc4	1.212	0.091	0.934	0.071	1.397	0.046	0.991	0.818
1387906_a_at	AF107845	GNAS complex locus	Gnas	0.493	0.001	0.434	0.001	0.586	0.003	0.320	0.012
1369897_s_at	BI277035	GNAS complex locus /// XLas protein	Gnas /// Xlas	0.703	0.193	0.391	0.000	0.671	0.109	0.339	0.010
1387367_at	NM_017211	golgi apparatus protein 1	Glg1	0.617	0.518	0.956	0.303	0.332	0.044	0.437	0.066
1374761_at	BM387073	golgi associated, gamma adaptin ear containing, ARF binding protein 1	Gga1	0.634	0.028	1.443	0.357	0.765	0.132	0.847	0.508
1372408_at	BI278620	golgi associated, gamma adaptin ear containing, ARF binding protein 2	Gga2	0.461	0.520	1.037	0.963	0.391	0.012	0.876	0.071
1379067_at	AA956006	golgi associated, gamma adaptin ear containing, ARF binding protein 3 (predicted)	Gga3_predicted	1.610	0.193	1.135	0.222	0.873	0.443	1.367	0.046
1375574_at	BE112983	golgi associated, gamma adaptin ear containing, ARF binding protein 3 (predicted)	Gga3_predicted	0.998	0.632	1.005	0.939	1.003	0.985	1.001	0.955
1381164_at	BF386935	Golgi autoantigen, golgin subfamily a, 1 (predicted)	Golga1_predicted	1.110	0.695	1.071	0.285	0.904	0.943	0.932	0.694
1378079_at	BI295829	golgi autoantigen, golgin subfamily a, 3 (predicted) /// similar to male-enhanced antigen-2 (predicted)	Golga3_predicted /// RGD1565361_predicted	1.178	0.094	3.096	0.003	1.149	0.177	1.842	0.015
1376650_at	BF399323	golgi autoantigen, golgin subfamily a, 5	Golga5	0.258	0.126	0.370	0.000	0.262	0.005	0.390	0.007
1398895_at	BM389419	golgi autoantigen, golgin subfamily a, 7	Golga7	0.931	0.644	1.164	0.442	0.821	0.238	1.232	0.905
1387979_at	D25543	golgi autoantigen, golgin subfamily b, macrogolgin 1	Golgb1	0.892	0.228	0.903	0.447	1.120	0.371	0.719	0.040
1390050_at	BI288898	golgi phosphoprotein 2 (predicted)	Golph2_predicted	0.560	0.150	0.674	0.223	0.344	0.011	0.590	0.040

1373754_at	AI599232	Golgi phosphoprotein 2 (predicted)	Golph2_predicted	0.504	0.201	0.609	0.002	0.249	0.001	0.428	0.022
1369571_at	NM_023977	golgi phosphoprotein 3	Golph3	0.998	0.989	0.996	0.977	0.998	0.986	1.004	0.985
1395291_at	BF396777	Golgi phosphoprotein 3-like	Golph3l	0.854	0.283	1.423	0.331	0.358	0.482	1.230	0.868
1378352_at	BM392166	golgi phosphoprotein 3-like	Golph3l	0.808	0.624	0.916	0.808	0.543	0.003	0.835	0.056
1398606_at	BM391878	golgi phosphoprotein 4	Golph4	0.594	0.230	0.662	0.003	0.572	0.034	0.524	0.008
1370325_at	AF110267	golgi reassembly stacking protein 2	Gorasp2	0.669	0.644	1.237	0.151	0.726	0.078	0.950	0.337
1388796_at	AI169291	Golgi SNAP receptor complex member 1	Gosr1	1.152	0.511	0.737	0.274	1.378	0.446	0.877	0.244
1395555_at	AW916706	golgi SNAP receptor complex member 1	Gosr1	0.995	0.992	1.156	0.309	1.023	0.923	1.002	0.949
1374900_at	BM388807	golgi SNAP receptor complex member 2	Gosr2	0.677	0.350	0.689	0.078	0.419	0.015	0.751	0.051
1375438_at	AA964687	golgi SNAP receptor complex member 2	Gosr2	0.625	0.548	0.882	0.240	0.551	0.009	0.794	0.017
1370031_at	NM_031685	golgi SNAP receptor complex member 2	Gosr2	0.828	0.974	1.313	0.877	0.390	0.029	1.091	0.968
1389077_at	AI179974	golgi transport 1 homolog B (S. cerevisiae) (predicted)	Golt1b_predicted	0.547	0.021	0.655	0.142	0.544	0.026	0.561	0.021
1383543_at	AW918220	golgi transport 1 homolog B (S. cerevisiae) (predicted)	Golt1b_predicted	0.958	0.733	1.024	0.433	1.067	0.467	0.935	0.145
1372330_at	BM391371	goliath	LOC652955	0.562	0.031	0.462	0.000	0.558	0.035	0.479	0.010
1368775_at	NM_133563	gonadotropin inducible ovarian transcription factor 1	Giot1	0.319	0.008	0.406	0.009	0.463	0.375	0.531	0.193
1370417_at	M15527	gonadotropin-releasing hormone 1	Gnrh1	1.936	0.827	1.628	0.057	3.565	0.024	1.995	0.017
1371939_at	AI171369	GPI-anchored membrane protein 1	Gpiap1	0.766	0.233	1.063	0.448	0.703	0.009	1.073	0.112
1395412_at	BF546337	GPI-anchored membrane protein 1	Gpiap1	0.919	0.834	1.226	0.780	0.562	0.115	1.071	0.937
1380358_at	AW529415	GPI-anchored membrane protein 1	Gpiap1	1.140	0.980	1.017	0.200	1.006	0.675	1.303	0.266
1387241_at	NM_031696	G-protein coupled receptor 88	Gpr88	0.877	0.502	0.672	0.302	0.781	0.265	0.583	0.244
1372383_at	AW435429	G-protein signalling modulator 1 (AGS3-like, C. elegans)	Gpsm1	0.109	0.005	0.405	0.000	0.062	0.017	0.545	0.033
1370590_at	AF107723	G-protein signalling modulator 1 (AGS3-like, C. elegans)	Gpsm1	0.889	0.993	0.567	0.021	0.999	0.993	0.572	0.031
1378128_at	BM383749	Grainyhead-like 1 (Drosophila) (predicted)	Grhl1_predicted	1.382	0.257	1.543	0.136	0.976	0.923	1.009	0.964
1382353_at	AA999160	grainyhead-like 1 (Drosophila) (predicted)	Grhl1_predicted	1.234	0.481	1.199	0.102	1.129	0.452	1.091	0.084
1385089_at	BM386731	Grainyhead-like 1 (Drosophila) (predicted)	Grhl1_predicted	0.950	0.708	1.530	0.355	0.688	0.059	1.012	0.965
1374043_at	AI317841	GRAM domain containing 3	Gramd3	1.492	0.054	0.590	0.003	2.235	0.005	1.030	0.512
1398664_at	C06752	GRAM domain containing 3	Gramd3	2.911	0.311	1.682	0.012	3.576	0.362	1.243	0.360
1384177_at	BI281497	GRAM domain containing 3	Gramd3	1.311	0.449	1.620	0.026	1.981	0.009	1.428	0.033
1386893_at	NM_017113	granulin	Grn	2.407	0.013	3.659	0.000	2.791	0.002	4.498	0.000
1371964_at	BM385050	G-rich RNA sequence binding factor 1	Grsf1	0.708	0.353	1.058	0.473	0.599	0.043	1.091	0.420
1368909_a_at	NM_053807	GRIP1 associated protein 1	Gripap1	1.765	0.005	1.273	0.120	2.393	0.015	1.123	0.068
1368288_at	NM_012564	group specific component	Gc	0.684	0.240	0.376	0.007	0.606	0.092	0.555	0.027
1368289_at	AA944965	group specific component	Gc	1.046	0.720	0.509	0.006	0.604	0.017	0.446	0.190
1379990_at	BG380925	Growth and transformation-dependent protein	LOC360721	0.960	0.101	1.417	0.013	1.060	0.115	1.078	0.185
1368947_at	NM_024127	growth arrest and DNA-damage-inducible 45 alpha	Gadd45a	1.115	0.766	2.456	0.036	0.831	0.049	2.212	0.068
1372016_at	BI287978	growth arrest and DNA-damage-inducible 45 beta	Gadd45b	44.522	0.000	131.035	0.000	21.005	0.006	38.806	0.007
1388792_at	AI599423	growth arrest and DNA-damage-inducible 45 gamma	Gadd45g	3.851	0.002	3.533	0.010	2.428	0.007	1.887	0.099
1371896_at	AI411436	growth arrest and DNA-damage-inducible, gamma interacting protein 1	Gadd45gip1	0.603	0.275	0.984	0.443	0.555	0.019	1.198	0.297
1392818_at	BM384139	growth arrest specific 5	Gas5	0.886	0.175	0.922	0.346	0.835	0.010	1.137	0.229
1373499_at	BF287008	growth arrest specific 5	Gas5	1.046	0.677	2.782	0.001	0.991	0.168	2.233	0.006
1383047_at	AA957335	growth arrest specific 6	Gas6	0.438	0.015	1.011	0.165	0.594	0.004	0.972	0.840
1369735_at	NM_057100	growth arrest specific 6	Gas6	0.777	0.169	0.410	0.010	0.708	0.052	0.542	0.032
1390791_at	AI172537	growth arrest-specific 2 like 1 (predicted)	Gas2l1_predicted	1.003	0.825	0.969	0.141	1.002	0.964	1.336	0.026
1367930_at	NM_017195	growth associated protein 43	Gap43	1.376	0.200	1.058	0.466	1.154	0.517	0.497	0.009
1382203_at	AI549010	growth differentiation factor 1 (predicted)	Gdf1_predicted	0.826	0.839	1.114	0.550	0.819	0.012	0.879	0.117
1374706_at	BF407916	Growth differentiation factor 11	Gdf11	0.565	0.018	0.543	0.001	0.557	0.028	0.581	0.002
1370153_at	NM_019216	growth differentiation factor 15	Gdf15	2.283	0.109	12.838	0.001	0.870	0.731	6.509	0.007
1368618_at	NM_031623	growth factor receptor bound protein 14	Grb14	0.998	0.996	0.998	0.272	1.014	0.970	1.004	0.971
1383246_at	AI146111	Growth factor receptor bound protein 2	Grb2	0.774	0.058	0.919	0.028	1.000	0.999	1.092	0.602
1368386_at	NM_030846	growth factor receptor bound protein 2	Grb2	1.139	0.115	1.104	0.932	0.842	0.490	0.777	0.025
1370617_at	D49847	growth factor receptor bound protein 2	Grb2	1.829	0.253	1.210	0.925	1.059	0.620	0.995	0.193
1368385_a_at	X62853	growth factor receptor bound protein 2	Grb2	1.239	0.320	2.715	0.002	0.753	0.377	1.516	0.017
1393098_at	BM386610	Growth factor receptor bound protein 2	Grb2	0.970	0.710	1.009	0.597	1.073	0.776	1.047	0.307
1374394_at	AI105305	Growth factor receptor bound protein 2	Grb2	1.051	0.985	2.316	0.016	1.510	0.505	1.893	0.015
1393857_at	AW253255	Growth factor receptor bound protein 2	Grb2	1.191	0.999	0.980	0.995	1.740	0.905	1.011	0.477
1368334_at	NM_053403	growth factor receptor bound protein 7	Grb7	0.999	0.989	1.001	0.127	0.788	0.145	0.871	0.131
1367867_at	NM_013222	growth factor, erv1 homolog (S. cerevisiae)	Gfer	0.907	0.102	7.168	0.002	0.507	0.010	3.663	0.011
1371574_at	BF284759	growth hormone inducible transmembrane protein	Ghitm	1.184	0.409	2.248	0.003	1.192	0.194	2.269	0.000
1373142_at	AA858928	Growth hormone inducible transmembrane protein	Ghitm	0.891	0.516	1.495	0.026	1.192	0.845	1.832	0.005
1368924_at	NM_017094	growth hormone receptor	Ghr	0.413	0.026	0.308	0.001	0.491	0.020	0.441	0.002
1373803_a_at	AI170771	growth hormone receptor	Ghr	0.611	0.159	0.491	0.034	0.635	0.011	0.456	0.019

1368552_at	NM_024487	GrpE-like 1, mitochondrial	Grpel1	0.624	0.771	1.297	0.207	0.596	0.149	1.372	0.020
1382351_at	AI069972	GTP binding protein (gene overexpressed in skeletal muscle) (predicted)	Gem_predicted	0.366	0.014	0.323	0.003	0.314	0.002	0.319	0.012
1374489_at	BF282573	GTP binding protein 2	Gtpbp2	2.714	0.001	8.708	0.000	2.020	0.010	6.777	0.004
1398438_at	BE118548	GTP binding protein 3	Gtpbp3	0.983	0.480	0.990	0.545	1.001	0.697	1.007	0.934
1370144_at	NM_053689	GTP binding protein 4	Gtpbp4	0.571	0.138	1.333	0.041	0.660	0.008	1.969	0.031
1372869_at	BE109202	GTP binding protein 4	Gtpbp4	0.823	0.435	1.930	0.000	1.015	0.739	1.398	0.014
1393326_s_at	BG378917	GTP binding protein 6 (putative) (predicted)	Gtpbp6_predicted	0.999	0.977	1.263	0.141	0.992	0.985	0.999	0.843
1380230_at	AI639457	GTP cyclohydrolase 1	Gch	2.034	0.042	1.120	0.517	1.184	0.014	0.514	0.075
1387221_at	NM_024356	GTP cyclohydrolase 1	Gch	1.670	0.052	1.898	0.029	1.299	0.090	1.506	0.126
1368503_at	AA859496	GTP cyclohydrolase 1	Gch	0.999	0.986	1.338	0.509	0.982	0.731	0.995	0.183
1375878_at	BE102596	GTPase activating protein and VPS9 domains 1 (predicted)	Gapvd1_predicted	0.759	0.365	1.115	0.040	0.889	0.996	1.002	0.966
1390217_at	BF283227	GTPase activating RANGAP domain-like 1	Garnl1	0.730	0.006	0.679	0.036	0.797	0.065	0.842	0.167
1387405_at	NM_020083	GTPase activating RANGAP domain-like 1	Garnl1	0.881	0.187	0.731	0.044	1.189	0.380	0.573	0.049
1395385_at	BF548145	GTPase activating RANGAP domain-like 1	Garnl1	0.951	0.205	0.541	0.035	1.130	0.771	0.745	0.082
1368994_a_at	AF041107	GTPase activating RANGAP domain-like 1	Garnl1	1.067	0.527	0.928	0.230	0.908	0.393	0.934	0.279
1392322_at	BM388319	GTPase, IMAP family member 7	Gimap7	1.177	0.394	1.141	0.092	1.207	0.521	0.995	0.981
1387659_at	AF245172	guanine deaminase	Gda	1.271	0.215	3.541	0.001	1.986	0.147	2.108	0.113
1377577_at	BI283031	guanine monphosphate synthetase	Gmps	0.749	0.214	1.805	0.001	0.738	0.013	1.482	0.006
1380373_at	BF397926	guanine monphosphate synthetase	Gmps	0.996	0.987	1.642	0.058	1.000	0.998	0.909	0.067
1388455_at	AA799996	guanine nucleotide binding protein (G protein), gamma 10	Gng10	0.708	0.537	0.490	0.001	0.596	0.129	0.423	0.021
1392471_at	BI302750	Guanine nucleotide binding protein (G protein), gamma 12	Gng12	1.956	0.034	1.528	0.024	1.658	0.009	1.269	0.072
1377739_at	AI576549	guanine nucleotide binding protein (G protein), gamma 12	Gng12	1.320	0.275	4.269	0.001	0.660	0.049	3.454	0.001
1387342_at	BM389548	guanine nucleotide binding protein (G protein), gamma 5 subunit	Gng5	1.244	0.117	3.770	0.001	1.033	0.620	3.387	0.001
1367844_at	M12672	guanine nucleotide binding protein, alpha inhibiting 2	Gnai2	0.726	0.858	0.780	0.194	0.600	0.360	0.788	0.057
1368030_at	J03219	guanine nucleotide binding protein, alpha inhibiting 3	Gnai3	1.199	0.322	2.248	0.093	1.002	0.833	0.999	0.242
1368029_at	NM_013106	guanine nucleotide binding protein, alpha inhibiting 3	Gnai3	1.278	0.424	1.804	0.016	1.678	0.301	1.488	0.010
1368879_a_at	AF413212	guanine nucleotide binding protein, alpha o	Gnao	0.628	0.207	0.982	0.938	0.706	0.079	0.825	0.306
1375902_at	AI231065	Guanine nucleotide binding protein, alpha o	Gnao	0.902	0.738	1.111	0.056	0.689	0.114	0.878	0.763
1383055_at	AW143805	Guanine nucleotide binding protein, alpha q polypeptide	Gnaq	0.567	0.035	0.447	0.001	0.604	0.012	0.624	0.042
1375745_at	BE117491	Guanine nucleotide binding protein, alpha q polypeptide	Gnaq	0.634	0.110	0.401	0.018	0.618	0.174	0.508	0.010
1385158_at	BI301125	Guanine nucleotide binding protein, alpha stimulating, olfactory type	Gnal	0.846	0.024	0.256	0.008	0.827	0.039	0.612	0.057
1382112_at	BM385698	Guanine nucleotide binding protein, alpha stimulating, olfactory type	Gnal	0.897	0.198	0.582	0.016	1.055	0.910	0.768	0.008
1382129_at	AI136136	Guanine nucleotide binding protein, alpha stimulating, olfactory type	Gnal	1.409	0.233	0.209	0.004	0.999	0.519	0.515	0.023
1384229_at	AI576080	Guanine nucleotide binding protein, alpha stimulating, olfactory type	Gnal	1.144	0.912	1.008	0.711	1.820	0.043	1.006	0.835
1368185_at	NM_013189	guanine nucleotide binding protein, alpha z subunit	Gnaz	1.543	0.033	0.595	0.005	1.453	0.007	0.725	0.188
1367732_at	U34958	guanine nucleotide binding protein, beta 1	Gnb1	1.251	0.162	2.879	0.001	1.136	0.614	2.601	0.003
1382982_at	AI230669	Guanine nucleotide binding protein, beta 1	Gnb1	1.077	0.682	1.317	0.280	1.368	0.992	1.081	0.810
1367731_at	NM_030987	guanine nucleotide binding protein, beta 1	Gnb1	0.904	0.704	0.617	0.016	0.715	0.179	0.563	0.021
1382105_at	AI603217	guanine nucleotide binding protein, beta 5	Gnb5	0.406	0.137	0.367	0.000	0.313	0.001	0.210	0.036
1370867_at	BM384381	guanine nucleotide binding protein, beta polypeptide 2	Gnb2	1.400	0.312	1.148	0.029	1.230	0.458	1.173	0.042
1398863_at	AF277892	guanine nucleotide binding protein, beta polypeptide 2	Gnb2	1.168	0.765	0.983	0.572	1.052	0.626	1.363	0.098
1398391_at	BG379297	guanine nucleotide binding protein-like 1	Gnl1	0.651	0.255	1.218	0.934	0.481	0.129	1.095	0.444
1374804_at	AI060050	guanine nucleotide binding protein-like 2 (nucleolar)	Gnl2	0.537	0.122	1.557	0.271	0.798	0.070	0.851	0.622
1388953_at	AA892598	guanine nucleotide binding protein-like 3 (nucleolar)	Gnl3	0.681	0.052	2.246	0.002	0.573	0.035	1.661	0.010
1387855_at	BI278628	guanosine diphosphate dissociation inhibitor 1	Gdi1	0.713	0.001	0.537	0.005	0.824	0.026	0.562	0.013
1387079_at	M57405	guanylate cyclase 1, soluble, alpha 3	Gucy1a3	1.151	0.688	1.307	0.264	1.073	0.368	0.758	0.260
1369162_at	NM_013170	guanylate cyclase 2C	Gucy2c	0.306	0.001	0.393	0.041	0.370	0.001	0.292	0.048
1375455_at	AI716086	guanylate cyclase activator 1a (retina) (predicted)	Guca1a_predicted	0.811	0.176	1.089	0.218	0.791	0.177	0.999	0.720
1371743_at	AA800291	guanylate kinase 1	Guk1	0.530	0.134	0.660	0.038	0.566	0.022	0.739	0.048
1368332_at	NM_133624	guanylate nucleotide binding protein 2	Gbp2	504.100	0.002	429.255	0.007	1223.375	0.004	615.861	0.004
1385051_at	BE108569	Guanylate nucleotide binding protein 4 (predicted)	Gbp4_predicted	127.686	0.000	41.990	0.001	427.678	0.000	123.393	0.000
1382950_at	AA901350	Guanylate nucleotide binding protein 4 (predicted)	Gbp4_predicted	355.187	0.007	55.935	0.004	407.518	0.005	74.146	0.002
1376285_at	BM390519	GULP, engulfment adaptor PTB domain containing 1	Gulp1	0.255	0.006	0.207	0.004	0.371	0.017	0.402	0.001
1367759_at	NM_012578	H1 histone family, member 0	H1f0	0.539	0.126	0.622	0.005	0.422	0.020	0.697	0.052
1380595_at	AI071495	H2A histone family, member V (predicted)	H2afv_predicted	0.986	0.600	1.013	0.485	0.960	0.602	0.961	0.664
1388827_at	AW523419	H2A histone family, member V (predicted) /// similar to H2A histone family, member V isoform 1 (predicted)	H2afv_predicted /// RGD1560813_predicted	0.993	0.975	0.964	0.074	1.477	0.064	1.440	0.712
1370004_at	M99065	H2A histone family, member Y	H2afy	0.713	0.639	1.697	0.010	0.852	0.330	1.347	0.513
1386861_at	NM_022674	H2A histone family, member Z	H2afz	0.687	0.287	1.062	0.456	0.628	0.116	1.009	0.093
1390019_at	BM390456	H3 histone, family 3B	H3f3b	0.860	0.230	0.575	0.105	0.840	0.253	0.573	0.002
1398888_at	AI408819	H3 histone, family 3B	H3f3b	0.951	0.510	1.175	0.010	0.901	0.837	1.415	0.002

1370190_at	BG663226	H3 histone, family 3B	H3f3b	1.066	0.694	1.380	0.012	0.898	0.372	1.479	0.002
1398849_at	AI177503	H3 histone, family 3B	H3f3b	0.752	0.887	2.316	0.004	0.459	0.284	1.866	0.018
1385988_at	BF287243	H6 homeo box 1 (predicted)	Hmx1_predicted	6.224	0.063	27.250	0.001	2.564	0.095	9.525	0.005
1387036_at	NM_024360	hairy and enhancer of split 1 (Drosophila)	Hes1	1.001	0.991	0.997	0.824	1.316	0.131	1.000	0.974
1374625_at	AI176616	hairy and enhancer of split 6 (Drosophila)	Hes6	0.387	0.019	0.955	0.490	0.370	0.169	0.886	0.634
1388729_at	BF282474	Harvey rat sarcoma oncogene, subgroup R (predicted)	Rras_predicted	1.011	0.611	2.342	0.006	1.301	0.049	1.871	0.177
1371255_at	BG379941	Harvey rat sarcoma viral (v-Ha-ras) oncogene homolog	Hras	0.690	0.655	1.794	0.020	0.411	0.014	1.583	0.023
1372344_at	AI175760	Hbs1-like (S. cerevisiae)	Hbs1l	1.390	0.012	2.558	0.001	1.267	0.013	1.928	0.000
1384378_at	BI293046	HCR (a-helix coiled-coil rod homolog)	Hcr	4.242	0.008	4.900	0.000	8.958	0.008	7.428	0.006
1383316_at	BF409313	HD domain containing 2 (predicted)	Hddc2_predicted	1.001	0.968	0.989	0.229	0.953	0.790	1.000	0.183
1372762_at	AA849729	HD domain containing 3 (predicted)	Hddc3_predicted	0.686	0.551	0.776	0.112	0.339	0.017	0.660	0.353
1383685_at	BI276972	HEAT repeat containing 1 (predicted)	Heatr1_predicted	0.489	0.069	1.426	0.046	0.638	0.019	2.203	0.038
1386898_at	NM_012966	heat shock 10 kDa protein 1 (chaperonin 10)	Hspe1	0.614	0.175	2.716	0.016	0.484	0.001	1.835	0.123
1388898_at	AI236601	heat shock 105kDa/110kDa protein 1	Hsph1	0.712	0.248	2.015	0.008	0.742	0.059	1.503	0.048
1385620_at	BF525282	heat shock 105kDa/110kDa protein 1	Hsph1	0.543	0.365	3.564	0.003	0.313	0.129	1.354	0.417
1388721_at	BG380282	heat shock 22kDa protein 8	Hspb8	35.812	0.006	9.021	0.006	12.673	0.003	5.919	0.017
1368247_at	NM_031971	heat shock 70kD protein 1A /// heat shock 70kD protein 1B (mapped)	Hspa1a /// Hspa1b_mapped	1.212	0.801	5.574	0.008	1.247	0.332	1.515	0.126
1370912_at	BI278231	heat shock 70kD protein 1B (mapped)	Hspa1b_mapped	1.189	0.982	6.148	0.010	1.171	0.574	2.034	0.098
1384295_at	AI111363	heat shock 70kDa protein 14	Hspa14	0.854	0.070	1.098	0.058	1.233	0.110	1.139	0.225
1394200_at	BF410146	heat shock 70kDa protein 2	Hspa2	1.067	0.467	0.946	0.924	0.632	0.166	1.267	0.376
1378002_at	BF401583	heat shock 70kDa protein 4-like (predicted)	Hspa4l_predicted	0.812	0.522	1.437	0.058	0.640	0.621	1.155	0.384
1375626_at	BF416562	Heat shock 70kDa protein 4-like (predicted)	Hspa4l_predicted	1.412	0.831	0.679	0.294	1.813	0.190	0.578	0.061
1370283_at	M14050	heat shock 70kDa protein 5 (glucose-regulated protein)	Hspa5	0.890	0.964	1.456	0.000	0.913	0.268	1.348	0.003
1383680_at	BG376339	heat shock 70kDa protein 5 binding protein 1	Hspa5bp1	1.143	0.610	0.808	0.064	1.084	0.234	1.014	0.121
1391915_at	BE120145	heat shock 70kDa protein 9A (predicted)	Hspa9a_predicted	1.038	0.040	7.122	0.011	1.375	0.193	2.590	0.041
1388851_at	BI282281	heat shock 70kDa protein 9A (predicted)	Hspa9a_predicted	0.796	0.443	1.971	0.004	0.689	0.194	1.910	0.008
1389930_at	AI598451	Heat shock 70kDa protein 9A (predicted)	Hspa9a_predicted	1.338	0.471	3.028	0.354	0.559	0.104	2.067	0.919
1370690_at	S75280	heat shock 70kDa protein 9A (predicted)	Hspa9a_predicted	0.616	0.578	2.418	0.069	0.432	0.353	1.926	0.108
1375336_at	AI237389	heat shock 90kDa protein 1, beta	Hspcb	0.747	0.239	1.543	0.047	0.591	0.102	1.191	0.818
1375335_at	BI285700	heat shock 90kDa protein 1, beta	Hspcb	0.792	0.419	1.739	0.032	0.788	0.029	1.198	0.571
1387430_at	NM_031694	heat shock factor 2	Hsf2	0.872	0.190	1.743	0.045	0.772	0.103	1.420	0.106
1382598_at	BE111342	heat shock factor 2	Hsf2	0.915	0.450	1.293	0.022	1.000	0.692	1.344	0.003
1371490_at	BG666149	heat shock factor binding protein 1	Hsbp1	0.745	0.768	0.361	0.046	0.745	0.166	0.473	0.000
1371783_at	AI009936	heat shock protein	LOC290549	0.634	0.552	1.066	0.250	0.794	0.213	0.909	0.053
1386894_at	NM_022229	heat shock protein 1 (chaperonin)	Hspd1	0.523	0.001	1.370	0.006	0.495	0.000	1.240	0.006
1372701_at	AI237597	heat shock protein 1, alpha	Hspca	0.765	0.053	2.787	0.001	0.757	0.429	1.627	0.006
1388850_at	BG671521	heat shock protein 1, alpha	Hspca	0.674	0.231	3.057	0.003	0.793	0.075	1.661	0.377
1370344_at	AF077354	heat shock protein 4	Hspa4	0.448	0.152	0.636	0.206	0.578	0.107	0.441	0.071
1394557_at	AW535242	Heat shock protein 4	Hspa4	0.914	0.581	1.061	0.844	0.878	0.648	1.195	0.481
1398240_at	NM_024351	heat shock protein 8	Hspa8	0.665	0.047	1.508	0.003	0.678	0.010	1.208	0.008
1387898_at	D29960	heat shock protein, alpha-crystallin-related, B6	Hspb6	0.420	0.014	0.200	0.004	0.410	0.016	0.411	0.029
1370917_at	AI172496	heat shock transcription factor 1	Hsf1	1.365	0.144	2.614	0.034	1.259	0.057	2.614	0.032
1368060_at	NM_031714	heat-responsive protein 12	Hrsp12	0.666	0.447	0.324	0.003	0.825	0.082	0.512	0.005
1374599_at	BM386001	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 (predicted)	Herc1_predicted	1.090	0.148	1.017	0.889	1.059	0.333	1.043	0.142
1394746_at	AI180352	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 (predicted)	Herc1_predicted	1.006	0.865	0.841	0.781	1.067	0.434	0.717	0.014
1390648_at	AW523544	Hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 2 (predicted)	Herc2_predicted	0.691	0.033	0.908	0.237	1.088	0.557	0.989	0.422
1381195_at	BF389423	Hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 2 (predicted)	Herc2_predicted	0.916	0.402	0.964	0.355	0.973	0.930	1.194	0.788
1375861_at	BE111332	Hect domain and RLD 3 (predicted)	Herc3_predicted	0.161	0.000	0.142	0.001	0.135	0.003	0.159	0.009
1389164_at	BI295026	hect domain and RLD 3 (predicted)	Herc3_predicted	1.662	0.090	0.361	0.009	1.688	0.274	0.719	0.366
1373381_at	AI236889	hect domain and RLD 4	Herc4	0.938	0.725	1.326	0.149	0.913	0.196	1.060	0.972
1371336_at	AA942716	hematological and neurological expressed sequence 1	Hn1	1.586	0.089	2.455	0.015	1.414	0.142	1.885	0.045
1388581_at	AI317868	hematological and neurological expressed sequence 1	Hn1	1.658	0.147	1.169	0.949	1.624	0.028	1.420	0.804
1372004_at	AI102065	heme binding protein 1 (predicted)	Hebp1_predicted	1.233	0.743	3.822	0.015	0.967	0.959	2.165	0.037
1382451_at	BM385477	heme binding protein 2 (predicted)	Hebp2_predicted	1.052	0.784	0.757	0.017	0.959	0.490	0.848	0.167
1370080_at	NM_012580	heme oxygenase (decycling) 1	Hmox1	0.732	0.888	9.148	0.004	0.428	0.050	7.135	0.001
1367903_at	J05405	heme oxygenase (decycling) 2	Hmox2	0.580	0.254	1.122	0.437	0.547	0.005	0.916	0.407

1384358_at	BM384625	Heme oxygenase (decycling) 2	Hmox2	0.975	0.891	0.988	0.968	0.997	0.745	0.989	0.975
1392330_at	BF417415	HemK methyltransferase family member 2 (predicted)	Hemk2_predicted	0.916	0.746	0.920	0.555	1.333	0.024	1.001	0.997
1381428_a_at	AI177364	Hemochromatosis	Hfe	0.737	0.331	0.544	0.003	0.711	0.048	0.888	0.838
1399067_at	AI229702	hemochromatosis	Hfe	0.790	0.740	0.834	0.021	0.793	0.457	0.923	0.042
1388608_x_at	AI577319	hemoglobin alpha, adult chain 1	Hba-a1	0.957	0.845	0.812	0.987	1.001	0.305	0.713	0.204
1370240_x_at	AI179404	hemoglobin alpha, adult chain 1 /// hemoglobin alpha 2 chain	Hba-a1 /// LOC360504	1.097	0.936	0.999	0.963	1.023	0.727	0.973	0.979
1370065_at	NM_053318	hemopexin	Hpx	4.995	0.002	10.770	0.006	12.095	0.000	12.106	0.001
1369204_at	NM_013185	hemopoietic cell kinase	Hck	0.998	0.604	0.997	0.115	1.005	0.489	0.999	0.495
1370834_at	AF177430	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	Hs3st1	1.299	0.036	1.005	0.937	0.999	0.987	1.120	0.062
1382101_at	AI714262	heparan sulfate 2-O-sulfotransferase 1	Hs2st1	1.004	0.178	0.687	0.369	1.286	0.105	0.849	0.420
1368983_at	NM_012945	heparin-binding EGF-like growth factor	Hbegf	0.721	0.235	6.398	0.008	0.830	0.230	3.133	0.044
1386366_at	AI231610	Hepatitis B virus x associated protein (predicted)	Hbxap_predicted	1.307	0.060	2.536	0.030	0.997	0.699	2.257	0.057
1394010_at	H32100	hepatitis B virus x associated protein (predicted)	Hbxap_predicted	1.002	0.893	1.040	0.598	0.966	0.272	0.789	0.212
1377622_at	AI717078	hepatitis B virus x associated protein (predicted)	Hbxap_predicted	0.915	0.958	1.151	0.644	0.616	0.002	0.927	0.916
1372076_at	BI294704	hepatitis B virus x interacting protein (predicted)	Hbxip_predicted	1.213	0.332	2.251	0.012	0.913	0.362	1.999	0.007
1367817_at	NM_053707	hepatoma-derived growth factor	Hdgf	0.993	0.741	2.049	0.000	0.818	0.033	1.723	0.006
1368026_at	NM_133548	hepatoma-derived growth factor, related protein 2	Hdgfrp2	1.683	0.045	1.740	0.003	1.029	0.953	1.464	0.013
1370458_at	AF389347	hepatoma-derived growth factor, related protein 3	Hdgfrp3	0.883	0.504	0.777	0.333	0.661	0.086	0.750	0.027
1382699_s_at	AW920326	Hermansky-Pudlak syndrome 1 homolog (human)	Hps1	0.637	0.112	0.821	0.492	0.917	0.487	1.039	0.217
1387096_at	NM_040669	Hermansky-Pudlak syndrome 1 homolog (human)	Hps1	0.993	0.976	0.989	0.904	0.953	0.508	0.982	0.960
1379443_at	BE120719	Hermansky-Pudlak syndrome 3 homolog (human) (predicted)	Hps3_predicted	0.993	0.128	1.017	0.911	1.025	0.481	1.219	0.073
1381919_at	BI290986	Hermansky-Pudlak syndrome 6	Hps6	1.152	0.783	1.335	0.420	0.550	0.153	0.654	0.852
1388613_at	BE113034	HESB like domain containing 2	Hbld2	0.522	0.001	0.971	0.121	0.686	0.058	0.882	0.026
1388603_a_at	BM384289	HESB like domain containing 2	Hbld2	0.570	0.068	1.424	0.002	0.479	0.017	1.376	0.004
1371637_at	AI411691	heterochromatin protein 1, binding protein 3	Hp1bp3	0.726	0.158	0.657	0.017	0.819	0.062	0.636	0.017
1395101_at	BF396757	Heterochromatin protein 1, binding protein 3	Hp1bp3	1.019	0.299	1.113	0.836	0.801	0.240	1.015	0.312
1370309_a_at	AJ238854	heterogeneous nuclear ribonucleoprotein A/B	Hnrpab	0.681	0.137	1.158	0.084	0.581	0.004	1.199	0.036
1372693_at	AI408833	heterogeneous nuclear ribonucleoprotein A1	Hnrpa1	1.580	0.012	1.353	0.016	1.387	0.008	1.352	0.055
1387872_at	BF396270	heterogeneous nuclear ribonucleoprotein A1	Hnrpa1	1.006	0.342	0.802	0.062	0.770	0.168	0.729	0.030
1398883_at	BI296284	heterogeneous nuclear ribonucleoprotein A2/B1 (predicted)	Hnrpa2b1_predicted	0.771	0.327	0.448	0.004	0.851	0.231	0.525	0.024
1395561_at	BG666358	heterogeneous nuclear ribonucleoprotein A2/B1 (predicted)	Hnrpa2b1_predicted	0.989	0.924	0.707	0.027	0.991	0.989	0.710	0.006
1374405_at	AI233336	heterogeneous nuclear ribonucleoprotein A3	Hnrpa3	0.700	0.362	2.257	0.002	0.851	0.420	1.692	0.011
1394741_at	AI409455	Heterogeneous nuclear ribonucleoprotein A3	Hnrpa3	0.864	0.853	1.907	0.132	1.090	0.578	0.985	0.684
1371505_at	BG381750	heterogeneous nuclear ribonucleoprotein C	Hnrpc	1.151	0.484	2.246	0.001	1.153	0.299	2.048	0.006
1369971_a_at	AB046616	heterogeneous nuclear ribonucleoprotein D	Hnrpd	0.734	0.340	1.470	0.039	0.741	0.387	1.203	0.002
1372810_at	BF281256	heterogeneous nuclear ribonucleoprotein D-like	Hnrpdl	1.504	0.007	1.689	0.000	1.249	0.013	1.336	0.016
1370844_at	BM387425	heterogeneous nuclear ribonucleoprotein F	Hnrpf	1.044	0.745	1.117	0.692	1.047	0.974	1.051	0.984
1367666_at	NM_080896	heterogeneous nuclear ribonucleoprotein H1	Hnrph1	1.005	0.751	0.803	0.078	1.063	0.223	0.744	0.119
1375019_at	AI101886	heterogeneous nuclear ribonucleoprotein H3 (2H9) (predicted)	Hnrph3_predicted	1.955	0.003	1.740	0.008	2.320	0.019	1.838	0.006
1398797_at	NM_057141	heterogeneous nuclear ribonucleoprotein K	Hnrpk	0.767	0.081	0.665	0.000	0.771	0.001	0.720	0.022
1367895_at	AI577321	heterogeneous nuclear ribonucleoprotein K	Hnrpk	1.036	0.298	1.004	0.960	0.848	0.474	1.030	0.165
1398873_at	BI279608	heterogeneous nuclear ribonucleoprotein L	Hnrpl	1.012	0.187	1.051	0.702	0.943	0.149	0.871	0.342
1391475_at	AI235307	heterogeneous nuclear ribonucleoprotein L-like (predicted)	Hnrpll_predicted	0.726	0.393	0.671	0.341	0.938	0.705	0.781	0.137
1397715_at	AI716475	Heterogeneous nuclear ribonucleoprotein M	Hnrpm	1.452	0.032	1.659	0.320	1.964	0.089	0.915	0.138
1370919_at	AI103467	heterogeneous nuclear ribonucleoprotein M	Hnrpm	0.845	0.149	0.785	0.009	0.807	0.077	0.777	0.007
1370536_at	AF059530	heterogeneous nuclear ribonucleoprotein methyltransferase-like 3 (S. cerevisiae)	Hrmt1l3	0.704	0.016	1.096	0.194	0.685	0.009	1.052	0.423
1382697_at	BF289134	Heterogeneous nuclear ribonucleoprotein methyltransferase-like 3 (S. cerevisiae)	Hrmt1l3	1.039	0.880	1.017	0.983	1.026	0.874	1.023	0.986
1373905_at	AI178441	heterogeneous nuclear ribonucleoprotein R	Hnrpr	0.521	0.566	0.705	0.022	0.503	0.035	0.690	0.061
1370171_at	AI058964	heterogeneous nuclear ribonucleoprotein U	Hnrpu	0.600	0.050	0.582	0.013	0.672	0.005	0.781	0.044
1370170_at	AI177494	heterogeneous nuclear ribonucleoprotein U	Hnrpu	0.780	0.145	0.826	0.080	0.740	0.076	0.800	0.016
1399099_at	BG381219	heterogeneous nuclear ribonucleoprotein U-like 1 (predicted)	Hnrpul1_predicted	1.150	0.695	0.916	0.850	1.105	0.274	1.334	0.416
1386897_at	NM_024363	heterogeneous nuclear ribonucleoproteins methyltransferase-like 2 (S. cerevisiae)	Hrmt1l2	0.707	0.474	2.144	0.011	0.665	0.038	1.756	0.002
1374732_at	BI275803	hexamthylene bis-acetamide inducible 2 (predicted)	Hexim2_predicted	0.554	0.429	0.368	0.235	0.983	0.904	0.519	0.167
AFFX_Rat_Hexo	AFFX_Rat_Hexo	hexokinase 1	Hk1	1.000	0.446	0.997	0.336	1.004	0.709	1.000	0.895
AFFX_Rat_Hexo	AFFX_Rat_Hexo	hexokinase 1	Hk1	0.999	0.451	0.997	0.194	1.002	0.611	0.998	0.231
AFFX_Rat_Hexo	AFFX_Rat_Hexo	hexokinase 1	Hk1	1.002	0.451	0.996	0.270	1.009	0.967	0.999	0.734
1383519_at	BI294137	Hexokinase 2	Hk2	4.988	0.011	16.768	0.002	17.219	0.011	20.434	0.001
1373222_at	AI230271	hexosaminidase A	Hexa	0.777	0.253	0.610	0.001	1.055	0.631	0.611	0.003
1374173_at	AA799841	Hexosaminidase B	Hexb	0.634	0.028	0.650	0.009	1.037	0.747	0.824	0.016
1372706_at	AA892845	hexosaminidase B	Hexb	0.699	0.460	1.082	0.453	0.624	0.238	0.901	0.338
1398933_at	AA894259	HIG1 domain family, member 2A (predicted)	Higd2a_predicted	0.764	0.809	0.940	0.690	0.519	0.026	0.951	0.711

1398859_at	U90725	high density lipoprotein binding protein	Hdlbp	0.644	0.507	1.167	0.232	0.806	0.189	1.020	0.596
1375309_at	BI296631	High density lipoprotein binding protein	Hdlbp	1.019	0.806	1.096	0.718	1.499	0.108	0.990	0.939
1372494_a_at	BM384171	high mobility group 20 B (predicted)	Hmg20b_predicted	1.004	0.865	1.001	0.991	1.109	0.728	1.000	0.991
1388309_at	BG378885	high mobility group AT-hook 1	Hmga1	1.277	0.189	2.387	0.020	1.705	0.035	2.783	0.037
1388783_at	BE107162	high mobility group box 1	Hmgb1	0.898	0.051	0.947	0.064	0.670	0.050	0.894	0.339
1368042_a_at	AF275734	high mobility group box 1 /// similar to High mobility group protein 1 (HMG-1) (predicted) /// similar to Hmgb1 protein (predicted) /// similar to High mobility group protein 1 (HMG-1) (predicted)	Hmgb1 /// RGD1562312_predicted /// RGD1563786_predicted /// RGD1563012_predicted	1.042	0.860	1.119	0.648	1.026	0.162	1.043	0.296
1367676_at	NM_017187	high mobility group box 2 /// similar to High mobility group protein 2 (HMG-2) (predicted) /// similar to High mobility group protein 2 (HMG-2) (predicted) /// similar to High mobility group protein 2 (HMG-2) (predicted)	Hmgb2 /// RGD1564519_predicted /// RGD1561694_predicted /// RGD1559962_predicted	1.599	0.239	2.112	0.165	1.337	0.163	1.551	0.454
1368549_at	NM_013221	high mobility group box transcription factor 1	Hbp1	0.649	0.840	1.788	0.052	1.310	0.462	0.935	0.818
1388314_at	BF281178	high mobility group nucleosomal binding domain 1	Hmgn1	0.699	0.013	1.803	0.003	0.441	0.002	1.562	0.005
1371352_at	BM391736	high mobility group nucleosomal binding domain 2	Hmgn2	0.669	0.002	1.134	0.124	0.663	0.003	1.219	0.006
1371989_at	BM386357	high mobility group nucleosomal binding domain 3	Hmgn3	0.753	0.162	0.461	0.001	0.900	0.795	0.590	0.009
1372179_at	BM389406	hippocalcin-like 1	Hpcal1	1.179	0.544	0.691	0.094	1.594	0.064	0.961	0.641
1374423_at	BE115866	hippocampus abundant gene transcript 1 (predicted)	Hiat1_predicted	0.718	0.127	0.812	0.103	0.637	0.020	0.869	0.131
1370520_at	AF260582	hippyragranin	LOC257650	0.945	0.434	0.577	0.023	0.941	0.733	0.705	0.289
1397362_at	AI071343	Hippyragranin	LOC257650	1.291	0.963	0.887	0.208	1.234	0.452	0.931	0.486
1371813_at	BI275598	HIRA interacting protein 3	Hirip3	0.370	0.038	0.716	0.185	0.353	0.048	0.796	0.487
1398932_at	AI227884	histidine triad nucleotide binding protein 1 (predicted)	Hint1_predicted	0.769	0.588	0.856	0.196	0.733	0.013	0.991	0.584
1379395_a_at	BI280018	histidine triad nucleotide binding protein 2 (predicted)	Hint2_predicted	0.561	0.432	0.553	0.010	0.537	0.000	0.597	0.098
1376094_at	AA925490	histidine triad nucleotide binding protein 3	Hint3	0.784	0.202	0.411	0.021	0.771	0.161	0.577	0.046
1388428_at	BF283222	histidyl tRNA synthetase 2 (predicted)	Hars2_predicted	0.664	0.052	1.367	0.049	0.672	0.032	0.989	0.722
1397548_at	BF417363	histocompatibility (minor) HA-1 (predicted)	Hmha1_predicted	0.998	0.973	1.001	0.603	0.999	0.980	1.001	0.462
1377578_at	AI072161	Histocompatibility 13 (predicted)	H13_predicted	0.706	0.090	0.557	0.004	1.024	0.891	0.612	0.041
1378250_at	BE104756	Histocompatibility 13 (predicted)	H13_predicted	0.740	0.185	0.649	0.053	0.976	0.267	0.576	0.049
1375334_at	AW533673	Histocompatibility 13 (predicted)	H13_predicted	0.893	0.570	1.178	0.615	1.224	0.085	1.042	0.502
1390021_at	BM391206	histone 1, H2bh	Hist1h2bh	0.729	0.583	1.283	0.883	0.393	0.984	1.564	0.206
1371332_at	AA848821	Histone 1, H4a (predicted)	Hist1h4a_predicted	1.014	0.218	1.015	0.324	0.467	0.009	1.182	0.237
1371959_at	AI235236	histone 2, H2aa (predicted) /// similar to Hist2h2aa1 protein (predicted)	Hist2h2aa_predicted /// RGD1566374_predicted	0.691	0.946	0.778	0.430	0.403	0.008	0.435	0.215
1384367_at	AI715140	histone 2, H3c2 (predicted) /// similar to histone protein Hist2h3c1 (predicted)	Hist2h3c2_predicted /// RGD1563516_predicted	0.346	0.029	0.990	0.941	0.346	0.029	0.993	0.963
1371765_at	AA850895	histone 2a	H2a	0.508	0.018	0.580	0.031	0.392	0.010	0.698	0.243
1381208_at	BE104595	histone 2a	H2a	0.748	0.145	0.653	0.178	0.413	0.001	1.416	0.685
1393647_at	BI285581	histone aminotransferase 1	Hat1	0.539	0.034	1.504	0.184	0.610	0.080	1.599	0.481
1389162_at	BI277328	histone cell cycle regulation defective interacting protein 5 (predicted)	Hirip5_predicted	1.022	0.664	3.203	0.005	1.118	0.104	2.610	0.001
1388761_at	AI180339	histone deacetylase 1 (predicted)	Hdac1_predicted	0.588	0.014	0.338	0.000	0.717	0.047	0.562	0.006
1396820_at	AW530195	histone deacetylase 1 (predicted)	Hdac1_predicted	0.966	0.929	0.539	0.003	0.988	0.948	0.559	0.004
1390700_s_at	BG378690	histone deacetylase 10	Hdac10	0.999	0.802	0.999	0.992	1.002	0.815	1.009	0.790
1370908_at	AA892297	histone deacetylase 2	Hdac2	0.610	0.001	0.732	0.023	0.966	0.420	0.823	0.001
1369060_a_at	NM_053448	histone deacetylase 3	Hdac3	0.606	0.328	0.543	0.001	0.677	0.001	0.510	0.026
1376761_at	BF419085	histone deacetylase 4 (predicted)	Hdac4_predicted	0.936	0.293	0.833	0.300	0.750	0.144	0.927	0.178
1371819_at	BF403027	histone deacetylase 5	Hdac5	0.726	0.191	1.025	0.291	0.570	0.087	0.913	0.719
1372592_at	AI411391	histone deacetylase 6	Hdac6	0.461	0.005	0.582	0.028	0.357	0.012	0.528	0.004
1378634_at	BE117008	histone deacetylase 8 (predicted)	Hdac8_predicted	0.592	0.040	1.059	0.391	0.833	0.256	1.005	0.245
1384652_at	AI555485	HIV TAT specific factor 1 (predicted)	Htatsf1_predicted	0.677	0.044	0.982	0.139	0.766	0.146	1.288	0.052
1390803_at	BE117639	HIV TAT specific factor 1 (predicted)	Htatsf1_predicted	0.525	0.214	1.398	0.023	0.399	0.032	0.857	0.065
1377400_at	BF391890	HIV-1 Rev binding protein 2 (predicted)	Hrb2_predicted	0.873	0.540	2.769	0.046	1.031	0.948	2.705	0.086
1397370_at	AI548338	HIV-1 Rev binding protein-like (predicted)	Hrbl_predicted	3.460	0.039	1.049	0.938	1.706	0.052	0.999	0.996
1390208_at	BG378579	HIV-1 tat interactive protein 2, homolog (human) (predicted)	Htatip2_predicted	0.434	0.188	0.709	0.014	0.338	0.004	1.099	0.395
1375154_at	BI291268	HIV-1 tat interactive protein, homolog (human)	Htatip	1.401	0.362	1.006	0.765	1.211	0.190	1.002	0.148
1372366_at	BI285597	HIV-1 tat interactive protein, homolog (human)	Htatip	0.963	0.697	1.628	0.038	1.188	0.209	1.277	0.526
1388536_at	BM391608	HLA-B associated transcript 2	Bat2	0.694	0.402	0.874	0.592	0.488	0.254	1.135	0.013
1371985_a_at	BE097389	HLA-B associated transcript 5	Bat5	1.479	0.008	1.655	0.000	1.786	0.013	2.067	0.029
1388158_at	BG057565	HLA-B-associated transcript 1A	Bat1a	1.478	0.571	1.843	0.000	1.240	0.889	1.663	0.000
1387175_a_at	NM_053609	HLA-B-associated transcript 3	Bat3	0.730	0.515	1.226	0.200	0.639	0.007	0.994	0.813
1372118_at	BI281674	HMP19 protein	MGC125201	0.369	0.279	0.241	0.018	0.441	0.016	0.293	0.018

1388363_at	BM389226	hnRNP-associated with lethal yellow	Raly	0.630	0.954	1.440	0.020	0.740	0.570	1.128	0.921
1390408_at	BF405032	holocytochrome c synthetase (predicted)	Hccs_predicted	0.593	0.437	1.198	0.481	0.713	0.081	1.216	0.612
1380442_at	AI235507	homeo box C8 (mapped)	Hoxc8_mapped	0.774	0.358	2.121	0.443	1.456	0.401	1.424	0.836
1385837_at	AA956624	homeo box D3 (mapped)	Hoxd3_mapped	0.875	0.600	0.849	0.946	0.695	0.614	0.939	0.977
1367816_at	NM_133621	homeobox only domain	Hod	1.035	0.684	2.052	0.156	7.093	0.013	10.509	0.008
1376692_at	BM392321	homeodomain interacting protein kinase 2 (predicted)	Hipk2_predicted	1.564	0.168	1.742	0.170	1.657	0.505	1.976	0.101
1369352_at	NM_031787	homeodomain interacting protein kinase 3	Hipk3	1.047	0.129	2.476	0.025	1.053	0.564	1.002	0.538
1399163_a_at	BM388880	homer homolog 1 (Drosophila)	Homer1	0.799	0.098	0.763	0.027	0.550	0.011	0.779	0.046
1370454_at	AB003726	homer homolog 1 (Drosophila)	Homer1	0.731	0.101	0.908	0.460	0.891	0.788	0.803	0.138
1385757_at	BF397258	Homer homolog 1 (Drosophila)	Homer1	1.049	0.965	0.837	0.489	2.913	0.022	0.895	0.767
1385573_at	AI070797	Homer homolog 3 (Drosophila)	Homer3	1.002	0.589	1.281	0.233	1.001	0.147	1.195	0.094
1370212_at	AW253366	homer homolog 3 (Drosophila)	Homer3	1.005	0.629	0.998	0.136	1.006	0.023	1.004	0.990
1367741_at	NM_053523	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	Herpud1	1.103	0.299	2.287	0.000	1.069	0.352	1.878	0.010
1371609_at	AI232270	homolog of zebrafish ES1	RGD1303003	0.448	0.140	0.956	0.766	0.479	0.018	0.980	0.909
1386689_at	BF563120	hook homolog 2 (Drosophila)	Hook2	0.992	0.995	1.071	0.350	1.001	0.955	1.037	0.307
1373126_at	AW918188	Hook homolog 3 (Drosophila)	Hook3	0.478	0.023	0.588	0.131	0.260	0.025	0.706	0.700
1385931_at	AW535564	hook homolog 3 (Drosophila)	Hook3	0.504	0.055	0.970	0.763	0.319	0.109	0.772	0.261
1380824_at	AI501458	Hook homolog 3 (Drosophila)	Hook3	0.666	0.150	0.886	0.508	0.663	0.003	0.879	0.474
1389384_at	BE111733	hormone-regulated proliferation associated protein 20	Hrpap20	1.289	0.222	3.200	0.007	1.473	0.025	4.073	0.002
1371510_at	AA944494	host cell factor C1 regulator 1 (XPO1-dependent)	Hcfc1r1	0.678	0.474	1.195	0.072	0.695	0.016	0.933	0.342
1392089_at	AW435314	host cell factor C2	Hcfc2	0.653	0.026	0.438	0.036	0.787	0.032	0.339	0.037
1383125_at	AW525401	HpaII tiny fragments locus 9c	Htf9c	0.614	0.053	1.763	0.052	0.379	0.107	0.999	0.991
1370202_at	BG378637	HRAS like suppressor 3	Hrasls3	17.671	0.020	7.711	0.028	39.971	0.002	52.873	0.003
1370316_at	AF187860	hsp70-interacting protein	Hspbp1	0.776	0.258	1.351	0.026	0.435	0.012	1.309	0.075
1368195_at	NM_134419	Hspb associated protein 1	Hspbap1	0.811	0.236	3.886	0.005	1.001	0.254	2.225	0.026
1368546_at	NM_024137	human immunodeficiency virus type I enhancer binding protein 2	Hivep2	4.159	0.040	1.227	0.024	3.257	0.037	1.161	0.381
1389132_at	AW253339	Huntingtin interacting protein 1	Hip1	0.642	0.018	0.386	0.030	0.941	0.844	0.676	0.020
1370994_at	BG381386	huntingtin interacting protein 1 related	Hip1r	1.017	0.272	1.013	0.833	0.721	0.101	0.678	0.002
1383820_at	AI072624	Huntingtin interacting protein 1 related	Hip1r	0.871	0.608	0.707	0.153	0.779	0.473	0.836	0.543
1378581_at	BI295536	huntingtin interacting protein 1 related	Hip1r	1.061	0.666	0.903	0.463	1.042	0.360	0.705	0.082
1385259_at	AI112792	huntingtin interacting protein 2 (predicted)	Hip2_predicted	1.213	0.512	0.834	0.175	1.312	0.802	0.763	0.109
1373063_at	BI277000	huntingtin interacting protein 2 (predicted)	Hip2_predicted	0.856	0.673	1.479	0.007	0.718	0.005	1.177	0.282
1369358_a_at	AI412750	huntingtin-associated protein 1	Hap1	0.337	0.071	0.136	0.000	0.675	0.123	0.210	0.012
1370395_at	U18650	Huntington disease gene homolog	Hdh	1.344	0.006	1.569	0.096	1.584	0.001	1.222	0.033
1378614_at	BI274329	Huntington disease gene homolog	Hdh	1.395	0.265	2.124	0.105	1.417	0.023	1.539	0.039
1386514_at	AA819731	Hyaluronan and proteoglycan link protein 4 (predicted)	Hapln4_predicted	0.952	0.333	0.418	0.052	1.226	0.505	0.412	0.075
1370462_at	AI171185	hyaluronan mediated motility receptor (RHAMM)	Hmmr	1.394	0.040	1.074	0.167	1.207	0.991	0.997	0.960
1389665_at	BG375619	hyaluronic acid binding protein 4 (predicted)	Habp4_predicted	0.296	0.003	0.760	0.039	0.294	0.002	0.659	0.094
1370370_at	AF034218	hyaluronoglucosaminidase 2	Hyal2	0.874	0.142	1.019	0.016	0.871	0.147	1.009	0.973
1396480_at	BG372249	Hyaluronoglucosaminidase 3	Hyal3	0.863	0.190	0.913	0.066	1.039	0.728	1.045	0.907
1369986_at	NM_033349	hydroxyacyl glutathione hydrolase	Hagh	0.465	0.423	0.370	0.002	0.465	0.049	0.297	0.004
1367662_at	NM_031682	hydroxyacyl-Coenzyme A dehydrogenase type II	Hadh2	0.422	0.299	0.844	0.935	0.368	0.131	0.724	0.275
1370164_at	AA800240	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	Hadha	1.377	0.262	1.078	0.299	1.943	0.024	1.361	0.012
1367694_at	NM_133618	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	Hadhb	0.904	0.676	1.393	0.005	1.031	0.385	1.375	0.007
1370433_at	AB000199	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	Hsd3b7	0.712	0.180	0.872	0.231	0.589	0.075	1.276	0.398
1386983_at	NM_013168	hydroxymethylbilane synthase	Hmbs	0.236	0.225	0.765	0.116	0.208	0.016	0.679	0.005
1376191_at	AA848820	hydroxyprostaglandin dehydrogenase 15 (NAD)	Hpgd	0.207	0.071	0.286	0.002	0.287	0.003	0.255	0.009
1387631_at	NM_024390	hydroxyprostaglandin dehydrogenase 15 (NAD)	Hpgd	0.420	0.343	0.080	0.006	0.992	0.318	0.095	0.000
1368051_at	NM_032066	hydroxysteroid (17-beta) dehydrogenase 12	Hsd17b12	0.632	0.181	0.721	0.003	0.819	0.475	0.747	0.004
1367672_at	NM_024392	hydroxysteroid (17-beta) dehydrogenase 4	Hsd17b4	0.291	0.123	0.190	0.003	0.478	0.001	0.312	0.032
1382492_a_at	AA866404	hydroxysteroid (17-beta) dehydrogenase 8	Hsd17b8	0.964	0.320	1.033	0.556	0.614	0.143	0.945	0.413
1379447_at	AW526204	hyperpolarization-activated cyclic nucleotide-gated potassium channel 3	Hcn3	0.846	0.082	1.592	0.070	0.545	0.160	1.482	0.004
1372087_at	BG666916	hypertrophic agonist responsive protein B64	Harpb64	1.480	0.470	0.877	0.274	1.850	0.021	1.434	0.035
1373671_at	AA944790	Hypothetical gene LOC554364	LOC554364	0.832	0.813	0.417	0.003	1.490	0.214	0.526	0.091
1372809_at	AI716200	hypothetical gene supported by AF152002	LOC290595	3.658	0.119	2.336	0.037	3.159	0.027	1.300	0.520
1368138_at	BI281170	hypothetical gene supported by NM_017212	LOC497674	0.538	0.040	0.910	0.069	0.689	0.087	0.670	0.030
1367778_at	NM_019331	hypothetical gene supported by NM_019331	LOC497733	0.804	0.070	0.666	0.002	0.508	0.000	0.567	0.000
1368174_at	NM_019371	hypothetical gene supported by NM_019371	LOC497816	1.035	0.718	3.909	0.010	0.687	0.951	2.891	0.063
1387000_at	NM_019385	hypothetical gene supported by NM_019385	LOC497835	0.717	0.107	1.624	0.015	0.884	0.229	1.149	0.421

1367853_at	NM_031798	hypothetical gene supported by NM_031798	LOC497723	0.345	0.000	0.287	0.001	0.353	0.016	0.398	0.033
1382264_at	AI714243	hypothetical gene supported by NM_133381	LOC497663	1.288	0.080	0.981	0.806	1.106	0.527	0.870	0.096
1393663_at	BI274126	hypothetical gene supported by NM_139339	LOC497667	1.279	0.928	0.725	0.365	1.051	0.846	1.399	0.379
1370517_at	U18772	hypothetical gene supported by NM_153735	LOC497675	0.095	0.014	0.095	0.008	0.118	0.007	0.086	0.049
1383768_at	BF563441	hypothetical gene supported by NM_173309	LOC497806	1.029	0.069	1.508	0.040	1.455	0.153	1.327	0.028
1372099_at	BI303661	hypothetical gene supported by NM_199207	LOC497793	0.890	0.552	1.782	0.036	0.939	0.192	1.352	0.200
1370872_at	BF288095	hypothetical gene supported by Y16641 (predicted) /// similar to Hnrpa3 protein (predicted) /// similar to Hnrpa3 protein (predicted)	RGD1564920_predicted /// RGD1562688_predicted /// RGD1563768_predicted	0.932	0.806	1.490	0.009	0.770	0.271	1.136	0.023
1370871_at	BM384165	hypothetical gene supported by Y16641; Y16641 (predicted)	RGD1561108_predicted	1.098	0.923	1.014	0.070	0.994	0.798	0.818	0.113
1374853_at	AI137833	hypothetical LOC287173	RGD1305622	1.220	0.287	2.331	0.010	1.065	0.589	1.917	0.006
1390503_at	BI301268	Hypothetical LOC287306 (predicted)	RGD1307036_predicted	1.363	0.136	1.110	0.109	1.009	0.870	1.030	0.529
1389203_at	BM387541	Hypothetical LOC287306 (predicted)	RGD1307036_predicted	1.011	0.373	0.821	0.450	1.025	0.888	0.693	0.488
1376912_at	BI290097	hypothetical LOC287388 (predicted)	RGD1310324_predicted	0.716	0.049	0.758	0.337	0.729	0.057	0.672	0.498
1377940_at	BF398271	hypothetical LOC287534	RGD1359691	1.041	0.923	1.002	0.991	1.105	0.821	0.999	0.997
1375425_at	BF395126	hypothetical LOC287541 (predicted)	RGD1309400_predicted	0.678	0.244	1.398	0.084	0.681	0.087	1.130	0.334
1374991_at	BE107630	hypothetical LOC287938	LOC287938	0.561	0.043	0.998	0.977	0.567	0.040	0.999	0.997
1397378_at	BE115240	Hypothetical LOC288354 (predicted)	RGD1308321_predicted	0.847	0.409	1.013	0.794	0.790	0.217	0.879	0.213
1393030_at	BE115641	hypothetical LOC291900 /// similar to spermatogenesis associated glutamate (E)-rich protein 4d /// hypothetical LOC317026 /// hypothetical LOC363325 /// LOC501316	LOC291900 /// LOC301986 /// LOC317026 /// LOC363325 /// LOC501316	0.598	0.056	0.349	0.006	0.491	0.038	0.335	0.058
1389338_at	AA875518	hypothetical LOC293114 (predicted)	RGD1308371_predicted	1.011	0.785	1.397	0.177	1.081	0.907	1.367	0.135
1399001_at	BI285943	hypothetical LOC294030	RGD1305481	0.890	0.597	1.236	0.029	0.973	0.266	1.300	0.077
1373136_at	AI013609	hypothetical LOC294390	RGD1307672	2.338	0.028	1.495	0.018	3.065	0.007	1.767	0.001
1374090_at	BI296363	hypothetical LOC295216 /// similar to DKFZP547E1010 protein	LOC295216 /// LOC361990	0.789	0.561	0.852	0.613	1.153	0.239	0.710	0.793
1384411_at	AA962968	Hypothetical LOC296884	LOC296884	1.239	0.949	0.863	0.116	1.115	0.815	0.816	0.892
1382218_at	AI012175	hypothetical LOC298077	RGD1305807	1.970	0.110	3.914	0.018	1.597	0.094	2.661	0.079
1372966_at	AI178784	hypothetical LOC298504 (predicted)	RGD1310174_predicted	0.373	0.001	0.535	0.077	0.579	0.005	0.575	0.127
1371745_at	AI179388	hypothetical LOC300361	RGD1310669	0.602	0.806	1.249	0.074	0.451	0.339	1.131	0.559
1372387_at	BF416240	hypothetical LOC300751 (predicted)	RGD1311874_predicted	1.387	0.811	1.139	0.319	1.001	0.911	1.011	0.995
1387909_at	U94904	hypothetical LOC301448	LOC301448	0.713	0.174	0.508	0.002	0.832	0.019	0.578	0.012
1376072_at	AI170779	hypothetical LOC301634 /// similar to RGD1309973_predicted protein	RGD1309973 /// LOC501188	0.997	0.682	0.553	0.010	1.922	0.602	0.590	0.085
1392547_at	AI716211	hypothetical LOC302884	MGC105649	85.708	0.000	21.055	0.004	47.224	0.000	19.230	0.001
1377938_at	AA859585	hypothetical LOC302941	RGD1359443	1.157	0.614	3.415	0.001	0.741	0.091	2.799	0.002
1375430_at	BM389077	hypothetical LOC303211	RGD1311260	0.079	0.012	1.126	0.059	0.276	0.009	1.115	0.419
1385088_at	AA891356	hypothetical LOC304650 (predicted)	RGD1310262_predicted	0.569	0.116	0.995	0.553	0.791	0.198	1.056	0.901
1382600_at	AA958022	Hypothetical LOC305452 (predicted)	RGD1309634_predicted	0.527	0.301	1.212	0.979	1.073	0.048	1.803	0.280
1374561_at	AW523899	hypothetical LOC305452 (predicted)	RGD1309634_predicted	1.220	0.341	1.456	0.415	1.086	0.747	1.252	0.897
1376309_at	BI296018	hypothetical LOC305452 (predicted)	RGD1309634_predicted	0.991	0.678	0.649	0.130	1.059	0.579	0.626	0.007
1380503_at	BI290590	hypothetical LOC305452 (predicted)	RGD1309634_predicted	1.037	0.726	0.970	0.836	1.002	0.932	0.810	0.128
1380263_at	BI290769	hypothetical LOC305452 (predicted)	RGD1309634_predicted	1.133	0.821	0.869	0.452	1.091	0.905	0.863	0.294
1381757_at	AA965058	hypothetical LOC305552 (predicted)	RGD1309501_predicted	0.553	0.007	0.803	0.194	0.579	0.013	1.092	0.194
1386143_at	AA799997	hypothetical LOC305552 (predicted)	RGD1309501_predicted	1.049	0.915	0.730	0.130	1.257	0.909	0.817	0.786
1371389_at	AI170668	hypothetical LOC306766	LOC306766	0.816	0.773	0.993	0.959	0.757	0.010	1.190	0.610
1398996_at	AI007987	hypothetical LOC308765 (predicted)	RGD1311021_predicted	0.753	0.452	0.966	0.913	0.640	0.110	1.107	0.218
1375435_at	AW251686	hypothetical LOC308765 (predicted)	RGD1311021_predicted	0.730	0.509	1.534	0.022	0.316	0.087	0.830	0.050
1384296_at	AI136388	hypothetical LOC312654 (predicted)	RGD1311909_predicted	1.410	0.162	0.525	0.009	0.897	0.525	0.801	0.024
1383793_at	BI274808	hypothetical LOC312654 (predicted)	RGD1311909_predicted	1.834	0.224	2.907	0.041	1.041	0.388	2.112	0.074
1396151_at	AA850797	hypothetical LOC312654 (predicted)	RGD1311909_predicted	0.779	0.758	0.770	0.991	1.869	0.148	0.830	0.911
1384066_at	AW921699	hypothetical LOC314168 (predicted)	RGD1307621_predicted	1.227	0.469	1.655	0.097	0.945	0.866	1.039	0.821
1379703_at	BF288207	hypothetical LOC315055 (predicted)	RGD1311559_predicted	2.667	0.030	1.654	0.953	4.574	0.003	1.206	0.191
1390619_at	AI178473	Hypothetical LOC315216 (predicted)	RGD1311907_predicted	0.806	0.096	0.905	0.111	0.825	0.230	0.905	0.179
1376156_at	BM391273	hypothetical LOC316091	RGD1304827	0.343	0.013	0.434	0.001	0.332	0.004	0.412	0.050
1382292_at	BF285343	hypothetical LOC361366	LOC361366	1.029	0.914	1.079	0.626	1.327	0.218	0.986	0.791
1388904_at	AI236597	hypothetical protein Dd25	Dd25	1.284	0.018	1.289	0.023	1.353	0.000	1.152	0.063
1376524_at	BG378747	hypothetical protein Dd25	Dd25	1.198	0.061	1.904	0.094	1.053	0.345	1.496	0.083
1375911_at	AI171772	hypothetical protein LK44	RGD735140	1.184	0.362	3.333	0.005	1.104	0.589	2.163	0.004
1393606_at	AI137411	hypothetical protein LK44	RGD735140	0.908	0.825	1.474	0.129	0.915	0.130	1.058	0.756
1377214_a_at	BF405050	hypothetical protein LOC292764	RGD1303117	0.879	0.995	0.891	0.416	0.729	0.209	0.999	0.990
1372217_at	BM385348	hypothetical protein LOC303332	LOC303332	0.586	0.059	1.484	0.015	0.568	0.006	1.453	0.036

1385268_at	BI289167	hypothetical protein LOC304743	LOC304743	1.841	0.046	3.562	0.000	2.160	0.008	2.840	0.000
1385269_s_at	BI289167	hypothetical protein LOC304743	LOC304743	1.102	0.661	3.291	0.002	1.603	0.066	2.046	0.004
1398988_at	BE110642	hypothetical protein LOC307347	LOC307347	0.951	0.898	0.821	0.155	0.850	0.291	0.951	0.602
1378914_a_at	AI059468	hypothetical protein LOC308990	LOC308990	0.912	0.905	0.953	0.191	1.033	0.089	0.962	0.763
1388817_at	BI284848	hypothetical protein LOC310665	LOC310665	0.831	0.260	1.042	0.630	0.546	0.008	0.930	0.285
1388985_at	AI012869	hypothetical protein LOC310926 /// LOC501211	LOC310926 /// LOC501211	0.574	0.051	0.772	0.507	0.604	0.565	1.017	0.947
1382234_at	BI286950	Hypothetical protein LOC311254	LOC311254	0.693	0.117	0.833	0.035	0.820	0.508	0.995	0.236
1398429_at	AA893184	hypothetical protein LOC311254	LOC311254	1.142	0.492	2.851	0.003	1.093	0.684	2.114	0.001
1394330_at	BF544149	hypothetical protein LOC361915 /// similar to LRRG00135 (predicted) /// similar to LRRG00135 /// similar to LRRGT00191 (predicted) /// similar to LRRGT00191 /// similar to LRRGT00174 /// similar to LRRG00135 /// similar to LRRG00135 (predicted) /// similar to LRRGT00150 /// similar to LRRGT00108 /// similar to LRRGT00014 /// similar to LRRGT00108 /// hypothetical protein LOC501130 /// similar to LRRG00135 /// similar to LRRG00135 /// similar to LRRG00135 (predicted) /// similar to LRRG00135	LOC361915 /// RGD1565352_predicted /// LOC498217 /// RGD1560298_predicted /// LOC498645 /// LOC499198 /// LOC499460 /// RGD1561567_predicted /// LOC499804 /// LOC500179 /// LOC500617 /// LOC500675 /// LOC501130 /// LOC501504 /// LOC501548 /// RGD1562616_predicted /// LOC501637	1.360	0.773	0.804	0.239	0.761	0.741	0.682	0.142
1385067_at	BE117752	hypothetical protein LOC361915 /// similar to LRRG00135 (predicted) /// similar to LRRG00135 /// similar to LRRGT00191 /// similar to LRRGT00174 /// similar to LRRG00135 /// similar to LRRG00135 (predicted) /// similar to LRRGT00150 /// similar to LRRGT00108 /// similar to LRRGT00014 /// similar to LRRGT00108 /// hypothetical protein LOC501130 /// similar to LRRG00135 /// similar to LRRG00135 /// similar to LRRG00135 (predicted) /// similar to LRRG00135 /// similar to LRRGT00057 (predicted) /// similar to LRRGT00088 /// similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH	LOC361915 /// RGD1565352_predicted /// LOC498217 /// LOC498645 /// LOC499198 /// LOC499460 /// RGD1561567_predicted /// LOC499804 /// LOC500179 /// LOC500617 /// LOC500675 /// LOC501130 /// LOC501504 /// LOC501548 /// RGD1562616_predicted /// LOC501637 /// RGD1564501_predicted /// LOC501760 /// LOC501761	1.189	0.449	0.902	0.458	0.655	0.265	0.841	0.084
1391152_at	AI412781	hypothetical protein LOC363306 /// similar to RIKEN cDNA 4930555G01 /// similar to RIKEN cDNA 1700001E04 (predicted)	LOC363306 /// LOC363318 /// RGD1561272_predicted	1.048	0.915	0.769	0.076	1.286	0.330	0.844	0.096
1383301_at	AI237554	hypothetical protein LOC498154	LOC498154	0.783	0.168	0.549	0.076	0.746	0.150	0.542	0.088
1389488_at	AA800750	hypothetical protein LOC498544	LOC498544	1.137	0.699	1.270	0.940	1.298	0.028	1.129	0.402
1389156_at	BM384589	hypothetical protein LOC498606	LOC498606	1.004	0.937	0.983	0.432	1.056	0.695	0.963	0.414
1389146_at	BF283267	hypothetical protein LOC498796	LOC498796	3.028	0.023	1.111	0.328	1.436	0.628	0.449	0.003
1375927_at	BE100774	Hypothetical protein LOC499120	LOC499120	0.455	0.002	0.481	0.007	0.667	0.074	0.595	0.009
1384258_at	AW920266	Hypothetical protein LOC499120	LOC499120	1.308	0.179	1.225	0.851	1.052	0.951	1.020	0.958
1377708_at	BF281491	hypothetical protein LOC499339	LOC499339	0.961	0.558	3.790	0.001	0.856	0.598	3.493	0.001
1390830_at	BE113228	hypothetical protein LOC499602	LOC499602	0.823	0.345	1.926	0.023	0.856	0.404	1.147	0.423
1393696_at	AA818846	hypothetical protein LOC499856	LOC499856	0.575	0.529	0.870	0.122	0.923	0.141	0.971	0.669
1380684_at	BI303657	Hypothetical protein LOC500086	LOC500086	1.225	0.232	1.239	0.277	1.012	0.273	1.333	0.067
1385950_at	AI454926	hypothetical protein LOC500102	LOC500102	3.775	0.014	1.090	0.958	1.541	0.053	1.002	0.156
1373476_at	AI410833	hypothetical protein LOC500251	LOC500251	1.131	0.103	1.244	0.010	0.998	0.637	1.118	0.105
1371640_at	BF289183	hypothetical protein LOC500855	LOC500855	1.231	0.500	1.291	0.156	0.931	0.847	1.268	0.191
1373819_at	AI232337	hypothetical protein LOC500855	LOC500855	0.664	0.842	0.772	0.030	0.831	0.904	0.654	0.019
1383662_at	AI043759	hypothetical protein LOC500956	LOC500956	3.188	0.001	2.108	0.002	3.162	0.002	2.097	0.002
1370684_s_at	U08214	hypothetical protein LOC501546	LOC501546	0.809	0.057	1.191	0.167	0.851	0.113	1.286	0.025
1389814_at	BI299841	hypothetical protein LOC501546	LOC501546	0.920	0.505	0.908	0.740	1.094	0.758	0.823	0.425
1372556_at	AA924509	hypothetical protein LOC502374	LOC502374	0.873	0.830	0.848	0.096	0.937	0.404	0.944	0.395
1371816_at	AI407560	Hypothetical protein LOC502684	LOC502684	1.254	0.467	0.827	0.265	0.664	0.582	0.902	0.121
1374777_at	BG380800	hypothetical protein LOC502894	LOC502894	2.388	0.073	1.501	0.952	0.881	0.953	1.319	0.600
1376496_at	AI717736	hypothetical protein LOC503164	LOC503164	14.856	0.017	4.075	0.007	37.491	0.002	13.818	0.015
1392908_at	BG381166	hypothetical protein LOC595134	LOC595134	1.163	0.526	1.230	0.002	0.893	0.810	1.450	0.031

1373011_at	BE109520	hypothetical protein LOC619558	LOC619558	1.855	0.000	1.270	0.022	0.881	0.590	0.938	0.076
1373012_at	BE109520	Hypothetical protein LOC619558	LOC619558	1.798	0.034	0.968	0.735	0.869	0.777	0.750	0.013
1375416_at	AI231165	hypothetical protein LOC619573	LOC619573	0.783	0.037	1.925	0.047	0.701	0.042	1.005	0.308
1372487_at	BI296006	hypothetical protein LOC619573	LOC619573	0.959	0.888	1.121	0.784	0.784	0.419	0.987	0.433
1373831_at	AW920524	hypothetical protein LOC619574	LOC619574	3.623	0.002	5.509	0.008	6.122	0.004	4.508	0.002
1373830_at	AA893539	hypothetical protein LOC619574	LOC619574	1.620	0.129	1.013	0.589	2.537	0.009	1.508	0.007
1388423_at	BM385163	hypothetical protein MGC:15854	RGD1302996	0.925	0.621	1.891	0.002	0.549	0.321	1.411	0.010
1372871_at	AA891821	hypothetical protein MGC:72616	RGD735175	1.387	0.245	1.831	0.037	1.147	0.571	1.430	0.041
1370947_at	AI228197	hypothetical protein RDA279	Rda279	0.818	0.306	1.916	0.029	0.696	0.109	1.635	0.043
1380334_at	AI555044	hypothetical RNA binding protein RGD1359713	RGD1359713	1.975	0.013	1.388	0.031	1.642	0.029	1.233	0.053
1376728_at	BM392264	Hypothetical RNA binding protein RGD1359713	RGD1359713	1.647	0.022	1.303	0.534	1.723	0.017	0.931	0.666
1376336_at	BM392257	Hypoxanthine guanine phosphoribosyl transferase	Hprt	1.048	0.458	0.554	0.078	1.797	0.030	0.726	0.052
1370280_at	M86443	hypoxanthine guanine phosphoribosyl transferase	Hprt	0.973	0.851	1.476	0.046	1.007	0.237	1.454	0.030
1370062_at	NM_080902	hypoxia induced gene 1	Hig1	1.124	0.322	2.730	0.028	1.104	0.437	1.769	0.048
1374105_at	H31665	hypoxia induced gene 1	Hig1	0.927	0.950	2.328	0.007	0.950	0.884	1.811	0.018
1387076_at	NM_024359	hypoxia inducible factor 1, alpha subunit	Hif1a	2.023	0.049	2.066	0.007	1.577	0.147	2.156	0.002
1371442_at	BI282904	hypoxia up-regulated 1	Hyou1	0.805	0.244	1.018	0.435	1.042	0.216	0.922	0.743
1370665_at	U41853	hypoxia up-regulated 1	Hyou1	0.794	0.952	0.959	0.181	0.571	0.936	0.808	0.187
1393047_at	BF416560	IBR domain containing 1 (predicted)	Ibrdc1_predicted	0.901	0.912	2.549	0.004	1.002	0.972	1.830	0.021
1382074_at	AI113237	IBR domain containing 3 (predicted)	Ibrdc3_predicted	6.731	0.004	4.072	0.000	5.969	0.001	4.836	0.001
1381709_at	BE098754	IBR domain containing 3 (predicted)	Ibrdc3_predicted	0.822	0.157	1.011	0.823	0.886	0.147	1.027	0.613
1389062_at	BE109152	IK cytokine	Ik	0.724	0.138	0.990	0.721	0.744	0.043	0.992	0.714
1373512_at	BI295737	ilvB (bacterial acetolactate synthase)-like (predicted)	Ilvbl_predicted	0.447	0.060	1.038	0.938	0.353	0.057	1.111	0.313
1397521_at	BF281905	ilvB (bacterial acetolactate synthase)-like (predicted)	Ilvbl_predicted	1.002	0.919	0.998	0.832	1.003	0.955	0.999	0.913
1374443_at	AW915478	immature colon carcinoma transcript 1 (predicted)	Ict1_predicted	0.682	0.483	1.218	0.109	0.522	0.169	1.368	0.040
1372389_at	BF420059	immediate early response 2	Ier2	1.096	0.481	1.181	0.140	1.016	0.920	1.176	0.132
1388587_at	AI176519	immediate early response 3	Ier3	1.512	0.440	5.579	0.032	1.677	0.198	4.015	0.012
1389355_at	BF285187	immediate early response 5	Ier5	9.029	0.000	4.314	0.001	6.519	0.003	5.362	0.005
1391489_at	AI407339	immunity-related GTPase family, M	Irgm	234.103	0.001	38.522	0.000	361.753	0.000	115.156	0.000
1390104_at	BI296551	immunity-related GTPase family, Q (predicted)	Irgq_predicted	0.786	0.605	0.390	0.163	1.068	0.865	0.759	0.621
1369981_at	NM_031624	immunoglobulin (CD79A) binding protein 1	Igbp1	0.824	0.180	1.086	0.916	0.747	0.025	1.000	0.635
1371262_at	AJ391299	immunoglobulin heavy chain (alpha polypeptide) (mapped) /// similar to immunoglobulin heavy chain variable region (predicted) /// gamma-2a immunoglobulin heavy chain /// similar to Immunoglobulin heavy chain (gamma polypeptide) (predicted) /// similar to immunoglobulin heavy chain variable region /// similar to immunoglobulin heavy chain variable region (predicted) /// similar to immunoglobulin heavy chain variable region (predicted) /// similar to immunoglobulin heavy chain variable region /// similar to immunoglobulin heavy chain variable region (predicted) /// similar to Ig heavy chain V region PJ14 precursor (predicted) /// similar to immunoglobulin heavy chain variable region (predicted)	Igha_mapped /// RGD1564658_predicted /// IgG-2a /// RGD1565478_predicted /// LOC500733 /// RGD1564392_predicted /// RGD1562780_predicted /// LOC500736 /// RGD1562606_predicted /// RGD1563394_predicted /// RGD1564251_predicted	0.689	0.644	0.611	0.057	1.236	0.092	0.574	0.037
1370594_at	AF322217	immunoglobulin superfamily, member 1	Igsf1	0.638	0.164	0.361	0.066	0.913	0.372	0.547	0.039
1370410_at	AF322216	immunoglobulin superfamily, member 1	Igsf1	0.854	0.302	0.457	0.039	0.822	0.428	0.494	0.023
1376733_at	AI407898	immunoglobulin superfamily, member 11	Igsf11	0.459	0.086	0.459	0.014	0.683	0.020	0.702	0.001
1377508_at	BI298836	Immunoglobulin superfamily, member 11	Igsf11	0.804	0.361	0.762	0.093	0.737	0.003	0.747	0.088
1376657_at	BE117767	immunoglobulin superfamily, member 4A	Igsf4a	1.058	0.138	0.934	0.103	0.824	0.833	0.803	0.051
1384132_at	H31111	immunoglobulin superfamily, member 4A	Igsf4a	1.022	0.930	0.827	0.205	0.685	0.257	0.849	0.219
1391887_at	BG372263	immunoglobulin superfamily, member 9 (predicted)	Igsf9_predicted	1.128	0.122	0.994	0.974	1.493	0.145	1.201	0.854
1388321_at	BG378108	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast) (predicted)	Imp3_predicted	0.395	0.002	0.853	0.024	0.416	0.013	0.875	0.187
1379407_at	BE104538	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	Imp4	0.515	0.380	1.221	0.130	0.535	0.355	1.147	0.206
1371957_at	BM388851	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	Imp4	0.913	0.798	1.215	0.091	0.775	0.095	1.184	0.043
1369868_at	NM_053946	implantation-associated protein	Iag2	0.640	0.323	0.786	0.044	0.695	0.117	0.628	0.008
1367876_at	NM_053778	importin 13	Ipo13	0.834	0.194	1.009	0.842	0.824	0.463	1.017	0.929
1374135_at	AI233262	importin 4 (predicted)	Ipo4_predicted	0.777	0.465	2.385	0.003	0.646	0.020	1.885	0.000
1375185_at	BM390183	importin 7 (predicted)	Ipo7_predicted	1.074	0.602	2.149	0.017	0.953	0.724	1.940	0.039
1380578_at	AA859349	Importin 7 (predicted)	Ipo7_predicted	0.918	0.890	2.102	0.868	1.268	0.608	1.140	0.232
1389984_at	AI072294	Importin 9 (predicted)	Ipo9_predicted	0.968	0.082	0.398	0.002	1.486	0.088	0.459	0.097
1372723_at	BF396318	Importin 9 (predicted)	Ipo9_predicted	1.073	0.311	0.642	0.001	1.110	0.658	0.811	0.037
1373972_at	BF387266	importin 9 (predicted)	Ipo9_predicted	1.174	0.944	1.354	0.954	1.260	0.393	0.992	0.998
1372193_at	AI408713	imprinted and ancient	Impact	1.619	0.056	1.454	0.006	1.732	0.062	1.334	0.010

1395339_at	BG664101	imprinted and ancient	Impact	0.933	0.651	0.997	0.325	1.000	0.419	0.736	0.744
1375754_at	AA850890	imprinted and ancient	Impact	0.999	0.721	1.811	0.269	0.938	0.418	1.539	0.081
1387608_at	NM_023973	indoleamine-pyrrole 2,3 dioxygenase	Indo	18.955	0.030	8.001	0.002	30.369	0.000	19.816	0.000
1370769_a_at	AB023133	inducible T-cell co-stimulator	Icos	1.054	0.794	0.993	0.647	0.913	0.534	1.002	0.847
1389521_at	AI408553	influenza virus NS1A binding protein (predicted)	Ivns1abp_predicted	0.683	0.127	0.726	0.012	0.620	0.064	0.663	0.002
1387124_at	NM_012590	inhibin alpha	Inha	0.777	0.245	0.979	0.913	0.775	0.247	0.982	0.993
1369238_at	NM_031815	inhibin beta E /// hypothetical gene supported by NM_031815	Inhbe /// LOC497821	0.867	0.662	0.966	0.488	0.865	0.417	0.897	0.651
1387028_a_at	M86708	inhibitor of DNA binding 1	Id1	1.048	0.931	0.996	0.982	0.959	0.964	0.998	0.750
1385923_at	AA944139	Inhibitor of DNA binding 4	Id4	1.731	0.335	2.234	0.109	1.072	0.382	1.368	0.375
1373457_at	AI170649	inhibitor of growth family, member 1	Ing1	0.937	0.291	0.998	0.050	0.987	0.797	0.625	0.028
1376758_at	AW532065	inhibitor of growth family, member 1	Ing1	1.110	0.311	1.373	0.196	1.231	0.267	0.891	0.418
1386129_at	BF523624	inhibitor of growth family, member 1-like (predicted)	Ing1l_predicted	0.967	0.182	1.176	0.112	0.568	0.009	1.158	0.836
1392165_at	AI071247	inhibitor of growth family, member 1-like (predicted)	Ing1l_predicted	0.738	0.206	1.522	0.007	0.502	0.001	1.040	0.703
1372945_at	BI296751	inhibitor of growth family, member 3	Ing3	1.208	0.710	1.410	0.404	1.036	0.145	1.103	0.087
1373817_at	BM391761	inhibitor of growth family, member 4	Ing4	0.984	0.807	1.259	0.190	0.992	0.983	1.052	0.019
1376812_at	BF419731	Inhibitor of growth family, member 5 (predicted)	Ing5_predicted	0.844	0.987	0.843	0.029	0.830	0.220	0.935	0.738
1387115_at	NM_080899	inhibitor of kappa light polypeptide enhancer in B-cells, kinase complex-associated protein	Ikbkap	0.967	0.054	1.498	0.012	0.869	0.467	1.131	0.120
1368424_at	NM_053355	inhibitor of kappaB kinase beta	Ikbkb	2.296	0.026	1.748	0.045	1.641	0.150	1.189	0.196
1383292_at	AI599126	inner centromere protein (predicted)	Incenp_predicted	0.999	0.994	0.997	0.920	1.003	0.971	0.994	0.962
1385423_at	AW521399	inner membrane protein, mitochondrial	Immt	0.529	0.019	0.543	0.132	0.607	0.014	0.475	0.090
1372080_at	BI287936	inner membrane protein, mitochondrial	Immt	0.613	0.025	0.904	0.134	0.610	0.000	0.900	0.673
1375597_at	BI300655	Inner membrane protein, mitochondrial	Immt	0.892	0.551	1.346	0.343	1.366	0.184	0.963	0.963
1388629_at	BF281278	inosine 5-monophosphate dehydrogenase 2	Impdh2	0.488	0.024	1.900	0.002	0.484	0.005	1.343	0.012
1372732_at	BM386917	inosine triphosphatase (nucleoside triphosphate pyrophosphatase) (mapped)	Itpa_mapped	0.785	0.131	0.896	0.324	0.610	0.040	0.810	0.538
1398808_at	NM_032057	Inositol (myo)-1(or 4)-monophosphatase 1	Impa1	0.433	0.064	0.562	0.012	0.466	0.026	0.563	0.009
1381016_at	BI288152	Inositol 1,3,4,5,6-pentakisphosphate 2-kinase	Ippk	0.661	0.463	0.683	0.024	0.290	0.003	0.466	0.006
1387907_at	J05510	inositol 1,4,5-triphosphate receptor 1	Itpr1	0.577	0.036	0.226	0.001	0.926	0.047	0.333	0.031
1378334_a_at	BF417289	Inositol 1,4,5-triphosphate receptor 2	Itpr2	0.488	0.077	0.627	0.119	0.422	0.068	0.520	0.159
1368005_at	NM_013138	inositol 1,4,5-triphosphate receptor 3	Itpr3	1.808	0.112	2.492	0.003	1.302	0.023	1.803	0.011
1388500_at	AI180252	Inositol 1,4,5-trisphosphate 3-kinase B	Itpkb	0.461	0.070	0.165	0.001	0.395	0.002	0.169	0.005
1373623_at	BI278809	inositol 1,4,5-trisphosphate 3-kinase C	Itpkc	1.377	0.967	1.296	0.016	1.415	0.112	1.102	0.029
1387904_at	AB049151	inositol hexaphosphate kinase 1	Ihpk1	1.060	0.359	1.333	0.027	1.710	0.039	1.454	0.007
1378212_at	BI303251	Inositol hexaphosphate kinase 1	Ihpk1	1.026	0.893	1.179	0.394	1.627	0.006	1.016	0.895
1387063_at	NM_021660	inositol hexaphosphate kinase 2	Ihpk2	0.729	0.256	0.528	0.006	1.033	0.710	0.629	0.000
1395036_at	BF386788	inositol monophosphatase domain containing 1	Impad1	0.696	0.120	1.525	0.009	1.212	0.486	1.499	0.017
1398652_at	BF396528	inositol monophosphatase domain containing 1	Impad1	0.872	0.897	0.392	0.036	0.637	0.905	0.476	0.049
1368340_at	NM_134417	inositol polyphosphate multikinase	Ipmk	0.479	0.042	1.400	0.062	0.387	0.020	1.064	0.746
1370651_a_at	AB011439	inositol polyphosphate phosphatase-like 1	Inppl1	1.003	0.160	0.999	0.736	1.017	0.917	0.990	0.997
1368022_at	NM_022944	inositol polyphosphate phosphatase-like 1	Inppl1	0.976	0.988	0.843	0.945	0.747	0.285	0.616	0.103
1399125_at	BI275516	inositol polyphosphate-1-phosphatase	Inpp1	9.327	0.007	5.154	0.000	7.429	0.000	3.293	0.001
1394340_at	BF523172	inositol polyphosphate-1-phosphatase	Inpp1	4.257	0.019	2.357	0.047	4.338	0.024	1.349	0.356
1387078_at	NM_031002	inositol polyphosphate-4-phosphatase, type 1	Inpp4a	1.606	0.189	0.663	0.036	1.577	0.283	0.413	0.008
1388697_at	BI279692	inositol polyphosphate-5-phosphatase A (predicted)	Inpp5a_predicted	0.561	0.238	0.797	0.511	0.616	0.341	1.127	0.864
1388502_at	AI412624	inositol polyphosphate-5-phosphatase B	Inpp5b	1.693	0.084	1.810	0.011	3.448	0.003	2.914	0.009
1370945_at	BF282728	inositol polyphosphate-5-phosphatase E	Inpp5e	0.838	0.533	0.974	0.970	0.421	0.122	1.287	0.871
1389176_at	BF282674	Inositol polyphosphate-5-phosphatase F (predicted)	Inpp5f_predicted	0.499	0.000	0.628	0.048	0.585	0.141	0.718	0.029
1391312_at	BE108090	inositol polyphosphate-5-phosphatase F (predicted)	Inpp5f_predicted	0.850	0.236	1.160	0.854	0.510	0.022	1.023	0.626
1387815_at	NM_019129	insulin 1	Ins1	0.937	0.180	0.745	0.003	1.036	0.613	0.789	0.001
1370077_at	NM_019130	insulin 2	Ins2	0.862	0.073	0.681	0.003	0.992	0.886	0.754	0.000
1387652_at	BI291249	insulin degrading enzyme	Ide	0.464	0.065	6.252	0.007	0.480	0.039	2.425	0.035
1367894_at	NM_022392	insulin induced gene 1	Insig1	0.545	0.322	1.225	0.040	0.509	0.117	0.987	0.955
1393690_at	AA818627	insulin induced gene 2	Insig2	1.749	0.225	2.207	0.008	1.771	0.884	2.021	0.017
1389377_at	AA851803	insulin induced gene 2	Insig2	0.494	0.234	1.371	0.106	0.815	0.150	1.366	0.063
1392043_at	BE116206	Insulin receptor	Insr	0.804	0.532	0.470	0.239	1.051	0.423	0.491	0.247
1369771_at	NM_012969	insulin receptor substrate 1	Irs1	0.957	0.923	0.748	0.060	1.383	0.348	0.428	0.006
1384500_at	BI288565	insulin responsive sequence DNA binding protein-1	Sned1	0.925	0.300	0.916	0.614	1.668	0.202	1.249	0.349
1394615_at	AI511008	Insulin responsive sequence DNA binding protein-1	Sned1	1.115	0.866	0.950	0.828	1.011	0.953	0.953	0.590
1380250_at	AI013978	insulin responsive sequence DNA binding protein-1	Sned1	1.090	0.896	0.906	0.418	1.676	0.031	0.829	0.165
1380971_at	BE120747	Insulin-like growth factor 1 receptor	Igf1r	2.656	0.038	1.534	0.022	2.279	0.057	1.082	0.510
1368123_at	NM_052807	insulin-like growth factor 1 receptor	Igf1r	1.366	0.048	1.855	0.003	1.349	0.006	1.369	0.028
1390671_at	AI044666	Insulin-like growth factor 1 receptor	Igf1r	1.592	0.173	1.995	0.006	1.777	0.012	1.712	0.021

1367571_a_at	NM_031511	insulin-like growth factor 2	Igf2	0.724	0.315	0.285	0.040	2.029	0.253	0.540	0.040
1372993_at	BI299621	Insulin-like growth factor 2 receptor	Igf2r	0.888	0.064	1.037	0.592	1.627	0.123	0.979	0.813
1367636_at	NM_012756	insulin-like growth factor 2 receptor	Igf2r	0.943	0.540	1.237	0.014	0.898	0.831	1.083	0.025
1386872_at	BI296290	insulin-like growth factor 2 receptor	Igf2r	1.001	0.706	1.903	0.037	0.925	0.928	1.609	0.130
1368160_at	NM_013144	insulin-like growth factor binding protein 1	Igfbp1	3.190	0.030	5.871	0.001	1.217	0.888	0.384	0.143
1370960_at	BE104060	insulin-like growth factor binding protein 5	Igfbp5	1.721	0.851	0.896	0.759	1.489	0.833	1.261	0.558
1371357_at	AI233246	insulin-like growth factor binding protein 7	Igfbp7	0.830	0.310	0.375	0.000	1.046	0.279	0.707	0.011
1371320_at	BF282337	integral membrane protein 2B	Itm2b	0.859	0.404	0.984	0.958	0.806	0.169	1.139	0.016
1371319_at	BI278308	integral membrane protein 2B	Itm2b	0.851	0.575	0.838	0.192	0.738	0.487	0.988	0.847
1391171_at	AW534352	Integral membrane protein 2B	Itm2b	1.012	0.986	1.710	0.042	1.150	0.928	0.966	0.788
1371334_at	BG668228	integral membrane protein 2C	Itm2c	0.746	0.600	0.486	0.043	0.815	0.201	0.632	0.005
1389282_at	BI292586	Integrin alpha 3 (predicted)	Itga3_predicted	1.246	0.118	1.581	0.128	2.073	0.041	1.637	0.047
1379530_at	AA964658	Integrin alpha 9	Itga9	2.221	0.110	1.043	0.842	1.198	0.467	1.026	0.915
1398736_at	BF399976	Integrin alpha 9	Itga9	1.467	0.139	2.600	0.023	1.087	0.285	1.455	0.029
1383880_at	BF418243	integrin alpha V (predicted)	Itgav_predicted	3.899	0.055	6.857	0.001	3.510	0.129	10.425	0.005
1386581_at	AW141214	integrin alpha V (predicted)	Itgav_predicted	1.144	0.699	3.697	0.007	1.035	0.859	5.253	0.002
1368819_at	AI177366	integrin beta 1 (fibronectin receptor beta)	Itgb1	0.808	0.636	0.858	0.210	0.978	0.832	0.884	0.043
1387346_at	NM_017022	integrin beta 1 (fibronectin receptor beta)	Itgb1	0.857	0.711	0.830	0.288	0.912	0.543	0.749	0.124
1398395_at	AW434272	integrin beta 1 binding protein 1 (predicted)	Itgb1bp1_predicted	0.731	0.091	0.911	0.768	0.502	0.015	0.899	0.124
1378448_at	BI295914	integrin beta 1 binding protein 1 (predicted)	Itgb1bp1_predicted	1.163	0.227	1.683	0.043	1.177	0.147	1.382	0.267
1390604_s_at	BM387863	integrin beta 3 binding protein (beta3-endonexin)	Itgb3bp	0.828	0.022	0.999	0.830	0.689	0.057	1.001	0.985
1377182_at	BM387863	integrin beta 3 binding protein (beta3-endonexin)	Itgb3bp	0.431	0.079	0.919	0.565	0.390	0.030	0.858	0.699
1388507_at	AI104279	integrin beta 4 binding protein	Itgb4bp	1.486	0.056	2.625	0.000	1.390	0.021	2.563	0.011
1377974_at	AI502837	Integrin beta 8 (predicted)	Itgb8_predicted	0.575	0.052	1.364	0.419	0.593	0.021	1.055	0.625
1387777_at	NM_133409	integrin linked kinase	Ilk	1.419	0.103	1.038	0.453	1.814	0.006	1.176	0.041
1370526_at	AF020045	integrin, alpha E, epithelial-associated	Itgae	0.378	0.071	0.674	0.026	0.362	0.010	0.828	0.029
1370801_at	AF336872	integrin, beta 5	Itgb5	1.157	0.419	1.033	0.644	1.207	0.181	0.982	0.120
1382439_at	AI070686	integrin, beta 6	Itgb6	2.217	0.048	1.294	0.230	2.470	0.004	1.106	0.427
1367921_at	NM_022606	integrin-linked kinase-associated serine/threonine phosphatase 2C	Ilkap	0.799	0.101	0.763	0.484	0.865	0.079	0.967	0.891
1383476_at	AW528065	Inter-alpha trypsin inhibitor, heavy chain 3	Itih3	5.966	0.000	3.093	0.001	7.760	0.000	3.259	0.003
1387202_at	NM_012967	intercellular adhesion molecule 1	Icam1	192.893	0.001	93.187	0.001	541.520	0.000	152.836	0.000
1398523_a_at	AA900618	interferon (alpha and beta) receptor 1 (predicted)	Ifnar1_predicted	1.007	0.977	0.974	0.909	1.001	0.981	1.042	0.770
1396163_at	BF563316	interferon gamma induced GTPase	Igtp	4.535	0.003	2.000	0.245	3.933	0.012	6.972	0.278
1375796_at	BI300770	interferon gamma induced GTPase /// similar to Ac2-233 (predicted)	Igtp /// RGD1566055_predicted	32.177	0.014	7.961	0.003	45.649	0.000	11.240	0.007
1372070_at	BM389261	interferon gamma inducible protein 30	Ifi30	0.596	0.287	1.840	0.052	0.765	0.067	2.035	0.014
1369956_at	NM_053783	interferon gamma receptor 1	Ifngr	1.471	0.119	1.811	0.012	1.461	0.069	1.738	0.001
1374601_at	BI274482	interferon gamma receptor 2 (predicted)	Ifngr2_predicted	1.716	0.010	1.494	0.026	4.218	0.001	2.180	0.017
1367696_at	NM_030833	interferon induced transmembrane protein 2 (1-8D)	Ifitm2	0.999	0.465	0.595	0.030	1.036	0.771	0.707	0.143
1387995_a_at	BI285494	interferon induced transmembrane protein 3	Ifitm3	1.141	0.083	1.164	0.034	7.296	0.004	9.552	0.000
1368073_at	NM_012591	interferon regulatory factor 1	Irf1	66.392	0.001	19.845	0.001	105.828	0.001	34.763	0.000
1371560_at	AA893384	interferon regulatory factor 3	Irf3	0.813	0.067	0.702	0.003	0.866	0.201	0.575	0.005
1377379_at	BF410603	interferon regulatory factor 6 (predicted)	Irf6_predicted	1.452	0.124	1.672	0.002	1.343	0.019	1.682	0.001
1386568_at	BF557891	interferon regulatory factor 6 (predicted)	Irf6_predicted	1.154	0.182	1.426	0.021	0.980	0.091	1.584	0.036
1383564_at	BF411036	interferon regulatory factor 7	Irf7	90.308	0.000	22.639	0.004	427.276	0.000	104.708	0.001
1372097_at	BF284262	Interferon regulatory factor 8	Irf8	81.264	0.000	12.276	0.000	57.633	0.001	3.574	0.084
1390507_at	BI296097	interferon stimulated exonuclease 20	Isg20	2.402	0.000	3.134	0.000	2.715	0.003	3.479	0.016
1383491_at	BM391709	interferon stimulated exonuclease gene 20-like 1 (predicted)	Isg20l1_predicted	1.295	0.277	7.085	0.000	0.802	0.223	5.863	0.001
1382792_at	BF412158	Interferon stimulated exonuclease gene 20-like 2	Isg20l2	1.443	0.005	0.993	0.458	1.210	0.073	0.979	0.864
1382314_at	BE096523	interferon, alpha-inducible protein (clone IFI-15K) (predicted)	G1p2_predicted	179.793	0.000	235.917	0.006	750.732	0.000	649.312	0.004
1382073_at	AI179042	Interferon, kappa (predicted)	Ifnk_predicted	0.978	0.943	1.023	0.236	1.220	0.199	0.905	0.119
1374551_at	BM388891	interferon-induced protein 35	Ifi35	3.427	0.090	2.301	0.010	5.642	0.008	2.992	0.012
1381014_at	BI274623	interferon-induced protein 44	Ifi44	9.795	0.000	7.773	0.000	27.596	0.000	16.137	0.000
1384180_at	BE118697	interferon-induced protein with tetratricopeptide repeats 2	Ifit2	13.497	0.008	2.122	0.074	183.348	0.001	30.924	0.002
1379568_at	AI009765	interferon-induced protein with tetratricopeptide repeats 2	Ifit2	1.570	0.220	1.127	0.589	8.735	0.001	4.530	0.002
1376908_at	AW531805	interferon-induced protein with tetratricopeptide repeats 3	Ifit3	1.019	0.976	1.018	0.105	87.295	0.001	24.041	0.029
1367795_at	NM_019242	interferon-related developmental regulator 1	Ifrd1	0.965	0.803	2.089	0.002	1.280	0.321	1.943	0.004
1373068_at	AI236977	interferon-related developmental regulator 2 (predicted)	Ifrd2_predicted	0.658	0.037	3.094	0.000	0.713	0.303	2.254	0.001
1371170_a_at	AJ245643	interleukin 1 alpha	Il1a	1.288	0.638	1.099	0.159	1.003	0.523	1.157	0.161
1387507_at	NM_012968	interleukin 1 receptor accessory protein	Il1rap	1.004	0.957	0.999	0.593	0.998	0.934	1.000	0.998
1370750_a_at	U14010	interleukin 1 receptor, type I	Il1r1	0.721	0.499	0.289	0.018	0.699	0.048	0.258	0.098

1387273_at	NM_013037	interleukin 1 receptor-like 1	Il1rl1	1.781	0.438	0.889	0.741	1.067	0.535	0.813	0.229
1387504_at	NM_133575	interleukin 1 receptor-like 2	Il1rl2	0.889	0.401	0.999	0.886	0.996	0.705	1.019	0.940
1388711_at	BF282650	interleukin 13 receptor, alpha 1	Il13ra1	3.091	0.069	2.075	0.005	3.098	0.005	3.214	0.000
1368375_a_at	AF015718	interleukin 15	Il15	10.358	0.000	6.836	0.000	32.084	0.000	20.423	0.003
1373611_at	BI279744	interleukin 17 receptor (predicted)	Il17r_predicted	2.150	0.033	2.159	0.052	1.626	0.079	1.316	0.111
1369665_a_at	AJ222813	interleukin 18	Il18	1.489	0.111	2.108	0.020	1.831	0.013	2.245	0.003
1369031_at	NM_053374	interleukin 18 binding protein	Il18bp	15.741	0.002	11.891	0.000	15.344	0.000	22.346	0.000
1391612_at	BF282190	interleukin 22 receptor, alpha 2	Il22ra2	1.160	0.950	0.990	0.848	3.318	0.033	1.000	0.994
1387642_at	NM_130410	Interleukin 23, alpha subunit p19	Il23a	1.711	0.265	5.895	0.019	1.000	0.997	4.709	0.024
1386987_at	NM_017020	interleukin 6 receptor, alpha	Il6ra	1.309	0.969	0.873	0.649	1.302	0.979	0.541	0.109
1371926_at	AI171807	Interleukin 6 signal transducer	Il6st	1.545	0.104	5.592	0.000	1.473	0.093	4.657	0.000
1383489_at	BG663025	Interleukin 6 signal transducer	Il6st	1.007	0.229	0.552	0.058	1.158	0.455	0.831	0.070
1373140_at	AA851740	Interleukin 6 signal transducer	Il6st	1.247	0.327	0.850	0.083	1.333	0.200	1.215	0.401
1370957_at	BM383427	interleukin 6 signal transducer	Il6st	0.988	0.953	1.619	0.334	1.363	0.698	1.457	0.437
1387366_at	NM_053412	interleukin enhancer binding factor 3	Ilf3	0.740	0.119	2.522	0.198	0.666	0.132	1.397	0.613
1383821_at	AA899489	Interleukin enhancer binding factor 3	Ilf3	0.830	0.189	0.825	0.312	0.645	0.575	0.764	0.195
1394933_at	AI409647	Interleukin enhancer binding factor 3	Ilf3	1.315	0.289	4.966	0.046	0.570	0.256	1.995	0.066
1375915_at	AI073247	interleukin-1 receptor-associated kinase 1 binding protein 1 (predicted)	Irak1bp1_predicted	0.334	0.010	0.991	0.871	0.349	0.008	0.883	0.420
1383474_at	BI274988	interleukin-1 receptor-associated kinase 2	Irak2	3.548	0.021	3.009	0.000	3.567	0.045	1.340	0.005
1387226_at	NM_019128	internexin, alpha	Inexa	0.285	0.047	0.480	0.002	0.314	0.001	0.397	0.008
1378817_at	AW434016	intersectin 1	Itsn1	2.730	0.024	1.127	0.234	1.001	0.935	1.225	0.901
1382858_at	BF397529	intimal thickness-related receptor	MGC94555	0.509	0.097	0.784	0.133	0.483	0.060	0.641	0.022
1372035_at	BG381014	Intraflagellar transport 52 homolog (Chlamydomonas) (predicted)	Ift52_predicted	0.758	0.028	1.568	0.036	1.093	0.587	1.614	0.026
1380548_at	BF420494	intraflagellar transport 57 homolog (Chlamydomonas) (predicted)	Ift57_predicted	1.295	0.090	3.718	0.001	2.390	0.021	4.007	0.007
1383876_at	BG376705	intraflagellar transport 74 homolog (Chlamydomonas)	Ift74	0.924	0.932	0.814	0.208	0.867	0.790	0.609	0.949
1390872_at	AI178134	Intraflagellar transport 80 homolog (Chlamydomonas)	Ift80	0.560	0.035	0.079	0.003	0.368	0.017	0.412	0.037
1391501_at	AA851404	intraflagellar transport 80 homolog (Chlamydomonas)	Ift80	0.993	0.301	0.691	0.064	0.996	0.847	0.762	0.050
1369433_at	NM_021741	IP63 protein	Ip63	0.514	0.031	0.618	0.068	0.502	0.025	0.588	0.062
1390162_at	AI234142	IQ calmodulin-binding motif containing 1 (predicted)	Iqcb1_predicted	1.091	0.114	1.236	0.052	0.848	0.519	1.168	0.533
1391585_at	AW253379	ischemia related factor NYW-1	Nyw1	0.481	0.055	0.287	0.025	0.800	0.543	0.939	0.427
1374923_at	BM386444	ischemia related factor NYW-1	Nyw1	1.245	0.379	1.204	0.431	1.075	0.549	1.165	0.221
1386018_at	AI176253	Ischemia related factor NYW-1	Nyw1	1.497	0.776	1.827	0.815	1.578	0.218	2.174	0.393
1389578_at	AA850740	ischemia/reperfusion inducible protein	Isrip	0.715	0.086	1.078	0.580	0.703	0.042	0.964	0.238
1369681_at	NM_017339	ISL1 transcription factor, LIM/homeodomain 1	Isl1	0.534	0.055	0.136	0.022	0.308	0.045	0.292	0.012
1387660_at	M25390	islet amyloid polypeptide	Iapp	0.865	0.553	0.485	0.004	0.850	0.316	0.601	0.013
1367787_at	NM_030844	islet cell autoantigen 1	Ica1	0.460	0.010	0.529	0.010	0.426	0.032	0.621	0.001
1379339_at	BM390448	isochorismatase domain containing 1	Isoc1	0.538	0.264	1.539	0.292	0.830	0.613	2.388	0.004
1372310_at	AI227941	isochorismatase domain containing 1	Isoc1	0.684	0.495	0.624	0.002	0.626	0.104	0.883	0.059
1369954_at	NM_031510	isocitrate dehydrogenase 1 (NADP+), soluble	Idh1	0.296	0.063	0.750	0.087	0.237	0.003	0.816	0.007
1370865_at	BI277627	isocitrate dehydrogenase 3 (NAD), gamma	Idh3g	0.609	0.006	0.565	0.001	0.609	0.005	0.663	0.009
1367911_at	NM_053638	isocitrate dehydrogenase 3 (NAD+) alpha	Idh3a	0.363	0.088	0.494	0.258	0.373	0.003	0.643	0.057
1388160_a_at	AI171793	isocitrate dehydrogenase 3 (NAD+) beta	Idh3B	0.671	0.689	1.303	0.122	0.738	0.016	1.387	0.000
1376418_a_at	AA859497	isoleucine-tRNA synthetase (predicted)	Iars_predicted	0.553	0.047	1.057	0.206	0.562	0.030	1.089	0.123
1380561_at	BI287928	isoleucine-tRNA synthetase 2, mitochondrial (predicted)	Iars2_predicted	0.981	0.874	0.421	0.006	0.824	0.163	0.501	0.012
1368878_at	NM_053539	isopentenyl-diphosphate delta isomerase	Idi1	0.537	0.232	0.597	0.000	0.521	0.167	0.444	0.006
1370232_at	AI102838	isovaleryl coenzyme A dehydrogenase	Ivd	0.810	0.250	0.848	0.040	0.858	0.219	0.844	0.186
1387905_at	AB062135	J domain protein 1	LOC619393	0.500	0.308	0.404	0.010	0.602	0.321	0.453	0.018
1368725_at	NM_019147	jagged 1	Jag1	1.381	0.178	4.895	0.001	1.728	0.048	5.248	0.000
1384060_at	BG663208	Janus kinase 1	Jak1	1.307	0.326	3.713	0.004	0.967	0.248	3.375	0.010
1383478_at	BG671504	Janus kinase 1	Jak1	1.062	0.702	2.708	0.001	0.977	0.941	2.742	0.001
1368856_at	NM_031514	Janus kinase 2	Jak2	9.737	0.001	4.233	0.006	17.885	0.004	5.788	0.011
1368251_at	NM_012855	Janus kinase 3	Jak3	1.463	0.043	0.990	0.954	3.240	0.000	1.526	0.022
1371983_at	AA945181	Josephin domain containing 1	Josd1	0.484	0.831	0.491	0.011	0.312	0.016	0.420	0.009
1385109_at	AA900775	Josephin domain containing 3	Josd3	0.778	0.023	2.322	0.014	1.160	0.915	1.438	0.016
1371498_at	AI412685	JTV1	MGC125271	0.579	0.105	1.572	0.003	0.442	0.011	1.413	0.031
1370975_at	AI172079	jumonji domain containing 1A /// hypothetical gene supported by NM_175764	Jmjd1a /// LOC497786	2.036	0.037	4.079	0.000	1.613	0.024	3.810	0.004
1388169_at	BE102096	jumonji domain containing 1C	Jmjd1c	1.138	0.028	1.559	0.032	1.611	0.031	1.397	0.016
1383911_at	AA924574	jumonji domain containing 2C (predicted)	Jmjd2c_predicted	1.094	0.093	1.868	0.000	1.731	0.069	1.472	0.001
1398811_at	NM_019213	jumping translocation breakpoint	Jtb	0.983	0.518	1.112	0.478	1.098	0.236	0.910	0.452
1393138_at	BE329377	Jun D proto-oncogene	Jund	1.307	0.073	2.251	0.002	1.426	0.069	1.827	0.001
1369788_s_at	NM_021835	Jun oncogene	Jun	4.713	0.018	7.391	0.000	6.296	0.014	6.651	0.000

1389528_s_at	BI288619	Jun oncogene	Jun	3.999	0.020	9.125	0.000	3.046	0.026	7.037	0.001
1374404_at	BI288619	Jun oncogene	Jun	2.175	0.139	4.952	0.008	2.441	0.112	2.763	0.011
1387061_at	NM_031047	junction plakoglobin	Jup	1.107	0.447	1.143	0.308	0.752	0.043	0.902	0.978
1381992_at	AI145378	kaptin (actin binding protein) (predicted)	Kptn_predicted	0.992	0.869	0.825	0.667	0.843	0.022	0.866	0.908
1377664_at	AI101205	KARP-1 binding protein 1	Kab	1.168	0.436	0.829	0.056	1.298	0.871	0.868	0.781
1372183_at	AI230596	Karyopherin (importin) alpha 1	Kpna1	0.788	0.332	1.546	0.002	0.641	0.030	1.295	0.112
1382756_at	AI101822	karyopherin (importin) alpha 1	Kpna1	0.762	0.418	1.918	0.003	0.563	0.007	1.186	0.066
1382251_at	BE120157	karyopherin (importin) alpha 1	Kpna1	0.809	0.774	3.064	0.004	0.710	0.151	2.350	0.406
1367683_at	NM_053483	karyopherin (importin) alpha 2	Kpna2	0.471	0.039	0.631	0.001	0.565	0.012	0.840	0.035
1373116_at	AA945320	Karyopherin (importin) alpha 3	Kpna3	1.386	0.101	1.462	0.037	1.745	0.017	1.179	0.300
1389001_at	AW433944	Karyopherin (importin) alpha 4	Kpna4	3.383	0.025	4.091	0.000	1.984	0.007	3.030	0.003
1368573_at	NM_017063	karyopherin (importin) beta 1	Kpnb1	0.983	0.958	1.790	0.093	0.917	0.559	1.652	0.718
1391086_at	BI302698	katanin p60 (ATPase-containing) subunit A1	Katna1	1.388	0.284	1.479	0.040	1.312	0.098	1.436	0.002
1396656_at	BF410595	Katanin p60 subunit A-like 1	Katnal1	0.986	0.941	1.151	0.942	1.017	0.125	1.165	0.986
1373214_at	AA945238	KDEL (Lys-Asp-Glu-Leu) containing 1	Kdelc1	0.723	0.297	0.832	0.713	0.535	0.629	0.796	0.336
1374704_at	BM384752	KDEL (Lys-Asp-Glu-Leu) containing 2	Kdelc2	1.038	0.738	1.796	0.174	0.879	0.696	0.923	0.267
1371514_at	BI278612	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	Kdelr1	0.679	0.015	1.012	0.297	0.786	0.014	0.915	0.060
1377269_at	BI288720	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	Kdelr2	0.866	0.093	1.003	0.930	0.867	0.101	1.009	0.953
1371780_at	AA850164	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	Kdelr2	0.661	0.546	0.894	0.248	0.706	0.087	0.876	0.129
1393321_at	AW525577	kelch domain containing 1 (predicted)	Klhdc1_predicted	0.850	0.973	1.022	0.869	1.004	0.989	0.930	0.920
1397716_at	AI547852	Kelch domain containing 2	Klhdc2	1.009	0.063	0.990	0.982	0.994	0.890	0.987	0.978
1374406_at	AA925512	kelch domain containing 2	Klhdc2	0.653	0.411	0.724	0.082	0.493	0.010	0.888	0.373
1371674_at	AA894104	kelch domain containing 3	Klhdc3	0.764	0.126	0.930	0.012	0.686	0.050	0.937	0.249
1388388_at	AI179127	Kelch domain containing 3	Klhdc3	0.970	0.937	1.551	0.179	0.891	0.087	1.234	0.044
1374983_at	BI289414	kelch domain containing 4 (predicted)	Klhdc4_predicted	0.689	0.889	1.328	0.074	1.377	0.692	1.331	0.123
1382230_at	BI296330	kelch domain containing 8A	Klhdc8a	0.607	0.042	0.656	0.039	0.608	0.122	0.918	0.289
1397746_at	BG371972	Kelch domain containing 8A	Klhdc8a	0.990	0.114	0.999	0.965	0.982	0.817	1.002	0.921
1371685_at	AI178043	Kelch repeat and BTB (POZ) domain containing 2 (predicted)	Kbtbd2_predicted	0.953	0.770	1.364	0.087	1.154	0.300	1.026	0.578
1396082_at	BG668869	kelch repeat and BTB (POZ) domain containing 3 (predicted)	Kbtbd3_predicted	0.605	0.121	1.180	0.583	0.863	0.181	0.906	0.596
1374614_at	BM385650	kelch repeat and BTB (POZ) domain containing 4 (predicted)	Kbtbd4_predicted	0.953	0.889	0.994	0.949	0.748	0.657	0.706	0.997
1390016_at	BF415854	Kelch repeat and BTB (POZ) domain containing 9 (predicted)	Kbtbd9_predicted	1.002	0.993	0.985	0.906	1.001	0.989	0.998	0.968
1374835_at	AA944485	Kelch-like 12 (Drosophila)	Klhl12	0.487	0.008	0.677	0.118	0.617	0.113	0.729	0.225
1378008_at	BF417386	Kelch-like 12 (Drosophila)	Klhl12	0.924	0.475	0.542	0.047	0.949	0.802	0.599	0.010
1373484_at	AI179828	kelch-like 13 (Drosophila)	Klhl13	0.463	0.033	0.515	0.057	1.145	0.626	0.633	0.145
1392446_at	AI145435	kelch-like 2, Mayven (Drosophila) (predicted)	Klhl2_predicted	0.710	0.005	0.624	0.001	0.825	0.237	0.749	0.145
1373884_at	BI298657	kelch-like 2, Mayven (Drosophila) (predicted)	Klhl2_predicted	1.006	0.756	0.895	0.045	1.003	0.112	0.992	0.216
1395182_at	AI411008	kelch-like 20 (Drosophila) (predicted)	Klhl20_predicted	0.901	0.830	1.202	0.563	1.192	0.486	1.088	0.714
1389478_at	BM392031	kelch-like 22 (Drosophila) (predicted)	Klhl22_predicted	0.428	0.002	1.001	0.375	0.207	0.000	1.019	0.477
1383300_at	BF550390	kelch-like 24 (Drosophila)	Klhl24	1.220	0.091	0.955	0.790	0.970	0.896	0.999	0.660
1386611_at	BG667175	kelch-like 24 (Drosophila)	Klhl24	1.076	0.580	1.371	0.006	0.818	0.603	1.402	0.136
1383110_at	BM385908	kelch-like 24 (Drosophila)	Klhl24	1.152	0.605	1.183	0.765	0.950	0.853	1.206	0.166
1377209_at	BI283664	kelch-like 25 (Drosophila)	Klhl25	0.644	0.019	1.002	0.974	0.655	0.035	0.999	0.311
1379258_at	AA998367	kelch-like 5 (Drosophila)	Klhl5	1.092	0.970	0.990	0.962	1.217	0.328	0.911	0.672
1388799_at	BG374559	kelch-like 7 (Drosophila)	Klhl7	0.683	0.003	0.511	0.002	0.630	0.028	0.558	0.003
1370066_at	NM_057152	Kelch-like ECH-associated protein 1	Keap1	0.976	0.784	0.924	0.577	1.298	0.214	1.000	0.995
1379709_at	AI599514	keratin associated protein 14 (predicted)	Krtap14_predicted	1.400	0.797	1.091	0.078	0.734	0.132	1.077	0.955
1388155_at	BI286012	keratin complex 1, acidic, gene 18	Krt1-18	1.118	0.539	2.531	0.005	0.708	0.151	1.888	0.007
1388433_at	BI279605	keratin complex 1, acidic, gene 19	Krt1-19	9.174	0.021	7.014	0.000	13.845	0.034	8.531	0.001
1373900_at	BI284344	keratin complex 2, basic, gene 7	Krt2-7	2.257	0.026	1.287	0.164	0.736	0.339	1.144	0.467
1371530_at	BF281337	keratin complex 2, basic, gene 8	Krt2-8	1.795	0.036	2.736	0.001	1.123	0.071	2.326	0.003
1371540_at	AI102711	keratinocyte associated protein 2 (predicted)	Krtcap2_predicted	0.746	0.543	0.976	0.346	0.654	0.079	0.933	0.572
1386896_at	AF393783	KH domain containing, RNA binding, signal transduction associated 1	Khdrbs1	0.883	0.490	2.150	0.001	0.823	0.101	1.662	0.002
1398773_at	NM_130405	KH domain containing, RNA binding, signal transduction associated 1	Khdrbs1	0.961	0.843	1.310	0.009	0.959	0.340	1.388	0.001
1387196_at	NM_022249	KH domain containing, RNA binding, signal transduction associated 3	Khdrbs3	0.753	0.076	1.000	0.366	0.824	0.201	1.335	0.093
1376525_at	BI296632	KH-type splicing regulatory protein	Khsrp	0.778	0.705	2.747	0.130	1.196	0.973	2.335	0.910
1375426_a_at	BI295086	KH-type splicing regulatory protein	Khsrp	1.030	0.861	1.058	0.598	0.975	0.868	1.165	0.382
1370592_at	AB019693	kidney expressed gene 1	Keg1	1.892	0.080	0.972	0.564	1.036	0.963	0.947	0.669
1371946_at	BG373288	kidney predominant protein NCU-G1	RGD1303130	0.948	0.394	1.084	0.381	0.748	0.047	1.255	0.945
1378060_at	BF399121	Kin of IRRE like 3 (Drosophila) (predicted)	Kirrel3_predicted	2.326	0.064	0.600	0.246	1.495	0.258	0.433	0.034
1384655_at	AW142820	kin of IRRE like 3 (Drosophila) (predicted)	Kirrel3_predicted	0.448	0.196	0.513	0.002	0.370	0.243	0.629	0.116
1387864_at	AI169232	kinase D-interacting substance 220	Kidins220	0.798	0.664	0.806	0.048	0.794	0.048	0.898	0.115

1370886_a_at	AA944723	kinesin 2	Kns2	0.537	0.037	0.952	0.326	0.926	0.215	0.649	0.078
1399126_at	AA964114	kinesin 2	Kns2	1.115	0.920	1.092	0.196	1.159	0.397	1.039	0.953
1391611_at	BI296819	kinesin family member 12	Kif12	0.888	0.164	0.656	0.011	0.845	0.230	0.635	0.036
1392197_at	BF392518	Kinesin family member 13A (predicted)	Kif13a_predicted	1.002	0.301	0.995	0.970	1.004	0.984	1.000	0.997
1396255_at	BF420465	kinesin family member 16B (predicted)	Kif16b_predicted	1.290	0.482	0.952	0.962	1.003	0.947	0.957	0.768
1378138_at	BI296233	kinesin family member 16B (predicted)	Kif16b_predicted	1.156	0.547	0.995	0.973	1.650	0.116	0.931	0.975
1394535_at	BF397930	kinesin family member 16B (predicted)	Kif16b_predicted	0.394	0.564	1.090	0.457	0.818	0.339	0.703	0.159
1384133_at	BF522755	kinesin family member 1A	Kif1a	0.610	0.009	0.955	0.837	0.413	0.019	0.812	0.307
1388670_at	BI286860	Kinesin family member 1A	Kif1a	0.611	0.032	0.652	0.028	0.447	0.002	0.668	0.035
1382785_at	BE105549	kinesin family member 1A	Kif1a	0.743	0.248	10.533	0.001	0.773	0.233	6.889	0.004
1397505_at	BE115743	kinesin family member 1A	Kif1a	0.598	0.413	0.815	0.835	0.499	0.155	0.618	0.030
1391906_at	BE113001	kinesin family member 1B	Kif1b	1.000	0.322	0.913	0.418	0.671	0.817	1.256	0.335
1376005_at	BE109334	Kinesin family member 1B	Kif1b	0.764	0.745	1.094	0.458	0.887	0.227	1.372	0.248
1392717_at	BE109171	Kinesin family member 1B	Kif1b	0.918	0.811	1.660	0.315	1.357	0.935	1.083	0.675
1388034_at	AB070355	kinesin family member 1B	Kif1b	1.015	0.967	1.832	0.073	1.088	0.366	1.181	0.613
1373722_at	BE111697	kinesin family member 20A (predicted)	Kif20a_predicted	0.666	0.101	0.474	0.022	0.566	0.010	0.518	0.003
1378186_at	BF408466	Kinesin family member 21A (predicted)	Kif21a_predicted	0.830	0.285	0.993	0.979	0.820	0.951	1.004	0.593
1381976_at	BE103004	kinesin family member 21A (predicted)	Kif21a_predicted	1.058	0.718	0.779	0.194	1.624	0.091	0.927	0.244
1372516_at	AI317842	kinesin family member 22	Kif22	0.401	0.000	0.884	0.183	0.393	0.001	0.823	0.592
1377025_at	BF563503	kinesin family member 3a	Kif3a	1.540	0.076	2.244	0.085	0.988	0.301	0.986	0.924
1374428_at	BI300933	kinesin family member 3B (predicted)	Kif3b_predicted	1.061	0.988	1.202	0.285	1.990	0.068	1.099	0.151
1369637_at	NM_053486	kinesin family member 3C	Kif3c	1.573	0.032	1.200	0.079	2.419	0.008	1.126	0.881
1386707_at	BF553488	Kinesin family member 3C	Kif3c	0.844	0.486	0.980	0.731	1.917	0.024	0.809	0.448
1378096_at	AA924572	kinesin family member 5B	Kif5b	1.034	0.567	3.683	0.053	0.946	0.592	1.416	0.103
1380206_at	BE096005	Kinesin family member 5C (predicted)	Kif5c_predicted	0.723	0.104	0.368	0.029	0.804	0.094	0.344	0.039
1380172_at	BE104278	kinesin family member 5C (predicted)	Kif5c_predicted	0.582	0.211	0.419	0.000	0.426	0.003	0.325	0.004
1373977_at	BE108253	Kinesin family member 5C (predicted)	Kif5c_predicted	0.663	0.278	0.386	0.011	0.397	0.004	0.486	0.033
1395997_at	BF392893	Kinesin family member 5C (predicted)	Kif5c_predicted	0.867	0.937	1.463	0.226	0.824	0.027	0.815	0.335
1372376_at	BF408879	kinesin family member 9 (predicted)	Kif9_predicted	1.862	0.162	2.591	0.009	1.787	0.032	1.742	0.019
1397163_s_at	BM392082	Kinesin family member 9 (predicted)	Kif9_predicted	1.936	0.901	0.825	0.952	1.121	0.612	0.848	0.523
1391697_at	BM392082	Kinesin family member 9 (predicted)	Kif9_predicted	1.292	0.985	1.062	0.815	1.039	0.587	1.000	0.708
1378197_at	AW433953	kinesin family member C2	KIFC2	0.570	0.678	0.326	0.025	0.525	0.263	0.361	0.014
1371125_at	BF564995	kinesin heavy chain family, member 2	Kif2	1.108	0.419	1.259	0.441	1.066	0.351	1.634	0.070
1383156_at	H31899	kinesin heavy chain family, member 2	Kif2	1.546	0.785	1.502	0.606	0.462	0.024	2.303	0.080
1389593_at	BM392287	Kinesin heavy chain family, member 2	Kif2	0.908	0.800	0.193	0.000	0.696	0.946	0.196	0.010
1373125_at	AW915749	kinesin light chain 2 (predicted)	Klc2_predicted	1.079	0.498	1.161	0.047	0.889	0.935	1.275	0.112
1372328_at	BM386079	kinesin light chain 4	Klc4	0.881	0.002	1.281	0.171	1.008	0.922	0.943	0.717
1374462_at	AA850935	kinesin-associated protein 3 (predicted)	Kifap3_predicted	0.860	0.077	0.953	0.514	0.853	0.027	1.110	0.341
1391618_at	AI227800	kinesin-associated protein 3 (predicted)	Kifap3_predicted	0.937	0.228	0.875	0.024	1.065	0.252	0.379	0.050
1397106_at	BE101327	KRAB box containing zinc finger protein	Krim1	1.651	0.504	1.164	0.727	0.767	0.305	1.005	0.984
1368650_at	NM_031135	Kruppel-like factor 10	Klf10	2.055	0.146	0.739	0.299	1.943	0.041	0.920	0.301
1368249_at	NM_053536	Kruppel-like factor 15	Klf15	1.014	0.761	2.075	0.058	1.011	0.943	1.019	0.610
1374231_at	AI103472	Kruppel-like factor 16 (predicted)	Klf16_predicted	1.094	0.727	2.328	0.008	0.621	0.031	1.874	0.074
1375248_at	BI294916	Kruppel-like factor 2 (lung) (predicted)	Klf2_predicted	1.014	0.990	1.005	0.847	0.985	0.999	1.013	0.929
1393150_at	BF562149	Kruppel-like factor 3 (basic) (mapped)	Klf3_mapped	1.500	0.132	2.067	0.051	1.013	0.581	1.040	0.837
1387260_at	NM_053713	Kruppel-like factor 4 (gut)	Klf4	1.542	0.259	1.537	0.091	1.125	0.128	1.140	0.268
1394039_at	BM382886	Kruppel-like factor 5	Klf5	14.598	0.000	15.032	0.000	17.794	0.000	17.546	0.000
1385961_at	BF561079	Kruppel-like factor 5	Klf5	13.909	0.000	11.562	0.000	16.864	0.000	11.264	0.000
1368363_at	NM_053394	Kruppel-like factor 5	Klf5	12.302	0.031	9.084	0.018	8.849	0.005	1.546	0.015
1387060_at	NM_031642	Kruppel-like factor 6	Klf6	8.126	0.001	16.152	0.001	5.932	0.001	4.080	0.006
1391471_at	BE116100	Kruppel-like factor 7 (ubiquitous) (predicted)	Klf7_predicted	1.247	0.245	2.255	0.069	2.141	0.013	1.131	0.550
1370209_at	BE101336	Kruppel-like factor 9	Klf9	1.186	0.128	2.140	0.004	1.081	0.934	1.655	0.017
1375341_at	BG664807	Kua homolog (predicted)	Kua_predicted	1.002	0.968	1.064	0.671	1.019	0.978	1.063	0.357
1374006_at	BI295878	kynurenine aminotransferase III	Kat3	2.391	0.016	0.995	0.691	3.407	0.015	2.143	0.003
1373702_at	AI171798	l(3)mbt-like 2 (Drosophila)	L3mbtl2	1.218	0.069	1.364	0.051	1.285	0.256	1.338	0.015
1370237_at	AA799574	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	Hadhsc	0.205	0.020	0.125	0.001	0.197	0.003	0.157	0.007
1389922_at	AA891362	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	Hadhsc	0.310	0.075	0.124	0.002	0.287	0.067	0.104	0.000
1392746_x_at	BF394189	La ribonucleoprotein domain family, member 1 (predicted)	Larp1_predicted	1.502	0.002	1.538	0.098	1.364	0.002	1.532	0.024
1382670_at	BF394189	La ribonucleoprotein domain family, member 1 (predicted)	Larp1_predicted	1.469	0.022	1.350	0.149	1.100	0.284	1.366	0.000
1390113_a_at	BI300539	La ribonucleoprotein domain family, member 1 (predicted)	Larp1_predicted	1.394	0.071	1.642	0.021	1.690	0.139	1.831	0.011
1389551_at	AI008160	lactamase, beta 2	Lactb2	0.926	0.624	4.289	0.032	0.463	0.164	4.750	0.061

1367586_at	NM_017025	lactate dehydrogenase A	Ldha	0.339	0.081	2.384	0.321	0.456	0.048	2.117	0.532
1370218_at	AA848319	lactate dehydrogenase B	Ldhb	0.298	0.000	0.479	0.032	0.235	0.000	0.456	0.020
1382061_at	AI501131	lactate dehydrogenase D	Ldhd	0.919	0.763	1.214	0.117	0.939	0.946	1.150	0.153
1374195_at	AA799544	ladinin (predicted)	Lad1_predicted	1.287	0.027	6.343	0.018	0.771	0.317	2.872	0.003
1377289_at	BF393969	ladybird homeobox 1 homolog (Drosophila) corepressor 1 (predicted)	Lbxcor1_predicted	1.139	0.306	1.022	0.989	2.208	0.036	2.314	0.086
1379340_at	BM385282	lamimin, gamma 2	Lamc2	14.205	0.001	28.303	0.002	13.586	0.003	27.167	0.004
1379889_at	AW527269	lamimin, gamma 2	Lamc2	3.363	0.040	1.626	0.293	2.202	0.270	2.180	0.175
1368054_at	NM_021755	lamin A	Lmna	1.626	0.198	1.426	0.135	0.951	0.507	1.047	0.286
1368055_a_at	BI282866	lamin A	Lmna	1.912	0.201	4.375	0.005	0.780	0.283	2.248	0.015
1392926_at	BI281952	laminin, alpha 1 (predicted)	Lama1_predicted	1.001	0.873	1.000	0.571	1.002	0.863	0.919	0.540
1370538_at	U61261	laminin, alpha 3	Lama3	1.049	0.902	1.607	0.050	1.509	0.617	1.937	0.204
1388932_at	BI274917	laminin, alpha 5	Lama5	0.995	0.885	1.000	0.690	0.993	0.791	0.995	0.543
1391022_at	BE101834	laminin, beta 3	Lamb3	0.880	0.910	1.139	0.545	1.004	0.947	1.115	0.286
1371322_at	BI275624	Laminin, gamma 1	Lamc1	2.409	0.056	2.325	0.005	1.045	0.754	2.345	0.042
1385064_at	BM384729	L-amino acid oxidase 1 (predicted)	Lao1_predicted	1.001	0.999	1.193	0.250	1.494	0.195	1.380	0.010
1374196_at	AI710389	lanC (bacterial lantibiotic synthetase component C)-like 1	Lancl1	0.471	0.001	0.640	0.010	0.597	0.036	0.546	0.049
1395354_at	BF549735	lanC (bacterial lantibiotic synthetase component C)-like 1	Lancl1	0.998	0.989	0.963	0.461	0.999	0.999	0.953	0.889
1389257_at	BI288578	LanC (bacterial lantibiotic synthetase component C)-like 2 (predicted)	Lancl2_predicted	0.567	0.590	0.530	0.001	0.653	0.238	0.559	0.011
1372973_at	BM390574	Lanosterol synthase	Lss	1.059	0.657	0.962	0.128	1.246	0.281	0.683	0.154
1391565_at	AA899663	large subunit GTPase 1 homolog (S. cerevisiae)	Lsg1	0.261	0.002	0.120	0.000	0.188	0.001	0.153	0.001
1373293_at	BM392010	large subunit GTPase 1 homolog (S. cerevisiae)	Lsg1	0.817	0.411	1.201	0.134	0.704	0.028	0.794	0.107
1398770_at	NM_031105	large subunit ribosomal protein L36a	Rpl36a	0.856	0.449	0.976	0.309	0.793	0.017	0.825	0.888
1373552_at	AW531852	LAS1-like (S. cerevisiae) (predicted)	Las1l_predicted	0.798	0.194	1.219	0.180	0.816	0.277	1.053	0.106
1367912_at	NM_021587	latent transforming growth factor beta binding protein 1	Ltbp1	1.062	0.887	1.197	0.993	1.706	0.074	1.161	0.336
1367768_at	NM_031655	latexin	Lxn	2.403	0.028	1.624	0.027	2.090	0.075	1.575	0.011
1369644_at	NM_134408	latrophilin 2	Lphn2	0.666	0.811	1.017	0.980	0.927	0.989	1.336	0.691
1386879_at	NM_031832	lectin, galactose binding, soluble 3	Lgals3	3.427	0.002	7.189	0.009	0.969	0.203	5.814	0.012
1369716_s_at	NM_012976	lectin, galactose binding, soluble 5 /// lectin, galactose binding, soluble 9	Lgals5 /// Lgals9	6.368	0.016	6.894	0.000	15.349	0.000	25.147	0.005
1387027_a_at	U72741	lectin, galactose binding, soluble 9	Lgals9	2.343	0.100	5.273	0.016	3.325	0.002	8.195	0.008
1368960_at	NM_053862	lectin, galactoside-binding, soluble 8	Lgals8	1.160	0.074	3.876	0.001	1.249	0.055	2.569	0.004
1389329_at	AI411914	lectin, galactoside-binding, soluble 8	Lgals8	1.015	0.724	1.505	0.006	1.273	0.012	1.500	0.010
1387946_at	AF065438	lectin, galactoside-binding, soluble, 3 binding protein	Lgals3bp	8.541	0.007	5.455	0.000	14.629	0.008	10.277	0.000
1378437_at	BM385012	Lectin, mannose-binding 2 (predicted)	Lman2_predicted	0.877	0.393	1.292	0.410	1.019	0.654	0.961	0.887
1373815_at	BI304064	lectin, mannose-binding 2 (predicted)	Lman2_predicted	0.717	0.428	1.487	0.052	0.615	0.058	1.244	0.129
1394716_at	AI011137	Lectin, mannose-binding 2-like (predicted)	Lman2l_predicted	1.501	0.074	2.006	0.023	0.386	0.002	1.294	0.102
1389027_at	BF284714	Lectin, mannose-binding 2-like (predicted)	Lman2l_predicted	0.591	0.216	1.036	0.163	0.746	0.026	0.932	0.280
1368848_at	NM_053886	lectin, mannose-binding, 1	Lman1	0.596	0.088	0.747	0.107	0.493	0.037	0.525	0.004
1368430_at	AF154349	legumain	Lgmn	1.331	0.224	1.289	0.003	1.233	0.205	1.313	0.005
1399136_at	BE103179	LEM domain containing 2	Lemd2	0.889	0.837	1.595	0.062	1.134	0.262	1.260	0.495
1371832_at	AW526333	Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	Leo1	0.961	0.957	0.718	0.288	0.363	0.032	0.676	0.052
1367967_at	NM_053667	leprecan 1	Lepre1	0.640	0.077	0.976	0.959	0.641	0.078	0.997	0.993
1373750_at	BF406832	leprecan-like 2 (predicted)	Leprel2_predicted	0.936	0.875	0.613	0.007	0.924	0.871	0.671	0.014
1388725_at	AA892288	leptin receptor overlapping transcript	Leprot	0.702	0.016	1.102	0.697	0.676	0.249	1.558	0.124
1369323_at	NM_020099	leptin receptor overlapping transcript	Leprot	0.922	0.631	0.997	0.376	0.899	0.109	1.496	0.084
1376579_at	AA945172	leucine aminopeptidase 3	Lap3	1.010	0.921	1.206	0.340	1.228	0.103	0.999	0.307
1388747_at	BG381002	leucine carboxyl methyltransferase 1	Lcmt1	0.741	0.050	1.122	0.299	0.708	0.284	1.065	0.703
1379282_at	AI145899	leucine rich repeat (in FLII) interacting protein 2	Lrrfip2	0.945	0.998	2.006	0.001	0.803	0.520	1.436	0.074
1397937_at	BF409772	Leucine rich repeat containing 35	Lrrc35	0.789	0.112	0.746	0.050	0.916	0.613	1.047	0.647
1372784_at	BM386669	leucine rich repeat containing 41	Lrrc41	0.764	0.290	1.119	0.348	0.519	0.046	0.937	0.249
1371879_at	BE110542	leucine rich repeat containing 42	Lrrc42	3.037	0.069	1.626	0.131	3.445	0.038	1.353	0.282
1373404_at	AI170354	Leucine rich repeat containing 46	Lrrc46	1.086	0.827	1.030	0.149	0.931	0.471	0.996	0.483
1375076_at	AI112007	leucine rich repeat containing 46	Lrrc46	1.023	0.992	1.007	0.655	0.975	0.513	1.001	0.984
1382479_at	AI029670	leucine rich repeat containing 4C (predicted)	Lrrc4c_predicted	1.039	0.615	0.763	0.617	0.998	0.140	0.771	0.300
1371445_at	BF285649	leucine rich repeat containing 59	Lrrc59	0.738	0.467	1.759	0.000	0.803	0.325	1.693	0.003
1373431_at	AI101427	leucine rich repeat containing 8 family, member D	Lrrc8d	1.676	0.003	1.215	0.090	1.317	0.042	1.009	0.804
1391601_at	AA964579	leucine rich repeat protein 2, neuronal (predicted)	Lrrn2_predicted	0.331	0.002	0.268	0.001	0.337	0.010	0.296	0.006
1392023_at	AW434002	Leucine zipper and CTNNBIP1 domain containing	Lzic	0.956	0.495	0.893	0.213	0.957	0.503	1.130	0.427
1383132_at	BG377939	leucine zipper and CTNNBIP1 domain containing	Lzic	1.127	0.654	1.513	0.006	0.971	0.990	0.952	0.672
1376957_at	AI178922	leucine zipper and CTNNBIP1 domain containing	Lzic	1.004	0.987	0.997	0.987	0.415	0.983	0.999	0.996
1372260_at	BI296304	leucine zipper domain protein	MGC116147	0.931	0.403	0.737	0.001	1.557	0.076	1.304	0.078
1375894_at	AI716087	leucine zipper transcription factor-like 1	Lztfl1	0.436	0.021	0.371	0.102	0.280	0.056	0.537	0.228

1387209_at	NM_053571	leucine zipper transcription regulator 2	Lztr2	1.122	0.397	0.460	0.083	1.094	0.902	0.834	0.187
1377171_at	AA875041	leucine zipper, putative tumor suppressor 1	Lzts1	0.883	0.529	1.247	0.958	0.945	0.333	1.378	0.021
1389190_at	BM392076	leucine zipper, putative tumor suppressor 2	Lzts2	1.000	0.966	1.002	0.959	1.001	1.000	1.102	0.452
1396013_at	BI293141	leucine zipper-EF-hand containing transmembrane protein 1	Letm1	0.795	0.314	2.120	0.032	0.820	0.259	1.858	0.013
1392273_at	BF402258	leucine zipper-EF-hand containing transmembrane protein 2	Letm2	1.095	0.334	0.463	0.026	1.104	0.937	0.817	0.032
1380128_at	AI237408	Leucine zipper-EF-hand containing transmembrane protein 2	Letm2	0.786	0.898	0.297	0.204	1.087	0.797	0.890	0.765
1398569_at	BF412229	Leucine-rich and death domain containing (predicted)	Lrdd_predicted	0.998	0.950	2.427	0.008	1.305	0.148	2.219	0.019
1373500_at	BI294727	leucine-rich PPR-motif containing	Lrpprc	0.440	0.007	1.273	0.269	0.475	0.001	0.979	0.751
1398209_at	BF413358	Leucine-rich PPR-motif containing	Lrpprc	1.214	0.982	1.289	0.454	1.070	0.784	1.057	0.877
1383459_at	AI764525	leucine-rich repeat LGI family, member 3 (predicted)	Lgi3_predicted	1.939	0.032	1.132	0.237	1.108	0.204	0.986	0.690
1382920_at	AA875002	leucine-rich repeat-containing 8	Lrrc8	0.928	0.115	0.735	0.343	0.899	0.024	0.863	0.089
1374296_at	BM387574	Leucine-rich repeat-containing 8	Lrrc8	0.748	0.990	0.399	0.012	0.495	0.046	0.513	0.004
1388104_at	BI300274	leucine-rich repeat-containing G protein-coupled receptor 4	Lgr4	0.893	0.074	1.702	0.044	1.001	0.603	0.955	0.563
1396947_at	BF404382	Leucine-rich repeat-containing G protein-coupled receptor 4	Lgr4	1.010	0.372	1.697	0.277	0.778	0.093	1.286	0.503
1397503_at	AI555886	Leucine-rich repeats and calponin homology (CH) domain containing 3 (predicted)	Lrch3_predicted	2.047	0.042	1.652	0.270	2.322	0.065	1.677	0.282
1380049_at	AI599448	Leucine-rich repeats and calponin homology (CH) domain containing 3 (predicted)	Lrch3_predicted	1.768	0.240	0.765	0.052	1.989	0.002	0.710	0.034
1374847_at	AI177438	leucine-zipper-like transcriptional regulator, 1 (predicted)	Lztr1_predicted	0.917	0.659	0.643	0.037	0.811	0.546	0.625	0.042
1395018_at	BE119004	leucyl-tRNA synthetase	Lars	1.340	0.265	0.863	0.230	1.507	0.279	0.967	0.541
1374118_at	AA944176	leucyl-tRNA synthetase	Lars	1.062	0.571	1.297	0.014	1.149	0.315	1.203	0.060
1390365_at	BI296415	leukocyte receptor cluster (LRC) member 1 (predicted)	Leng1_predicted	1.003	0.979	1.210	0.145	1.007	1.000	1.074	0.317
1372680_at	AI406310	Leukocyte receptor cluster (LRC) member 4 (predicted)	Leng4_predicted	1.102	0.261	0.828	0.412	1.690	0.046	0.966	0.808
1392932_at	BI279191	leukocyte receptor cluster (LRC) member 8	Leng8	0.687	0.008	0.488	0.004	1.240	0.663	0.642	0.070
1389010_at	AW918009	leukotriene A4 hydrolase	Lta4h	0.399	0.102	0.469	0.025	0.205	0.022	0.940	0.325
1388102_at	U66322	leukotriene B4 12-hydroxydehydrogenase	Ltb4dh	1.005	0.509	0.989	0.902	1.229	0.825	0.992	0.957
1387438_at	NM_053639	leukotriene C4 synthase	Ltc4s	1.002	0.832	0.999	0.352	1.002	1.000	1.000	0.484
1378633_at	BE106297	leupaxin	Lpxn	1.552	0.009	0.658	0.148	0.651	0.171	0.462	0.028
1391155_at	AW528765	Ligand of numb-protein X 1 (predicted)	Lnx1_predicted	0.711	0.346	0.201	0.005	0.699	0.067	0.200	0.012
1368204_at	NM_030855	ligase I, DNA, ATP-dependent	Lig1	0.674	0.122	1.200	0.377	1.000	0.153	1.054	0.939
1379195_s_at	AI556346	ligase I, DNA, ATP-dependent	Lig1	0.986	0.721	1.282	0.023	0.679	0.898	1.342	0.233
1374010_at	BI275032	Ligase III, DNA, ATP-dependent	Lig3	0.995	0.175	1.143	0.516	1.009	0.246	0.933	0.161
1391874_at	AW528103	Like-glycosyltransferase (predicted)	Large_predicted	1.002	0.999	0.997	0.959	0.999	0.066	1.027	0.796
1388566_at	AI102215	LIM and SH3 protein 1	Lasp1	1.945	0.015	1.418	0.046	1.380	0.231	0.835	0.498
1371317_at	BI296590	LIM domain binding 1 (predicted)	Ldb1_predicted	0.804	0.091	0.538	0.061	0.709	0.071	0.635	0.106
1383824_at	AI029445	LIM domain binding 2 (predicted)	Ldb2_predicted	0.801	0.406	0.740	0.254	1.129	0.389	0.501	0.046
1389885_at	BI294855	LIM domain containing 2	Limd2	0.991	0.650	0.829	0.123	0.561	0.018	0.746	0.032
1383863_at	BF288303	LIM domain only 2	Lmo2	9.160	0.002	3.216	0.003	19.140	0.000	5.876	0.001
1373374_at	BM389691	LIM domain only 4	Lmo4	1.115	0.235	3.291	0.026	1.172	0.601	2.062	0.061
1396470_at	BF561077	LIM domain only 4	Lmo4	1.238	0.614	1.803	0.017	0.695	0.971	2.048	0.015
1375726_at	BI284480	LIM domain only protein 7	LMO7	0.747	0.032	0.951	0.571	0.765	0.033	0.854	0.312
1381798_at	BE114958	LIM domain only protein 7	LMO7	1.021	0.698	1.662	0.595	1.216	0.410	1.492	0.219
1377206_at	BI282093	LIM homeobox protein 1	Lhx1	1.428	0.208	1.791	0.179	1.019	0.059	1.016	0.909
1389982_at	BF419586	LIM homeobox protein 1	Lhx1	1.069	0.653	1.984	0.000	1.143	0.959	1.445	0.007
1394567_at	AW535805	LIM homeobox protein 3	Lhx3	0.644	0.099	0.995	0.957	0.747	0.102	0.938	0.177
1384740_at	BF412896	LIM homeobox protein 3	Lhx3	0.768	0.521	0.815	0.811	0.681	0.056	1.064	0.495
1369149_at	NM_031727	LIM motif-containing protein kinase 1	Limk1	0.661	0.307	0.979	0.805	0.701	0.404	0.885	0.493
1387090_a_at	NM_024135	LIM motif-containing protein kinase 2	Limk2	1.014	0.994	0.997	0.968	0.993	0.629	0.999	0.992
1379505_at	BG380642	limb expression 1 homolog (chicken) (predicted) /// similar to limb expression 1	Lix1_predicted /// LOC500376	1.015	0.986	0.724	0.220	0.983	0.744	0.991	0.989
1396959_at	BM382853	Limbic system-associated membrane protein	Lsamp	1.151	0.695	0.999	0.974	0.997	0.988	0.991	0.841
1367865_at	NM_133421	limkain b1	Lkap	1.424	0.004	1.017	0.322	1.693	0.005	1.046	0.193
1369610_at	NM_021851	lin-7 homolog C (C. elegans)	Lin7c	0.577	0.386	2.037	0.090	0.628	0.056	1.785	0.136
1367723_a_at	NM_031621	linker of T-cell receptor pathways	Lnk	0.829	0.230	1.017	0.169	0.534	0.083	0.920	0.399
1382465_at	AW533397	lipase, hormone sensitive	Lipe	0.999	0.987	0.997	0.945	0.999	0.884	0.993	0.906
1377599_at	BM385286	lipin 1	Lpin1	0.701	0.581	1.180	0.214	0.285	0.003	1.070	0.631
1391378_at	BF418338	Lipin 2 (predicted)	Lpin2_predicted	1.838	0.041	1.225	0.231	1.826	0.033	1.182	0.468
1387011_at	NM_130741	lipocalin 2	Lcn2	134.500	0.006	1482.998	0.000	1.648	0.854	34.096	0.003
1368368_a_at	NM_032616	lipolysis stimulated lipoprotein receptor	Lsr	1.698	0.043	1.373	0.884	1.723	0.015	1.927	0.049
1375158_at	BI291441	Lipolysis stimulated lipoprotein receptor	Lsr	0.696	0.362	1.000	0.996	1.418	0.491	1.002	0.974
1376664_at	BM386170	liver regeneration-related protein	LOC246187	0.931	0.704	1.121	0.321	1.054	0.611	1.032	0.762
1397153_at	BE115262	LMBR1 domain containing 1	Lmbrd1	1.470	0.170	1.885	0.014	1.758	0.207	1.480	0.064
1373051_at	BM383988	LMBR1 domain containing 1	Lmbrd1	0.819	0.336	0.768	0.018	0.881	0.160	0.993	0.399

1387757_at	NM_139189	LMBR1 domain containing 1	Lmbrd1	0.758	0.698	0.799	0.114	0.453	0.303	0.927	0.694
1383230_at	BI282204	LOC360664 (predicted)	RGD1311078_predicted	0.787	0.163	1.731	0.153	0.738	0.099	1.177	0.427
1392866_at	AI044609	LOC360791 (predicted)	RGD1307391_predicted	0.979	0.661	0.651	0.515	1.002	0.993	0.761	0.185
1396257_at	BF389756	LOC360791 (predicted)	RGD1307391_predicted	0.820	0.914	0.916	0.585	1.123	0.549	1.141	0.685
1373983_at	AI168986	LOC360807	LOC360807	1.431	0.000	2.048	0.001	1.202	0.031	1.587	0.003
1382415_at	BI289373	LOC360807	LOC360807	1.333	0.240	1.905	0.023	1.810	0.756	1.324	0.373
1390435_at	AA996717	LOC361111 (predicted)	RGD1307583_predicted	0.370	0.005	1.029	0.786	0.321	0.037	0.862	0.543
1390409_at	BI294742	LOC361774 (predicted)	RGD1306116_predicted	1.109	0.471	1.957	0.009	1.036	0.649	1.700	0.050
1383432_at	AI716676	LOC362136 (predicted)	RGD1309610_predicted	0.281	0.001	0.084	0.002	0.248	0.006	0.149	0.003
1388706_at	BF524995	LOC362678 (predicted)	RGD1308923_predicted	0.989	0.729	0.923	0.390	0.990	0.979	0.615	0.258
1372843_at	BG377188	LOC363020 (predicted)	RGD1309410_predicted	0.650	0.009	1.209	0.118	0.576	0.013	1.540	0.010
1376372_at	BI301069	LOC498083	LOC498083	1.065	0.672	0.956	0.867	0.863	0.630	1.543	0.886
1372023_at	BI279581	LOC498674	LOC498674	0.438	0.159	0.516	0.063	0.490	0.177	0.852	0.998
1371715_at	AI012212	LOC500651	MGC112883	0.425	0.088	0.604	0.002	0.411	0.032	0.590	0.007
1382882_x_at	AA963228	LOC500720 /// RGD1564761 (predicted)	LOC500720 /// RGD1564761_predicted	0.780	0.027	0.513	0.002	0.783	0.076	0.445	0.004
1394693_at	AW919728	LOC500720 /// RGD1564761 (predicted)	LOC500720 /// RGD1564761_predicted	0.668	0.059	0.393	0.006	0.706	0.037	0.403	0.078
1392166_at	BE099838	LOC500720 /// RGD1564761 (predicted)	LOC500720 /// RGD1564761_predicted	0.766	0.265	0.520	0.003	0.826	0.159	0.479	0.012
1398716_at	BG670822	LOC500720 /// RGD1564761 (predicted)	LOC500720 /// RGD1564761_predicted	0.963	0.320	0.472	0.008	0.793	0.317	0.432	0.051
1397700_x_at	BG670822	LOC500720 /// RGD1564761 (predicted)	LOC500720 /// RGD1564761_predicted	0.832	0.461	0.547	0.005	0.907	0.435	0.402	0.015
1397007_at	BI278529	LOC501214	LOC501214	1.048	0.990	1.078	0.151	1.271	0.337	0.884	0.126
1395590_at	BF391746	LOC501485	LOC501485	0.858	0.725	0.792	0.105	0.986	0.950	0.903	0.071
1371444_at	BI284504	Longevity assurance homolog 2 (S. cerevisiae)	Lass2	0.452	0.242	0.604	0.051	0.507	0.039	0.613	0.015
1371676_at	BG380464	longevity assurance homolog 5 (S. cerevisiae) (predicted)	Lass5_predicted	0.547	0.257	1.455	0.030	0.380	0.005	1.041	0.792
1372443_at	AI409038	low density lipoprotein receptor-related protein 11 (predicted)	Lrp11_predicted	2.602	0.004	1.895	0.006	1.430	0.133	1.172	0.032
1384069_at	BG670059	low density lipoprotein receptor-related protein 11 (predicted)	Lrp11_predicted	2.026	0.041	2.135	0.021	1.538	0.810	1.059	0.244
1368239_at	NM_053541	low density lipoprotein receptor-related protein 3	Lrp3	0.866	0.424	0.906	0.014	0.955	0.475	1.022	0.540
1370932_at	AI070976	low density lipoprotein receptor-related protein 4	Lrp4	0.989	0.974	0.552	0.050	1.001	0.958	0.548	0.049
1381363_at	BF388580	Low density lipoprotein receptor-related protein 6 (predicted)	Lrp6_predicted	1.315	0.034	0.766	0.033	1.033	0.707	0.516	0.009
1376725_at	BM391816	low density lipoprotein receptor-related protein 6 (predicted)	Lrp6_predicted	0.589	0.197	1.035	0.843	0.446	0.030	0.709	0.128
1388148_a_at	AI232268	low density lipoprotein receptor-related protein associated protein 1	Lrpap1	0.605	0.235	0.597	0.044	0.590	0.107	0.677	0.025
1374108_at	BM388942	low density lipoprotein-related protein 12 (predicted)	Lrp12_predicted	0.759	0.006	0.529	0.000	0.763	0.018	0.573	0.009
1371417_at	AI233054	low molecular mass ubiquinone-binding protein	Qpc	0.641	0.364	0.874	0.072	0.697	0.015	0.572	0.103
1386878_at	AI104234	low-density lipoprotein receptor-related protein 10	Lrp10	0.828	0.321	0.837	0.237	0.948	0.114	0.836	0.011
1370928_at	BI284739	LPS-induced TN factor	Litaf	1.726	0.196	2.186	0.000	1.626	0.064	2.046	0.004
1374495_at	BM388121	LPS-responsive beige-like anchor (predicted)	Lrba_predicted	0.798	0.613	0.706	0.008	1.062	0.965	0.592	0.103
1378988_at	BE117226	LPS-responsive beige-like anchor (predicted)	Lrba_predicted	0.958	0.846	0.998	0.987	0.999	0.620	0.995	0.991
1381970_at	AA945865	LSM14 homolog A (SCD6, S. cerevisiae) (predicted)	Lsm14a_predicted	1.544	0.026	1.648	0.012	1.366	0.042	2.085	0.004
1377905_at	BF417956	LSM14 homolog A (SCD6, S. cerevisiae) (predicted)	Lsm14a_predicted	1.889	0.097	1.377	0.033	1.610	0.072	1.177	0.044
1388488_at	AA943742	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)	Lsm3_predicted	1.750	0.354	3.145	0.032	1.426	0.181	2.829	0.032
1371683_at	AI103250	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)	Lsm4_predicted	1.055	0.755	1.406	0.033	0.996	0.487	1.557	0.403
1376483_at	AW251852	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)	Lsm5_predicted	0.738	0.065	1.586	0.015	0.828	0.445	1.553	0.004
1388772_at	AI177016	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)	Lsm8_predicted	0.408	0.039	0.537	0.015	0.503	0.009	0.773	0.004
1372312_at	AI176212	LTV1 homolog (S. cerevisiae)	Ltv1	0.459	0.088	1.066	0.272	0.476	0.011	0.991	0.937
1392207_at	BG373449	LUC7-like (S. cerevisiae)	Luc7l	0.995	0.788	1.357	0.132	1.088	0.622	0.943	0.711
1392425_x_at	BI275713	LUC7-like (S. cerevisiae)	Luc7l	0.838	0.871	2.691	0.003	1.652	0.162	1.484	0.212
1372309_at	BI296558	LUC7-like 2 (S. cerevisiae) (predicted)	Luc7l2_predicted	0.789	0.331	0.757	0.299	0.904	0.698	0.758	0.194
1394283_at	AW144132	LUC7-like 2 (S. cerevisiae) (predicted)	Luc7l2_predicted	0.933	0.710	1.664	0.007	1.025	0.337	1.620	0.013
1384146_at	AI236895	LUC7-like 2 (S. cerevisiae) (predicted)	Luc7l2_predicted	0.908	0.844	1.216	0.252	0.892	0.358	1.101	0.660
1387423_at	NM_012978	luteinizing hormone/choriogonadotropin receptor	Lhcgr	1.005	0.942	1.000	0.953	0.979	0.721	0.998	0.970
1389510_at	BE111765	Ly1 antibody reactive clone	Lyar	0.276	0.054	0.961	0.854	0.232	0.039	0.960	0.565
1377459_at	AI764114	lymphocyte antigen 6 complex, locus G6E	Ly6g6e	0.999	0.866	0.998	0.904	1.001	0.978	1.000	0.995
1389210_at	BE109711	lymphocyte cytosolic protein 1	Lcp1	12.590	0.029	21.249	0.005	6.948	0.001	3.300	0.046
1383785_at	BE115061	Lymphoid enhancer binding factor 1	Lef1	0.973	0.684	0.658	0.069	0.912	0.267	0.621	0.141
1379499_at	BF282228	lymphotoxin B	Ltb	3.881	0.024	5.380	0.011	36.253	0.002	47.983	0.000
1372914_at	AI705656	lymphotoxin B receptor	Ltbr	0.802	0.799	1.238	0.087	0.882	0.417	1.146	0.075
1373904_at	AI103948	LysM, putative peptidoglycan-binding, domain containing 2 (predicted)	Lysmd2_predicted	0.883	0.749	1.897	0.000	0.610	0.097	1.619	0.020

1376436_at	AI071181	LysM, putative peptidoglycan-binding, domain containing 3	Lysmd3	1.674	0.019	3.172	0.005	1.896	0.018	3.089	0.024
1367832_at	NM_013006	lysophospholipase 1	Lypla1	0.679	0.189	0.659	0.001	0.813	0.041	0.838	0.443
1367458_at	NM_031342	lysophospholipase 2	Lypla2	0.998	0.888	1.001	0.949	0.940	0.929	0.998	0.940
1375034_at	AI410383	lysophospholipase 3	Lypla3	1.178	0.672	0.877	0.091	0.761	0.243	0.834	0.075
1372281_at	AA819059	lysophospholipase-like 1 (predicted)	Lyplal1_predicted	0.482	0.263	0.490	0.006	0.831	0.046	0.524	0.022
1368075_at	NM_012732	lysosomal acid lipase 1	Lip1	2.223	0.043	2.907	0.046	7.842	0.001	7.198	0.003
1368504_at	NM_012857	lysosomal membrane glycoprotein 1	Lamp1	1.014	0.507	1.251	0.000	0.916	0.144	1.271	0.001
1383080_at	BI292252	Lysosomal membrane glycoprotein 2	Lamp2	1.427	0.013	1.159	0.356	1.656	0.002	1.328	0.228
1370010_at	NM_017068	lysosomal membrane glycoprotein 2	Lamp2	0.964	0.246	1.104	0.277	1.250	0.012	1.147	0.095
1380097_at	BE098726	Lysosomal-associated protein transmembrane 4A	Laptm4a	1.624	0.128	2.024	0.030	2.258	0.007	1.709	0.044
1388748_at	AW525776	lysosomal-associated protein transmembrane 4A	Laptm4a	1.044	0.496	1.333	0.045	1.435	0.307	1.556	0.008
1388728_at	BI282923	lysosomal-associated protein transmembrane 4B	Laptm4b	0.538	0.122	0.453	0.001	0.618	0.014	0.510	0.002
1372006_at	BM391274	Lysyl oxidase-like 2 (predicted)	Loxl2_predicted	0.669	0.369	0.193	0.001	0.880	0.322	0.292	0.004
1388849_at	BG375145	Lysyl oxidase-like 3 (predicted)	Loxl3_predicted	0.891	0.246	1.173	0.020	0.819	0.191	1.036	0.541
1371662_at	AA892250	lysyl-tRNA synthetase	Kars	2.751	0.002	2.687	0.000	3.415	0.004	3.449	0.005
1393136_at	BF393285	macoilin	LOC313618	0.617	0.060	2.031	0.018	0.583	0.046	1.520	0.049
1371734_at	BI282245	macrophage erythroblast attacher	Maea	0.727	0.137	1.780	0.000	0.623	0.005	1.249	0.022
1367609_at	NM_031051	macrophage migration inhibitory factor	Mif	0.398	0.300	1.636	0.156	0.349	0.020	1.211	0.193
1389373_at	AI029555	MAD homolog 1 (Drosophila)	Smad1	2.921	0.037	2.013	0.001	2.914	0.018	1.597	0.011
1369174_at	NM_013130	MAD homolog 1 (Drosophila)	Smad1	1.175	0.101	1.006	0.977	1.013	0.852	1.108	0.095
1396061_at	AI511079	MAD homolog 1 (Drosophila)	Smad1	1.190	0.446	1.497	0.099	1.363	0.028	1.094	0.600
1368214_at	NM_019191	MAD homolog 2 (Drosophila)	Smad2	0.974	0.553	2.073	0.011	1.145	0.459	1.804	0.051
1390827_at	AA997679	MAD homolog 3 (Drosophila)	Smad3	0.746	0.117	1.020	0.906	0.580	0.004	0.837	0.372
1386984_at	NM_019275	MAD homolog 4 (Drosophila)	Smad4	1.773	0.069	2.412	0.000	1.740	0.006	2.275	0.001
1367910_at	AB010954	MAD homolog 4 (Drosophila)	Smad4	1.034	0.183	1.750	0.043	1.022	0.316	1.561	0.131
1385928_at	AI175564	MAD homolog 6 (Drosophila) (predicted)	Smad6_predicted	1.424	0.383	0.988	0.571	0.950	0.926	1.000	0.882
1368896_at	NM_030858	MAD homolog 7 (Drosophila)	Madh7	1.214	0.206	1.642	0.100	2.011	0.067	1.762	0.022
1374146_at	BF419366	MAD2 mitotic arrest deficient-like 2 (yeast)	Mad2l2	0.967	0.512	2.373	0.105	1.132	0.283	1.552	0.187
1372409_at	BI286562	MAD2L1 binding protein	Mad2l1bp	1.007	0.582	1.460	0.139	1.022	0.930	1.613	0.102
1371374_at	AI172177	MAF1 homolog (S. cerevisiae)	Maf1	0.722	0.045	0.999	0.988	0.985	0.674	1.149	0.283
1372815_at	BG673028	mago-nashi homolog, proliferation-associated (Drosophila) (predicted)	Magoh_predicted	0.669	0.039	0.850	0.052	0.634	0.013	0.944	0.543
1370904_at	BI301490	major histocompatibility complex, class II, DM alpha	Hla-dma	1.206	0.152	1.013	0.817	1.008	0.541	1.170	0.013
1370882_at	AI171966	major histocompatibility complex, class II, DM beta	Hla-dmb	1.001	0.930	1.126	0.045	1.009	0.945	2.808	0.004
1372293_at	AF023090	Major histocompatibility complex-like mRNA, partial sequence	---	0.614	0.271	1.312	0.069	0.655	0.047	0.849	0.339
1367925_at	NM_022715	major vault protein	Mvp	2.514	0.010	2.072	0.003	2.135	0.030	2.216	0.002
1398804_at	NM_133324	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	Mak10	0.861	0.683	1.119	0.747	0.575	0.139	1.001	0.992
1397556_at	BF563329	Mak3 homolog (S. cerevisiae) (predicted)	Mak3_predicted	0.923	0.454	5.264	0.000	0.686	0.374	3.219	0.014
1389382_at	BI277034	makorin, ring finger protein, 2	Mkrn2	0.999	0.995	0.726	0.687	1.000	0.994	0.812	0.901
1384361_at	BF555523	mal, T-cell differentiation protein 2	Mal2	0.627	0.130	0.752	0.527	1.040	0.651	1.012	0.969
1372755_at	AI102073	mal, T-cell differentiation protein 2	Mal2	0.860	0.842	0.788	0.155	0.776	0.139	0.835	0.553
1372790_at	BG671530	Malate dehydrogenase 1, NAD (soluble)	Mdh1	0.465	0.027	0.196	0.002	0.535	0.013	0.293	0.006
1367653_a_at	NM_033235	malate dehydrogenase 1, NAD (soluble)	Mdh1	0.665	0.297	0.517	0.000	0.662	0.051	0.518	0.011
1369927_at	NM_031151	malate dehydrogenase, mitochondrial	Mor1	0.530	0.300	0.864	0.006	0.477	0.005	0.787	0.071
1382430_at	AI172357	male-specific lethal 2-like 1 (Drosophila) (predicted)	Msl2l1_predicted	1.408	0.092	1.135	0.168	1.347	0.075	1.356	0.341
1372320_at	BE103894	male-specific lethal-3 homolog 1 (Drosophila)	Msl31	0.883	0.692	1.634	0.017	0.824	0.170	1.190	0.266
1370870_at	M30596	malic enzyme 1	Me1	0.513	0.165	0.540	0.001	0.573	0.001	0.668	0.030
1370067_at	NM_012600	malic enzyme 1	Me1	0.556	0.385	0.557	0.010	0.631	0.200	0.835	0.007
1381403_at	AI575071	malic enzyme 2, NAD(+)-dependent, mitochondrial (predicted)	Me2_predicted	0.308	0.103	0.687	0.078	0.253	0.053	0.811	0.070
1389572_at	AI410864	malic enzyme 3, NADP(+)-dependent, mitochondrial (predicted)	Me3_predicted	1.572	0.156	1.870	0.008	1.068	0.463	1.988	0.039
1393738_s_at	AI136864	malignant fibrous histiocytoma amplified sequence 1 (predicted)	Mfhas1_predicted	0.635	0.508	0.990	0.999	0.894	0.397	0.799	0.756
1398648_at	AI136864	malignant fibrous histiocytoma amplified sequence 1 (predicted)	Mfhas1_predicted	1.010	0.950	1.002	0.968	1.013	0.206	1.000	0.966
1388660_at	BI295915	malignant T cell amplified sequence 1	Mcts1	0.510	0.302	0.659	0.020	0.542	0.008	0.691	0.020
1367638_at	NM_053477	malonyl-CoA decarboxylase	Mlycd	0.539	0.242	0.692	0.028	0.488	0.269	0.790	0.293
1379363_at	BF283311	Maltase-glucoamylase (predicted)	Mgam_predicted	0.994	0.227	0.311	0.094	1.035	0.783	0.513	0.138
1396289_at	BI283720	MAM domain containing glycosylphosphatidylinositol anchor 1 (predicted)	Mdga1_predicted	0.878	0.304	1.096	0.329	1.090	0.617	1.000	1.000
1388588_at	AI236101	mammary tumor virus receptor 2	Mtvr2	1.461	0.391	1.604	0.045	1.371	0.111	1.549	0.029
1377041_at	AA891664	manic fringe homolog (Drosophila)	Mfng	0.240	0.006	0.623	0.071	0.366	0.026	1.025	0.056
1373681_at	AA799505	mannose phosphate isomerase (mapped)	Mpi_mapped	0.984	0.958	0.973	0.846	0.981	0.896	0.621	0.030
1371495_at	AA943990	mannose-6-phosphate receptor, cation dependent	M6pr	0.717	0.128	1.014	0.167	0.910	0.585	1.063	0.043
1371655_at	BI281806	mannose-P-dolichol utilization defect 1	Mpdu1	0.768	0.556	0.990	0.385	0.707	0.063	1.110	0.119
1383574_at	AI502956	mannosidase 1, alpha (predicted)	Man1a_predicted	0.403	0.056	3.691	0.009	0.557	0.109	4.732	0.003

1371988_at	AA892549	mannosidase 1, alpha (predicted)	Man1a_predicted	0.612	0.191	0.690	0.070	0.697	0.087	0.782	0.053
1377463_at	BE099244	Mannosidase 2, alpha 2 (predicted)	Man2a2_predicted	1.929	0.002	2.040	0.009	1.889	0.003	2.175	0.001
1376674_at	BI274940	Mannosidase 2, alpha 2 (predicted)	Man2a2_predicted	1.522	0.129	1.110	0.122	2.401	0.005	1.380	0.075
1374110_at	BI278556	Mannosidase 2, alpha 2 (predicted)	Man2a2_predicted	1.284	0.278	1.226	0.214	1.261	0.579	1.017	0.625
1388699_at	BE114558	mannosidase 2, alpha B1	Man2b1	0.625	0.021	0.510	0.003	0.632	0.123	0.445	0.000
1381779_s_at	BG380027	mannosidase, alpha, class 2C, member 1	Man2c1	0.812	0.132	0.887	0.872	0.777	0.367	0.925	0.993
1387920_at	M57547	mannosidase, alpha, class 2C, member 1	Man2c1	0.952	0.322	0.534	0.062	0.892	0.985	0.809	0.030
1371875_at	BM388852	mannosidase, beta A, lysosomal	Manba	2.457	0.018	3.344	0.000	1.993	0.002	2.973	0.002
1367796_at	NM_030861	mannoside acetylglucosaminyltransferase 1	Mgat1	0.498	0.007	0.702	0.054	0.413	0.005	0.623	0.011
1379088_x_at	BF392858	Mannoside acetylglucosaminyltransferase 1	Mgat1	1.658	0.152	0.830	0.922	1.482	0.123	0.624	0.149
1386982_at	NM_053604	mannoside acetylglucosaminyltransferase 2	Mgat2	0.383	0.104	0.271	0.000	0.395	0.043	0.331	0.028
1397027_at	BF396069	Mannoside acetylglucosaminyltransferase 5	Mgat5	1.298	0.672	0.744	0.271	1.166	0.086	0.685	0.245
1371446_at	BI283703	MAP kinase-activated protein kinase 2	Mapkapk2	1.522	0.101	2.337	0.019	0.851	0.512	1.596	0.014
1372038_at	BM383395	MAP kinase-interacting serine/threonine kinase 2	Mknk2	0.740	0.573	0.321	0.006	0.420	0.007	0.428	0.052
1368710_at	NM_021699	MAP/microtubule affinity-regulating kinase 2	Mark2	1.614	0.002	1.730	0.035	1.392	0.024	1.657	0.365
1368831_at	NM_130749	MAP/microtubule affinity-regulating kinase 3	Mark3	1.011	0.667	1.879	0.006	1.114	1.000	1.589	0.018
1383245_at	AI454309	MAP3K12 binding inhibitory protein 1 (predicted)	Mbip_predicted	1.096	0.357	0.594	0.417	1.066	0.241	0.770	0.996
1372580_at	BF283599	MAP-kinase activating death domain	Madd	0.588	0.020	0.721	0.038	0.753	0.390	0.772	0.014
1369066_at	NM_053585	MAP-kinase activating death domain	Madd	0.743	0.132	0.538	0.045	0.726	0.041	0.585	0.026
1369944_at	NM_030862	MARCKS-like 1	Marcksl1	1.230	0.533	1.031	0.457	1.663	0.248	0.938	0.856
1372342_at	AI176583	MARVEL (membrane-associating) domain containing 1	Mrvldc1	0.628	0.249	0.566	0.085	0.636	0.258	0.525	0.070
1380036_at	BE101298	MARVEL (membrane-associating) domain containing 1	Mrvldc1	0.967	0.847	0.975	0.938	1.004	0.457	0.960	0.638
1387002_at	NM_053556	maternal G10 transcript	G10	0.681	0.503	0.822	0.049	0.824	0.026	0.682	0.016
1380579_at	BM384214	matrilin 1, cartilage matrix protein	Matn1	0.735	0.306	0.885	0.542	0.745	0.025	1.017	0.834
1368151_at	NM_019149	matrin 3	Matr3	1.201	0.050	1.227	0.001	1.039	0.032	1.385	0.027
1382522_at	AI169689	matrin 3 /// similar to Matrin 3 (predicted)	Matr3 /// RGD1560749_predicted	3.551	0.017	1.919	0.055	1.592	0.049	1.235	0.022
1368595_at	NM_031757	matrix metallopeptidase 24	Mmp24	0.382	0.033	0.274	0.003	0.265	0.013	0.249	0.009
1368657_at	NM_133523	matrix metallopeptidase 3	Mmp3	6.711	0.007	4.527	0.019	1.365	0.398	0.987	0.638
1370320_at	AY083160	MAWD binding protein	Mawbp	0.507	0.103	0.509	0.056	0.526	0.064	0.745	0.127
1390993_at	AW532101	MAWD binding protein	Mawbp	0.457	0.116	0.556	0.025	0.388	0.012	0.718	0.093
1375929_at	BI289109	max binding protein (predicted)	Mnt_predicted	0.900	0.416	1.807	0.007	0.978	0.965	1.595	0.003
1372093_at	AI409308	Max interacting protein 1	Mxi1	0.444	0.041	1.011	0.680	0.792	0.177	0.916	0.787
1368963_at	NM_013160	Max interacting protein 1	Mxi1	1.008	0.522	1.026	0.892	1.009	0.989	1.026	0.284
1387646_a_at	NM_022210	Max protein	Max	0.995	0.982	1.011	0.270	1.231	0.070	1.015	1.000
1371929_at	BI278563	MAX-like protein X	Mlx	0.489	0.121	0.756	0.153	0.544	0.048	0.750	0.024
1385443_at	AI549299	MAX-like protein X	Mlx	0.469	0.603	0.971	0.436	0.600	0.062	0.860	0.227
1391849_at	BF547270	MBD2-interacting zinc finger (predicted)	Mizf_predicted	1.044	0.835	1.534	0.016	1.428	0.505	1.641	0.026
1369820_at	NM_053951	mcf.2 transforming sequence-like	Mcf2l	1.110	0.959	0.706	0.151	0.284	0.031	0.484	0.055
1389168_at	AI412239	McKusick-Kaufman syndrome protein	Mkks	0.488	0.215	0.863	0.091	0.255	0.026	0.957	0.655
1389433_at	BI298816	McKusick-Kaufman syndrome protein	Mkks	0.683	0.440	0.200	0.008	0.936	0.805	0.407	0.014
1386479_at	AI071163	McKusick-Kaufman syndrome protein	Mkks	0.988	0.634	0.598	0.323	0.588	0.164	0.635	0.033
1375382_at	BE120346	mediator of DNA damage checkpoint 1	Mdc1	0.471	0.078	0.886	0.175	0.606	0.098	0.902	0.248
1388368_at	BM389891	mediator of RNA polymerase II transcription, subunit 28 homolog (yeast) (predicted)	Med28_predicted	1.711	0.060	3.093	0.016	1.594	0.043	3.092	0.015
1393276_at	BF418487	mediator of RNA polymerase II transcription, subunit 31 homolog (yeast) (predicted)	Med31_predicted	0.603	0.305	1.193	0.984	0.689	0.066	1.352	0.473
1392659_at	AI045496	Mediator of RNA polymerase II transcription, subunit 31 homolog (yeast) (predicted)	Med31_predicted	1.002	0.985	1.400	0.065	0.919	0.066	1.145	0.055
1376196_a_at	BG375059	mediator of RNA polymerase II transcription, subunit 4 homolog (yeast)	Med4	0.818	0.741	2.484	0.004	0.771	0.361	2.414	0.021
1372269_at	AI229534	mediator of RNA polymerase II transcription, subunit 6 homolog (yeast) (predicted)	Med6_predicted	0.771	0.963	1.251	0.576	0.605	0.016	1.169	0.376
1378977_at	AI178197	Mediator of RNA polymerase II transcription, subunit 8 homolog (yeast) (predicted)	Med8_predicted	0.899	0.404	0.670	0.112	0.767	0.053	0.827	0.038
1374629_at	AI713147	mediator of RNA polymerase II transcription, subunit 8 homolog (yeast) (predicted)	Med8_predicted	1.657	0.686	2.660	0.029	0.760	0.165	1.880	0.038
1394624_at	AW528017	Megakaryoblastic leukemia (translocation) 1 (predicted)	Mkl1_predicted	0.832	0.055	0.954	0.807	1.077	0.567	1.350	0.342
1373189_at	AW143154	megakaryoblastic leukemia (translocation) 1 (predicted)	Mkl1_predicted	0.706	0.890	0.434	0.107	0.756	0.337	1.074	0.111
1384308_at	AW532697	Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (predicted)	Meis1_predicted	1.232	0.433	0.472	0.005	2.217	0.015	0.879	0.222
1375392_at	BF405277	Meis1, myeloid ecotropic viral integration site 1 homolog 2 (predicted)	Meis2_predicted	0.853	0.107	0.825	0.925	1.153	0.668	1.016	0.992
1389728_at	BE104098	Meis1, myeloid ecotropic viral integration site 1 homolog 2 (predicted)	Meis2_predicted	0.934	0.971	0.509	0.016	0.868	0.415	0.771	0.552
1372800_at	BF416139	Meis1, myeloid ecotropic viral integration site 1 homolog 3 (mouse) (predicted)	Meis3_predicted	0.757	0.287	0.990	0.911	1.002	0.632	1.085	0.614
1386895_at	NM_053409	melanoma antigen, family D, 1	Maged1	0.624	0.002	0.655	0.006	0.499	0.000	0.573	0.000
1367744_at	NM_080479	melanoma antigen, family D, 2	Maged2	1.141	0.479	0.328	0.003	1.321	0.120	0.366	0.022
1377267_at	BF402385	melanoma antigen, family E, 1 (predicted)	Magee1_predicted	0.860	0.846	0.433	0.009	1.566	0.085	0.792	0.158
1395316_at	H32543	melanoma antigen, family H, 1	Mageh1	0.402	0.002	0.355	0.001	0.448	0.016	0.375	0.020
1394409_at	BE097621	melanoma associated antigen (mutated) 1 (predicted)	Mum1_predicted	0.769	0.663	0.863	0.020	0.927	0.997	0.690	0.009

1388905_at	AI230770	membralin	RGD1311136	0.741	0.101	1.692	0.213	0.849	0.209	1.469	0.437
1396872_at	AI555260	Membrane associated guanylate kinase 1 b NT-short isoform	LOC500261	1.523	0.260	1.000	0.925	0.878	0.196	1.183	0.694
1398866_at	AF255614	membrane associated guanylate kinase, WW and PDZ domain containing 3	Magi3	1.154	0.639	2.363	0.001	1.027	0.532	1.716	0.170
1368927_at	NM_017249	membrane bound C2 domain containing protein	Mbc2	2.148	0.105	1.683	0.139	1.024	0.249	1.050	0.995
1398296_at	NM_032615	membrane interacting protein of RGS16	Mir16	0.695	0.149	0.287	0.000	0.412	0.022	0.225	0.005
1374156_at	BE108018	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5) (predicted)	Mpp5_predicted	0.728	0.002	0.880	0.405	0.744	0.020	1.060	0.685
1382363_at	AI072027	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5) (predicted)	Mpp5_predicted	0.732	0.256	2.429	0.082	0.450	0.177	1.183	0.295
1397535_at	BF555544	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5) (predicted)	Mpp5_predicted	1.044	0.637	1.260	0.089	0.659	0.015	1.341	0.067
1398205_at	BF392849	Membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5) (predicted)	Mpp5_predicted	1.890	0.749	2.574	0.016	1.489	0.436	1.311	0.161
1380062_at	BE097259	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6) (predicted)	Mpp6_predicted	1.303	0.231	1.398	0.017	1.164	0.159	1.369	0.288
1383606_at	BI302544	membrane targeting (tandem) C2 domain containing 1	Mtac2d1	0.920	0.964	0.546	0.023	1.017	0.616	0.629	0.033
1372798_at	BF282715	membrane-associated DHHC16 zinc finger protein	LOC654495	0.575	0.052	0.448	0.064	0.863	0.118	0.620	0.021
1372448_at	D86711	membrane-associated DHHC5 zinc finger protein	LOC362156	0.892	0.993	0.767	0.026	0.807	0.323	0.712	0.037
1372571_at	AW143187	membrane-associated ring finger (C3HC4) 2	March2	0.564	0.471	0.525	0.001	0.341	0.128	0.648	0.062
1384285_at	BI298096	membrane-associated ring finger (C3HC4) 3	March3	0.769	0.999	0.764	0.022	0.464	0.091	1.360	0.977
1385790_at	BF560024	membrane-associated ring finger (C3HC4) 5 (predicted)	March5_predicted	1.923	0.008	2.956	0.010	2.576	0.013	3.227	0.002
1388491_at	AI234849	membrane-associated ring finger (C3HC4) 5 (predicted)	March5_predicted	1.650	0.015	1.464	0.028	2.255	0.003	2.095	0.013
1390485_at	BI290680	membrane-associated ring finger (C3HC4) 5 (predicted)	March5_predicted	2.693	0.040	4.901	0.000	3.483	0.004	6.912	0.002
1373087_at	AI175452	Membrane-associated ring finger (C3HC4) 7	March7	1.342	0.086	1.937	0.017	1.122	0.004	1.856	0.019
1381651_at	BE100638	Membrane-associated ring finger (C3HC4) 7	March7	1.232	0.954	1.243	0.503	1.195	0.895	1.367	0.681
1398833_at	NM_053569	membrane-bound transcription factor peptidase, site 1	Mbtps1	0.754	0.031	0.587	0.004	0.698	0.039	0.695	0.004
1383621_at	AW526365	Membrane-bound transcription factor peptidase, site 2	Mbtps2	1.529	0.045	1.170	0.262	1.884	0.022	1.775	0.013
1381854_at	BF418164	Membrane-spanning 4-domains, subfamily A, member 8B (predicted)	Ms4a8b_predicted	1.529	0.098	0.521	0.088	1.001	0.302	0.509	0.084
1376359_at	BG375355	membrane-spanning 4-domains, subfamily A, member 8B (predicted)	Ms4a8b_predicted	1.427	0.204	1.531	0.049	0.698	0.176	0.853	0.289
1375956_at	AI104569	menage a trois 1	Mnat1	1.094	0.690	1.753	0.000	1.057	0.233	1.102	0.061
1370129_at	NM_131904	meningioma expressed antigen 5 (hyaluronidase)	Mgea5	3.234	0.019	9.749	0.005	1.133	0.765	6.054	0.000
1375217_at	BI296680	Meningioma expressed antigen 5 (hyaluronidase)	Mgea5	1.213	0.020	1.411	0.288	0.869	0.771	1.453	0.488
1395741_at	BF548107	Meningioma expressed antigen 5 (hyaluronidase)	Mgea5	1.717	0.143	0.550	0.119	0.999	0.514	0.580	0.002
1376009_at	BI300199	meningioma expressed antigen 6 (coiled-coil proline-rich) (predicted)	Mgea6_predicted	0.815	0.126	0.985	0.217	0.828	0.313	1.145	0.844
1375452_at	AI177180	meningioma expressed antigen 6 (coiled-coil proline-rich) (predicted)	Mgea6_predicted	0.817	0.539	1.257	0.046	1.060	0.604	1.346	0.105
1368236_at	NM_013143	meprin 1 alpha	Mep1a	0.989	0.899	0.922	0.896	0.991	0.995	1.007	0.469
1370811_at	D50564	mercaptopyruvate sulfurtransferase	Mpst	0.708	0.685	0.576	0.323	0.747	0.210	0.980	0.789
1389178_at	BE329043	mesenchymal stem cell protein DSC92	Ngrn	0.867	0.016	0.814	0.718	0.903	0.579	1.003	0.979
1371820_at	BI282064	mesoderm development candiate 2	Mesdc2	0.926	0.836	1.124	0.217	1.377	0.779	1.451	0.008
1394616_at	AI013798	mesoderm development candiate 2	Mesdc2	1.020	0.933	1.003	0.927	1.009	0.972	0.964	0.863
1377696_at	AI407755	mesoderm development candidate 1	Mesdc1	1.578	0.405	0.836	0.941	2.145	0.033	1.652	0.624
1368441_at	NM_031658	mesothelin	Msln	0.655	0.010	0.456	0.003	0.720	0.036	0.657	0.021
1374065_at	BG378920	Met proto-oncogene	Met	4.281	0.014	1.298	0.149	3.189	0.140	1.136	0.017
1370262_at	AI706785	metadherin	Mtdh	0.728	0.524	1.429	0.002	0.776	0.067	1.207	0.252
1395194_at	BF413525	Metal response element binding transcription factor 1 (predicted)	Mtf1_predicted	1.133	0.581	1.649	0.472	1.812	0.068	1.225	0.241
1391792_at	BF398762	Metal response element binding transcription factor 2	Mtf2	1.058	0.636	1.140	0.672	1.292	0.022	0.946	0.363
1391050_at	BI294718	metal response element binding transcription factor 2	Mtf2	1.041	0.721	0.963	0.834	0.719	0.704	0.962	0.606
1384516_at	AI072919	Metal response element binding transcription factor 2	Mtf2	0.962	0.901	0.972	0.098	1.112	0.839	1.087	0.445
1378394_at	BE113263	metallophosphoesterase 1 (predicted)	Mppe1_predicted	1.713	0.045	0.822	0.089	4.676	0.007	1.416	0.004
1371237_a_at	AF411318	metallothionein 1a	Mt1a	3.019	0.057	36.702	0.000	4.035	0.066	40.644	0.000
1388267_a_at	M24327	metallothionein 1a	Mt1a	2.408	0.091	26.361	0.000	3.614	0.135	30.521	0.000
1389313_at	AI137972	Metastasis associated 1	Mta1	0.713	0.326	0.584	0.032	0.762	0.135	0.693	0.038
1385433_at	AI576354	metastasis suppressor 1 (predicted)	Mtss1_predicted	1.190	0.064	13.180	0.018	0.793	0.085	6.242	0.035
1392086_at	BE115673	Metastasis suppressor 1 (predicted)	Mtss1_predicted	1.037	0.412	1.567	0.043	1.036	0.396	0.971	0.443
1373103_at	BM386922	metastasis-associated gene family, member 2	Mta2	0.980	0.901	1.004	0.560	1.184	0.418	1.166	0.497
1388766_at	AI409049	metaxin 2	Mtx2	0.794	0.063	1.766	0.021	0.748	0.208	1.478	0.098
1389911_at	BM389126	meteorin, glial cell differentiation regulator-like	Metrnl	0.478	0.056	0.455	0.073	0.387	0.022	0.612	0.099
1371031_at	AI454484	methionine adenosyltransferase I, alpha	Mat1a	2.341	0.019	4.976	0.006	1.789	0.083	3.470	0.018
1398798_at	NM_022539	methionine aminopeptidase 2	Metap2	0.901	0.819	1.265	0.083	0.825	0.389	1.277	0.293
1372828_at	BM389609	methionine sulfoxide reductase B2	Msrb2	0.622	0.510	1.095	0.670	1.066	0.585	0.908	0.480
1389733_at	BM384125	methionine-tRNA synthetase (predicted)	Mars_predicted	0.855	0.055	0.940	0.247	0.680	0.022	0.949	0.878
1389634_at	AI101470	methionyl aminopeptidase 1 (predicted)	Metap1_predicted	1.395	0.301	1.932	0.006	0.854	0.670	1.561	0.024
1399137_at	AW527547	methionyl aminopeptidase 1 (predicted)	Metap1_predicted	0.905	0.725	0.748	0.018	0.868	0.066	0.649	0.048
1369277_at	NM_022673	methyl CpG binding protein 2	Mecp2	1.172	0.958	1.538	0.274	1.002	0.986	1.531	0.545
1395975_at	AI235040	Methyl CpG binding protein 2	Mecp2	1.276	0.971	0.904	0.879	1.856	0.157	0.886	0.920
1392885_at	BF281957	methyl-CpG binding domain protein 1	Mbd1	0.952	0.145	1.241	0.090	1.191	0.903	1.471	0.018

1381404_at	AW524425	Methyl-CpG binding domain protein 1	Mbd1	0.874	0.561	2.253	0.024	1.081	0.601	2.332	0.031
1375232_at	BM388847	methyl-CpG binding domain protein 6 (predicted)	Mbd6_predicted	1.138	0.487	0.902	0.214	1.042	0.689	0.977	0.809
1376852_at	BI274460	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	Mccc1	0.391	0.062	0.571	0.003	0.429	0.066	0.556	0.004
1377060_at	AI410674	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	Mccc2	0.467	0.010	0.496	0.034	0.531	0.025	0.724	0.002
1368181_at	NM_022508	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthase	Mthfd1	3.342	0.006	4.917	0.003	4.242	0.009	5.213	0.001
1377302_a_at	AI145027	methylmalonic aciduria (cobalamin deficiency) cblA type (predicted)	Mmaa_predicted	1.427	0.125	1.602	0.006	1.508	0.177	1.254	0.029
1376592_at	BG379780	methylmalonyl CoA epimerase (predicted)	Mcee_predicted	1.000	1.000	0.416	0.051	0.774	0.282	0.544	0.939
1379858_at	AA955134	methyltransferase like 2 (predicted)	Mettl2_predicted	0.569	0.181	1.380	0.035	0.698	0.153	1.624	0.012
1397176_at	AI104417	methyltransferase like 6	Mettl6	1.198	0.343	1.097	0.637	1.816	0.028	1.300	0.111
1371479_at	AA946026	methyltransferase like 7A /// LOC500939	Mettl7a /// LOC500939	1.055	0.169	1.353	0.030	1.341	0.007	1.444	0.011
1376986_at	BF412656	methyltransferase-like 3	Mettl3	0.894	0.943	1.172	0.002	0.923	0.243	1.018	0.094
1368020_at	NM_031062	mevalonate (diphospho) decarboxylase	Mvd	0.782	0.451	2.687	0.002	0.433	0.924	0.919	0.218
1371770_at	AW434268	MHC class II region expressed gene KE2	Ke2	0.611	0.645	1.411	0.081	0.823	0.610	1.453	0.128
1368528_at	NM_134459	MIC2 like 1	Mic2l1	0.893	0.105	0.446	0.003	0.900	0.125	0.548	0.034
1390063_at	BG380473	microfibrillar-associated protein 3	Mfap3	0.738	0.689	0.377	0.015	0.483	0.103	0.701	0.522
1398185_at	BF410350	microfibrillar-associated protein 3-like	Mfap3l	0.855	0.266	0.618	0.107	2.867	0.130	0.638	0.010
1397032_at	BF404482	Microrchidia 3 (predicted)	Morc3_predicted	1.157	0.097	1.082	0.904	1.238	0.061	0.999	0.936
1367612_at	NM_134349	microsomal glutathione S-transferase 1	Mgst1	0.960	0.188	1.252	0.152	0.477	0.022	1.044	0.708
1372599_at	BI290559	microsomal glutathione S-transferase 2 (predicted)	Mgst2_predicted	0.955	0.741	2.460	0.018	1.002	0.988	1.106	0.285
1372413_at	BI278800	microspherule protein 1	Mcrs1	1.289	0.142	1.221	0.119	1.075	0.853	0.793	0.478
1388399_at	BE106597	microtubule associated serine/threonine kinase 2 (predicted)	Mast2_predicted	1.232	0.058	2.097	0.009	1.581	0.111	1.281	0.060
1367882_at	NM_030995	microtubule-associated protein 1 A	Mtap1a	0.455	0.008	0.517	0.057	0.354	0.003	0.662	0.068
1371682_at	AI177372	microtubule-associated protein 1 light chain 3 alpha	Map1lc3a	0.755	0.031	0.879	0.235	0.771	0.085	0.710	0.318
1382199_at	BF288776	Microtubule-associated protein 1 light chain 3 beta	Map1lc3b	1.085	0.525	1.557	0.174	0.918	0.286	0.692	0.129
1367669_a_at	AI233190	microtubule-associated protein 1 light chain 3 beta	Map1lc3b	0.715	0.682	1.628	0.225	0.533	0.268	1.137	0.130
1373363_at	BI281702	microtubule-associated protein 1b	Map1b	1.330	0.145	1.194	0.100	1.080	0.563	1.062	0.032
1395172_at	BE096402	Microtubule-associated protein 1b	Map1b	1.622	0.164	1.540	0.142	1.471	0.104	0.898	0.410
1395357_at	BG672052	microtubule-associated protein 1b	Map1b	3.397	0.274	0.939	0.624	1.197	0.364	0.535	0.121
1371003_at	BG378086	microtubule-associated protein 1b	Map1b	0.962	0.318	1.861	0.018	0.622	0.061	1.497	0.068
1368411_a_at	X74211	microtubule-associated protein 2	Mtap2	0.816	0.012	0.602	0.103	0.687	0.013	0.546	0.090
1388152_at	BG374290	microtubule-associated protein 2	Mtap2	0.361	0.031	0.332	0.000	0.397	0.007	0.349	0.005
1373268_at	BM383953	microtubule-associated protein 4	LOC367171	0.897	0.878	1.101	0.449	0.835	0.037	0.865	0.125
1371607_at	AI230787	microtubule-associated protein 4	LOC367171	1.014	0.879	0.624	0.026	0.915	0.122	0.650	0.045
1371087_a_at	AJ002556	microtubule-associated protein 6	Mtap6	0.714	0.098	0.980	0.080	0.820	0.083	0.992	0.163
1368345_at	NM_017204	microtubule-associated protein 6	Mtap6	0.712	0.211	0.987	0.947	0.897	0.627	0.774	0.159
1376907_at	AW521452	Microtubule-associated protein 6	Mtap6	0.998	0.989	0.938	0.160	0.865	0.162	0.973	0.780
1392916_at	BM386695	microtubule-associated protein 7 (predicted)	Mtap7_predicted	1.351	0.024	0.847	0.018	0.977	0.610	0.824	0.044
1380120_at	BG374192	microtubule-associated protein 7 (predicted)	Mtap7_predicted	1.763	0.065	2.195	0.033	1.188	0.511	1.284	0.111
1383719_at	AW531489	microtubule-associated protein 7 (predicted)	Mtap7_predicted	1.328	0.433	0.939	0.313	1.342	0.470	1.026	0.655
1397364_at	AW521314	Microtubule-associated protein tau	Mapt	1.011	0.981	0.796	0.763	1.004	0.968	0.944	0.890
1387071_a_at	BE107978	microtubule-associated protein tau /// hypothetical gene supported by NM_017212	Mapt /// LOC497674	0.513	0.022	1.013	0.078	0.553	0.015	0.820	0.374
1368137_at	NM_017212	microtubule-associated protein tau /// hypothetical gene supported by NM_017212	Mapt /// LOC497674	1.491	0.127	0.998	0.986	0.897	0.915	0.704	0.698
1375525_at	BI294783	microtubule-associated protein, RP/EB family, member 1	Mapre1	0.758	0.061	1.186	0.061	0.750	0.051	1.038	0.127
1370792_at	U75920	microtubule-associated protein, RP/EB family, member 1	Mapre1	0.931	0.478	1.733	0.284	0.995	0.952	1.677	0.152
1373397_at	AI180161	microtubule-associated protein, RP/EB family, member 1	Mapre1	0.890	0.989	3.230	0.002	0.659	0.201	1.926	0.006
1374062_x_at	AA946204	microtubule-associated protein, RP/EB family, member 3	Mapre3	0.367	0.000	0.469	0.000	0.395	0.070	0.398	0.038
1372091_at	BI275959	MID1 interacting G12-like protein	Mig12	0.533	0.093	0.697	0.005	0.481	0.029	0.644	0.008
1379417_at	AA956668	midasin homolog (yeast)	Mdn1	0.817	0.520	1.474	0.008	0.779	0.285	1.306	0.044
1389303_at	AI411019	MIF4G domain containing	Mif4gd	0.971	0.829	0.988	0.847	0.611	0.988	0.986	0.830
1397745_at	BF414336	Mindbomb homolog 1 (Drosophila) (predicted)	Mib1_predicted	0.948	0.885	0.984	0.879	1.082	0.714	1.008	0.953
1381298_at	AI103253	Minichromosome maintenance deficient 10 (S. cerevisiae) (predicted)	Mcm10_predicted	0.719	0.145	0.987	0.301	1.120	0.363	1.000	0.303
1374053_at	AI235774	minichromosome maintenance deficient 3 (S. cerevisiae) associated protein (predicted)	Mcm3ap_predicted	0.936	0.993	1.266	0.023	1.160	0.259	1.145	0.232
1388744_at	AI599678	minichromosome maintenance deficient 7 (S. cerevisiae)	Mcm7	0.338	0.015	2.227	0.021	0.778	0.048	2.152	0.037
1385819_at	BF287803	misato homolog 1 (Drosophila) (predicted)	Msto1_predicted	0.636	0.212	1.089	0.517	0.984	0.164	1.121	0.100
1373929_at	BI279787	mitchondrial ribosomal protein S7	Mrps7	0.634	0.592	1.162	0.918	0.557	0.094	0.846	0.146
1384115_at	BF555448	Mitochondrial acyl-CoA thioesterase 1	Mte1	0.657	0.043	1.532	0.001	0.711	0.016	1.230	0.022
1391433_at	AA899721	mitochondrial acyl-CoA thioesterase 1	Mte1	0.604	0.049	1.373	0.110	0.646	0.008	1.037	0.693
1382446_at	AA799829	mitochondrial ATP synthase regulatory component factor B	Atp5s	0.500	0.087	1.391	0.058	0.655	0.119	1.004	0.991
1382688_at	AI229706	Mitochondrial carrier domain containing protein RGD1359361	RGD1359361	1.701	0.081	6.591	0.000	1.145	0.981	2.025	0.020
1371474_at	BG665132	mitochondrial carrier homolog 1 (C. elegans)	Mtch1	0.616	0.006	0.729	0.024	0.661	0.008	0.733	0.027

1372566_at	AI412014	mitochondrial carrier homolog 2 (C. elegans) (predicted)	Mtch2_predicted	0.559	0.312	0.400	0.057	0.622	0.134	0.342	0.015
1375131_at	BF284715	mitochondrial carrier homolog 2 (C. elegans) (predicted)	Mtch2_predicted	0.871	0.944	1.685	0.010	0.839	0.044	1.538	0.013
1379456_at	AA957383	mitochondrial carrier triple repeat 1	Mcart1	0.810	0.087	0.971	0.528	0.342	0.005	0.935	0.479
1386478_at	H33101	mitochondrial carrier triple repeat 1	Mcart1	0.657	0.131	0.844	0.224	0.597	0.024	0.818	0.071
1393239_at	BI296413	Mitochondrial fission regulator 1 (predicted)	Mtfr1_predicted	1.119	0.492	1.443	0.010	1.325	0.052	1.437	0.017
1369023_at	NM_031052	mitochondrial intermediate peptidase	Mipep	1.002	0.944	0.813	0.143	0.999	0.998	0.998	0.337
1377096_at	AW251803	mitochondrial methionyl-tRNA formyltransferase	Mtfmt	0.924	0.777	0.578	0.023	0.689	0.164	0.511	0.073
1388661_at	AA943734	mitochondrial protein, 18 kDa	MGC94604	0.542	0.022	2.159	0.128	0.289	0.098	1.715	0.082
1389125_at	BI293704	mitochondrial ribosomal protein L1 (predicted)	Mrpl1_predicted	1.065	0.800	1.299	0.095	0.625	0.049	1.261	0.179
1367506_at	BF283488	mitochondrial ribosomal protein L11	mrpl11	0.998	0.983	0.867	0.233	0.877	0.123	0.848	0.100
1388931_at	AA799440	mitochondrial ribosomal protein L13	Mrpl13	0.569	0.452	0.822	0.544	0.492	0.002	0.703	0.265
1372597_at	BE113348	mitochondrial ribosomal protein L14 (predicted)	Mrpl14_predicted	2.321	0.114	4.606	0.044	3.920	0.032	4.764	0.017
1395063_at	AA851300	Mitochondrial ribosomal protein L14 (predicted)	Mrpl14_predicted	1.282	0.197	1.036	0.256	1.401	0.161	1.413	0.192
1398891_at	AI103129	mitochondrial ribosomal protein L15 (predicted)	Mrpl15_predicted	0.794	0.702	1.307	0.142	0.570	0.014	1.272	0.038
1371967_at	AI410349	mitochondrial ribosomal protein L16	Mrpl16	0.681	0.056	1.062	0.589	0.492	0.004	1.153	0.587
1369013_a_at	AI103095	mitochondrial ribosomal protein L17	Mrpl17	0.780	0.173	1.201	0.001	0.797	0.254	1.152	0.076
1394722_at	AA964121	mitochondrial ribosomal protein L17	Mrpl17	0.933	0.192	0.858	0.068	0.820	0.038	1.025	0.907
1399058_at	BI288800	mitochondrial ribosomal protein L18 (predicted)	Mrpl18_predicted	0.620	0.458	0.789	0.547	0.404	0.007	0.905	0.486
1396808_at	AI501314	Mitochondrial ribosomal protein L18 (predicted)	Mrpl18_predicted	1.296	0.504	0.801	0.391	1.297	0.236	0.736	0.080
1398911_at	AI171870	mitochondrial ribosomal protein L2	Mrpl2	0.854	0.046	1.047	0.840	0.683	0.182	0.905	0.294
1367502_at	BI287857	mitochondrial ribosomal protein L21 (predicted)	Mrpl21_predicted	0.582	0.635	1.435	0.040	0.763	0.106	0.937	0.215
1388860_at	AI175327	mitochondrial ribosomal protein L22 (predicted)	Mrpl22_predicted	0.667	0.280	1.078	0.550	0.556	0.157	1.188	0.013
1368004_at	NM_022529	mitochondrial ribosomal protein L23	Mrpl23	0.558	0.504	1.321	0.121	0.501	0.008	0.978	0.430
1371888_at	AA892843	mitochondrial ribosomal protein L24	mrpl24	1.022	0.151	2.498	0.007	0.766	0.055	1.741	0.015
1399047_at	BF283001	mitochondrial ribosomal protein L27 (predicted)	Mrpl27_predicted	0.669	0.543	1.969	0.028	0.478	0.060	1.974	0.029
1371709_at	BI279024	mitochondrial ribosomal protein L3 (predicted)	Mrpl3_predicted	0.852	0.833	1.615	0.036	0.923	0.803	1.507	0.036
1398983_at	AW435012	mitochondrial ribosomal protein L30 (predicted)	Mrpl30_predicted	0.859	0.296	1.357	0.056	0.859	0.312	1.181	0.208
1389327_at	BF282675	mitochondrial ribosomal protein L32 (predicted)	Mrpl32_predicted	0.816	0.250	0.985	0.354	1.030	0.135	0.965	0.692
1371604_at	AA858969	mitochondrial ribosomal protein L34	Mrpl34	0.562	0.185	0.934	0.095	0.340	0.001	0.940	0.635
1371955_at	BF408394	mitochondrial ribosomal protein L35 (predicted)	Mrpl35_predicted	0.546	0.382	0.875	0.249	0.474	0.022	1.123	0.044
1371553_at	BF288120	mitochondrial ribosomal protein L36 (predicted)	Mrpl36_predicted	0.189	0.018	0.544	0.029	0.312	0.004	0.575	0.082
1398921_at	BE110549	mitochondrial ribosomal protein L37	Mrpl37	0.578	0.324	1.219	0.415	1.263	0.664	1.737	0.045
1383618_at	BG378538	mitochondrial ribosomal protein L38	Mrpl38	0.609	0.227	2.447	0.006	0.840	0.133	1.944	0.014
1388366_at	BI275903	mitochondrial ribosomal protein L4 (predicted)	Mrpl4_predicted	0.613	0.093	1.036	0.395	0.592	0.078	1.117	0.337
1388517_at	AI599474	mitochondrial ribosomal protein L40	Mrpl40	0.398	0.190	0.881	0.651	0.292	0.009	0.881	0.909
1374931_at	AA943496	mitochondrial ribosomal protein L40	Mrpl40	0.928	0.312	0.852	0.066	1.053	0.698	1.145	0.930
1371423_at	AA800010	mitochondrial ribosomal protein L41	Mrpl41	0.605	0.032	0.706	0.030	0.767	0.047	0.756	0.026
1371853_at	AI176602	mitochondrial ribosomal protein L42 (predicted) /// similar to RIKEN cDNA 2900055D03	Mrpl42_predicted /// LOC367117	0.431	0.014	0.654	0.070	0.362	0.008	0.730	0.768
1367546_at	BM390298	mitochondrial ribosomal protein L43 (predicted)	Mrpl43_predicted	0.747	0.248	1.751	0.055	0.790	0.238	1.491	0.290
1383157_at	AW520344	mitochondrial ribosomal protein L44	Mrpl44	0.604	0.079	1.369	0.566	0.623	0.011	1.264	0.323
1371790_at	BI277658	mitochondrial ribosomal protein L45 (predicted)	Mrpl45_predicted	0.686	0.091	2.275	0.058	0.996	0.253	1.203	0.236
1373155_at	BI283167	mitochondrial ribosomal protein L46	Mrpl46	0.723	0.440	1.912	0.040	0.626	0.032	1.663	0.107
1382144_at	AW520527	mitochondrial ribosomal protein L47	Mrpl47	0.491	0.137	1.329	0.160	0.363	0.001	1.362	0.186
1379306_at	BE111794	mitochondrial ribosomal protein L48 (predicted)	Mrpl48_predicted	0.906	0.410	0.734	0.047	0.827	0.089	0.784	0.064
1371586_at	AF209972	mitochondrial ribosomal protein L48 (predicted)	Mrpl48_predicted	0.762	0.549	1.576	0.051	0.633	0.110	1.083	0.183
1372619_at	AI172185	mitochondrial ribosomal protein L49	Mrpl49	0.384	0.064	0.333	0.009	0.242	0.039	0.354	0.071
1372927_at	AA891839	mitochondrial ribosomal protein L50 (predicted)	Mrpl50_predicted	0.528	0.118	0.531	0.011	0.565	0.000	0.631	0.026
1376585_at	BF395602	mitochondrial ribosomal protein L50 (predicted)	Mrpl50_predicted	0.981	0.466	1.030	0.198	0.993	0.853	0.805	0.238
1390188_at	BF419327	mitochondrial ribosomal protein L51 (predicted)	Mrpl51_predicted	0.577	0.048	1.236	0.189	0.567	0.020	1.342	0.045
1374411_at	BF414649	Mitochondrial ribosomal protein L52 (predicted)	Mrpl52_predicted	0.517	0.503	1.406	0.197	0.532	0.102	1.039	0.590
1388654_at	AI409180	Mitochondrial ribosomal protein L52 (predicted)	Mrpl52_predicted	0.786	0.612	0.502	0.017	0.641	0.395	0.583	0.033
1367477_at	BM386162	mitochondrial ribosomal protein L53 (predicted)	Mrpl53_predicted	0.761	0.665	1.220	0.390	0.764	0.138	1.082	0.349
1388853_at	BI285231	mitochondrial ribosomal protein L54 (predicted)	Mrpl54_predicted	0.999	0.988	1.662	0.052	1.238	0.247	1.486	0.061
1375161_at	BM386389	mitochondrial ribosomal protein L55 (predicted)	Mrpl55_predicted	0.476	0.456	0.657	0.235	0.679	0.149	0.706	0.447
1398912_at	BM389259	mitochondrial ribosomal protein L9	mrpl9	1.031	0.331	1.762	0.026	0.812	0.410	1.767	0.142
1372128_at	BI294944	mitochondrial ribosomal protein S12 (predicted)	Mrps12_predicted	0.628	0.243	0.818	0.532	0.672	0.098	1.039	0.799
1377937_at	AA859719	mitochondrial ribosomal protein S14 (predicted)	Mrps14_predicted	0.702	0.027	0.630	0.013	0.680	0.018	1.002	0.241
1383090_at	BF548676	mitochondrial ribosomal protein S14 (predicted)	Mrps14_predicted	0.755	0.137	1.136	0.545	0.672	0.087	1.188	0.110
1372697_at	AW254612	mitochondrial ribosomal protein S15	Mrps15	0.384	0.138	1.056	0.438	0.315	0.001	0.926	0.923
1399002_at	BM384239	mitochondrial ribosomal protein S17 (predicted)	Mrps17_predicted	0.722	0.185	0.481	0.020	0.648	0.040	0.657	0.353

1371591_at	AA858667	mitochondrial ribosomal protein S18A	Mrps18a	1.010	0.974	0.953	0.433	0.610	0.062	0.856	0.286
1371809_at	BM389296	mitochondrial ribosomal protein S18B	Mrps18b	0.923	0.923	4.527	0.000	1.249	0.150	3.436	0.002
1379378_at	AI071605	mitochondrial ribosomal protein S18C (predicted)	Mrps18c_predicted	0.487	0.163	1.103	0.068	0.442	0.130	1.284	0.050
1380447_a_at	AI071722	mitochondrial ribosomal protein S18C (predicted)	Mrps18c_predicted	1.011	0.222	1.776	0.000	0.535	0.019	1.537	0.007
1372116_at	AI008955	Mitochondrial ribosomal protein S2 (predicted)	Mrps2_predicted	0.499	0.001	1.183	0.107	0.284	0.020	1.152	0.076
1373609_at	AI232274	mitochondrial ribosomal protein S21 (predicted) /// similar to chromosome 1 open reading frame 51 (predicted)	Mrps21_predicted /// RGD1559569_predicted	0.665	0.304	0.540	0.006	0.708	0.009	0.651	0.033
1371661_at	AI411153	mitochondrial ribosomal protein S23 (predicted)	Mrps23_predicted	0.893	0.863	0.935	0.664	1.063	0.860	1.030	0.367
1388910_at	BI285944	mitochondrial ribosomal protein S24 (predicted)	Mrps24_predicted	1.023	0.887	2.274	0.061	1.063	0.459	1.751	0.001
1371548_at	BI289416	mitochondrial ribosomal protein S25	Mrps25	0.855	0.598	1.006	0.958	0.680	0.016	1.041	0.362
1367526_at	AI180224	mitochondrial ribosomal protein S26 (predicted)	Mrps26_predicted	0.420	0.004	0.822	0.038	0.395	0.032	0.642	0.074
1372916_at	BI295139	mitochondrial ribosomal protein S27 (predicted)	Mrps27_predicted	0.402	0.099	1.149	0.242	0.321	0.105	0.820	0.354
1384579_at	AA901191	Mitochondrial ribosomal protein S27 (predicted)	Mrps27_predicted	1.219	0.261	0.979	0.782	1.669	0.021	1.329	0.110
1373069_at	BG378230	mitochondrial ribosomal protein S30 (predicted)	Mrps30_predicted	0.572	0.025	1.415	0.136	0.391	0.005	1.333	0.160
1372214_at	AI104277	mitochondrial ribosomal protein S33 (predicted)	Mrps33_predicted	0.393	0.135	0.737	0.120	0.349	0.019	0.818	0.150
1371608_at	BI275958	mitochondrial ribosomal protein S34 (predicted)	Mrps34_predicted	1.191	0.654	2.401	0.017	1.816	0.041	2.868	0.003
1372839_at	BG379352	mitochondrial ribosomal protein S35 (predicted)	Mrps35_predicted	0.477	0.071	1.053	0.147	0.423	0.044	0.979	0.169
1371576_at	AW142276	mitochondrial ribosomal protein S36 (predicted)	Mrps36_predicted	0.447	0.001	0.735	0.116	0.455	0.006	0.836	0.073
1388877_at	BM386940	mitochondrial ribosomal protein S5 (predicted)	Mrps5_predicted	0.665	0.026	0.954	0.443	0.731	0.055	1.263	0.383
1396142_at	BI274476	mitochondrial ribosomal protein S9	Mrps9	0.734	0.457	0.623	0.457	0.778	0.452	0.588	0.149
1373002_at	AI009481	mitochondrial ribosomal protein S9	Mrps9	0.809	0.506	1.047	0.778	0.589	0.026	1.032	0.315
1396227_at	BG374845	mitochondrial ribosome recycling factor	Mrrf	0.816	0.232	1.008	0.518	0.733	0.167	0.722	0.105
1376415_at	BE114114	mitochondrial ribosome recycling factor	Mrrf	0.665	0.977	1.322	0.229	0.557	0.299	1.141	0.590
1398252_at	NM_017209	mitochondrial trans-2-enoyl-CoA reductase	Mecr	0.759	0.120	0.997	0.986	0.759	0.211	0.997	0.990
1387732_at	NM_053499	mitochondrial transcription termination factor 1	Mterf	1.468	0.104	2.102	0.001	1.248	0.264	2.021	0.022
1377493_at	BM386301	mitochondrial translation optimization 1 homolog (S. cerevisiae) (predicted)	Mto1_predicted	0.498	0.062	2.589	0.021	0.282	0.011	3.249	0.014
1384314_at	BM383771	mitochondrial translational initiation factor 2	Mtif2	1.436	0.003	1.015	0.758	1.655	0.175	0.980	0.313
1392654_at	BF413389	mitochondrial translational release factor 1-like (predicted) /// similar to mitochondrial translational release factor 1-like	Mtrf1l_predicted /// LOC361473	1.062	0.661	1.104	0.947	1.168	0.326	1.106	0.577
1372457_at	BF284182	mitochondrial tumor suppressor 1	Mtus1	0.852	0.130	0.338	0.023	0.519	0.022	0.417	0.012
1376058_at	AI705731	mitochondrial tumor suppressor 1	Mtus1	0.735	0.605	1.063	0.364	0.398	0.055	0.838	0.861
1380321_at	BI287786	mitochondrial tumor suppressor 1	Mtus1	1.112	0.687	0.480	0.008	0.693	0.382	0.485	0.047
1387919_at	U41803	mitofusin 2	Mfn2	1.234	0.038	1.516	0.004	0.755	0.062	1.108	0.013
1380238_at	BE117357	Mitogen activated protein kinase 14	Mapk14	1.163	0.410	1.303	0.915	1.235	0.661	1.255	0.764
1367697_at	NM_031020	mitogen activated protein kinase 14	Mapk14	1.139	0.789	1.227	0.016	0.986	0.926	0.962	0.530
1387771_a_at	AF155236	mitogen activated protein kinase 3	Mapk3	1.373	0.305	1.316	0.115	0.839	0.402	0.806	0.294
1387971_a_at	AF092450	mitogen activated protein kinase 8 interacting protein	Mapk8ip	1.005	0.300	0.502	0.049	0.578	0.180	0.554	0.005
1386973_a_at	NM_053777	mitogen activated protein kinase 8 interacting protein	Mapk8ip	0.511	0.428	0.714	0.033	0.582	0.013	0.672	0.033
1367760_at	D13341	mitogen activated protein kinase kinase 1	Map2k1	0.879	0.447	1.403	0.011	0.976	0.570	1.327	0.055
1398834_at	D14592	mitogen activated protein kinase kinase 2	Map2k2	0.630	0.012	0.624	0.027	0.563	0.017	0.727	0.022
1388858_at	BI283843	mitogen activated protein kinase kinase 3	Map2k3	1.789	0.200	2.190	0.013	1.260	0.168	1.548	0.160
1377621_at	AI413033	Mitogen activated protein kinase kinase 4	Map2k4	1.055	0.133	0.982	0.778	0.986	0.799	0.943	0.599
1386959_a_at	NM_017246	mitogen activated protein kinase kinase 5	Map2k5	0.677	0.312	0.697	0.029	0.767	0.237	0.794	0.577
1390372_at	BF521975	Mitogen activated protein kinase kinase kinase 12	Map3k12	0.702	0.076	0.511	0.033	0.754	0.042	0.540	0.019
1368886_at	NM_013055	mitogen activated protein kinase kinase kinase 12	Map3k12	0.886	0.199	0.638	0.005	0.884	0.548	0.497	0.002
1377607_at	BM385631	mitogen activated protein kinase kinase kinase 3 (predicted)	Map3k3_predicted	0.977	0.865	1.512	0.181	0.621	0.063	0.959	0.378
1382046_at	AA963495	mitogen activated protein kinase kinase kinase 3 (predicted)	Map3k3_predicted	0.763	0.914	1.412	0.118	0.656	0.201	0.998	0.981
1378791_at	BF398201	mitogen activated protein kinase kinase kinase 4 (predicted)	Map3k4_predicted	0.898	0.554	1.084	0.585	1.034	0.670	1.359	0.084
1399075_at	AI146037	Mitogen activated protein kinase kinase kinase 7 (predicted)	Map3k7_predicted	0.979	0.678	0.773	0.168	1.032	0.677	1.050	0.960
1398297_at	NM_021746	mitogen-activated protein kinase 12	Mapk12	0.819	0.465	1.741	0.136	0.577	0.196	1.681	0.272
1368273_at	NM_031622	mitogen-activated protein kinase 6	Mapk6	2.988	0.043	3.366	0.000	3.035	0.075	2.278	0.000
1388593_at	AI176465	mitogen-activated protein kinase 8 interacting protein 3	Mapk8ip3	1.611	0.025	1.795	0.013	1.624	0.157	1.235	0.054
1397809_at	AW920788	Mitogen-activated protein kinase 8 interacting protein 3	Mapk8ip3	1.411	0.173	1.674	0.016	1.016	0.965	1.128	0.220
1384190_at	BF553848	mitogen-activated protein kinase 8 interacting protein 3	Mapk8ip3	0.960	0.987	1.001	0.985	1.052	0.975	1.014	0.923
1371587_at	AA817829	mitogen-activated protein kinase kinase 1 interacting protein 1	Map2k1ip1	1.289	0.015	3.343	0.002	1.168	0.090	2.718	0.002
1387809_at	NM_053703	mitogen-activated protein kinase kinase 6	Map2k6	1.243	0.172	1.145	0.809	1.909	0.149	1.103	0.464
1398934_at	BE107454	mitogen-activated protein kinase kinase kinase 7 interacting protein 2	Map3k7ip2	1.158	0.481	1.341	0.760	1.000	0.697	1.257	0.925
1369393_at	NM_053847	mitogen-activated protein kinase kinase kinase 8	Map3k8	7.730	0.001	3.282	0.001	5.144	0.029	1.461	0.044
1373719_at	AA819812	mitogen-activated protein kinase kinase kinase kinase 3	Map4k3	1.020	0.273	0.762	0.003	1.023	0.630	0.851	0.057
1371042_at	BG664160	mitogen-activated protein kinase kinase kinase kinase 3	Map4k3	0.826	0.982	1.124	0.121	0.672	0.072	1.198	0.567
1373863_at	BF398680	mitogen-activated protein kinase kinase kinase kinase 4 (predicted)	Map4k4_predicted	1.022	0.601	2.120	0.073	1.108	0.527	1.547	0.195

1372804_at	AI175555	MMR_HSR1 domain containing protein RGD1359460	RGD1359460	0.761	0.352	1.124	0.403	1.055	0.561	1.160	0.088
1372904_at	BI285628	MOB1, Mps One Binder kinase activator-like 2B (yeast) (predicted)	Mobkl2b_predicted	5.090	0.011	1.775	0.132	3.958	0.014	1.401	0.121
1368071_at	NM_134410	MOCO sulphurase C-terminal domain containing 2	Mosc2	0.541	0.174	0.665	0.006	0.706	0.211	0.573	0.004
1372177_at	AI180033	molybdenum cofactor synthesis 2	Mocs2	1.228	0.278	0.937	0.325	1.931	0.017	1.841	0.063
1380666_at	BI284181	MON1 homolog b (yeast) (predicted)	Mon1b_predicted	0.997	0.986	0.994	0.955	1.002	0.994	0.997	0.977
1393189_at	BF414655	Monoamine oxidase A	Maoa	0.553	0.140	1.044	0.094	0.719	0.323	1.333	0.807
1370678_s_at	D00688	monoamine oxidase A	Maoa	0.611	0.165	1.046	0.341	0.586	0.640	0.983	0.912
1368514_at	NM_013198	monoamine oxidase B	Maob	0.408	0.039	0.146	0.000	0.461	0.008	0.178	0.013
1371883_at	BG376037	monocyte to macrophage differentiation-associated	Maf	1.003	0.393	1.111	0.924	1.633	0.259	0.854	0.223
1388311_at	AA799550	Morf4 family associated protein 1	Mrfap1	0.835	0.777	0.824	0.021	0.803	0.300	0.794	0.001
1386004_s_at	BF286548	mortality factor 4 like 1	Morf4l1	0.951	0.250	1.012	0.062	0.965	0.928	1.135	0.060
1399057_at	BE109080	mortality factor 4 like 1	Morf4l1	0.838	0.988	1.941	0.001	0.855	0.624	1.642	0.002
1371422_at	BM392210	mortality factor 4 like 2	Morf4l2	1.053	0.165	1.151	0.024	1.121	0.389	1.109	0.112
1372210_at	BM388609	motile sperm domain containing 3	Mospd3	0.806	0.359	1.060	0.681	0.749	0.384	1.306	0.538
1382161_at	AA817668	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein) (predicted)	Mphosph10_predicted	0.356	0.115	2.578	0.037	1.008	0.831	2.406	0.052
1375442_at	BG375380	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein) (predicted)	Mphosph10_predicted	0.925	0.407	2.588	0.051	1.002	0.429	1.004	0.924
1382918_at	AA956561	MRNA CSG245, partial sequence	---	1.002	0.951	1.011	0.735	0.962	0.982	0.997	0.983
1368525_at	NM_024001	MRS2-like, magnesium homeostasis factor (S. cerevisiae)	Mrs2l	0.653	0.121	0.925	0.915	0.522	0.034	1.029	0.770
1387299_at	NM_053337	Msx-interacting-zinc finger	Miz1	0.709	0.325	0.486	0.374	0.678	0.890	0.476	0.007
1373383_at	AA848807	MTERF domain containing 1	Mterfd1	0.781	0.247	1.444	0.026	0.814	0.023	1.332	0.105
1382085_at	BI293662	MTERF domain containing 2	Mterfd2	0.463	0.089	0.773	0.635	0.427	0.003	0.731	0.699
1378034_at	BF552141	MTERF domain containing 3	Mterfd3	1.065	0.645	0.286	0.000	0.975	0.913	0.278	0.001
1367888_at	NM_053572	MT-protocadherin	Pcdh21	3.731	0.058	5.873	0.010	6.766	0.002	11.742	0.004
1389032_at	AI408501	mucolipin 1 (predicted)	Mcoln1_predicted	1.269	0.197	1.483	0.044	0.917	0.002	1.189	0.152
1369906_s_at	BG378265	multiple coagulation factor deficiency 2	Mcfd2	0.902	0.966	1.124	1.000	0.829	0.925	0.743	0.215
1398785_at	NM_019208	multiple endocrine neoplasia 1	Men1	0.687	0.074	1.875	0.006	1.039	0.932	1.525	0.020
1375914_at	BI285504	multiple endocrine neoplasia 1	Men1	1.235	0.110	0.819	0.264	1.006	0.733	1.357	0.128
1388126_at	BG380493	multiple inositol polyphosphate histidine phosphatase 1	Minpp1	0.848	0.404	0.795	0.129	0.800	0.375	0.814	0.005
1368133_at	NM_019196	multiple PDZ domain protein	Mpdz	0.730	0.071	0.736	0.007	0.845	0.025	0.684	0.004
1387368_at	NM_012981	muscle and microspikes RAS	Mras	1.776	0.102	2.419	0.034	1.978	0.010	1.617	0.133
1375675_at	AA892813	Muscleblind-like 2 (predicted)	Mbnl2_predicted	0.571	0.027	0.615	0.002	0.586	0.018	0.815	0.004
1377208_at	BI291457	Muscleblind-like 2 (predicted)	Mbnl2_predicted	0.766	0.165	0.946	0.611	0.782	0.479	0.873	0.302
1375140_at	AA818999	muscleblind-like 2 (predicted)	Mbnl2_predicted	0.939	0.834	0.222	0.015	0.980	0.626	0.300	0.004
1394931_at	AI180361	muscleblind-like 2 (predicted)	Mbnl2_predicted	0.985	0.927	0.499	0.150	0.998	0.981	0.495	0.162
1373032_at	AW251450	musculoskeletal, embryonic nuclear protein 1	Mustn1	0.998	0.999	1.001	0.911	1.307	0.358	1.003	0.977
1368018_at	NM_031359	muskelin 1, intracellular mediator containing kelch motifs	Mkln1	1.542	0.165	1.450	0.014	1.159	0.996	1.470	0.218
1369965_at	NM_031053	mutL homolog 1 (E. coli) /// hypothetical gene supported by NM_031053	Mlh1 /// LOC497834	0.873	0.043	1.122	0.013	1.029	0.354	0.922	0.964
1368002_at	NM_031058	mutS homolog 2 (E. coli)	Msh2	0.799	0.137	0.778	0.121	0.627	0.640	0.780	0.121
1377846_a_at	AA819391	mutS homolog 6 (E. coli) (predicted)	Msh6_predicted	0.825	0.210	0.887	0.800	0.675	0.012	0.823	0.147
1387779_at	NM_031668	MYB binding protein (P160) 1a	Mybbp1a	0.536	0.067	2.122	0.001	0.523	0.027	1.882	0.004
1394511_at	BF419160	myb-like, SWIRM and MPN domains 1 (predicted)	Mysm1_predicted	1.192	0.274	1.762	0.019	1.112	0.325	1.254	0.128
1386075_at	AI710379	Myc induced nuclear antigen	Mina	0.784	0.004	0.504	0.001	0.759	0.056	0.572	0.036
1392743_at	BI278157	myc induced nuclear antigen	Mina	0.631	0.032	0.786	0.009	0.668	0.000	0.846	0.336
1386074_at	AA850705	myc induced nuclear antigen	Mina	0.820	0.109	0.502	0.002	0.606	0.010	0.552	0.008
1368810_a_at	BG666632	myelin basic protein	Mbp	1.372	0.065	0.802	0.409	1.003	0.911	1.049	0.855
1379526_at	BG374506	Myelin basic protein	Mbp	1.690	0.334	2.139	0.062	0.852	0.893	1.496	0.057
1372327_at	BF552877	myelin basic protein expression factor 2, repressor	Myef2	0.839	0.366	0.363	0.001	0.949	0.606	0.456	0.003
1373153_at	AI230720	Myelin oligodendrocyte glycoprotein	Mog	0.516	0.021	0.429	0.012	1.182	0.683	0.849	0.288
1398257_at	NM_022668	myelin oligodendrocyte glycoprotein	Mog	1.002	0.748	0.881	0.024	1.002	0.988	0.689	0.033
1392332_at	AI070390	myelin transcription factor 1 (predicted)	Myt1_predicted	0.982	0.085	0.621	0.021	0.774	0.097	0.647	0.046
1395161_at	AW531604	myelin transcription factor 1 (predicted)	Myt1_predicted	0.831	0.274	0.341	0.024	0.643	0.080	0.706	0.152
1370535_at	U48809	myelin transcription factor 1-like	Myt1l	0.998	0.148	0.984	0.800	0.998	0.021	0.991	0.865
1385132_at	AI044253	myeloblastosis oncogene-like 1 (predicted)	Mybl1_predicted	0.966	0.092	1.663	0.096	1.005	0.923	1.498	0.029
1368308_at	NM_012603	myelocytomatosis viral oncogene homolog (avian)	Myc	2.272	0.083	49.603	0.001	0.468	0.057	33.833	0.001
1372520_at	AI172056	myeloid cell leukemia sequence 1	Mcl1	2.684	0.002	3.576	0.000	2.498	0.005	2.793	0.000
1370174_at	BI284349	myeloid differentiation primary response gene 116	Myd116	6.114	0.026	21.458	0.001	6.549	0.059	9.671	0.017
1374468_at	AI236590	myeloid differentiation primary response gene 88	Myd88	1.251	0.504	0.719	0.159	1.476	0.051	1.041	0.627
1371359_at	BG381670	myeloid leukemia factor 2 (predicted)	Mlf2_predicted	1.005	0.997	0.957	0.558	0.776	0.958	0.965	0.464
1381069_at	BF413433	myeloid/lymphoid or mixed-lineage leukemia (mapped)	Mll_mapped	2.004	0.014	1.915	0.037	2.465	0.013	2.061	0.035
1393752_at	BE101697	myeloid/lymphoid or mixed-lineage leukemia (mapped)	Mll_mapped	1.057	0.463	1.006	0.943	1.004	0.439	0.989	0.823
1373038_at	AI145989	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	Mllt10	1.488	0.104	1.432	0.005	1.364	0.378	1.439	0.020

1383512_at	AW918674	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	Mllt10	1.021	0.889	2.496	0.008	1.022	0.832	2.119	0.014
1371692_at	AI009661	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	Mllt11	0.320	0.002	0.532	0.004	0.288	0.006	0.559	0.005
1372274_at	AI009727	Myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	Mll5	1.185	0.108	0.922	0.806	1.317	0.268	0.877	0.198
1375573_at	BE120038	Myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	Mll5	1.175	0.250	1.697	0.119	0.983	0.990	1.635	0.122
1392564_at	BI299176	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	Mll5	1.181	0.579	1.054	0.370	1.265	0.568	1.574	0.083
1377321_at	BF415831	Myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	Mll5	1.310	0.733	1.000	0.954	1.301	0.433	0.953	0.265
1384125_at	BF547275	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	Mll5	1.028	0.872	1.091	0.347	1.020	0.929	1.142	0.600
1375703_at	BE117891	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	Mll5	0.835	0.948	1.146	0.276	0.814	0.392	0.546	0.008
1385422_at	BF396651	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	Mll5	0.988	0.972	1.062	0.351	0.802	0.510	0.819	0.189
1368279_at	NM_053718	myeloid/lymphoid or mixed-lineage leukemia,translocated to, 3 (trithorax homolog, Drosophila)	Mllt3	1.165	0.102	2.205	0.068	2.707	0.013	2.241	0.018
1385953_at	AI454608	Myeloid/lymphoid or mixed-lineage leukemia,translocated to, 3 (trithorax homolog, Drosophila)	Mllt3	1.397	0.139	1.282	0.077	1.912	0.011	1.200	0.063
1384478_at	BF549837	Myeloid/lymphoid or mixed-lineage leukemia,translocated to, 3 (trithorax homolog, Drosophila)	Mllt3	0.938	0.708	1.450	0.038	1.969	0.064	1.039	0.148
1388453_at	BI296048	myeloid-associated differentiation marker	Myadm	0.852	0.029	0.416	0.024	0.826	0.460	0.542	0.022
1388434_at	AA818018	MYG1 protein	C12orf10	0.487	0.090	1.051	0.911	0.362	0.038	1.157	0.993
1392676_at	AI548984	myocardial ischemic preconditioning upregulated 1	Mip1	1.187	0.683	0.440	0.005	1.086	0.759	0.401	0.005
1378482_at	AI411065	MyoD family inhibitor domain containing (predicted)	Mdfic_predicted	1.407	0.164	0.957	0.811	1.161	0.982	0.953	0.856
1387181_at	NM_013172	myogenic factor 6	Myf6	0.598	0.324	0.625	0.075	0.811	0.568	1.675	0.567
1368310_at	NM_017115	myogenin	Myog	0.997	0.993	0.997	0.348	1.007	0.980	1.004	0.761
1394804_at	AI599871	Myopalladin (predicted)	Mypn_predicted	1.132	0.804	0.554	0.767	1.059	0.708	0.903	0.911
1368355_at	NM_017083	myosin 5B	Myo5b	1.182	0.567	0.868	0.472	1.134	0.597	0.602	0.047
1370478_at	AY004215	myosin heavy chain Myr 8	Myr8	0.124	0.002	0.204	0.011	0.169	0.000	0.236	0.048
1397590_at	AA859008	myosin Ib	Myo1b	3.691	0.020	2.538	0.118	2.488	0.066	1.968	0.555
1369720_at	NM_053986	myosin Ib	Myo1b	3.070	0.045	7.124	0.000	1.918	0.112	3.192	0.002
1395485_s_at	AA859008	myosin Ib	Myo1b	2.564	0.068	1.008	0.423	1.960	0.106	1.062	0.141
1388917_at	BI279786	myosin ID	Myo1d	0.495	0.175	0.247	0.000	0.582	0.072	0.353	0.024
1370933_at	BI275813	myosin IE	Myo1e	2.032	0.117	0.931	0.651	3.728	0.006	1.051	0.468
1376098_a_at	BF282304	myosin IG	Myo1g	0.959	0.070	6.836	0.002	1.154	0.596	5.672	0.003
1387866_at	AI178160	myosin IXb	Myo9b	6.124	0.002	5.392	0.005	5.975	0.003	2.505	0.001
1388114_at	X05566	myosin light chain, regulatory B	Mrlcb	1.664	0.018	3.283	0.001	1.656	0.046	2.279	0.000
1386996_at	D14688	myosin light chain, regulatory B	Mrlcb	0.822	0.208	0.950	0.031	1.006	0.993	1.010	0.057
1390067_at	BF403821	Myosin phosphatase-Rho interacting protein	Mrip	1.123	0.107	0.999	0.705	1.101	0.613	0.998	0.979
1369980_s_at	NM_053814	myosin phosphatase-Rho interacting protein	Mrip	1.221	0.135	1.137	0.030	1.405	0.020	1.597	0.015
1368450_at	NM_022178	myosin Va	Myo5a	0.881	0.255	2.634	0.022	0.617	0.081	1.363	0.023
1376848_at	AI137988	Myosin X (predicted)	Myo10_predicted	2.674	0.013	1.377	0.074	1.861	0.039	1.351	0.001
1393639_at	AI044576	myosin X (predicted)	Myo10_predicted	1.019	0.418	1.088	0.119	0.999	0.443	1.305	0.100
1370158_at	AA946388	myosin, heavy polypeptide 10, non-muscle	Myh10	0.408	0.000	0.232	0.001	0.451	0.001	0.299	0.003
1380613_at	BM390334	Myosin, heavy polypeptide 11, smooth muscle	Myh11	1.389	0.578	0.858	0.140	1.563	0.199	1.254	0.354
1384264_at	AI578120	myosin, heavy polypeptide 14	Myh14	1.023	0.912	0.994	0.519	1.245	0.360	1.011	0.981
1396165_at	AI601887	Myosin, heavy polypeptide 7, cardiac muscle, beta	Myh7	1.527	0.515	1.319	0.799	1.017	0.831	1.331	0.628
1393540_at	AA924346	Myosin, heavy polypeptide 7, cardiac muscle, beta	Myh7	1.001	0.998	1.002	0.432	1.240	0.195	0.999	0.987
1371725_at	BM392410	Myosin, heavy polypeptide 9, non-muscle	Myh9	2.572	0.012	1.909	0.004	1.491	0.152	1.772	0.004
1387402_at	NM_013194	myosin, heavy polypeptide 9, non-muscle	Myh9	1.782	0.170	1.676	0.300	2.178	0.229	1.057	0.903
1371541_at	AI177055	Myosin, light polypeptide kinase (predicted)	Mylk_predicted	0.663	0.150	0.467	0.011	1.123	0.281	0.699	0.263
1371841_at	AI228667	myotrophin	Mtpn	0.786	0.015	1.016	0.666	0.693	0.029	1.082	0.686
1387785_at	U21661	myotrophin	Mtpn	0.636	0.046	2.310	0.007	0.510	0.021	1.505	0.035
1383071_at	BG667380	myotrophin	Mtpn	0.635	0.347	0.715	0.025	0.495	0.093	0.768	0.012
1387786_at	AI711244	myotrophin	Mtpn	0.538	0.712	0.990	0.285	0.527	0.080	1.099	0.691
1377422_at	AI029466	myotubularin related protein 1 (predicted)	Mtmr1_predicted	0.681	0.106	1.840	0.052	0.629	0.020	2.684	0.015
1391512_at	AI029734	Myotubularin related protein 1 (predicted)	Mtmr1_predicted	0.977	0.869	1.136	0.202	1.058	0.426	0.916	0.931
1373589_at	BM385209	myotubularin related protein 3	Mtmr3	1.085	0.064	1.399	0.030	1.152	0.188	1.098	0.436
1372287_at	AI236780	Myotubularin related protein 6 (predicted)	Mtmr6_predicted	0.671	0.042	0.848	0.027	0.675	0.030	0.917	0.196
1391225_at	BF392551	Myotubularin related protein 7 (predicted)	Mtmr7_predicted	0.740	0.022	0.395	0.001	0.791	0.090	0.432	0.024
1374883_at	BF392344	myotubularin related protein 7 (predicted)	Mtmr7_predicted	0.971	0.832	0.699	0.089	0.589	0.022	0.611	0.018
1389116_at	BE111884	myotubularin related protein 9	Mtmr9	0.789	0.599	0.830	0.819	0.772	0.932	0.871	0.487
1373432_at	BE111604	myristoylated alanine rich protein kinase C substrate	Marcks	0.670	0.046	0.454	0.003	0.685	0.017	0.450	0.075
1370949_at	M59859	myristoylated alanine rich protein kinase C substrate	Marcks	1.091	0.479	0.659	0.003	0.728	0.053	0.443	0.020
1370948_a_at	M59859	myristoylated alanine rich protein kinase C substrate	Marcks	1.013	0.980	0.937	0.510	0.594	0.091	0.628	0.188
1399016_at	BG671507	MYST histone acetyltransferase 2	Myst2	1.078	0.888	1.459	0.114	0.972	0.392	1.146	0.451
1371015_at	X52711	myxovirus (influenza virus) resistance 1	Mx1	7.248	0.003	3.361	0.001	71.772	0.000	31.540	0.000
1369202_at	NM_017028	myxovirus (influenza virus) resistance 2	Mx2	21.174	0.005	3.319	0.041	47.527	0.003	12.513	0.001
1387283_at	NM_134350	myxovirus (influenza virus) resistance 2	Mx2	2.682	0.006	3.121	0.007	17.385	0.001	12.222	0.001

1373939_at	AI236719	N-acetylglucosamine kinase	Nagk	0.999	0.709	0.854	0.444	0.407	0.009	0.654	0.287
1374790_at	AW433892	N-acetylglucosamine-1-phosphotransferase, gamma subunit	Gnptg	0.644	0.125	0.669	0.009	0.765	0.085	0.677	0.024
1372401_at	AA859401	N-acetylneuraminic acid synthase (sialic acid synthase) (predicted)	Nans_predicted	0.980	0.123	1.677	0.017	1.478	0.150	1.932	0.025
1372402_at	AW435213	N-acetylneuraminic acid synthase (sialic acid synthase) (predicted)	Nans_predicted	1.167	0.433	1.299	0.043	1.334	0.157	1.526	0.111
1397963_x_at	BE106401	N-acetylneuraminic acid synthase (sialic acid synthase) (predicted)	Nans_predicted	0.864	0.853	0.978	0.798	1.020	0.673	1.071	0.477
1368434_at	NM_053853	N-acetyltransferase 1 (arylamine N-acetyltransferase)	Nat1	1.092	0.737	0.838	0.005	1.351	0.314	1.045	0.999
1387187_a_at	U17260	N-acetyltransferase 1 (arylamine N-acetyltransferase)	Nat1	1.012	0.921	0.992	0.965	1.003	0.490	0.995	0.976
1388352_at	BI296716	N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae) (predicted)	Nat5_predicted	1.630	0.093	0.854	0.113	2.113	0.038	0.948	0.495
1392627_x_at	BI282114	N-acetyltransferase 8 (camello like)	Nat8	1.042	0.924	0.992	0.229	1.168	0.190	0.945	0.161
1375230_at	AA800192	N-acetyltransferase 8 (camello like)	Nat8	1.045	0.950	1.171	0.270	1.176	0.180	1.332	0.264
1376192_at	AI070138	N-acetyltransferase 9 (predicted)	Nat9_predicted	0.824	0.198	0.955	0.572	0.568	0.037	1.078	0.420
1383922_a_at	BG375634	N-acetyltransferase ARD1 homolog (S. cerevisiae) (predicted)	Ard1_predicted	0.685	0.497	0.910	0.414	0.889	0.298	0.920	0.310
1384340_a_at	AA997134	N-acetyltransferase ARD1 homolog (S. cerevisiae) (predicted)	Ard1_predicted	0.592	0.927	0.721	0.045	1.028	0.817	0.782	0.196
1369077_at	NM_053407	N-acylsphingosine amidohydrolase 1	Asah1	1.578	0.867	0.406	0.008	0.823	0.803	0.368	0.016
1374770_at	AA800062	N-acylsphingosine amidohydrolase 1	Asah1	1.008	0.929	0.775	0.028	1.067	0.491	0.842	0.287
1391791_at	AI137826	N-acylsphingosine amidohydrolase 3-like (predicted)	Asah3l_predicted	1.095	0.708	1.000	0.877	1.002	0.250	0.999	0.952
1379472_at	AI232666	NAD synthetase 1	Nadsyn1	0.807	0.178	0.859	0.415	0.961	0.825	0.864	0.984
1392988_at	BF407232	NAD(P) dependent steroid dehydrogenase-like	Nsdhl	0.709	0.114	0.916	0.140	0.809	0.206	0.817	0.655
1387599_a_at	J02679	NAD(P)H dehydrogenase, quinone 1	Nqo1	0.556	0.038	3.715	0.005	0.453	0.010	3.812	0.012
1374959_at	AA945624	NAD(P)H dehydrogenase, quinone 2	Nqo2	6.196	0.008	1.670	0.318	9.031	0.001	1.625	0.422
1389334_at	BI277594	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10 /// NADH dehydrogenase 1 alpha subcomplex 10-like protein	Ndufa10 /// LOC316632	0.619	0.093	0.861	0.109	0.492	0.001	0.855	0.125
1375220_at	AA818971	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11	Ndufa11	0.713	0.565	0.700	0.084	0.546	0.014	0.934	0.226
1386951_at	NM_012985	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 5	Ndufa5	0.870	0.046	1.266	0.020	0.782	0.069	1.086	0.311
1388391_at	AA996544	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 (predicted)	Ndufa1_predicted	0.991	0.968	0.754	0.010	0.825	0.197	0.774	0.192
1391126_at	BG379351	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12 (predicted)	Ndufa12_predicted	0.279	0.009	0.220	0.001	0.397	0.009	0.222	0.000
1371605_at	AI710281	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12 (predicted)	Ndufa12_predicted	0.687	0.237	0.823	0.080	0.612	0.048	0.717	0.329
1388362_at	BM390197	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13 (predicted)	Ndufa13_predicted	0.941	0.948	1.131	0.067	0.972	0.328	1.575	0.003
1389288_at	BI279838	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (predicted)	Ndufa2_predicted	0.523	0.335	0.489	0.018	0.370	0.015	0.622	0.007
1379243_at	AA819547	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14) (predicted)	Ndufa6_predicted	0.637	0.030	0.798	0.371	0.640	0.055	0.618	0.401
1395045_at	BM384525	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a) (predicted)	Ndufa7_predicted	0.636	0.119	0.843	0.155	0.599	0.052	0.875	0.495
1375411_at	BI277002	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a) (predicted)	Ndufa7_predicted	0.831	0.375	0.902	0.146	0.717	0.211	0.910	0.740
1371355_at	BI280270	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	Ndufa8	0.742	0.611	1.291	0.084	0.820	0.146	1.610	0.126
1388323_at	BG381033	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	Ndufa9	0.656	0.100	0.822	0.035	0.623	0.009	0.838	0.230
1393689_at	BE097322	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1 (predicted)	Ndufaf1_predicted	0.733	0.165	1.025	0.918	0.676	0.084	1.986	0.046
1373041_at	AI555535	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3 (predicted)	Ndufb3_predicted	0.600	0.120	0.723	0.005	0.519	0.025	0.615	0.042
1388315_at	BI282661	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11 (predicted)	Ndufb11_predicted	0.791	0.892	0.709	0.053	0.565	0.163	0.754	0.060
1389012_at	BM386606	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 (predicted)	Ndufb2_predicted	0.948	0.802	0.799	0.165	0.742	0.156	0.990	0.923
1371371_at	AW434041	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa	Ndufb4	0.768	0.026	0.773	0.076	0.687	0.020	0.810	0.034
1388304_at	BI281307	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (predicted)	Ndufb5_predicted	0.595	0.270	0.563	0.000	0.529	0.010	0.477	0.033
1371346_at	AI104528	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (predicted)	Ndufb6_predicted	0.725	0.585	0.592	0.029	0.530	0.041	0.666	0.002
1388343_at	AI575943	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (predicted)	Ndufb7_predicted	0.539	0.228	1.079	0.524	0.681	0.051	0.986	0.399
1371701_at	BG666921	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (predicted)	Ndufb9_predicted	0.618	0.124	1.164	0.246	0.560	0.003	1.097	0.158
1389964_at	AA944343	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1 (predicted)	Ndufab1_predicted	0.558	0.476	0.921	0.221	0.452	0.027	0.889	0.388
1375516_at	AA891171	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	Ndufc2	0.679	0.264	0.787	0.056	0.647	0.120	0.761	0.001
1381520_at	BE105072	NADH dehydrogenase (ubiquinone) Fe-S protein 1	Ndufs1	1.212	0.180	0.844	0.165	0.599	0.140	1.223	0.149
1371577_at	AI171362	NADH dehydrogenase (ubiquinone) Fe-S protein 1	Ndufs1	0.616	0.263	0.585	0.000	0.472	0.059	0.704	0.001
1371482_at	AA851675	NADH dehydrogenase (ubiquinone) Fe-S protein 2	Ndufs2	0.598	0.339	0.603	0.001	0.592	0.157	0.672	0.020
1388364_at	BG381650	NADH dehydrogenase (ubiquinone) Fe-S protein 3 (predicted)	Ndufs3_predicted	0.543	0.325	0.984	0.752	0.498	0.188	1.082	0.378
1372147_at	BM387802	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	Ndufs4	0.884	0.503	1.175	0.287	0.898	0.162	1.224	0.114
1388414_at	AI410498	NADH dehydrogenase (ubiquinone) Fe-S protein 5b, 15kDa (NADH-coenzyme Q reductase)	Ndufs5b	0.749	0.739	0.593	0.027	0.787	0.084	0.715	0.220
1370006_at	NM_019223	NADH dehydrogenase (ubiquinone) Fe-S protein 6	Ndufs6	0.942	0.563	1.048	0.612	0.866	0.429	0.989	0.944
1371912_at	AI231358	NADH dehydrogenase (ubiquinone) Fe-S protein 7	Ndufs7	0.539	0.177	0.982	0.918	0.601	0.129	1.000	0.998
1388326_at	AA799479	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (predicted)	Ndufs8_predicted	0.738	0.616	1.158	0.331	0.578	0.053	1.149	0.560
1371416_at	AI231746	NADH dehydrogenase (ubiquinone) flavoprotein 1	Ndufv1	0.542	0.196	0.880	0.044	0.710	0.006	0.708	0.105
1371041_at	M22756	NADH dehydrogenase (ubiquinone) flavoprotein 2	Ndufv2	0.625	0.139	0.959	0.151	0.633	0.006	0.925	0.102
1368566_a_at	AA964381	NADH dehydrogenase (ubiquinone) flavoprotein 3-like	Ndufv3l	1.086	0.608	0.774	0.111	0.948	0.062	0.695	0.108
1368567_at	NM_022607	NADH dehydrogenase (ubiquinone) flavoprotein 3-like	Ndufv3l	0.588	0.815	1.291	0.167	0.430	0.567	1.086	0.665
1387311_at	NM_053683	NADPH oxidase 1	Nox1	0.998	0.405	0.688	0.045	1.003	0.628	0.995	0.977
1387110_at	NM_012993	nardilysin, N-arginine dibasic convertase 1	Nrd1	0.907	0.756	0.846	0.070	1.092	0.767	0.937	0.010
1382673_at	BE115812	Nardilysin, N-arginine dibasic convertase 1	Nrd1	0.931	0.983	1.250	0.270	0.914	0.074	1.116	0.046

1368153_a_at	AJ293698	nasal embryonic LHRH factor	Nelf	1.177	0.460	0.565	0.042	0.827	0.447	0.811	0.089
1371435_at	BI279561	nascent-polypeptide-associated complex alpha polypeptide (predicted)	Naca_predicted	0.904	0.737	1.182	0.844	0.654	0.197	1.036	0.918
1391425_at	AW528585	NCK interacting protein with SH3 domain (predicted)	Nckipsd_predicted	0.992	0.842	1.187	0.766	0.832	0.917	1.206	0.819
1371407_at	AI178285	NCK-associated protein 1	Nckap1	0.868	0.315	0.816	0.007	0.871	0.062	0.885	0.011
1388196_at	BM383722	NCK-associated protein 1	Nckap1	1.038	0.796	0.864	0.024	1.194	0.684	0.833	0.042
1398319_at	AI071000	Nclone10 mRNA	---	2.035	0.003	2.006	0.008	1.293	0.088	1.995	0.006
1374827_at	BI276137	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2 (predicted)	Ndst2_predicted	0.916	0.553	1.215	0.002	1.054	0.993	0.999	0.987
1389532_at	AW252250	Nebulette (predicted)	Nebl_predicted	2.480	0.021	1.472	0.074	0.919	0.549	1.014	0.647
1394666_at	AI549596	Nebulin (predicted)	Neb_predicted	1.320	0.786	1.614	0.883	1.155	0.354	1.235	0.510
1372082_at	BM391772	NECAP endocytosis associated 2	Necap2	0.569	0.042	0.848	0.222	1.116	0.531	0.770	0.051
1371947_at	BG671865	necdin	Ndn	0.794	0.901	0.336	0.011	0.873	0.203	0.625	0.021
1394181_at	AI176506	Necdin-like 2	Ndnl2	0.643	0.006	0.974	0.903	0.783	0.007	1.041	0.140
1376704_a_at	BM390112	necdin-like 2	Ndnl2	0.616	0.116	0.963	0.462	0.768	0.205	1.035	0.702
1398893_at	BG671512	Nedd4 family interacting protein 1	Ndfip1	0.728	0.249	0.632	0.000	0.650	0.068	0.621	0.000
1395345_at	BF282156	Nedd4 family interacting protein 1	Ndfip1	1.416	0.310	0.806	0.896	0.883	0.081	0.912	0.371
1389364_at	BF406709	Nedd4 family interacting protein 2 (predicted)	Ndfip2_predicted	1.528	0.169	4.782	0.000	1.049	0.675	3.074	0.001
1373861_at	AI228114	Nedd4 family interacting protein 2 (predicted)	Ndfip2_predicted	1.218	0.196	2.164	0.001	1.249	0.007	1.910	0.001
1373775_at	AI232313	NEDD8 ultimate buster-1	Nub1	3.986	0.001	2.518	0.007	4.866	0.000	3.598	0.001
1393654_at	BM391891	nei endonuclease VIII-like 1 (E. coli)	Neil1	0.558	0.070	0.598	0.014	0.832	0.073	0.621	0.032
1372497_at	AI104094	neighbor of Brca1 gene 1	Nbr1	1.042	0.890	0.925	0.850	0.875	0.147	0.848	0.069
1381509_at	BF393724	neighbor of Brca1 gene 1	Nbr1	1.001	0.988	9.171	0.010	0.932	0.076	3.960	0.014
1368120_at	NM_031069	NEL-like 1 (chicken)	Nell1	0.997	0.060	0.864	0.195	0.753	0.955	1.412	0.197
1392770_at	BF415817	neogenin	Neo1	0.530	0.006	0.615	0.018	0.497	0.003	0.715	0.024
1371056_at	U68726	neogenin	Neo1	1.082	0.833	0.580	0.025	1.029	0.905	0.453	0.004
1374508_at	BG663343	nephronophthisis 1 (juvenile) homolog (human) (predicted)	Nphp1_predicted	0.674	0.036	2.410	0.066	0.457	0.009	1.728	0.028
1369948_at	NM_053401	nerve growth factor receptor (TNFRSF16) associated protein 1	Ngfrap1	0.666	0.069	0.924	0.063	0.362	0.005	0.819	0.009
1385534_at	BG381021	nerve growth factor receptor (TNFRSF16) associated protein 1	Ngfrap1	0.844	0.187	0.937	0.271	0.685	0.079	0.965	0.024
1367961_at	NM_031523	nerve growth factor, gamma	Ngfg	1.199	0.693	0.541	0.025	0.224	0.051	0.522	0.013
1372528_at	AI102069	N-ethylmaleimide sensitive fusion protein	Nsf	0.282	0.118	0.466	0.004	0.493	0.030	0.667	0.029
1369689_at	AF142097	N-ethylmaleimide sensitive fusion protein	Nsf	0.677	0.174	0.505	0.161	0.646	0.175	0.520	0.198
1369690_at	AI547471	N-ethylmaleimide sensitive fusion protein	Nsf	1.021	0.403	0.506	0.001	0.842	0.317	0.530	0.001
1398782_at	NM_080585	N-ethylmaleimide sensitive fusion protein attachment protein alpha	Napa	0.642	0.077	1.044	0.503	0.642	0.008	0.863	0.021
1368320_at	NM_031521	neural cell adhesion molecule 1	Ncam1	0.480	0.030	1.147	0.808	0.434	0.009	0.689	0.569
1391235_at	BF394807	Neural cell adhesion molecule 1	Ncam1	0.997	0.663	1.005	0.600	1.022	0.321	0.993	0.936
1396764_at	BF400138	Neural cell adhesion molecule 1	Ncam1	1.665	0.868	0.691	0.629	1.009	0.955	0.945	0.314
1396893_at	AI576209	Neural cell adhesion molecule 1	Ncam1	0.997	0.992	0.936	0.615	0.997	0.978	0.934	0.689
1397120_at	BF409530	Neural cell adhesion molecule 1	Ncam1	0.991	0.992	0.558	0.527	1.010	0.585	0.993	0.772
1389507_at	AI072446	neural precursor cell expressed, developmentally down-regulated 4-like	Nedd4l	0.850	0.397	1.373	0.124	0.581	0.016	1.078	0.769
1379457_at	AI013407	neural precursor cell expressed, developmentally down-regulated gene 1 (predicted)	Nedd1_predicted	1.000	0.968	0.996	0.930	1.001	0.993	0.998	0.163
1395157_at	BI286685	neural precursor cell expressed, developmentally down-regulated gene 4A	Nedd4a	0.740	0.010	0.248	0.304	0.954	0.976	0.411	0.100
1383899_at	BI277849	neural precursor cell expressed, developmentally down-regulated gene 4A	Nedd4a	0.924	0.050	1.374	0.334	1.056	0.996	1.305	0.501
1375119_at	BI284798	neural precursor cell expressed, developmentally down-regulated gene 4A	Nedd4a	0.472	0.130	0.780	0.073	0.634	0.074	0.707	0.014
1371314_at	BM389736	neural precursor cell expressed, developmentally down-regulated gene 4A	Nedd4a	0.555	0.191	0.417	0.005	0.664	0.185	0.422	0.001
1386263_at	AI227677	neural precursor cell expressed, developmentally down-regulated gene 4A	Nedd4a	0.706	0.314	0.642	0.051	0.679	0.176	0.592	0.021
1398860_at	AF095740	neural precursor cell expressed, developmentally down-regulated gene 8	Nedd8	0.858	0.804	1.071	0.706	0.740	0.279	1.140	0.351
1374650_at	BM392374	neural precursor cell expressed, developmentally down-regulated gene 9	Nedd9	0.663	0.039	0.486	0.014	0.448	0.006	0.532	0.015
1372773_at	BM389728	neural proliferation, differentiation and control, 1	Npdc1	0.901	0.763	1.151	0.020	0.912	0.655	1.057	0.158
1375684_at	BE111846	neuraminidase 1	Neu1	0.629	0.171	0.979	0.471	0.584	0.148	0.965	0.398
1369081_at	NM_031522	neuraminidase 1	Neu1	0.981	0.902	1.825	0.099	0.983	0.914	0.862	0.291
1369404_a_at	NM_021767	neurexin 1	Nrxn1	0.997	0.530	1.128	0.953	1.136	0.883	1.083	0.563
1386697_at	BF567897	neurexophilin 1	Nxph1	0.992	0.976	0.977	0.962	0.992	0.978	1.016	0.997
1389663_at	BI278423	neurobeachin-like 2 (predicted)	Nbeal2_predicted	0.774	0.298	0.671	0.025	0.621	0.376	0.795	0.261
1387678_at	NM_080766	neuroblastoma ras oncogene	Nras	1.211	0.123	0.779	0.062	0.916	0.558	0.846	0.064
1372953_at	AI101330	neurocalcin delta	Ncald	0.238	0.018	0.168	0.000	0.228	0.004	0.201	0.003
1392581_at	BF420172	neurocalcin delta	Ncald	0.391	0.036	0.137	0.000	0.308	0.047	0.139	0.000
1367956_at	NM_053543	neurochondrin	Ncdn	0.511	0.060	0.582	0.008	0.450	0.001	0.573	0.006
1372000_at	AI180187	neuroepithelial cell transforming gene 1	Net1	1.371	0.121	1.385	0.013	0.939	0.849	1.259	0.039
1370876_at	BI285436	neurofascin	Nfasc	1.578	0.071	1.778	0.013	1.000	0.272	1.294	0.077
1392822_at	AA957509	Neurofibromatosis 1	Nf1	0.760	0.608	1.649	0.072	1.010	0.985	0.825	0.989
1375994_at	BE107324	Neurofibromatosis 1	Nf1	1.011	0.969	0.612	0.031	0.999	0.994	0.711	0.057
1397682_at	AW917689	Neurofibromatosis 1	Nf1	1.008	0.979	1.017	0.326	0.904	0.635	0.493	0.102

1367845_at	NM_017029	neurofilament 3, medium	Nef3	2.314	0.018	3.538	0.000	3.604	0.009	4.292	0.001
1370815_at	AF031879	neurofilament, heavy polypeptide	Nefh	0.274	0.000	0.913	0.253	0.271	0.001	0.904	0.515
1387288_at	NM_019218	neurogenic differentiation 1	Neurod1	1.130	0.032	0.518	0.013	0.969	0.796	0.583	0.061
1397705_at	BF542792	neuroligin 2	Nlgn2	1.220	0.565	1.035	0.920	1.079	0.937	0.796	0.678
1368895_at	NM_053992	neuroligin 2	Nlgn2	1.057	0.914	0.587	0.009	0.974	0.900	0.515	0.029
1369669_at	NM_053970	neurolysin (metallopeptidase M3 family)	Nln	4.484	0.006	2.845	0.006	4.342	0.007	2.974	0.012
1375991_at	BE120163	neuromedin B (predicted)	Nmb_predicted	0.813	0.299	1.191	0.036	0.633	0.083	1.049	0.777
1369717_at	M94555	neuromedin U	Nmu	0.908	0.974	0.977	0.966	0.998	0.953	1.003	0.982
1375381_at	AW252503	Neuron derived neurotrophic factor	Nenf	0.809	0.106	0.899	0.399	0.997	0.156	0.990	0.843
1381184_at	BF396578	Neuron navigator 2	Nav2	1.069	0.855	0.403	0.320	0.960	0.828	0.810	0.293
1387817_at	NM_024128	neuron specific gene family member 1	Nsg1	0.423	0.007	0.095	0.000	0.552	0.012	0.080	0.020
1398024_at	BE110250	Neuronal PAS domain protein 2 (predicted)	Npas2_predicted	0.896	0.811	1.001	0.995	0.916	0.059	0.998	0.990
1376362_at	BG380575	neuronal pentraxin receptor	Nptxr	0.461	0.004	0.677	0.093	0.383	0.002	0.454	0.002
1371412_a_at	BE107450	Neuronal regeneration related protein	Nrep	0.701	0.270	0.179	0.007	0.427	0.303	0.197	0.019
1369999_a_at	NM_053601	neuronatin	Nnat	0.607	0.544	0.288	0.006	0.925	0.257	0.296	0.014
1371036_at	BG671431	neuron-glia-CAM-related cell adhesion molecule	Nrcam	1.280	0.024	1.543	0.007	0.530	0.004	1.077	0.708
1381621_at	BF386153	Neuron-glia-CAM-related cell adhesion molecule	Nrcam	1.719	0.380	1.639	0.173	0.736	0.299	1.324	0.290
1377001_at	AI406747	neuron-glia-CAM-related cell adhesion molecule	Nrcam	1.093	0.642	0.881	0.700	0.906	0.066	0.676	0.318
1392734_at	AI145667	neuron-glia-CAM-related cell adhesion molecule	Nrcam	1.241	0.698	2.068	0.018	0.499	0.043	0.892	0.561
1395083_at	AA926313	Neuro-oncological ventral antigen 1	Nova1	0.341	0.011	0.223	0.000	0.679	0.064	0.370	0.010
1377049_at	BE107890	neuropathy target esterase like 1	Ntel1	0.766	0.307	4.050	0.036	1.046	0.833	1.982	0.056
1387154_at	NM_012614	neuropeptide Y	Npy	0.960	0.870	0.888	0.670	0.656	0.079	0.765	0.024
1373577_at	BE116566	Neuropilin 1	Nrp1	3.881	0.001	1.271	0.738	5.087	0.023	1.280	0.715
1382995_at	AA859669	Neuropilin 2	Nrp2	1.576	0.397	1.488	0.075	1.640	0.191	1.456	0.071
1395070_at	AI136959	Neurotrimin	Hnt	0.566	0.098	0.786	0.368	0.647	0.053	0.669	0.358
1368255_at	NM_017354	neurotrimin /// hypothetical gene supported by NM_017354	Hnt /// LOC360435	0.166	0.000	0.266	0.004	0.204	0.023	0.352	0.002
1369000_at	NM_021589	neurotrophic tyrosine kinase, receptor, type 1	Ntrk1	0.206	0.017	0.231	0.228	0.266	0.034	0.270	0.026
1375615_at	AI575310	Neurotrophic tyrosine kinase, receptor, type 1	Ntrk1	0.514	0.297	0.405	0.019	0.789	0.145	0.405	0.012
1370687_a_at	M55292	neurotrophic tyrosine kinase, receptor, type 2	Ntrk2	0.397	0.050	0.290	0.091	0.465	0.010	0.330	0.109
1383135_at	BG669126	Neurotrophic tyrosine kinase, receptor, type 2	Ntrk2	0.647	0.059	0.126	0.005	0.977	0.176	0.265	0.000
1397246_at	BE102996	Neurotrophic tyrosine kinase, receptor, type 2	Ntrk2	0.998	0.223	0.239	0.007	1.017	0.868	0.252	0.005
1368939_a_at	L14447	neurotrophic tyrosine kinase, receptor, type 3	Ntrk3	1.002	0.818	0.994	0.974	1.158	0.315	0.828	0.923
1377080_at	AI598730	neurotrophin receptor associated death domain	Nradd	0.970	0.105	0.842	0.166	0.884	0.414	0.706	0.147
1372039_at	AI406810	NFKB inhibitor interacting Ras-like protein 2 (predicted)	Nkiras2_predicted	1.229	0.174	1.076	0.831	1.008	0.971	0.985	0.961
1377091_at	AW524733	NG5 protein	Ng5	1.137	0.648	1.172	0.228	0.959	0.310	1.147	0.180
1369409_at	NM_022856	Ngfi-A binding protein 1	Nab1	1.886	0.010	1.665	0.046	1.973	0.009	1.590	0.014
1393172_at	AA848648	Ngfi-A binding protein 1	Nab1	2.825	0.013	1.399	0.136	2.748	0.009	1.464	0.012
1374925_at	AI102530	Ngfi-A binding protein 2	Nab2	1.150	0.169	1.680	0.207	1.817	0.189	1.073	0.755
1383289_at	BG373214	Ngg1 interacting factor 3-like 1 (S. pombe)	Nif3l1	1.177	0.569	0.997	0.538	0.758	0.058	1.430	0.332
1387977_at	AF218575	nibrin	Nbn	1.264	0.439	1.592	0.001	1.564	0.038	1.683	0.005
1374497_at	AI102943	nicalin homolog (zebrafish)	Ncln	0.633	0.067	0.893	0.425	0.958	0.605	0.676	0.043
1396543_at	BE099968	nicastrin	Ncstn	1.289	0.534	0.783	0.102	1.023	0.773	0.508	0.055
1367511_at	BI285459	nicastrin	Ncstn	0.997	0.994	0.552	0.005	0.964	0.432	0.580	0.021
1398610_at	BG375744	nicolin 1	Nicn1	0.547	0.005	0.594	0.040	0.385	0.000	0.646	0.012
1383065_at	AW434166	nicolin 1	Nicn1	0.958	0.830	0.849	0.486	0.830	0.751	0.954	0.297
1394718_at	BF396080	Nicotinamide nucleotide adenylyltransferase 2 (predicted)	Nmnat2_predicted	1.684	0.328	0.782	0.765	2.109	0.098	1.084	0.773
1374025_at	AA963282	nicotinamide nucleotide adenylyltransferase 3 /// similar to Nicotinamide nucleotide adenylyltransferase 3	Nmnat3 /// LOC501040	0.854	0.526	2.105	0.016	1.162	0.577	2.091	0.058
1371483_at	AA891872	nicotinamide nucleotide transhydrogenase (mapped)	Nnt_mapped	0.552	0.280	0.490	0.001	0.443	0.039	0.634	0.005
1381261_at	BE113729	Nicotinamide nucleotide transhydrogenase (mapped)	Nnt_mapped	1.531	0.921	0.534	0.456	1.221	0.257	0.516	0.548
1375436_at	BF416417	nicotinate phosphoribosyltransferase domain containing 1	Naprt1	0.618	0.106	1.419	0.554	0.680	0.156	0.886	0.280
1395411_at	AW916787	nicotinate phosphoribosyltransferase domain containing 1	Naprt1	0.981	0.959	0.910	0.240	1.003	0.982	0.626	0.159
1371032_at	BG372942	nidogen 1	Nid1	0.670	0.060	0.551	0.004	0.681	0.087	0.574	0.001
1388618_at	BM389302	nidogen 2	Nid2	0.942	0.625	1.035	0.770	0.925	0.631	1.000	0.999
1398892_at	BI287960	Niemann Pick type C2	Npc2	0.978	0.747	1.280	0.085	0.908	0.834	1.195	0.137
1375271_at	BE118382	NIMA (never in mitosis gene a)- related kinase 9 (predicted)	Nek9_predicted	1.011	0.969	0.998	0.876	0.990	0.921	1.002	0.984
1397316_at	AI179830	NIMA (never in mitosis gene a)- related kinase 9 (predicted)	Nek9_predicted	0.994	0.991	1.035	0.950	1.764	0.314	1.047	0.787
1389996_at	AI406369	NIMA (never in mitosis gene a)-related expressed kinase 1 (predicted)	Nek1_predicted	0.840	0.946	0.725	0.010	0.658	0.067	0.628	0.010
1382284_at	AW525175	NIMA (never in mitosis gene a)-related expressed kinase 3 (predicted)	Nek3_predicted	1.518	0.101	0.993	0.960	0.946	0.996	1.074	0.207
1374565_at	BF282365	NIMA (never in mitosis gene a)-related expressed kinase 6	Nek6	1.638	0.422	1.288	0.246	0.978	0.878	0.988	0.934
1388878_at	BI279756	nin one binding protein	Nob1p	1.371	0.399	2.157	0.003	0.916	0.716	1.894	0.009
1370348_at	U72660	ninjurin 1	Ninj1	0.764	0.733	3.304	0.006	1.095	0.871	2.909	0.007

1384801_at	AA963592	Nipped-B homolog (Drosophila)	NIPBL	1.864	0.006	1.398	0.019	1.689	0.056	1.861	0.003
1392470_at	AI180223	Nipped-B homolog (Drosophila)	NIPBL	1.434	0.035	0.917	0.702	1.599	0.139	1.411	0.049
1380371_at	BE117361	Nipped-B homolog (Drosophila)	NIPBL	0.788	0.186	1.309	0.631	1.008	0.465	1.918	0.402
1395923_at	BF416343	Nipped-B homolog (Drosophila)	NIPBL	1.005	0.438	0.742	0.138	1.002	0.881	0.615	0.140
1371782_at	BF283798	nipsnap homolog 3A (C. elegans)	Nipsnap3a	0.621	0.216	1.166	0.299	0.279	0.041	0.996	0.997
1374566_at	AI237243	Nischarin	Nisch	0.636	0.070	0.448	0.005	0.759	0.010	0.636	0.043
1371558_at	BI282284	nischarin	Nisch	0.963	0.166	0.744	0.020	0.948	0.994	0.769	0.023
1382686_at	BF285846	Nischarin	Nisch	1.270	0.537	0.792	0.241	1.094	0.635	0.720	0.172
1394957_at	BE108587	nischarin	Nisch	0.784	0.998	0.574	0.142	1.002	0.999	0.820	0.036
1387667_at	L12562	nitric oxide synthase 2, inducible	Nos2	374.969	0.000	113.753	0.000	109.349	0.004	57.801	0.003
1371397_at	AI104068	nitric oxide synthase interacting protein (predicted)	Nosip_predicted	0.998	0.977	1.190	0.992	1.002	0.997	1.001	0.999
1388324_at	BG668463	nitrilase 1	Nit1	0.561	0.028	0.665	0.017	0.487	0.003	0.701	0.033
1398049_at	BF405475	nitrilase 1	Nit1	0.957	0.810	0.374	0.010	0.993	0.207	0.559	0.006
1372438_at	AI411100	nitrilase family, member 2	Nit2	0.388	0.400	0.477	0.007	0.397	0.172	0.221	0.037
1387859_at	AI410876	nitrogen fixation gene 1 (S. cerevisiae)	Nfs1	0.608	0.014	0.444	0.000	0.784	0.078	0.481	0.002
1385387_at	AA925143	NK2 transcription factor related, locus 2 (Drosophila) (predicted)	Nkx2-2_predicted	1.234	0.332	0.232	0.000	1.179	0.997	0.434	0.091
1368998_at	NM_031737	NK6 transcription factor related, locus 1 (Drosophila)	Nkx6-1	0.823	0.103	0.465	0.000	0.493	0.005	0.567	0.005
1393248_at	BF407833	NMD3 homolog (S. cerevisiae) (predicted)	Nmd3_predicted	0.885	0.339	2.106	0.000	0.897	0.166	1.795	0.001
1372558_at	AI177404	NMDA receptor-regulated gene 1 (predicted)	Narg1_predicted	0.854	0.320	1.465	0.002	1.141	0.173	1.298	0.124
1393078_at	BG671648	NMDA receptor-regulated gene 1 (predicted)	Narg1_predicted	0.999	0.446	1.483	0.040	0.993	0.780	1.362	0.975
1383514_s_at	BG671648	NMDA receptor-regulated gene 1 (predicted)	Narg1_predicted	0.814	0.872	1.695	0.196	0.814	0.068	1.133	0.870
1393881_at	AW527638	NMDA receptor-regulated gene 1 (predicted)	Narg1_predicted	1.027	0.900	2.240	0.064	0.828	0.280	2.099	0.234
1368410_at	NM_012601	N-methylpurine-DNA glycosylase	Mpg	0.361	0.006	0.589	0.040	0.455	0.001	0.590	0.063
1393144_at	BM388202	N-myc (and STAT) interactor	Nmi	4.707	0.002	7.363	0.000	12.694	0.001	9.040	0.000
1381875_at	BM386847	N-myc (and STAT) interactor	Nmi	19.101	0.007	14.404	0.001	18.039	0.001	18.040	0.001
1391458_at	BE120446	N-myc downstream regulated gene 1	Ndrg1	0.689	0.035	1.582	0.343	0.645	0.044	1.014	0.963
1371360_at	BM384099	N-myc downstream regulated gene 1	Ndrg1	1.153	0.445	1.141	0.438	0.730	0.115	1.134	0.202
1370229_at	BG666709	N-myc downstream regulated gene 4	Ndrg4	0.533	0.000	1.808	0.020	0.465	0.001	1.621	0.032
1375522_at	AI010491	N-myristoyltransferase 1	Nmt1	1.358	0.193	4.460	0.001	1.488	0.107	2.863	0.001
1384878_at	AI501085	N-myristoyltransferase 2	Nmt2	1.419	0.084	3.795	0.000	1.230	0.217	1.717	0.024
1380305_at	BE106776	NOD3-like protein	nod3l	0.526	0.351	0.232	0.041	0.527	0.337	0.193	0.043
1389658_at	BI283104	NOL1/NOP2/Sun domain family, member 2 (predicted)	Nsun2_predicted	0.830	0.026	1.829	0.003	0.827	0.014	1.250	0.042
1373509_at	BE113288	NOL1/NOP2/Sun domain family, member 4 (predicted)	Nsun4_predicted	0.570	0.000	0.600	0.021	0.570	0.009	0.525	0.058
1389061_at	AI171164	NOL1/NOP2/Sun domain family, member 5 (predicted)	Nsun5_predicted	0.803	0.069	2.739	0.677	1.084	0.787	1.770	0.587
1380165_at	AI234713	Non-catalytic region of tyrosine kinase adaptor protein 1 (predicted)	Nck1_predicted	1.237	0.534	1.596	0.480	1.262	0.792	1.194	0.440
1373940_at	BM386507	non-catalytic region of tyrosine kinase adaptor protein 1 (predicted)	Nck1_predicted	0.773	0.901	1.500	0.406	0.946	0.694	1.594	0.336
1398441_at	AA957410	non-catalytic region of tyrosine kinase adaptor protein 2 (predicted)	Nck2_predicted	1.510	0.207	1.694	0.012	0.934	0.640	1.633	0.001
1368863_at	NM_053507	non-metastatic cell expressed protein 3	Nme3	0.294	0.073	0.199	0.001	0.277	0.006	0.221	0.022
1370446_at	AF202049	non-metastatic cells 7, protein expressed in	Nme7	0.554	0.006	0.573	0.045	0.668	0.007	0.675	0.075
1398904_at	AI599066	non-POU domain containing, octamer-binding /// similar to Nono protein (predicted)	Nono /// RGD1561770_predicted	0.902	0.255	0.916	0.543	1.286	0.216	1.090	0.148
1384257_at	BF555394	non-POU domain containing, octamer-binding /// similar to Nono protein (predicted)	Nono /// RGD1561770_predicted	1.095	0.429	2.480	0.011	1.067	0.688	2.037	0.011
1390426_at	BF389398	Notch gene homolog 1 (Drosophila)	Notch1	2.337	0.013	1.511	0.031	4.955	0.002	1.866	0.005
1398362_at	AI011448	Notch gene homolog 2 (Drosophila)	Notch2	1.959	0.019	2.476	0.014	1.356	0.148	2.150	0.113
1389765_at	BI276730	notchless homolog 1 (Drosophila) (predicted)	Nle1_predicted	1.003	0.950	1.237	0.264	0.645	0.824	1.011	0.887
1372932_at	BI302258	novel nuclear protein 1	Nnp1	0.384	0.045	0.843	0.047	0.469	0.038	0.847	0.012
1388340_at	BF281153	NS5A (hepatitis C virus) transactivated protein 9	Ns5atp9	0.985	0.875	0.337	0.012	0.866	0.848	0.606	0.033
1398772_at	NM_031981	NSFL1 (p97) cofactor (p47)	Nsfl1c	0.840	0.606	1.672	0.084	0.661	0.032	1.213	0.547
1371908_at	AA891920	NTF2-related export protein 1 (predicted)	Nxt1_predicted	0.492	0.005	2.582	0.064	0.605	0.191	2.145	0.090
1376553_at	BI284353	nth (endonuclease III)-like 1 (E.coli) (predicted)	Nthl1_predicted	0.650	0.076	1.104	0.517	0.663	0.073	0.683	0.199
1383614_at	BI295051	NUAK family, SNF1-like kinase, 2	Nuak2	3.365	0.002	2.158	0.065	7.166	0.001	2.136	0.067
1378264_at	BG375928	Nuclear autoantigenic sperm protein (histone-binding)	Nasp	1.068	0.623	0.961	0.045	0.935	0.890	1.110	0.240
1377299_at	AI137618	nuclear autoantigenic sperm protein (histone-binding)	Nasp	1.001	0.993	1.259	0.038	0.740	0.777	1.081	0.492
1373978_at	AI410277	nuclear cap binding protein subunit 1, 80kDa	Ncbp1	0.434	0.034	1.388	0.036	0.516	0.012	1.554	0.018
1383965_at	BI282103	nuclear cap binding protein subunit 2 (predicted)	Ncbp2_predicted	0.844	0.140	0.995	0.570	1.343	0.043	1.098	0.452
1396264_at	BF397752	Nuclear cap binding protein subunit 2 (predicted)	Ncbp2_predicted	0.827	0.267	1.146	0.304	1.961	0.024	1.174	0.454
1385553_at	AI136699	nuclear cap binding protein subunit 2 (predicted)	Ncbp2_predicted	0.962	0.798	1.810	0.008	0.670	0.055	1.593	0.030
1392858_at	BM387770	nuclear cap binding protein subunit 2 (predicted)	Ncbp2_predicted	0.700	0.805	0.731	0.455	0.987	0.437	0.996	0.708
1368436_at	NM_017271	nuclear distribution gene C homolog (Aspergillus)	Nudc	0.632	0.123	1.931	0.004	0.667	0.009	1.912	0.004
1398105_at	AI548809	Nuclear factor I/A	Nfia	1.358	0.234	0.993	0.927	1.114	0.564	0.984	0.929

1369678_a_at	D78017	nuclear factor I/A	Nfia	0.998	0.758	1.002	0.717	0.820	0.556	0.724	0.478
1369679_a_at	AB060652	nuclear factor I/A	Nfia	0.947	0.962	0.797	0.318	0.918	0.309	1.006	0.962
1371202_a_at	AB012232	nuclear factor I/B	Nfib	4.143	0.001	1.474	0.049	1.565	0.919	1.090	0.623
1388250_at	AB012232	nuclear factor I/B	Nfib	0.994	0.181	0.994	0.956	0.838	0.208	0.997	0.961
1394778_at	BE116111	Nuclear factor I/B	Nfib	1.618	0.248	0.994	0.127	2.095	0.047	1.316	0.267
1375342_at	BG381296	Nuclear factor I/C	Nfic	1.008	0.579	1.676	0.093	1.094	0.279	1.146	0.375
1370968_at	AA858801	nuclear factor of kappa light chain gene enhancer in B-cells 1, p105	Nfkb1	19.062	0.003	7.672	0.001	17.755	0.000	7.481	0.002
1389538_at	AW672589	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha	Nfkbia	55.162	0.000	25.927	0.000	82.838	0.000	20.087	0.000
1367943_at	NM_030867	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, beta	Nfkbib	4.401	0.056	7.259	0.001	5.777	0.005	5.671	0.002
1375989_a_at	AI170362	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2, p49/p100	Nfkb2	12.319	0.000	10.630	0.000	18.223	0.000	11.327	0.000
1378724_at	BI291716	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1	Nfkbil1	1.135	0.942	2.499	0.146	0.818	0.065	1.033	0.900
1376325_at	BM388975	Nuclear factor related to kappa B binding protein (predicted)	Nfrkb_predicted	1.120	0.527	1.010	0.299	1.135	0.387	0.797	0.214
1367826_at	NM_031789	nuclear factor, erythroid derived 2, like 2	Nfe2l2	0.744	0.715	2.525	0.001	0.890	0.435	2.345	0.002
1378543_at	BE108222	Nuclear factor, erythroid derived 2, like 3 (predicted)	Nfe2l3_predicted	0.574	0.010	0.728	0.055	0.686	0.048	0.588	0.171
1373278_at	BM391303	nuclear factor, erythroid derived 2,-like 1 (predicted)	Nfe2l1_predicted	1.671	0.050	1.266	0.109	1.420	0.104	1.080	0.207
1375253_at	BF403837	nuclear factor, erythroid derived 2,-like 1 (predicted)	Nfe2l1_predicted	1.062	0.589	2.341	0.027	1.058	0.740	1.534	0.330
1390068_at	AI179123	nuclear factor, erythroid derived 2,-like 1 (predicted)	Nfe2l1_predicted	1.376	0.640	1.574	0.063	1.253	0.726	1.625	0.103
1368488_at	NM_053727	nuclear factor, interleukin 3 regulated	Nfil3	0.908	0.321	9.018	0.000	1.350	0.862	5.977	0.009
1397114_at	BF388191	Nuclear fragile X mental retardation protein interacting protein 1	Nufip1	1.862	0.005	1.447	0.284	1.828	0.019	1.818	0.024
1376250_at	BI284814	nuclear fragile X mental retardation protein interacting protein 1	Nufip1	1.374	0.089	2.910	0.003	2.933	0.005	3.854	0.000
1394371_at	BF556765	nuclear fragile X mental retardation protein interacting protein 1	Nufip1	1.420	0.330	1.804	0.019	2.860	0.018	2.997	0.008
1387950_at	AF158186	nuclear import 7 homolog (S. cerevisiae)	Nip7	0.995	0.474	2.448	0.001	0.818	0.203	1.714	0.005
1398913_at	AI599394	nuclear mitotic apparatus protein 1	Numa1	0.829	0.217	0.867	0.036	0.811	0.075	0.987	0.076
1382109_at	BI301006	nuclear NF-kappaB activating protein	2610020o08rik	0.982	0.632	0.936	0.763	0.936	0.506	1.250	0.406
1368654_at	NM_012991	nuclear pore associated protein	Npap60	0.877	0.673	1.527	0.264	1.059	0.867	1.072	0.276
1386957_at	NM_053622	nuclear pore membrane glycoprotein 121	Pom121	0.674	0.174	0.902	0.027	0.708	0.038	0.981	0.307
1367919_at	NM_053322	nuclear pore membrane glycoprotein 210	Pom210	1.035	0.643	0.954	0.912	0.865	0.132	0.676	0.062
1372295_at	BF551356	Nuclear prelamin A recognition factor	Narf	0.496	0.001	0.505	0.004	0.553	0.001	0.667	0.009
1384009_at	AI535383	nuclear prelamin A recognition factor	Narf	0.684	0.044	0.547	0.012	0.761	0.041	0.493	0.010
1398958_at	BI278849	nuclear prelamin A recognition factor-like	Narfl	0.681	0.190	1.233	0.155	0.864	0.806	1.139	0.404
1367847_at	NM_053611	nuclear protein 1	Nupr1	0.723	0.318	1.453	0.061	1.356	0.163	1.873	0.058
1368230_a_at	U95161	nuclear protein E3-3	RGD708545	0.495	0.324	1.224	0.348	0.382	0.001	1.133	0.183
1381624_at	BF391717	Nuclear protein in the AT region (predicted)	Npat_predicted	1.133	0.492	4.201	0.012	0.978	0.927	2.007	0.023
1393244_at	AW435274	Nuclear protein localization 4 homolog (S. cerevisiae)	Nploc4	0.650	0.829	0.713	0.164	0.761	0.077	0.754	0.043
1374996_at	AI172269	nuclear protein localization 4 homolog (S. cerevisiae)	Nploc4	0.793	0.914	0.949	0.829	0.686	0.121	0.876	0.088
1387921_at	AB032932	nuclear protein UKp68	Npuk68	1.613	0.005	3.109	0.002	1.500	0.006	2.729	0.000
1387152_at	NM_022186	nuclear receptor binding factor 2	Nrbf2	0.907	0.704	1.233	0.292	0.999	0.458	1.036	0.792
1379560_at	BE099674	nuclear receptor binding SET domain protein 1 (predicted)	Nsd1_predicted	1.224	0.030	2.328	0.022	0.896	0.455	2.184	0.007
1390010_at	AI454081	nuclear receptor coactivator 1 (predicted)	Ncoa1_predicted	0.989	0.531	1.291	0.408	0.871	0.285	1.038	0.449
1396254_at	BF401989	Nuclear receptor coactivator 2	Ncoa2	1.473	0.055	1.734	0.034	1.523	0.045	1.257	0.100
1380638_at	BI294907	nuclear receptor coactivator 3	Ncoa3	1.170	0.645	1.864	0.044	1.249	0.237	1.634	0.042
1388549_at	AI228248	nuclear receptor coactivator 4 (predicted)	Ncoa4_predicted	0.536	0.145	0.620	0.015	0.541	0.054	0.562	0.002
1389028_at	BI291460	nuclear receptor coactivator 6	Ncoa6	1.192	0.052	1.620	0.003	1.290	0.074	1.389	0.011
1392175_at	AA956966	Nuclear receptor co-repressor 1	Ncor1	1.298	0.032	1.413	0.107	0.984	0.210	1.019	0.493
1398976_at	AA848674	nuclear receptor co-repressor 1	Ncor1	1.115	0.302	1.599	0.009	1.027	0.742	1.185	0.029
1384293_at	BE100543	nuclear receptor co-repressor 1	Ncor1	0.885	0.374	1.022	0.710	0.773	0.106	0.915	0.037
1372102_at	BF390024	nuclear receptor co-repressor 1	Ncor1	0.903	0.665	1.764	0.026	1.107	0.763	1.878	0.104
1392392_at	AI012510	Nuclear receptor co-repressor 1	Ncor1	0.893	0.933	0.982	0.918	0.797	0.041	0.996	0.623
1372196_at	BI284203	nuclear receptor co-repressor 2 (predicted)	Ncor2_predicted	1.689	0.009	0.849	0.592	1.129	0.690	1.580	0.066
1379982_at	BE117278	nuclear receptor interacting protein 1 (predicted)	Nrip1_predicted	1.907	0.000	1.891	0.002	1.224	0.167	1.314	0.007
1370816_at	M25804	nuclear receptor subfamily 1, group D, member 1	Nr1d1	3.122	0.010	13.653	0.002	2.307	0.038	7.741	0.007
1370541_at	U20796	nuclear receptor subfamily 1, group D, member 2	Nr1d2	1.430	0.504	1.580	0.251	1.490	0.357	1.581	0.422
1389854_at	AA956855	Nuclear receptor subfamily 1, group H, member 2	Nr1h2	1.328	0.115	1.542	0.008	1.512	0.165	1.360	0.044
1369073_at	NM_021745	nuclear receptor subfamily 1, group H, member 4	Nr1h4	0.782	0.245	0.227	0.013	0.720	0.346	0.403	0.020
1380135_at	AW531996	Nuclear receptor subfamily 2, group C, member 2	Nr2c2	1.076	0.109	0.913	0.302	0.999	0.318	1.005	0.629
1392219_at	AI145523	Nuclear receptor subfamily 2, group C, member 2	Nr2c2	0.732	0.346	0.669	0.131	0.600	0.190	0.648	0.157
1389998_at	BE113958	Nuclear receptor subfamily 2, group F, member 2	Nr2f2	0.954	0.684	0.992	0.620	1.206	0.337	0.981	0.981
1397004_at	BF394158	Nuclear receptor subfamily 3, group C, member 1	Nr3c1	2.556	0.001	1.448	0.128	2.254	0.003	1.195	0.255
1368221_at	NM_012576	nuclear receptor subfamily 3, group C, member 1	Nr3c1	1.899	0.200	0.950	0.639	2.390	0.002	1.202	0.165
1368476_at	NM_013131	nuclear receptor subfamily 3, group C, member 2	Nr3c2	1.038	0.861	2.198	0.779	1.145	0.046	1.462	0.878
1369217_at	NM_017352	nuclear receptor subfamily 4, group A, member 3	Nr4a3	1.176	0.564	0.753	0.133	1.364	0.455	0.817	0.572

1393389_at	BF396237	Nuclear receptor subfamily 4, group A, member 3	Nr4a3	1.009	0.990	0.961	0.909	1.078	0.836	0.891	0.854
1381895_at	AW435074	nuclear respiratory factor 1 (predicted)	Nrf1_predicted	0.603	0.055	6.540	0.004	0.978	0.841	4.701	0.002
1385617_at	BE096654	Nuclear respiratory factor 1 (predicted)	Nrf1_predicted	0.880	0.325	1.311	0.027	1.129	0.995	1.165	0.958
1398861_at	AF093139	nuclear RNA export factor 1	Nxf1	1.293	0.969	1.274	0.093	1.161	0.839	1.033	0.198
1382718_at	AA900547	Nuclear transcription factor, X-box binding 1	Nfx1	1.349	0.034	2.791	0.003	1.051	0.263	2.154	0.000
1378637_at	BG374464	nuclear transcription factor, X-box binding 1	Nfx1	1.316	0.102	2.483	0.001	1.101	0.076	1.898	0.001
1382082_at	AI145337	nuclear transcription factor-Y beta	Nfyb	2.036	0.039	0.507	0.078	1.821	0.013	0.530	0.035
1387452_a_at	NM_031553	nuclear transcription factor-Y beta	Nfyb	1.013	0.999	0.781	0.449	0.991	0.947	0.644	0.354
1368820_at	NM_012866	nuclear transcription factor-Y gamma	Nfyc	1.107	0.150	0.976	0.503	1.109	0.278	0.880	0.166
1398268_at	BI296061	nuclear transcription factor-Y gamma	Nfyc	0.964	0.274	1.347	0.012	1.220	0.140	1.265	0.007
1371246_at	BE109988	nuclear transport factor 2	NTF2	0.751	0.197	0.795	0.314	0.847	0.198	1.038	0.463
1376112_a_at	AI231712	nuclear transport factor 2	NTF2	0.569	0.482	0.346	0.008	0.656	0.043	0.429	0.011
1369775_at	NM_022799	nuclear ubiquitous casein kinase and cyclin-dependent kinase substrate	Nucks	0.998	0.875	1.044	0.154	0.987	0.910	1.012	0.942
1377676_at	AI599187	nuclear ubiquitous casein kinase and cyclin-dependent kinase substrate	Nucks	0.816	0.990	2.293	0.003	0.675	0.177	2.060	0.042
1389314_at	AW915489	nuclear VCP-like (predicted)	Nvl_predicted	3.599	0.051	2.410	0.051	1.126	0.596	1.382	0.046
1370199_at	Z36277	nucleobindin 1	Nucb1	0.927	0.701	0.998	0.981	1.194	0.401	1.212	0.400
1370000_at	NM_021663	nucleobindin 2	Nucb2	0.702	0.326	0.468	0.001	0.769	0.166	0.475	0.015
1368032_at	M94288	nucleolar and coiled-body phosphoprotein 1	Nolc1	0.962	0.051	2.117	0.019	0.535	0.010	1.550	0.096
1368031_at	NM_022869	nucleolar and coiled-body phosphoprotein 1	Nolc1	0.524	0.237	0.630	0.037	0.462	0.000	0.848	0.056
1392732_at	AI711233	nucleolar and spindle associated protein 1 (predicted)	Nusap1_predicted	0.980	0.900	0.920	0.911	0.982	0.912	0.920	0.716
1377760_at	AA956374	nucleolar complex associated 4 homolog (S. cerevisiae)	Noc4l	1.116	0.646	1.461	0.000	0.807	0.116	1.362	0.077
1383752_at	BG375714	nucleolar protein 1 (predicted)	Nol1_predicted	0.638	0.011	2.458	0.000	0.425	0.088	1.623	0.001
1380201_at	BF412675	nucleolar protein 10	Nol10	0.888	0.028	0.723	0.110	0.784	0.025	1.051	0.217
1368544_a_at	NM_053516	nucleolar protein 3 (apoptosis repressor with CARD domain)	Nol3	0.680	0.161	1.391	0.008	0.477	0.023	1.026	0.015
1368173_at	NM_021754	nucleolar protein 5	Nol5	0.847	0.088	1.973	0.005	0.984	0.056	1.864	0.000
1388622_at	AW535890	nucleolar protein 5A	Nol5a	0.563	0.036	1.266	0.030	0.622	0.032	1.070	0.026
1373445_at	BI296198	nucleolar protein 8 (predicted)	Nol8_predicted	1.085	0.648	1.114	0.240	1.041	0.435	1.857	0.022
1385009_at	BI291860	nucleolar protein 8 (predicted)	Nol8_predicted	0.692	0.846	1.629	0.037	1.062	0.168	1.318	0.525
1395642_at	BG372596	nucleolar protein 9	Nol9	0.885	0.480	1.541	0.072	1.050	0.745	1.395	0.098
1371539_at	AW921151	nucleolar protein family A, member 2 (predicted)	Nola2_predicted	0.678	0.012	2.358	0.005	0.474	0.001	2.081	0.006
1398832_at	NM_012749	nucleolin	Ncl	0.650	0.064	2.420	0.003	0.675	0.027	1.894	0.000
1399158_a_at	J04943	nucleophosmin 1	Npm1	0.813	0.027	1.391	0.082	0.470	0.050	1.247	0.480
1398757_at	NM_012992	nucleophosmin 1	Npm1	0.782	0.256	1.699	0.009	0.699	0.010	1.385	0.046
1398756_at	J04943	nucleophosmin 1 /// similar to Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Numatrin) (Nucleolar protein NO38)	Npm1 /// LOC300303	0.705	0.269	2.869	0.005	0.636	0.001	2.061	0.013
1395212_at	BE105805	Nucleophosmin/nucleoplasmin 2	Npm2	0.854	0.069	0.641	0.010	0.773	0.043	0.574	0.007
1387151_at	NM_053830	nucleoporin 107	Nup107	1.242	0.752	1.156	0.270	1.270	0.345	1.210	0.131
1375071_at	BE119719	nucleoporin 133 (predicted)	Nup133_predicted	0.492	0.149	1.159	0.345	0.541	0.102	1.194	0.923
1370934_at	L06821	nucleoporin 153	Nup153	1.014	0.644	1.640	0.010	1.025	0.519	1.585	0.019
1382413_at	AA874825	Nucleoporin 155	Nup155	1.002	0.784	0.699	0.048	0.806	0.982	0.634	0.004
1398259_at	NM_053952	nucleoporin 155	Nup155	1.347	0.837	3.485	0.001	0.385	0.042	1.821	0.017
1382661_at	AI230642	nucleoporin 160 (predicted)	Nup160_predicted	1.173	0.291	1.238	0.268	0.677	0.071	0.832	0.947
1372021_at	AI102685	nucleoporin 188	Nup188	1.002	0.137	1.002	0.977	1.001	1.000	1.003	0.990
1376722_at	AI409108	nucleoporin 205kDa (predicted)	Nup205_predicted	0.712	0.148	1.024	0.880	0.854	0.072	0.724	0.854
1379476_at	AA963457	nucleoporin 35	Nup35	0.743	0.534	1.523	0.136	0.470	0.004	1.282	0.308
1386364_at	H31217	Nucleoporin 37 (predicted)	Nup37_predicted	1.010	0.152	0.998	0.990	1.004	0.705	1.000	0.179
1376703_at	AI501977	nucleoporin 37 (predicted)	Nup37_predicted	0.402	0.171	0.954	0.048	0.473	0.013	0.593	0.036
1367803_at	NM_017361	nucleoporin 54	Nup54	1.770	0.167	4.232	0.002	1.485	0.054	2.745	0.001
1379937_at	AW526968	Nucleoporin 62	Nup62	0.772	0.417	0.996	0.867	0.752	0.333	1.000	0.953
1370909_at	BI286040	nucleoporin 62	Nup62	1.031	0.980	0.887	0.544	0.926	0.745	0.792	0.981
1368199_at	NM_053616	nucleoporin 88	Nup88	0.732	0.671	0.697	0.089	0.626	0.202	0.657	0.001
1372519_at	AI169375	nucleoporin 93	Nup93	1.405	0.268	1.101	0.534	1.083	0.421	0.922	0.189
1398901_at	AA799609	nucleoporin 98	Nup98	1.254	0.039	1.598	0.022	1.240	0.153	1.383	0.000
1379001_at	AA945695	Nucleoporin 98	Nup98	0.788	0.960	1.113	0.543	1.581	0.027	1.033	0.952
1388073_a_at	AF000901	nucleoporin like 1	Nupl1	0.629	0.081	0.934	0.136	0.700	0.091	0.999	0.950
1370437_at	U63839	nucleoporin like 1	Nupl1	0.858	0.339	0.842	0.482	0.634	0.077	1.071	0.224
1388198_at	AF000899	nucleoporin like 1	Nupl1	0.619	0.479	1.156	0.717	0.687	0.059	0.990	0.981
1370711_a_at	AF000900	nucleoporin like 1	Nupl1	0.998	0.861	0.995	0.070	0.975	0.878	0.753	0.058
1388337_at	AI102495	nucleoside phosphorylase (mapped)	Np_mapped	3.507	0.035	0.714	0.234	5.503	0.000	1.109	0.636
1370826_at	AF062594	nucleosome assembly protein 1-like 1	Nap1l1	0.874	0.590	1.001	0.469	0.669	0.187	1.088	0.248
1373473_a_at	BM386384	nucleosome assembly protein 1-like 1	Nap1l1	0.898	0.820	1.330	0.012	0.740	0.177	1.241	0.021

1383673_at	BI288925	nucleosome assembly protein 1-like 2	Nap1l2	0.285	0.001	0.288	0.002	0.270	0.016	0.298	0.013
1387407_at	NM_133402	nucleosome assembly protein 1-like 3	Nap1l3	0.896	0.070	0.519	0.152	0.774	0.371	0.635	0.027
1388438_at	AI230346	nucleosome assembly protein 1-like 4	Nap1l4	0.937	0.791	1.748	0.001	0.855	0.096	1.502	0.010
1373433_at	BE108745	nucleosome binding protein 1 (predicted) /// similar to Nucleosome binding protein 1	Nsbp1_predicted /// LOC501603	0.605	0.000	0.554	0.011	0.855	0.330	0.483	0.006
1371503_at	BI289647	nucleotide binding protein 1	Nubp1	1.081	0.776	1.574	0.001	1.239	0.251	2.063	0.002
1379743_at	BF397271	Nucleotide binding protein 2	Nubp2	1.688	0.010	0.994	0.037	1.246	0.427	1.145	0.991
1372607_at	BM384157	nucleotide binding protein 2	Nubp2	0.865	0.614	0.889	0.367	0.837	0.077	1.377	0.291
1376288_at	AI408455	NudC domain containing 1 (predicted)	Nudcd1_predicted	1.061	0.159	0.849	0.429	1.794	0.052	0.988	0.614
1393753_at	BE114265	NudC domain containing 1 (predicted)	Nudcd1_predicted	0.831	0.880	1.750	0.000	0.919	0.190	1.729	0.004
1372939_at	AI010173	NudC domain containing 2	Nudcd2	0.785	0.291	1.508	0.023	1.276	0.663	1.819	0.008
1367761_at	NM_133320	nudE nuclear distribution gene E homolog like 1 (A. nidulans)	Ndel1	1.022	0.849	1.693	0.001	0.917	0.394	1.509	0.011
1373230_at	AI145851	nudix (nucleoside diphosphate linked moiety X)-type motif 18	Nudt18	0.940	0.600	1.626	0.203	1.037	0.871	1.497	0.246
1371919_at	BF414021	nudix (nucleoside diphosphate linked moiety X)-type motif 19	Nudt19	0.492	0.269	0.768	0.025	0.475	0.106	0.860	0.035
1377602_at	BF284944	nudix (nucleoside diphosphate linked moiety X)-type motif 2	Nudt2	0.858	0.722	1.165	0.607	0.837	0.504	1.255	0.132
1367507_at	BI281661	nudix (nucleoside diphosphate linked moiety X)-type motif 22	Nudt22	1.140	0.944	1.445	0.371	2.519	0.000	1.259	0.091
1370180_at	AA891213	nudix (nucleoside diphosphate linked moiety X)-type motif 4	Nudt4	0.736	0.044	0.489	0.001	0.674	0.006	0.859	0.108
1398847_at	BG376935	nudix (nucleoside diphosphate linked moiety X)-type motif 4	Nudt4	0.357	0.205	1.132	0.039	0.607	0.025	0.999	0.214
1375584_at	BG376873	Nudix (nucleoside diphosphate linked moiety X)-type motif 5	Nudt5	1.125	0.202	0.949	0.535	1.274	0.050	0.952	0.715
1373138_at	AA858886	nudix (nucleoside diphosphate linked moiety X)-type motif 5	Nudt5	0.584	0.218	1.635	0.045	0.484	0.024	1.192	0.278
1370435_a_at	U58289	nudix (nucleoside diphosphate linked moiety X)-type motif 6	Nudt6	0.921	0.556	0.693	0.410	0.786	0.905	0.694	0.456
1389251_at	AA944380	nudix (nucleoside diphosphate linked moiety X)-type motif 7 (predicted)	Nudt7_predicted	0.300	0.155	0.252	0.003	0.342	0.062	0.410	0.040
1373840_at	BM384191	nudix (nucleoside diphosphate linked moiety X)-type motif 9	Nudt9	0.905	0.270	2.377	0.008	1.891	0.150	1.719	0.035
1383957_at	BG376322	nudix (nucleotide diphosphate linked moiety X)-type motif 3	Nudt3	1.447	0.042	3.568	0.006	1.394	0.046	1.656	0.018
1372074_at	BI276000	nudix (nucleotide diphosphate linked moiety X)-type motif 3	Nudt3	0.956	0.625	1.219	0.172	0.876	0.564	1.296	0.105
1375536_at	BI287975	Numb gene homolog (Drosophila)	Numb	0.689	0.434	1.026	0.858	0.970	0.878	1.261	0.874
1382392_at	AI045633	Numb gene homolog (Drosophila)	Numb	0.888	0.785	1.054	0.880	0.749	0.602	0.755	0.819
1385048_at	BF398257	Numb-like	Numbl	0.726	0.054	1.200	0.964	1.266	0.223	1.089	0.440
1368311_at	NM_012861	O-6-methylguanine-DNA methyltransferase	Mgmt	0.771	0.750	4.506	0.003	0.621	0.040	3.725	0.003
1376813_at	BI295955	O-acyltransferase (membrane bound) domain containing 5	Oact5	1.279	0.122	0.789	0.016	0.828	0.217	0.816	0.002
1393915_at	BE128627	O-acyltransferase (membrane bound) domain containing 5	Oact5	0.885	0.694	0.652	0.042	0.726	0.405	0.747	0.139
1388612_at	AI599462	OCIA domain containing 1	Ociad1	0.643	0.229	0.878	0.081	0.615	0.038	0.887	0.016
1381408_at	BI275477	OCIA domain containing 1	Ociad1	1.531	0.978	0.973	0.618	1.470	0.307	0.899	0.376
1383283_at	BM385645	oculocerebrorenal syndrome of Lowe (mapped)	Ocrl_mapped	0.624	0.041	0.542	0.006	0.397	0.054	0.359	0.015
1391692_at	AI229519	Odd Oz/ten-m homolog 2 (Drosophila)	Odz2	1.014	0.921	0.465	0.970	1.005	0.978	0.720	0.496
1395836_at	BF400594	Odd Oz/ten-m homolog 2 (Drosophila)	Odz2	0.999	0.996	0.626	0.355	1.016	0.914	0.694	0.220
1387927_a_at	U03415	olfactomedin 1	Olfm1	0.914	0.365	0.830	0.072	1.617	0.071	0.885	0.985
1369008_a_at	NM_053573	olfactomedin 1	Olfm1	0.953	0.392	1.932	0.021	0.839	0.758	1.950	0.018
1389295_at	AI411761	olfactomedin-like 2B (predicted)	Olfml2b_predicted	1.031	0.723	0.848	0.157	0.831	0.011	0.968	0.343
1392896_at	AI111675	olfactory receptor 1188 (predicted)	Olr1188_predicted	0.844	0.831	1.441	0.083	0.738	0.467	1.134	0.982
1370735_at	AF010293	olfactory receptor 1278	Olr1278	0.999	0.996	0.949	0.302	2.250	0.016	1.031	0.994
1388091_at	M64391	olfactory receptor 1500	Olr1500	1.021	0.898	0.987	0.916	2.013	0.058	0.999	0.992
1370741_at	AF034896	olfactory receptor 1696	Olr1696	0.999	0.997	1.002	0.867	1.353	0.261	1.023	0.760
1394670_at	AA859595	oligonucleotide/oligosaccharide-binding fold containing 1	Obfc1	1.332	0.570	1.182	0.873	1.033	0.892	0.999	0.289
1373295_at	BI281889	oligonucleotide/oligosaccharide-binding fold containing 1	Obfc1	1.002	0.785	0.932	0.082	0.973	0.364	0.994	0.074
1374631_at	AW914202	oligonucleotide/oligosaccharide-binding fold containing 2B	Obfc2b	0.875	0.733	1.197	0.460	0.879	0.215	1.128	0.714
1370543_at	U76557	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	Ogt	0.805	0.077	0.345	0.000	1.007	0.964	0.453	0.001
1380360_at	AA891814	OMA1 homolog, zinc metallopeptidase (S. cerevisiae) (predicted)	Oma1_predicted	0.574	0.146	0.760	0.198	1.128	0.907	1.131	0.906
1373737_at	BG376997	open reading frame 19	ORF19	1.208	0.125	1.098	0.164	1.195	0.881	0.737	0.772
1373717_at	BF409265	Opioid binding protein/cell adhesion molecule-like	Opcml	1.346	0.587	1.170	0.918	1.272	0.569	0.798	0.107
1369417_a_at	NM_053848	opioid binding protein/cell adhesion molecule-like	Opcml	0.920	0.822	1.495	0.307	0.891	0.191	0.713	0.102
1387961_at	M88709	opioid binding protein/cell adhesion molecule-like	Opcml	0.594	0.930	0.925	0.214	0.723	0.461	0.854	0.185
1394987_at	BE120450	Opioid binding protein/cell adhesion molecule-like	Opcml	0.991	0.985	0.981	0.869	1.299	0.193	0.990	0.914
1386986_at	NM_053340	opioid growth factor receptor	Ogfr	4.323	0.051	1.871	0.022	10.693	0.004	2.154	0.081
1386918_a_at	AF087827	opioid receptor, sigma 1	Oprs1	0.628	0.043	0.690	0.686	0.645	0.040	0.858	0.731
1387225_at	NM_133585	optic atrophy 1 homolog (human)	Opa1	1.002	0.924	1.387	0.011	1.359	0.010	1.456	0.004
1388432_at	BI294994	optineurin	Optn	3.127	0.006	3.119	0.000	3.025	0.013	2.948	0.000
1370618_at	AB069907	optineurin	Optn	2.612	0.014	6.136	0.003	2.057	0.084	6.595	0.012
1389141_at	BF288111	origin recognition complex, subunit 2-like (S. cerevisiae)	Orc2l	1.084	0.645	1.501	0.004	1.052	0.291	1.734	0.002
1393745_at	BE118179	origin recognition complex, subunit 3-like (S. cerevisiae)	Orc3l	0.874	0.394	1.751	0.006	0.854	0.032	1.499	0.036

1395192_at	BF392026	origin recognition complex, subunit 3-like (S. cerevisiae)	Orc3l	0.844	0.684	1.427	0.041	0.857	0.639	1.376	0.055
1390478_at	BE103926	origin recognition complex, subunit 4	Orc4	1.147	0.041	0.704	0.127	0.977	0.181	0.999	0.942
1391703_at	BF414253	origin recognition complex, subunit 4-like (S. cerevisiae)	Orc4l	1.360	0.090	1.949	0.002	0.889	0.170	1.868	0.007
1376316_at	AI070593	Origin recognition complex, subunit 6-like (S. cerevisiae)	Orc6l	0.553	0.054	0.443	0.007	0.563	0.023	0.511	0.017
1398439_a_at	AI070593	origin recognition complex, subunit 6-like (S. cerevisiae)	Orc6l	0.637	0.070	0.184	0.019	0.535	0.046	0.163	0.020
1376317_at	BI282917	origin recognition complex, subunit 6-like (S. cerevisiae)	Orc6l	0.589	0.287	0.665	0.010	0.396	0.073	0.292	0.027
1398907_at	BI296182	ORM1-like 2 (S. cerevisiae) (predicted)	Ormdl2_predicted	0.422	0.099	0.473	0.004	0.497	0.019	0.457	0.004
1370163_at	BF281299	ornithine decarboxylase 1	Odc1	1.189	0.340	4.861	0.001	1.107	0.425	4.343	0.000
1372241_at	AI411388	ornithine decarboxylase antizyme 1	Oaz1	0.737	0.166	0.773	0.095	0.726	0.052	0.695	0.110
1368731_at	NM_053288	orosomucoid 1	Orm1	1.004	0.861	6.398	0.005	1.004	0.884	1.000	0.981
1389117_at	AW532161	O-sialoglycoprotein endopeptidase	Osgep	0.895	0.421	0.672	0.147	0.928	0.821	0.878	0.128
1372246_at	BI294750	osteoclast stimulating factor 1	Ostf1	0.598	0.312	0.782	0.182	0.633	0.033	0.944	0.147
1387197_at	NM_031817	osteomodulin	Omd	1.386	0.418	1.010	0.063	1.569	0.075	1.039	0.080
1397207_at	AI171260	OTU domain containing 4	Otud4	1.098	0.050	3.015	0.001	0.999	0.804	1.163	0.134
1373231_at	BG665102	OTU domain containing 5	Otud5	1.360	0.042	0.850	0.440	1.598	0.083	0.925	0.369
1372958_at	BE111986	OTU domain, ubiquitin aldehyde binding 1 (predicted)	Otub1_predicted	0.521	0.779	0.474	0.254	0.559	0.055	0.296	0.174
1376118_at	BE109604	OTU domain, ubiquitin aldehyde binding 2 (predicted)	Otub2_predicted	0.358	0.016	0.197	0.007	0.215	0.013	0.175	0.009
1385154_at	BE121382	OTU domain, ubiquitin aldehyde binding 2 (predicted)	Otub2_predicted	1.323	0.706	1.619	0.019	1.002	0.980	1.454	0.993
1382263_at	AI511280	outer dense fiber of sperm tails 2-like (predicted)	Odf2l_predicted	0.448	0.066	0.871	0.498	1.267	0.284	0.964	0.238
1367869_at	NM_057153	oxidation resistance 1	Oxr1	0.391	0.008	0.203	0.006	0.641	0.233	0.366	0.006
1374911_at	AW251534	oxidative stress responsive gene	RGD1303142	1.005	0.128	8.435	0.003	0.998	0.943	6.506	0.005
1380687_at	BI295176	Oxidative-stress responsive 1 (predicted)	Oxsr1_predicted	1.011	0.263	0.906	0.937	0.949	0.891	1.253	0.344
1388909_at	AA891742	oxidoreductase NAD-binding domain containing 1 (predicted)	Oxnad1_predicted	0.612	0.246	0.615	0.009	0.509	0.003	0.792	0.060
1380220_at	AW534345	Oxysterol binding protein 2 (predicted)	Osbp2_predicted	0.760	0.025	0.992	0.904	0.557	0.045	0.894	0.970
1375209_at	AA893228	Oxysterol binding protein-like 11 (predicted)	Osbpl11_predicted	1.381	0.780	1.470	0.081	1.087	0.782	0.867	0.889
1383830_a_at	AI070135	oxysterol binding protein-like 1A	Osbpl1a	0.999	0.809	0.895	0.809	1.057	0.819	1.001	0.783
1367519_at	BG373087	oxysterol binding protein-like 2	Osbpl2	0.955	0.620	1.459	0.079	0.599	0.026	1.022	0.843
1378814_at	BF387902	Oxysterol binding protein-like 2	Osbpl2	1.083	0.850	2.097	0.050	1.280	0.364	1.722	0.044
1393368_at	BG372522	oxysterol binding protein-like 5	Osbpl5	2.443	0.018	1.718	0.209	2.437	0.013	1.435	0.322
1371978_at	AI406375	Oxysterol binding protein-like 9 (predicted)	Osbpl9_predicted	1.149	0.348	1.743	0.003	0.893	0.105	1.876	0.003
1387636_a_at	NM_134395	P11 protein	Cdtw1	0.470	0.444	0.398	0.016	0.299	0.016	0.606	0.036
1368902_at	NM_019210	p21 (CDKN1A)-activated kinase 3	Pak3	0.657	0.376	0.363	0.086	0.785	0.377	0.276	0.088
1378380_at	BE098920	P21 (CDKN1A)-activated kinase 4 (predicted)	Pak4_predicted	1.426	0.074	2.251	0.016	1.736	0.107	1.386	0.078
1382781_at	AI764741	P21 (CDKN1A)-activated kinase 6 (predicted)	Pak6_predicted	1.065	0.984	0.677	0.011	1.981	0.118	0.695	0.043
1375205_at	Z83046	p300/CBP-associated factor	Pcaf	3.516	0.001	1.420	0.106	3.053	0.002	1.271	0.071
1387109_at	NM_031576	P450 (cytochrome) oxidoreductase	Por	0.891	0.621	1.641	0.022	0.894	0.201	1.051	0.533
1368213_at	AI407454	P450 (cytochrome) oxidoreductase	Por	1.030	0.990	1.001	0.233	0.934	0.302	1.004	0.984
1372941_at	BI273897	p53 and DNA damage regulated 1	Pdrg1	2.006	0.122	2.610	0.005	1.300	0.011	2.072	0.005
1371812_at	BI284223	P55	LOC362855	0.895	0.629	1.148	0.064	0.862	0.847	1.113	0.212
1389963_at	BI283388	p55 protein	LOC652956	1.103	0.055	1.020	0.847	1.146	0.240	0.874	0.856
1382758_at	AA955094	P7 protein	P7	1.037	0.887	0.974	0.913	0.651	0.985	0.800	0.237
1373455_at	BE115648	Paf1, RNA polymerase II associated factor, homolog (S. cerevisiae)	Paf1	0.801	0.019	0.835	0.925	0.782	0.109	0.791	0.670
1395094_at	BF549339	Paired box gene 3	Pax3	1.022	0.943	1.125	0.433	1.220	0.455	1.397	0.172
1369242_at	NM_013001	paired box gene 6	Pax6	0.497	0.000	0.350	0.001	0.520	0.027	0.525	0.007
1387238_at	NM_053869	paired-like homeobox 2a	Phox2a	1.009	0.157	0.998	0.431	1.001	0.293	0.999	0.856
1376894_at	AA849956	pallidin	Pldn	0.751	0.102	0.429	0.012	0.619	0.152	0.620	0.102
1370236_at	AI234353	palmitoyl-protein thioesterase 1	Ppt1	0.665	0.482	0.384	0.000	0.603	0.045	0.419	0.000
1390423_at	BE104245	pam, highwire, rpm 1 (predicted)	Phr1_predicted	1.899	0.012	1.471	0.162	2.427	0.007	1.611	0.062
1372863_at	BF409872	pam, highwire, rpm 1 (predicted)	Phr1_predicted	1.794	0.014	1.665	0.013	1.978	0.020	2.314	0.002
1369516_at	NM_022852	pancreatic and duodenal homeobox gene 1	Pdx1	1.012	0.965	0.215	0.011	0.490	0.001	0.249	0.029
1369196_at	NM_012626	pancreatic polypeptide	Ppy	0.959	0.798	0.228	0.062	0.812	0.255	0.264	0.120
1369030_at	NM_012635	pancreatic trypsin 1	Prss1	0.833	0.993	0.483	0.306	1.026	0.957	0.576	0.082
1368238_at	NM_053289	pancreatitis-associated protein	Pap	1.177	0.992	1.095	0.365	1.001	0.983	0.918	0.936
1382934_at	AI136392	Pannexin 1	Panx1	0.680	0.085	1.691	0.081	0.430	0.089	1.364	0.355
1382924_at	AA850195	pantothenate kinase 1 (predicted)	Pank1_predicted	0.388	0.077	0.623	0.016	0.309	0.077	0.450	0.117
1396994_at	BM382872	pantothenate kinase 2 (Hallervorden-Spatz syndrome) (predicted)	Pank2_predicted	1.846	0.100	0.805	0.480	2.946	0.013	1.000	0.887
1395209_at	BM387740	Pantothenate kinase 2 (Hallervorden-Spatz syndrome) (predicted)	Pank2_predicted	0.963	0.595	1.110	0.314	1.168	0.335	1.226	0.884
1392033_a_at	AW142000	pantothenate kinase 2 (Hallervorden-Spatz syndrome) (predicted)	Pank2_predicted	1.056	0.782	1.101	0.628	1.197	0.073	1.064	0.137
1392831_at	AA891438	Pantothenate kinase 2 (Hallervorden-Spatz syndrome) (predicted)	Pank2_predicted	0.979	0.865	1.335	0.151	0.694	0.919	0.770	0.444
1378378_at	BI276838	pantothenate kinase 2 (Hallervorden-Spatz syndrome) (predicted)	Pank2_predicted	1.016	0.907	1.571	0.043	1.045	0.584	1.340	0.067
1374987_at	AI232974	Pantothenate kinase 3 (predicted)	Pank3_predicted	0.528	0.027	0.550	0.008	0.584	0.033	0.722	0.011

1394706_at	AI044545	Pantothenate kinase 3 (predicted)	Pank3_predicted	0.513	0.150	1.230	0.293	0.415	0.014	1.237	0.193
1369938_at	NM_133531	pantothenate kinase 4	Pank4	1.069	0.840	1.802	0.078	0.998	0.971	1.165	0.186
1394136_at	AI176017	PAP associated domain containing 1 (predicted)	Papd1_predicted	0.999	0.652	2.965	0.025	0.994	0.944	1.862	0.025
1373653_at	BF550883	PAP associated domain containing 1 (predicted)	Papd1_predicted	0.613	0.670	1.260	0.042	1.116	0.543	1.853	0.008
1384352_at	AI547390	PAP associated domain containing 4	Papd4	1.723	0.130	4.471	0.001	1.045	0.749	3.740	0.002
1374612_at	AI170664	PAP associated domain containing 5 (predicted)	Papd5_predicted	0.841	0.162	0.876	0.023	0.874	0.437	1.098	0.042
1383109_at	BG669807	papillary renal cell carcinoma (translocation-associated) (predicted)	Prcc_predicted	1.007	0.757	0.707	0.318	0.988	0.466	0.537	0.133
1390299_at	BF405880	Papillary renal cell carcinoma (translocation-associated) (predicted)	Prcc_predicted	0.993	0.982	0.761	0.515	1.496	0.161	0.895	0.178
1395613_at	BF408015	Par-3 (partitioning defective 3) homolog (C. elegans)	Pard3	2.496	0.014	1.746	0.102	2.835	0.024	0.907	0.911
1379138_at	BF391688	Par-3 (partitioning defective 3) homolog (C. elegans)	Pard3	1.078	0.347	0.998	0.984	1.021	0.464	0.675	0.168
1381590_at	BI295719	Par-3 (partitioning defective 3) homolog (C. elegans)	Pard3	1.184	0.898	1.014	0.937	1.263	0.867	0.999	0.985
1383224_at	BF525012	par-6 (partitioning defective 6) homolog beta (C. elegans) (predicted)	Pard6b_predicted	0.754	0.375	1.541	0.107	0.497	0.219	1.334	0.035
1375848_at	BG668051	paraoxonase 2	Pon2	0.361	0.001	0.245	0.001	0.532	0.014	0.241	0.025
1384465_at	AI136693	paraspeckle protein 1	Pspc1	0.346	0.003	0.930	0.032	0.446	0.002	0.639	0.119
1386892_at	NM_031975	parathymosin	Ptms	1.320	0.907	0.851	0.791	1.087	0.707	0.791	0.435
1368653_a_at	BI281756	Parkinson disease (autosomal recessive, early onset) 7	Park7	0.620	0.427	0.684	0.010	0.507	0.040	0.638	0.041
1389919_at	BI296756	parvin, beta (predicted)	Parvb_predicted	1.000	1.000	1.000	0.998	1.001	0.146	0.997	0.986
1371697_at	BI278288	patatin-like phospholipase domain containing 2 (predicted)	Pnpla2_predicted	1.385	0.048	1.886	0.040	2.121	0.004	2.491	0.012
1390655_at	BF420653	paternally expressed 3 (predicted)	Peg3_predicted	0.686	0.027	0.437	0.025	0.807	0.275	0.433	0.128
1382118_at	BE104676	paternally expressed 3 (predicted)	Peg3_predicted	0.713	0.066	0.514	0.007	1.010	0.359	0.658	0.007
1376598_at	AI179993	PAX interacting (with transcription-activation domain) protein 1 (predicted)	Paxip1_predicted	0.653	0.071	0.407	0.000	1.178	0.995	0.533	0.016
1371664_at	BG673589	paxillin	Pxn	1.093	0.474	1.392	0.050	0.936	0.457	1.151	0.283
1373350_at	H31668	PC4 and SFRS1 interacting protein 1	Psip1	1.240	0.053	0.661	0.123	1.037	0.628	0.809	0.226
1393267_at	BI276726	PC4 and SFRS1 interacting protein 1	Psip1	1.256	0.054	1.069	0.560	1.336	0.048	1.082	0.494
1383588_at	BE098610	PC4 and SFRS1 interacting protein 1	Psip1	0.558	0.082	0.852	0.054	0.543	0.081	0.908	0.159
1370326_at	U36444	PCTAIRE-motif protein kinase 1	Pctk1	1.065	0.752	0.735	0.006	1.092	0.464	0.714	0.017
1382345_at	AA955299	PCTAIRE-motif protein kinase 2	Pctk2	1.212	0.083	1.018	0.872	1.222	0.084	1.042	0.534
1398810_at	NM_022595	PDGFA associated protein 1	Pdap1	0.678	0.357	0.830	0.984	0.489	0.004	0.683	0.394
1369946_at	NM_024384	PDRP protein	Pdrp	1.868	0.008	2.002	0.042	1.187	0.096	1.263	0.001
1367946_at	NM_017365	PDZ and LIM domain 1 (elfin)	Pdlim1	1.793	0.813	0.610	0.216	1.428	0.736	0.826	0.365
1372745_at	BE112453	PDZ and LIM domain 5	Pdlim5	0.998	0.897	2.044	0.024	1.007	0.983	1.252	0.376
1368703_at	NM_053326	PDZ and LIM domain 5	Pdlim5	0.993	0.935	1.103	0.162	1.010	0.858	1.081	0.344
1370347_at	AF095585	PDZ and LIM domain 7	Pdlim7	1.240	0.334	1.044	0.905	1.229	0.277	0.996	0.797
1371950_at	AI008961	PDZ domain containing 11 (predicted)	Pdzd11_predicted	0.852	0.609	0.738	0.036	0.819	0.014	0.942	0.157
1379650_at	AI231443	PDZ domain containing 8 (predicted)	Pdzk8_predicted	1.076	0.612	1.301	0.224	0.815	0.190	0.879	0.483
1373748_at	AW532566	PDZ domain containing RING finger 3 (predicted)	Pdzrn3_predicted	0.129	0.003	0.060	0.002	0.050	0.007	0.050	0.022
1368209_at	NM_130401	PDZK1 interacting protein 1	Pdzk1ip1	8.833	0.051	1.319	0.042	1.234	0.952	1.069	1.000
1399034_at	AI009650	pecanex homolog (Drosophila)	Pcnx	1.828	0.050	1.480	0.041	1.983	0.003	1.625	0.002
1375451_at	BE105268	pecanex-like 3 (Drosophila)	Pcnxl3	1.264	0.366	0.783	0.149	1.101	0.625	0.785	0.113
1372174_at	AI009656	PEF protein with a long N-terminal hydrophobic domain	Peflin	0.939	0.892	1.817	0.048	0.859	0.613	1.400	0.124
1390814_at	AA848897	pellino homolog 1 (Drosophila)	Peli1	1.945	0.052	1.273	0.096	3.446	0.014	1.112	0.063
1382476_x_at	AI060133	Pellino homolog 3 (Drosophila) (predicted)	Peli3_predicted	0.681	0.046	1.014	0.905	0.639	0.035	0.978	0.851
1371684_at	AA799330	pelota homolog	Pelo	1.608	0.088	4.613	0.001	0.937	0.688	3.880	0.001
1376348_at	BM386015	pentatricopeptide repeat domain 2 (predicted)	Ptcd2_predicted	0.796	0.663	1.162	0.591	0.872	0.390	0.887	0.218
1371008_at	BE099971	peptidase (mitochondrial processing) alpha	Pmpca	0.366	0.039	0.928	0.633	0.430	0.004	0.856	0.944
1387781_at	NM_022395	peptidase (mitochondrial processing) beta	Pmpcb	0.694	0.868	0.622	0.010	0.670	0.625	0.637	0.005
1398792_at	NM_057123	peptidase (prosome, macropain) 26S subunit, ATPase 1	Psmc1	0.590	0.241	0.681	0.003	0.501	0.045	0.785	0.068
1381035_at	AI235476	Peptidase (prosome, macropain) 26S subunit, ATPase 1	Psmc1	1.141	0.604	1.817	0.097	1.101	0.802	1.591	0.018
1367833_at	NM_031149	peptidase (prosome, macropain) 26S subunit, ATPase 5	Psmc5	0.531	0.117	0.985	0.691	0.423	0.011	0.889	0.527
1393907_at	AA998735	peptide YY (mapped)	Pyy_mapped	0.493	0.169	0.068	0.006	0.365	0.001	0.077	0.049
1367687_a_at	M25719	peptidylglycine alpha-amidating monooxygenase	Pam	0.822	0.009	0.342	0.000	0.913	0.033	0.422	0.004
1372517_at	BI283851	peptidylprolyl isomerase (cyclophilin)-like 1	Ppil1	1.982	0.203	0.642	0.661	1.032	0.909	0.891	0.964
1375440_at	BI283709	peptidylprolyl isomerase (cyclophilin)-like 2	Ppil2	1.168	0.777	0.639	0.016	1.334	0.054	0.930	0.410
1375686_at	AI706907	peptidylprolyl isomerase (cyclophilin)-like 3	Ppil3	0.772	0.231	1.789	0.251	0.485	0.009	1.024	0.855
1375061_at	BM383803	Peptidylprolyl isomerase (cyclophilin)-like 4 (predicted)	Ppil4_predicted	0.743	0.157	0.540	0.021	0.727	0.173	0.982	0.855
1398850_at	BG671399	peptidylprolyl isomerase A	Ppia	0.819	0.763	0.810	0.030	0.676	0.215	0.811	0.024
1369934_at	NM_022536	peptidylprolyl isomerase B	Ppib	0.706	0.274	1.113	0.839	0.721	0.011	0.799	0.071
1372827_at	AA957342	peptidylprolyl isomerase D (cyclophilin D)	Ppid	0.720	0.005	0.947	0.298	0.587	0.001	0.846	0.048
1380893_at	BF416306	peptidylprolyl isomerase D (cyclophilin D) /// similar to peptidylprolyl isomerase D (predicted)	Ppid /// RGD1560149_predicted	0.976	0.909	1.374	0.636	1.074	0.695	0.945	0.529
1379665_at	AI177835	peptidylprolyl isomerase domain and WD repeat containing 1 (predicted)	Ppwd1_predicted	1.157	0.444	1.949	0.014	1.318	0.454	1.753	0.001

1389055_at	AI104479	peptidylprolyl isomerase E (cyclophilin E)	Ppie	1.048	0.832	2.379	0.002	0.982	0.855	1.294	0.021
1370319_at	U68544	peptidylprolyl isomerase F (cyclophilin F)	Ppif	0.853	0.047	1.173	0.119	1.107	0.891	1.323	0.019
1380020_at	BF395860	Peptidylprolyl isomerase G	Ppig	0.831	0.572	0.858	0.547	1.089	0.348	0.847	0.077
1370096_at	NM_017330	perforin 1 (pore forming protein)	Prf1	0.996	0.397	1.243	0.918	1.532	0.350	1.020	0.862
1390650_at	BI290593	pericentrin 1	Pcnt1	0.665	0.095	1.056	0.119	0.493	0.010	1.078	0.845
1371064_at	U95920	pericentriolar material 1	Pcm1	0.460	0.265	0.683	0.329	0.574	0.029	0.648	0.016
1374956_at	BE101520	pericentriolar material 1	Pcm1	0.961	0.721	0.858	0.236	1.338	0.977	0.848	0.228
1374855_at	BI279017	period homolog 1 (Drosophila)	Per1	0.796	0.435	3.662	0.002	1.223	0.123	4.019	0.001
1368303_at	NM_031678	period homolog 2 (Drosophila)	Per2	3.140	0.005	1.591	0.001	1.826	0.046	1.450	0.023
1370247_a_at	AA943163	peripheral myelin protein 22	Pmp22	1.425	0.341	0.996	0.896	0.999	0.938	0.998	0.798
1389547_at	BE107375	periphilin 1 (predicted)	Pphln1_predicted	1.031	0.892	0.816	0.658	1.001	0.979	0.997	0.919
1370833_at	AF324454	peroxin 2	Pex2	0.130	0.136	1.559	0.278	0.201	0.023	1.309	0.310
1379753_at	BE121134	peroxin 2	Pex2	0.894	0.917	1.561	0.078	1.276	0.997	1.946	0.076
1367613_at	NM_057114	peroxiredoxin 1	Prdx1	0.788	0.554	1.044	0.181	0.712	0.291	1.022	0.911
1367578_at	NM_017169	peroxiredoxin 2	Prdx2	0.849	0.564	0.756	0.032	0.852	0.151	0.859	0.298
1367591_at	NM_022540	peroxiredoxin 3	Prdx3	0.508	0.043	0.634	0.049	0.619	0.345	0.609	0.004
1387891_at	BI282076	peroxiredoxin 4	Prdx4	0.697	0.504	0.293	0.017	0.721	0.399	0.540	0.038
1367677_at	NM_053610	peroxiredoxin 5	Prdx5	0.810	0.996	1.341	0.060	0.559	0.221	0.760	0.858
1367969_at	AF014009	peroxiredoxin 6	Prdx6	0.510	0.418	2.847	0.064	0.866	0.564	1.220	0.512
1379361_at	BI273703	peroxisomal biogenesis factor 11A	Pex11a	1.046	0.750	1.050	0.136	1.005	0.995	0.995	0.756
1372923_at	BG377340	Peroxisomal biogenesis factor 11b	Pex11b	0.861	0.072	0.772	0.030	0.968	0.607	0.832	0.232
1369070_at	NM_053921	peroxisomal biogenesis factor 12	Pex12	0.721	0.442	0.819	0.366	0.711	0.183	1.143	0.532
1374638_at	AI012951	peroxisomal biogenesis factor 13 (predicted)	Pex13_predicted	0.547	0.009	0.770	0.032	0.637	0.015	1.034	0.458
1397996_at	BF387766	Peroxisomal biogenesis factor 13 (predicted)	Pex13_predicted	1.177	0.879	0.944	0.552	1.137	0.298	0.850	0.694
1368526_at	NM_031350	peroxisomal biogenesis factor 3	Pex3	0.918	0.430	0.593	0.093	0.771	0.165	0.668	0.234
1388908_at	BI278268	peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase	Peci	0.526	0.127	0.516	0.003	0.750	0.059	0.545	0.028
1372765_a_at	BM390774	peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase /// similar to RIKEN cDNA 1810022C23	Peci /// RGD1310224	0.456	0.091	0.444	0.118	0.400	0.075	0.765	0.591
1396866_s_at	AA850928	peroxisomal membrane protein 3	Pxmp3	0.802	0.130	0.972	0.387	0.640	0.088	0.910	0.290
1387064_at	NM_017234	peroxisomal membrane protein 3	Pxmp3	0.667	0.182	0.848	0.160	0.597	0.031	1.021	0.380
1383117_at	AI232414	peroxisomal membrane protein 4	Pxmp4	0.486	0.179	0.525	0.292	0.500	0.261	0.511	0.050
1368016_at	NM_133299	peroxisomal trans-2-enoyl-CoA reductase	Pecr	0.683	0.017	0.729	0.123	0.338	0.024	0.791	0.132
1388350_at	BG377475	peroxisome biogenesis factor 19	Pex19	1.179	0.138	1.495	0.283	0.727	0.082	1.265	0.411
1371431_at	BI296577	Peroxisome biogenesis factor 5 (predicted)	Pex5_predicted	0.723	0.573	1.378	0.009	1.045	0.509	1.322	0.057
1379784_at	AA997675	peroxisome biogenesis factor 7	Pex7	0.370	0.027	0.245	0.000	0.479	0.153	0.488	0.056
1370089_at	NM_031347	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	Ppargc1a	0.288	0.017	3.939	0.040	0.421	0.042	2.434	0.003
1392715_at	BE113289	peroxisome proliferative activated receptor, gamma, coactivator 1 beta	Ppargc1b	0.778	0.831	1.417	0.157	1.354	0.232	0.574	0.017
1379312_at	AI706508	peroxisome proliferative activated receptor, gamma, coactivator-related 1 (predicted)	Pprc1_predicted	1.297	0.228	3.340	0.014	1.239	0.146	2.221	0.054
1395733_at	AI717063	Peroxisome proliferative activated receptor, gamma, coactivator-related 1 (predicted)	Pprc1_predicted	1.040	0.998	1.239	0.088	1.031	0.792	1.033	0.448
1374914_at	AI230294	Peroxisome proliferator activated receptor delta	Ppard	1.725	0.062	0.940	0.467	1.390	0.101	0.855	0.483
1372423_at	BI286396	PERP, TP53 apoptosis effector (predicted)	Perp_predicted	1.351	0.577	0.950	0.843	1.014	0.688	0.964	0.801
1389177_at	AI598971	PERP, TP53 apoptosis effector (predicted)	Perp_predicted	1.205	0.734	1.270	0.582	0.572	0.247	0.876	0.612
1382357_at	AI713784	PERQ amino acid rich, with GYF domain 1 (predicted)	Perq1_predicted	1.559	0.043	0.802	0.266	1.102	0.057	0.662	0.086
1381469_a_at	AW526967	PERQ amino acid rich, with GYF domain 1 (predicted)	Perq1_predicted	1.189	0.301	1.016	0.854	1.013	0.822	1.014	0.244
1390241_at	BI296888	PERQ amino acid rich, with GYF domain 1 (predicted)	Perq1_predicted	1.191	0.361	0.900	0.912	1.163	0.417	0.862	0.196
1374326_at	AI178019	peter pan homolog (Drosophila)	Ppan	0.588	0.009	2.936	0.004	0.493	0.066	1.882	0.017
1374747_at	BM384279	PFTAIRE protein kinase 1 (predicted)	Pftk1_predicted	0.496	0.071	0.136	0.004	0.344	0.014	0.292	0.002
1368262_at	NM_021657	PH domain and leucine rich repeat protein phosphatase	Phlpp	0.580	0.472	3.206	0.000	0.704	0.193	2.239	0.003
1389201_at	BG373545	PHD finger protein 10	Phf10	0.817	0.018	0.672	0.001	0.821	0.015	0.910	0.189
1376121_at	BE107051	PHD finger protein 10	Phf10	1.152	0.158	0.653	0.005	0.538	0.092	0.524	0.012
1394906_at	BF289997	PHD finger protein 10	Phf10	0.622	0.675	0.395	0.033	0.243	0.022	0.677	0.014
1382546_at	AW920026	PHD finger protein 11	Phf11	1.967	0.181	1.307	0.172	21.633	0.000	8.487	0.017
1394014_at	AA924840	PHD finger protein 12	Phf12	0.903	0.175	0.825	0.147	1.070	0.441	0.960	0.060
1374032_at	AA998886	PHD finger protein 12	Phf12	0.986	0.527	0.683	0.033	0.665	0.106	0.924	0.856
1373446_at	AI102512	PHD finger protein 13 (predicted)	Phf13_predicted	1.269	0.255	2.563	0.010	0.972	0.917	1.318	0.460
1385671_at	AA956689	PHD finger protein 15 (predicted)	Phf15_predicted	1.379	0.088	0.552	0.007	1.377	0.081	0.747	0.034
1384759_at	AW534015	PHD finger protein 17 (predicted)	Phf17_predicted	1.751	0.351	2.431	0.049	0.702	0.503	1.595	0.079
1381246_at	BI293437	PHD finger protein 21B (predicted)	Phf21b_predicted	1.345	0.077	1.230	0.013	2.377	0.009	1.590	0.000
1383570_at	BF547887	PHD finger protein 3 (predicted)	Phf3_predicted	1.665	0.138	1.505	0.015	0.954	0.495	1.626	0.106
1371463_at	AI233239	PHD finger protein 5A	Phf5a	0.571	0.493	1.348	0.470	0.446	0.073	1.185	0.507
1387034_at	NM_012619	phenylalanine hydroxylase	Pah	0.665	0.094	0.723	0.393	0.996	0.425	1.024	0.390
1390267_at	AW915175	phenylalanine-tRNA synthetase 2 (mitochondrial)	Fars2	1.034	0.800	2.021	0.009	0.981	0.819	1.662	0.023

1371453_at	BE113146	phenylalanine-tRNA synthetase-like, beta subunit	Farslb	0.894	0.611	1.483	0.009	0.750	0.013	1.318	0.002
1386990_at	NM_057137	phenylalkylamine Ca2+ antagonist (emopamil) binding protein	Ebp	0.722	0.594	0.606	0.074	0.505	0.213	0.732	0.053
1378143_at	AI170625	phosducin-like	Pdcl	0.991	0.401	0.830	0.047	1.564	0.046	0.958	0.220
1387499_a_at	NM_022247	phosducin-like	Pdcl	1.002	0.985	0.914	0.914	1.011	0.825	1.014	0.271
1377779_at	AI137175	phosducin-like 3	Pdcl3	1.922	0.163	1.924	0.025	0.951	0.379	1.651	0.064
1373052_at	BI275649	phosducin-like 3	Pdcl3	1.767	0.213	3.651	0.005	1.178	0.016	2.890	0.007
1374153_at	AI236359	Phosducin-like 3	Pdcl3	2.494	0.302	1.775	0.162	1.459	0.425	0.785	0.644
1396588_at	BF405168	Phosphatase and actin regulator 1	Phactr1	1.148	0.273	0.994	0.236	2.723	0.039	1.165	0.102
1394534_at	AW532329	Phosphatase and actin regulator 1	Phactr1	1.254	0.627	0.903	0.994	1.405	0.874	1.049	0.655
1382303_at	AA996943	phosphatase and actin regulator 1	Phactr1	1.078	0.695	0.801	0.124	1.031	0.899	0.997	0.124
1378172_at	AI008119	Phosphatase and actin regulator 2	Phactr2	1.494	0.311	2.338	0.133	3.622	0.092	3.631	0.014
1392105_at	AW527533	Phosphatase and actin regulator 2	Phactr2	1.365	0.429	0.498	0.048	1.960	0.082	0.715	0.423
1370112_at	NM_031606	phosphatase and tensin homolog	Pten	1.412	0.333	2.167	0.012	1.022	0.437	1.486	0.063
1389299_at	BG673255	Phosphate cytidylyltransferase 1, choline, alpha isoform	Pcyt1a	1.420	0.161	2.564	0.004	1.294	0.001	1.629	0.005
1368100_at	NM_053568	phosphate cytidylyltransferase 2, ethanolamine	Pcyt2	0.875	0.543	1.220	0.011	0.793	0.110	1.111	0.072
1369961_at	NM_022538	phosphatidic acid phosphatase 2a	Ppap2a	0.389	0.118	1.125	0.771	0.787	0.261	1.068	0.723
1382772_at	BF289261	Phosphatidic acid phosphatase 2a	Ppap2a	1.370	0.602	1.657	0.128	2.015	0.152	0.796	0.705
1373083_at	AW915681	phosphatidic acid phosphatase type 2 domain containing 2	Ppapdc2	0.843	0.323	0.456	0.015	0.701	0.084	0.753	0.093
1372101_at	AI177031	phosphatidic acid phosphatase type 2B	Ppap2b	3.706	0.008	1.377	0.434	4.392	0.008	1.316	0.134
1388913_at	AA893191	phosphatidic acid phosphatase type 2c	Ppap2c	0.949	0.182	1.629	0.146	1.002	0.994	1.281	0.373
1387058_at	NM_017225	phosphatidylcholine transfer protein	Pctp	1.080	0.819	1.143	0.036	1.092	0.387	1.459	0.081
1373845_at	AA944773	Phosphatidylethanlomine binding protein 2	Pbp2	0.755	0.352	0.911	0.404	0.699	0.022	1.397	0.092
1386891_at	NM_017236	phosphatidylethanolamine binding protein 1	Pebp1	0.623	0.439	0.714	0.097	0.470	0.007	0.838	0.512
1393755_at	BE109926	phosphatidylinositol 3-kinase catalytic delta polypeptide (predicted)	Pik3cd_predicted	1.163	0.726	1.009	0.916	1.002	0.999	0.998	0.999
1369050_at	NM_053923	phosphatidylinositol 3-kinase, C2 domain containing, gamma polypeptide	Pik3c2g	3.003	0.018	2.450	0.046	5.039	0.018	4.046	0.023
1382366_at	AI578786	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	Pik3ca	1.054	0.122	0.980	0.817	1.320	0.046	0.792	0.393
1379041_at	BG381034	Phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	Pik3ca	1.169	0.143	0.795	0.054	0.939	0.239	0.786	0.033
1393499_at	AA964375	Phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	Pik3ca	1.005	0.202	1.267	0.592	1.174	0.543	1.079	0.324
1374232_at	BI290699	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	Pik3ca	1.179	0.679	1.634	0.045	1.317	0.630	1.120	0.262
1369177_at	NM_053735	phosphatidylinositol 4-kinase type 2 alpha	Pi4k2a	0.863	0.310	1.011	0.212	1.191	0.336	1.813	0.048
1370318_at	U39572	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	Pik4ca	0.870	0.897	0.684	0.049	0.743	0.019	0.640	0.001
1374689_at	AI102103	phosphatidylinositol 4-kinase, catalytic, beta polypeptide	Pik4cb	1.494	0.025	0.713	0.015	1.338	0.325	0.848	0.304
1384062_at	AI072443	Phosphatidylinositol 4-kinase, catalytic, beta polypeptide	Pik4cb	0.873	0.492	0.865	0.085	0.693	0.185	0.640	0.007
1382414_at	AI043787	Phosphatidylinositol 4-kinase, catalytic, beta polypeptide	Pik4cb	0.989	0.961	1.199	0.611	1.110	0.089	1.065	0.593
1369039_at	NM_031083	phosphatidylinositol 4-kinase, catalytic, beta polypeptide	Pik4cb	0.698	0.993	0.283	0.002	0.941	0.837	0.318	0.000
1373877_at	BF401685	Phosphatidylinositol binding clathrin assembly protein	Picalm	1.137	0.062	1.411	0.010	1.208	0.481	1.209	0.032
1396561_x_at	BF409296	phosphatidylinositol glycan, class A (mapped)	Piga_mapped	1.007	0.606	1.588	0.015	1.156	0.553	1.603	0.246
1373664_at	AI228670	phosphatidylinositol glycan, class C	Pigc	0.692	0.084	0.753	0.041	0.614	0.307	0.580	0.093
1373101_at	AI236743	phosphatidylinositol glycan, class K	Pigk	0.417	0.199	0.469	0.008	0.808	0.074	0.555	0.014
1398309_at	D88364	phosphatidylinositol glycan, class L	Pigl	0.498	0.001	0.897	0.437	1.484	0.427	0.974	0.932
1369042_at	NM_024144	phosphatidylinositol glycan, class M	Pigm	0.968	0.793	0.319	0.099	0.784	0.308	0.532	0.070
1382724_at	AW433604	Phosphatidylinositol glycan, class O (predicted)	Pigo_predicted	0.842	0.062	1.196	0.152	0.726	0.112	1.001	0.996
1375600_at	AI535065	Phosphatidylinositol glycan, class O (predicted)	Pigo_predicted	0.645	0.877	1.003	0.965	0.734	0.926	1.596	0.632
1396415_at	BF387862	Phosphatidylinositol glycan, class P (predicted)	Pigp_predicted	0.916	0.457	0.996	0.486	0.969	0.785	1.013	0.454
1371948_at	BF415030	phosphatidylinositol glycan, class P (predicted)	Pigp_predicted	0.934	0.725	0.990	0.484	0.985	0.707	1.308	0.076
1388793_at	AI408261	phosphatidylinositol glycan, class Q	Pigq	0.406	0.071	0.252	0.024	0.530	0.039	0.250	0.005
1373099_at	BI284221	phosphatidylinositol glycan, class S	Pigs	0.686	0.471	0.460	0.001	0.579	0.088	0.553	0.003
1372900_at	BI274156	phosphatidylinositol glycan, class T (predicted)	Pigt_predicted	0.421	0.001	0.476	0.005	0.476	0.004	0.588	0.019
1374571_at	AI172192	phosphatidylinositol glycan, class X	Pigx	0.496	0.114	0.381	0.028	0.369	0.034	0.294	0.008
1398806_at	NM_017231	phosphatidylinositol transfer protein, alpha	Pitpna	0.570	0.152	0.796	0.071	0.494	0.011	0.754	0.013
1367674_at	NM_053742	phosphatidylinositol transfer protein, beta	Pitpnb	1.076	0.280	0.829	0.408	1.093	0.150	0.828	0.474
1389347_at	BE100607	phosphatidylinositol transfer protein, membrane-associated 1	Pitpnm1	0.849	0.111	0.536	0.012	2.067	0.121	0.923	0.459
1379352_at	BF406008	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	Pip5k1a	0.380	0.105	0.766	0.100	0.302	0.033	0.631	0.078
1372861_at	BG380713	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	Pip5k1c	1.083	0.305	0.796	0.064	1.128	0.132	0.767	0.150
1370025_at	NM_080480	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma	Pip5k2c	0.740	0.336	1.186	0.545	0.762	0.463	1.217	0.163
1374632_at	AI232697	phosphatidylserine receptor	Ptdsr	0.590	0.278	2.645	0.001	1.011	0.947	2.131	0.002
1374077_at	AI172029	Phosphatidylserine synthase 1	Ptdss1	0.596	0.064	0.293	0.020	0.709	0.790	0.388	0.017
1367497_at	AA851302	phosphatidylserine synthase 1	Ptdss1	0.414	0.180	1.090	0.643	0.366	0.016	0.881	0.727
1372663_at	BI289419	phosphatidylserine synthase 2 (predicted)	Ptdss2_predicted	0.805	0.173	1.026	0.358	0.805	0.174	1.010	0.823
1391295_at	AI136393	Phosphodiesterase 10A	Pde10a	0.237	0.003	0.588	0.100	0.154	0.009	0.560	0.092
1368438_at	NM_022236	phosphodiesterase 10A	Pde10a	0.419	0.004	0.439	0.003	0.456	0.009	0.384	0.003

1370669_a_at	AB027156	phosphodiesterase 10A	Pde10a	0.376	0.037	0.199	0.015	0.284	0.035	0.231	0.019
1388020_a_at	AF328800	phosphodiesterase 1C	Pde1c	1.195	0.016	1.053	0.694	1.568	0.045	1.215	0.072
1371219_a_at	AF328797	phosphodiesterase 1C	Pde1c	1.537	0.080	1.139	0.953	1.348	0.104	0.854	0.701
1394973_at	BF410175	Phosphodiesterase 1C	Pde1c	1.383	0.145	0.752	0.055	1.001	0.888	0.676	0.064
1369157_at	NM_017229	phosphodiesterase 3B	Pde3b	0.780	0.119	0.766	0.028	0.760	0.187	0.764	0.080
1394872_x_at	AI235078	Phosphodiesterase 3B	Pde3b	1.031	0.933	0.988	0.926	1.137	0.112	0.985	0.904
1376565_at	AI029179	Phosphodiesterase 4A, cAMP specific	Pde4a	0.487	0.187	0.609	0.162	0.489	0.192	0.610	0.121
1368670_a_at	L36467	phosphodiesterase 4A, cAMP specific	Pde4a	1.002	0.668	0.998	0.592	1.000	0.536	0.806	0.383
1378077_at	BF412632	Phosphodiesterase 4B, cAMP specific	Pde4b	1.126	0.870	1.064	0.277	0.836	0.434	1.001	0.997
1384400_at	BM389421	Phosphodiesterase 4C, cAMP-specific	Dpde1	1.529	0.114	2.067	0.006	2.751	0.014	2.618	0.008
1382254_at	BI295944	Phosphodiesterase 4D interacting protein (myomegalin)	Pde4dip	1.098	0.435	0.746	0.047	1.106	0.421	1.035	0.511
1379811_at	AI763912	Phosphodiesterase 4D interacting protein (myomegalin)	Pde4dip	0.956	0.855	0.608	0.005	1.298	0.331	0.775	0.017
1370569_at	BF565001	phosphodiesterase 4D, cAMP specific	Pde4d	0.562	0.010	0.851	0.211	0.964	0.956	0.799	0.088
1393573_at	AI575628	phosphodiesterase 6B, cGMP, rod receptor, beta polypeptide (predicted)	Pde6b_predicted	1.303	0.792	1.129	0.642	1.106	0.619	1.214	0.979
1388512_at	BM391512	phosphodiesterase 6D, cGMP-specific, rod, delta (predicted)	Pde6d_predicted	0.979	0.897	1.154	0.593	0.678	0.065	1.235	0.731
1371044_at	BF410284	phosphodiesterase 7A	Pde7a	1.637	0.011	1.575	0.066	1.205	0.531	1.504	0.209
1382518_at	BM386012	phosphodiesterase 8A	Pde8a	0.672	0.078	0.951	0.896	0.723	0.251	0.869	0.795
1392088_at	BF399382	Phosphodiesterase 8B	Pde8b	0.835	0.570	0.804	0.126	1.942	0.287	0.401	0.142
1374452_at	BF399743	phosphodiesterase 9A	Pde9a	2.340	0.125	1.723	0.047	2.453	0.013	1.101	0.500
1375213_at	BM384604	phosphoenolpyruvate carboxykinase 2 (mitochondrial) (predicted)	Pck2_predicted	0.376	0.005	0.820	0.129	0.373	0.015	0.521	0.007
1391451_at	AI228633	Phosphoenolpyruvate carboxykinase 2 (mitochondrial) (predicted)	Pck2_predicted	0.590	0.080	0.523	0.000	0.422	0.039	0.709	0.037
1376247_at	BF403197	phosphoenolpyruvate carboxykinase 2 (mitochondrial) (predicted)	Pck2_predicted	0.625	0.164	1.153	0.100	0.479	0.074	0.895	0.596
1367743_at	NM_013190	phosphofructokinase, liver, B-type	Pfkl	0.387	0.218	1.889	0.016	0.587	0.134	1.600	0.097
1367864_at	NM_031715	phosphofructokinase, muscle	Pfkm	0.464	0.075	0.207	0.004	0.430	0.032	0.232	0.034
1372182_at	BM389769	phosphofructokinase, platelet	Pfkp	4.975	0.001	7.762	0.000	4.954	0.000	6.087	0.000
1367924_at	NM_134406	phosphofurin acidic cluster sorting protein 1	Pacs1	0.968	0.352	1.097	0.094	0.999	0.984	1.070	0.479
1388634_at	BI277505	phosphoglucomutase 1	Pgm1	0.398	0.035	1.200	0.285	0.499	0.029	1.152	0.336
1369473_at	NM_017033	phosphoglucomutase 1	Pgm1	0.476	0.243	1.060	0.435	0.307	0.023	1.045	0.589
1373769_at	AI176913	phosphoglucomutase 1 (predicted)	Pgm1_predicted	1.324	0.165	1.331	0.415	1.436	0.034	1.045	0.508
1382103_at	AI549036	phosphoglucomutase 3 (predicted)	Pgm3_predicted	0.910	0.046	0.828	0.426	0.926	0.210	0.877	0.081
1371646_at	AI008441	phosphogluconate dehydrogenase (mapped)	Pgd_mapped	1.424	0.139	1.977	0.016	1.392	0.134	2.131	0.003
1371846_at	BM391894	phosphoglycerate dehydrogenase like 1	Phgdhl1	0.505	0.149	1.441	0.097	0.390	0.024	1.435	0.092
1385466_at	AI146067	phosphoglycerate dehydrogenase like 1	Phgdhl1	0.955	0.892	1.267	0.138	0.991	0.417	0.999	0.529
1388318_at	BI279760	phosphoglycerate kinase 1	Pgk1	0.814	0.097	2.084	0.001	0.700	0.072	1.611	0.026
1387361_s_at	NM_053291	phosphoglycerate kinase 1	Pgk1	0.735	0.309	1.993	0.014	0.605	0.020	1.562	0.049
1386864_at	NM_053290	phosphoglycerate mutase 1	Pgam1	0.711	0.214	1.527	0.006	0.702	0.040	1.515	0.005
1391577_at	BI293450	phosphoglycerate mutase family member 5	Pgam5	1.121	0.766	1.562	0.001	0.904	0.020	1.521	0.014
1378382_at	AI230014	Phosphoglycerate mutase family member 5	Pgam5	1.054	0.826	1.639	0.001	0.913	0.265	1.609	0.006
1369655_at	NM_022958	phosphoinositide-3-kinase, class 3	Pik3c3	1.761	0.033	1.346	0.535	1.405	0.174	0.662	0.133
1389723_at	AI172265	phosphoinositide-3-kinase, regulatory subunit 4, p150 (predicted)	Pik3r4_predicted	0.291	0.000	0.295	0.001	0.484	0.022	0.395	0.005
1396714_at	BF394289	Phospholipase A2, activating protein	Plaa	0.663	0.313	4.654	0.118	0.633	0.449	3.619	0.099
1368668_at	NM_053866	phospholipase A2, activating protein	Plaa	0.753	0.485	1.779	0.008	0.595	0.075	1.246	0.007
1370257_at	AI234860	phospholipase A2, group IB	Pla2g1b	0.695	0.305	0.388	0.070	0.893	0.957	0.637	0.119
1368128_at	NM_031598	phospholipase A2, group IIA (platelets, synovial fluid)	Pla2g2a	4.045	0.002	8.301	0.000	2.247	0.049	1.086	0.216
1377323_at	AW434922	phospholipase A2, group IVB (cytosolic) (predicted)	Pla2g4b_predicted	1.370	0.158	2.092	0.058	1.056	0.906	1.542	0.190
1370385_at	U51898	phospholipase A2, group VI	Pla2g6	2.176	0.007	0.937	0.784	1.877	0.008	0.937	0.655
1371014_at	BE097028	phospholipase C, beta 1	Plcb1	0.820	0.102	0.505	0.006	0.683	0.203	0.608	0.010
1381133_at	BF409213	Phospholipase C, beta 1	Plcb1	0.988	0.578	0.742	0.015	0.769	0.211	0.827	0.127
1397388_at	AI555001	Phospholipase C, beta 1	Plcb1	1.002	0.967	0.870	0.405	1.004	0.993	0.764	0.473
1388156_at	AW526098	phospholipase C, beta 3	Plcb3	0.838	0.902	0.857	0.398	0.927	0.920	1.000	1.000
1386962_at	NM_024353	phospholipase C, beta 4	Plcb4	0.948	0.693	0.288	0.006	1.522	0.134	0.514	0.046
1381747_at	BM385105	Phospholipase C, delta 3 (predicted)	Plcd3_predicted	0.942	0.363	1.219	0.506	1.030	0.994	1.115	0.594
1387065_at	NM_080688	phospholipase C, delta 4	Plcd4	1.003	0.955	1.001	0.980	1.008	0.968	1.004	0.995
1368183_at	NM_013187	phospholipase C, gamma 1	Plcg1	1.459	0.112	1.353	0.050	1.535	0.333	1.134	0.065
1374590_at	BF420110	phospholipase C-like 2 (predicted)	Plcl2_predicted	0.542	0.031	0.746	0.017	0.537	0.018	0.770	0.058
1392099_at	AI549022	phospholipase C-like 3 (predicted)	Plcl3_predicted	7.880	0.011	1.153	0.069	6.555	0.000	1.438	0.084
1371961_at	BF287282	phospholipase D family, member 3	Pld3	1.098	0.562	0.805	0.037	0.878	0.446	0.759	0.147
1370531_a_at	U69550	phospholipase D1	Pld1	2.432	0.007	3.428	0.004	2.259	0.002	2.066	0.027
1370530_a_at	AB000779	phospholipase D1	Pld1	2.588	0.023	2.856	0.008	2.802	0.017	2.840	0.001
1370529_a_at	AB003171	phospholipase D1	Pld1	0.981	0.934	1.838	0.049	1.402	0.621	1.002	0.975
1368954_at	D88672	phospholipase D2	Pld2	1.014	0.279	0.995	0.963	1.299	0.885	1.009	0.985

1369029_at	NM_057194	phospholipid scramblase 1	Plscr1	6.280	0.005	3.217	0.016	12.282	0.003	3.218	0.006
1373417_at	BI285973	phospholipid scramblase 3	Plscr3	1.954	0.023	3.094	0.004	2.512	0.015	3.351	0.001
1371455_at	AI411429	phosphomannomutase 1	Pmm1	0.571	0.687	2.078	0.005	0.311	0.002	2.014	0.031
1397458_at	AW533978	phosphomannomutase 2 (predicted)	Pmm2_predicted	1.361	0.094	0.741	0.243	0.966	0.842	0.799	0.031
1371535_at	AI411161	phosphomannomutase 2 (predicted)	Pmm2_predicted	0.776	0.647	1.538	0.002	0.761	0.240	1.484	0.025
1373243_at	BG378288	phosphomevalonate kinase	Pmvk	0.541	0.143	1.239	0.551	0.301	0.029	0.852	0.084
1388756_at	AI231606	phosphopantothenoylcysteine synthetase	Ppcs	0.431	0.029	0.716	0.054	0.293	0.028	0.748	0.067
1388339_at	BE112895	phosphoprotein enriched in astrocytes 15	Pea15	1.520	0.269	2.503	0.013	0.765	0.894	1.621	0.048
1371441_at	BG662875	phosphoprotein enriched in astrocytes 15	Pea15	0.993	0.971	1.221	0.156	0.693	0.189	0.760	0.274
1369785_at	NM_057198	phosphoribosyl pyrophosphate amidotransferase	Ppat	1.008	0.147	0.880	0.082	0.854	0.152	0.772	0.134
1368165_at	NM_017243	phosphoribosyl pyrophosphate synthetase 1	Prps1	1.245	0.713	1.274	0.117	1.388	0.340	1.377	0.063
1387085_at	M29392	phosphoribosyl pyrophosphate synthetase 1	Prps1	1.273	0.742	0.961	0.508	1.371	0.357	0.869	0.300
1398262_at	NM_012634	phosphoribosyl pyrophosphate synthetase 2	Prps2	0.549	0.062	0.555	0.200	0.871	0.064	0.732	0.185
1367750_at	NM_022545	phosphoribosyl pyrophosphate synthetase-associated protein 1	Prpsap1	0.698	0.032	0.983	0.240	0.763	0.096	0.981	0.050
1369978_at	NM_057131	phosphoribosyl pyrophosphate synthetase-associated protein 2	Prpsap2	0.717	0.019	0.772	0.036	0.674	0.022	0.769	0.155
1387790_at	NM_080910	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoribosylaminoimidazole succinocarboxamide synthetase	Paics	0.525	0.200	1.090	0.018	0.439	0.002	1.180	0.023
1388641_at	AI410319	phosphoribosylglycinamide formyltransferase	Gart	0.357	0.016	1.546	0.187	0.314	0.006	0.997	0.959
1394839_at	AA850773	Phosphoribosylglycinamide formyltransferase	Gart	1.113	0.849	1.393	0.363	0.841	0.197	1.071	0.738
1390210_at	BF418932	Phosphorylase kinase alpha 1	Phka1	0.624	0.022	0.531	0.024	1.004	0.733	0.807	0.105
1369357_at	NM_022626	phosphorylase kinase alpha 1	Phka1	0.842	0.059	0.999	0.099	0.840	0.041	0.998	0.965
1389180_at	AI175035	Phosphorylase kinase, beta	Phkb	0.781	0.050	0.237	0.078	0.858	0.513	0.575	0.077
1367788_at	NM_080584	phosphorylase kinase, gamma 2 (testis)	Phkg2	1.015	0.411	1.173	0.004	1.230	0.763	1.152	0.092
1388180_at	AI044239	phosphorylated adaptor for RNA export	Phax	0.720	0.269	1.035	0.710	0.689	0.004	0.907	0.065
1372665_at	AI230228	phosphoserine aminotransferase 1	Psat1	0.616	0.211	0.728	0.198	0.637	0.023	0.694	0.085
1375964_at	BF282282	phosphoserine phosphatase	Psph	0.491	0.212	0.809	0.136	0.296	0.022	0.698	0.022
1371012_at	AJ245707	phytanoyl-CoA 2-hydroxylase 2	Phyh2	0.180	0.026	0.278	0.001	0.273	0.040	0.399	0.008
1398042_at	BF400265	Phytanoyl-CoA dioxygenase domain containing 1	Phyhd1	1.006	0.518	1.067	0.958	1.204	0.331	1.069	0.884
1393245_at	AI029057	Phytanoyl-CoA hydroxylase	Phyh	0.598	0.024	0.661	0.006	0.589	0.001	0.593	0.032
1387271_at	NM_053674	phytanoyl-CoA hydroxylase	Phyh	0.376	0.129	0.530	0.006	0.298	0.001	0.467	0.001
1387399_at	NM_020098	piccolo (presynaptic cytomatrix protein)	Pclo	0.282	0.006	0.205	0.008	0.168	0.004	0.218	0.011
1398271_at	AF138789	piccolo (presynaptic cytomatrix protein)	Pclo	0.259	0.035	1.143	0.762	0.250	0.035	0.901	0.848
1389597_at	BI293445	piggyBac transposable element derived 5 (predicted)	Pgbd5_predicted	0.815	0.188	0.633	0.076	0.803	0.051	0.565	0.095
1391269_at	BG372987	pim-2 oncogene (predicted)	Pim2_predicted	3.587	0.002	1.908	0.183	0.729	0.422	0.306	0.108
1377662_at	AI176041	pirin	Pir	0.536	0.058	1.475	0.185	0.242	0.013	1.417	0.028
1378017_at	AI408960	pitrilysin metallepetidase 1 (predicted)	Pitrm1_predicted	0.744	0.692	1.554	0.021	0.901	0.158	1.275	0.002
1389903_at	AA799616	pituitary tumor-transforming 1 interacting protein	Pttg1ip	0.931	0.906	1.618	0.004	0.774	0.253	1.247	0.078
1388539_at	BE113268	plakophilin 2	Pkp2	0.655	0.688	1.748	0.095	0.722	0.092	1.270	0.060
1378689_at	BF409044	Plakophilin 4 (predicted)	Pkp4_predicted	1.153	0.023	1.014	0.888	1.964	0.001	0.958	0.581
1372744_at	BE113437	plakophilin 4 (predicted)	Pkp4_predicted	0.832	0.981	0.787	0.945	1.000	0.205	1.167	0.640
1368399_a_at	NM_031640	plasma glutamate carboxypeptidase	Pgcp	0.814	0.388	0.555	0.005	1.096	0.629	0.640	0.013
1367800_at	NM_013151	plasminogen activator, tissue	Plat	3.309	0.002	21.701	0.008	1.975	0.115	7.907	0.020
1385981_at	BF394800	plasticity related gene 1	Prg1	0.441	0.023	0.305	0.009	0.180	0.004	0.290	0.014
1379374_at	AW526088	plasticity related gene 1	Prg1	0.345	0.024	0.395	0.000	0.288	0.000	0.325	0.008
1389654_at	BM392070	Plastin 1 (I isoform) (predicted)	Pls1_predicted	0.793	0.744	0.546	0.001	0.766	0.103	0.530	0.012
1372947_at	BG672591	plastin 3 (T-isoform)	Pls3	0.991	0.384	1.283	0.059	1.028	0.691	1.383	0.011
1396071_at	AI502944	Plastin 3 (T-isoform)	Pls3	1.362	0.588	0.917	0.752	0.972	0.889	1.017	0.358
1391394_s_at	AI071374	platelet derived growth factor receptor, beta polypeptide	Pdgfrb	1.077	0.811	0.999	0.933	0.816	0.046	0.998	0.994
1379375_at	BE100812	Platelet derived growth factor, alpha	Pdgfa	8.595	0.000	2.479	0.007	7.316	0.002	2.018	0.076
1370427_at	L06238	platelet derived growth factor, alpha	Pdgfa	6.643	0.004	3.490	0.000	6.154	0.003	2.892	0.016
1369963_at	NM_053654	platelet-activating factor acetylhydrolase, isoform 1b, alpha1 subunit	Pafah1b3	1.026	0.119	1.592	0.007	1.384	0.136	2.264	0.018
1369641_at	AF016048	platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit	Pafah1b2	0.924	0.451	1.847	0.040	0.759	0.411	1.061	0.654
1369642_at	BM392366	platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit	Pafah1b2	0.725	0.780	1.147	0.283	0.666	0.129	0.715	0.068
1387807_at	NM_031763	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa	Pafah1b1	1.167	0.211	1.979	0.010	0.998	1.000	1.813	0.015
1392890_at	BG663460	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa	Pafah1b1	0.800	0.949	0.398	0.019	0.491	0.153	0.407	0.002
1383372_at	BF407234	platelet-activating factor receptor	Ptafr	1.001	0.460	0.998	0.615	1.170	0.071	1.077	0.133
1374616_at	BM384311	platelet-derived growth factor receptor-like	Pdgfrl	1.524	0.101	0.632	0.003	1.333	0.209	1.171	0.994
1373272_at	AI009219	Pleckstrin homology domain containing, family A member 5	Plekha5	0.456	0.186	0.755	0.094	0.851	0.101	0.895	0.287
1379536_at	BF547014	Pleckstrin homology domain containing, family A member 6 (predicted)	Plekha6_predicted	1.798	0.002	3.168	0.011	1.373	0.057	2.301	0.012
1370334_at	AF081582	pleckstrin homology domain containing, family B (evectins) member 1	Plekhb1	1.000	0.998	0.266	0.001	1.003	0.884	0.322	0.027
1375631_at	AI177176	pleckstrin homology domain containing, family B (evectins) member 2 (predicted)	Plekhb2_predicted	1.652	0.090	1.679	0.005	1.431	0.021	1.627	0.002

1398327_at	BM386598	pleckstrin homology domain containing, family C (with FERM domain) member 1	Plekhc1	2.344	0.001	1.265	0.007	1.954	0.004	1.037	0.119
1384182_at	BE128738	pleckstrin homology domain containing, family C (with FERM domain) member 1	Plekhc1	1.094	0.949	1.140	0.773	1.001	0.980	0.998	0.919
1372824_at	AI103367	pleckstrin homology domain containing, family F (with FYVE domain) member 2 (predicted)	Plekhf2_predicted	1.662	0.065	2.583	0.004	1.505	0.061	2.732	0.000
1395020_at	BI275435	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1 (predicted)	Plekhh1_predicted	2.039	0.021	2.320	0.008	1.488	0.029	1.413	0.182
1374215_at	AA848429	pleckstrin homology domain containing, family J member 1	Plekhj1	0.583	0.037	1.015	0.839	0.768	0.223	1.073	0.105
1380867_a_at	BM383086	pleckstrin homology domain containing, family M (with RUN domain) member 1	Plekhm1	3.014	0.006	1.048	0.784	2.445	0.013	1.641	0.010
1388609_at	AI406723	pleckstrin homology domain containing, family M (with RUN domain) member 2 (predicted)	Plekhm2_predicted	1.264	0.035	2.259	0.011	1.330	0.401	1.089	0.561
1377735_at	AI176309	Pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 3	Plekha3	1.066	0.217	0.753	0.427	1.321	0.121	0.907	0.234
1398641_at	AI058924	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 3	Plekha3	1.387	0.782	0.886	0.976	1.133	0.745	1.250	0.279
1367727_at	NM_053911	pleckstrin homology, Sec7 and coiled-coil domains 2	Pscd2	0.952	0.516	1.266	0.023	0.756	0.094	1.291	0.032
1368860_at	NM_017180	pleckstrin homology-like domain, family A, member 1	Phlda1	1.528	0.056	1.229	0.044	0.999	0.992	0.445	0.844
1378106_at	AI029402	pleckstrin homology-like domain, family A, member 2 (predicted)	Phlda2_predicted	3.784	0.011	2.244	0.206	1.019	1.000	0.996	0.896
1375224_at	AW520812	pleckstrin homology-like domain, family A, member 3	Phlda3	1.002	0.744	5.182	0.014	0.999	0.864	3.289	0.039
1386941_at	NM_022401	plectin 1	Plec1	0.988	0.391	0.988	0.699	0.997	0.725	1.038	0.800
1387122_at	NM_012760	pleiomorphic adenoma gene-like 1	Plagl1	0.221	0.047	0.291	0.004	0.258	0.000	0.270	0.002
1369968_at	NM_017066	pleiotrophin	Ptn	1.196	0.741	0.827	0.037	1.476	0.775	0.902	0.136
1387823_at	NM_021757	pleiotropic regulator 1, PRL1 homolog (Arabidopsis)	Plrg1	0.678	0.865	1.150	0.019	0.578	0.034	1.045	0.667
1376139_at	BI295513	Plexin A3 (mapped)	Plxna3_mapped	0.891	0.177	1.037	0.749	0.930	0.362	0.819	0.040
1374444_at	BI288540	Plexin B1 (predicted)	Plxnb1_predicted	0.757	0.299	0.994	0.294	1.288	0.872	0.862	0.452
1371411_at	BG380275	plexin B2	Plxnb2	1.322	0.322	1.137	0.244	1.569	0.214	0.995	0.238
1387929_at	AB020504	PMF32 protein	Pmf31	1.038	0.933	0.584	0.163	0.908	0.656	0.656	0.084
1386913_at	NM_019358	podoplanin	Pdpn	0.941	0.471	1.981	0.005	0.673	0.413	0.851	0.515
1384349_at	AI577326	pogo transposable element with ZNF domain (predicted)	Pogz_predicted	1.040	0.211	1.028	0.964	1.027	0.958	0.934	0.948
1393594_at	AI030196	Pogo transposable element with ZNF domain (predicted)	Pogz_predicted	1.805	0.222	0.706	0.041	1.340	0.041	0.858	0.088
1370177_at	AI548856	poliovirus receptor	PVR	14.720	0.001	12.733	0.010	19.862	0.000	13.030	0.007
1398745_at	BM389610	Poliovirus receptor-related 1	Pvrl1	0.996	0.944	0.890	0.620	0.991	0.980	0.893	0.053
1380849_at	BI274299	Poliovirus receptor-related 1	Pvrl1	0.992	0.968	1.002	0.755	1.028	0.878	1.027	0.987
1389681_at	BI296388	Poliovirus receptor-related 2 (herpesvirus entry mediator B)	Pvrl2	2.599	0.048	1.459	0.128	1.818	0.025	1.575	0.087
1375216_at	AA850909	poliovirus receptor-related 2 (herpesvirus entry mediator B)	Pvrl2	2.868	0.056	0.648	0.038	4.696	0.005	0.664	0.546
1389899_at	BE102426	Poliovirus receptor-related 2 (herpesvirus entry mediator B)	Pvrl2	0.540	0.678	0.843	0.758	1.440	0.090	1.185	0.590
1378027_at	AW525315	poliovirus receptor-related 3 (predicted)	Pvrl3_predicted	0.709	0.358	1.581	0.063	0.802	0.142	1.812	0.013
1397363_at	AI103913	poliovirus receptor-related 3 (predicted)	Pvrl3_predicted	0.652	0.512	1.226	0.163	0.644	0.182	1.726	0.200
1368106_at	NM_031821	polo-like kinase 2 (Drosophila)	Plk2	1.318	0.016	1.461	0.019	1.705	0.004	1.674	0.003
1373080_at	BI284422	poly (A) polymerase alpha (predicted)	Papola_predicted	0.669	0.334	0.737	0.040	0.670	0.331	0.835	0.129
1393546_at	BF394642	Poly (A) polymerase alpha (predicted)	Papola_predicted	0.875	0.453	0.948	0.704	0.600	0.031	1.291	0.661
1384573_at	BE108853	poly (A) polymerase alpha (predicted)	Papola_predicted	0.741	0.502	0.971	0.472	0.747	0.359	1.031	0.074
1370354_at	AB019366	poly (ADP-ribose) glycohydrolase	Parg	0.817	0.063	0.800	0.010	0.770	0.007	0.806	0.365
1369969_at	NM_013063	poly (ADP-ribose) polymerase family, member 1	Parp1	1.512	0.556	0.726	0.322	1.347	0.062	0.944	0.924
1380071_at	BI285978	Poly (ADP-ribose) polymerase family, member 12 (predicted)	Parp12_predicted	7.040	0.007	2.887	0.000	8.872	0.001	4.962	0.001
1374693_at	BM388613	poly (ADP-ribose) polymerase family, member 16	Parp16	1.698	0.152	1.242	0.225	1.002	0.992	1.422	0.323
1383251_at	AW524533	poly (ADP-ribose) polymerase family, member 2 (predicted)	Parp2_predicted	0.988	0.781	1.224	0.005	0.773	0.697	1.401	0.004
1376144_at	AA819679	poly (ADP-ribose) polymerase family, member 9 (predicted)	Parp9_predicted	27.680	0.000	15.173	0.000	48.249	0.000	22.399	0.000
1371777_at	BM383696	poly A binding protein, cytoplasmic 4	Pabpc4	1.153	0.049	1.739	0.001	1.130	0.137	1.876	0.002
1369952_at	NM_134353	poly(A) binding protein, cytoplasmic 1	Pabpc1	1.055	0.175	1.261	0.047	1.135	0.538	1.225	0.964
1382922_at	BG375109	Poly(A) binding protein, nuclear 1	Pabpn1	0.488	0.005	0.451	0.004	0.537	0.006	0.493	0.148
1392480_at	BE100901	poly(A) binding protein, nuclear 1	Pabpn1	0.519	0.049	0.795	0.170	0.634	0.231	1.021	0.935
1379481_at	AW525563	poly(A) binding protein, nuclear 1	Pabpn1	0.410	0.051	0.509	0.059	0.525	0.164	0.675	0.013
1371958_at	BM392148	poly(A) binding protein, nuclear 1	Pabpn1	1.030	0.924	0.291	0.000	1.733	0.382	0.238	0.002
1380101_at	BE109349	poly(A) polymerase gamma (predicted)	Papolg_predicted	1.072	0.885	0.691	0.031	2.003	0.013	1.006	0.932
1391685_at	AW521201	poly(A)-specific ribonuclease (PARN)-like domain containing 1	Pnldc1	0.996	0.294	0.999	0.509	1.021	0.871	0.998	0.487
1395792_at	AI549034	Poly(rC) binding protein 2	Pcbp2	1.039	0.235	1.589	0.202	0.970	0.788	1.066	0.493
1398941_at	AI170413	poly(rC) binding protein 2	Pcbp2	1.058	0.742	1.077	0.333	1.013	0.398	0.869	0.139
1383274_at	AA956005	poly(rC) binding protein 3	Pcbp3	1.207	0.372	1.136	0.665	1.220	0.250	1.553	0.259
1383273_a_at	AA956005	poly(rC) binding protein 3	Pcbp3	1.112	0.788	1.205	0.383	0.839	0.394	1.741	0.182
1371915_at	AW523679	poly(rC) binding protein 4 (predicted)	Pcbp4_predicted	1.187	0.796	1.010	0.902	1.313	0.968	1.017	0.866
1372212_at	BI285445	polyamine oxidase (predicted)	Paox_predicted	0.541	0.349	0.946	0.813	0.572	0.188	1.183	0.645
1372335_at	BE114641	Polycomb group ring finger 1	Pcgf1	0.913	0.276	0.958	0.888	0.998	0.347	0.957	0.998
1390352_at	AA926371	polycomb group ring finger 1	Pcgf1	1.023	0.535	0.982	0.790	1.088	0.992	0.899	0.168
1392892_at	AA955814	polycomb group ring finger 2 (predicted)	Pcgf2_predicted	0.705	0.987	1.736	0.138	0.999	0.993	0.950	0.558
1389760_at	AA858786	polycomb group ring finger 6	Pcgf6	0.708	0.091	1.212	0.275	0.751	0.126	1.645	0.074
1371029_at	AW916437	polycystic kidney disease 1 homolog	Pkd1	1.042	0.793	1.035	0.285	1.032	0.971	0.840	0.308

1372797_at	BM383862	polyglutamine binding protein 1	Pqbp1	0.442	0.078	0.423	0.056	0.588	0.025	0.476	0.023
1371800_at	AI230538	polyhomeotic-like 2 (Drosophila)	Phc2	2.422	0.062	0.991	0.188	4.086	0.003	1.718	0.147
1393674_at	BF396736	Polyhomeotic-like 2 (Drosophila)	Phc2	1.240	0.184	0.672	0.109	1.798	0.032	0.793	0.196
1371987_at	BI274697	polymerase (DNA directed) sigma (predicted)	Pols_predicted	1.010	0.752	0.756	0.281	1.935	0.109	0.745	0.231
1387142_at	NM_017141	polymerase (DNA directed), beta	Polb	1.025	0.283	0.925	0.961	0.875	0.321	1.068	0.355
1373935_at	AI102751	polymerase (DNA directed), delta 2, regulatory subunit	Pold2	0.711	0.021	2.091	0.096	0.898	0.129	1.774	0.065
1370045_at	NM_053528	polymerase (DNA directed), gamma	Polg	0.796	0.006	1.472	0.019	0.726	0.102	1.163	0.134
1375504_at	BM390747	Polymerase (DNA directed), gamma 2, accessory subunit (predicted)	Polg2_predicted	0.600	0.127	0.947	0.972	0.970	0.893	1.188	0.675
1384265_at	BI278347	polymerase (DNA-directed), delta 3, accessory subunit	Pold3	1.734	0.054	5.134	0.008	1.531	0.005	3.952	0.013
1388883_at	BF281976	polymerase (DNA-directed), delta 4	Pold4	0.500	0.130	0.184	0.003	0.327	0.003	0.235	0.013
1371920_at	AA851255	polymerase (DNA-directed), delta interacting protein 2 (predicted)	Poldip2_predicted	0.449	0.057	0.489	0.008	0.543	0.002	0.603	0.010
1383037_at	AI232159	polymerase (DNA-directed), delta interacting protein 2 (predicted)	Poldip2_predicted	1.000	1.000	0.779	0.314	0.887	0.420	0.858	0.131
1388367_at	AI178241	polymerase (DNA-directed), epsilon 4 (p12 subunit) (predicted)	Pole4_predicted	0.855	0.046	1.428	0.064	0.808	0.239	1.473	0.041
1376001_at	BG380440	polymerase (RNA) I associated factor 1 (predicted)	Praf1_predicted	0.629	0.012	2.062	0.014	0.794	0.328	1.635	0.040
1388808_at	AW531224	polymerase (RNA) II (DNA directed) polypeptide A (mapped)	Polr2a_mapped	0.554	0.082	0.744	0.139	0.823	0.458	1.077	0.219
1382976_at	BM387928	Polymerase (RNA) II (DNA directed) polypeptide A (mapped)	Polr2a_mapped	0.639	0.826	1.161	0.443	0.912	0.670	1.534	0.134
1372083_at	BI289658	polymerase (RNA) II (DNA directed) polypeptide B (predicted)	Polr2b_predicted	0.634	0.489	0.729	0.012	0.950	0.234	0.813	0.109
1398899_at	AI170414	polymerase (RNA) II (DNA directed) polypeptide C	Polr2c	1.035	0.220	1.182	0.113	0.814	0.269	1.364	0.037
1379832_at	BF544977	polymerase (RNA) II (DNA directed) polypeptide D (predicted)	Polr2d_predicted	0.624	0.157	0.878	0.049	0.751	0.137	0.847	0.078
1367471_at	BI279090	polymerase (RNA) II (DNA directed) polypeptide E (predicted)	Polr2e_predicted	0.605	0.625	1.493	0.114	0.501	0.009	1.296	0.180
1391699_at	AI556892	polymerase (RNA) II (DNA directed) polypeptide F	Polr2f	0.665	0.141	1.009	0.975	0.773	0.106	1.027	0.916
1369996_at	NM_031335	polymerase (RNA) II (DNA directed) polypeptide F	Polr2f	0.823	0.850	1.691	0.662	0.422	0.079	1.118	0.555
1367769_at	NM_053948	polymerase (RNA) II (DNA directed) polypeptide G	Polr2g	0.561	0.029	0.792	0.085	0.338	0.003	0.746	0.222
1373668_at	BG373075	polymerase (RNA) II (DNA directed) polypeptide I (predicted)	Polr2i_predicted	0.952	0.906	1.568	0.090	0.708	0.327	1.334	0.144
1398914_at	AW530341	polymerase (RNA) II (DNA directed) polypeptide J (predicted)	Polr2j_predicted	0.430	0.178	0.868	0.633	0.435	0.013	0.785	0.508
1380256_at	BE103946	polymerase (RNA) III (DNA directed) polypeptide C	Polr3c	1.827	0.044	1.234	0.114	2.203	0.012	2.045	0.005
1371822_at	BI275831	polymerase (RNA) III (DNA directed) polypeptide D	Polr3d	0.545	0.676	1.198	0.076	0.702	0.081	1.139	0.428
1374415_at	BF416982	polymerase (RNA) III (DNA directed) polypeptide E (predicted)	Polr3e_predicted	0.950	0.989	1.459	0.048	0.511	0.027	0.796	0.412
1399035_at	BE097233	polymerase (RNA) III (DNA directed) polypeptide H (predicted)	Polr3h_predicted	0.701	0.024	0.610	0.021	0.392	0.007	0.579	0.007
1374295_at	AI233096	polymerase (RNA) mitochondrial (DNA directed) (predicted)	Polrmt_predicted	0.972	0.995	1.880	0.185	0.999	0.928	0.992	0.691
1371099_at	U07886	Polymeric immunoglobulin receptor AATTAA-containing 3'UTR Group 1 mRNA sequence	---	2.542	0.841	5.273	0.034	0.999	0.514	0.892	0.307
1393367_at	AW520745	polynucleotide kinase 3'-phosphatase	Pnkp	0.595	0.217	1.090	0.067	0.471	0.053	1.386	0.115
1367931_a_at	X60790	polypyrimidine tract binding protein 1	Ptbp1	0.665	0.115	0.832	0.762	0.604	0.000	0.731	0.038
1378038_at	BF393884	Polypyrimidine tract binding protein 2	Ptbp2	1.577	0.000	2.806	0.012	1.284	0.002	2.326	0.034
1375844_at	AI406370	polypyrimidine tract binding protein 2	Ptbp2	1.226	0.005	1.318	0.019	1.398	0.111	1.163	0.018
1373913_at	BF282271	polyribonucleotide nucleotidyltransferase 1	Pnpt1	1.178	0.208	0.997	0.983	1.820	0.019	1.435	0.101
1380587_at	BF404982	Polyribonucleotide nucleotidyltransferase 1	Pnpt1	1.002	0.979	0.898	0.184	0.985	0.883	0.876	0.096
1370274_at	D16554	polyubiquitin	Ubb	0.876	0.959	1.080	0.041	0.793	0.248	1.014	0.655
1386852_x_at	D16554	polyubiquitin	Ubb	0.893	0.983	1.047	0.375	0.910	0.197	0.962	0.515
1376646_at	BF285164	popeye domain containing 2	Popdc2	1.224	0.826	1.696	0.049	1.038	0.906	1.027	0.568
1388847_at	AI177083	Positive cofactor 2, multiprotein complex, glutamine/Q-rich-associated protein (predicted)	Pcqap_predicted	1.364	0.130	2.549	0.002	1.343	0.264	2.046	0.012
1389183_at	BI281709	postmeiotic segregation increased 2 (S. cerevisiae) (predicted)	Pms2_predicted	0.653	0.109	1.438	0.183	1.050	0.181	1.885	0.065
1387222_at	NM_019907	postsynaptic protein Cript	Cript	0.705	0.690	0.849	0.672	0.711	0.106	0.877	0.467
1379276_at	AW919982	Potassium channel modulatory factor 1	Kcmf1	0.986	0.853	0.453	0.025	0.744	0.214	0.503	0.023
1394690_at	AA900721	Potassium channel regulator (predicted)	Kcnrg_predicted	1.009	0.681	0.952	0.542	1.011	0.406	0.934	0.642
1370317_at	U78090	potassium channel regulator 1	LOC245960	0.988	0.970	0.969	0.532	0.897	0.164	0.732	0.059
1377768_at	BE107485	potassium channel tetramerisation domain containing 1	Kctd1	0.745	0.188	0.566	0.003	0.694	0.045	0.746	0.114
1392785_at	AA800908	potassium channel tetramerisation domain containing 12 (predicted)	Kctd12_predicted	2.507	0.053	3.061	0.007	1.030	0.906	1.381	0.342
1373045_at	AI235230	potassium channel tetramerisation domain containing 13	Kctd13	0.809	0.310	2.457	0.000	0.587	0.313	1.645	0.027
1376211_a_at	AI235964	potassium channel tetramerisation domain containing 6 (predicted)	Kctd6_predicted	0.955	0.904	1.373	0.256	1.223	0.309	1.112	0.239
1374582_at	AI175423	potassium channel tetramerisation domain containing 9 (predicted)	Kctd9_predicted	1.466	0.432	1.254	0.105	1.015	0.929	1.206	0.105
1371857_at	AI010108	potassium channel tetramerization domain containing 10	Kctd10	1.012	0.237	0.724	0.157	1.485	0.914	0.858	0.716
1370342_at	AF385402	potassium channel, subfamily K, member 2	Kcnk2	0.792	0.301	0.582	0.140	0.779	0.826	0.331	0.048
1387441_at	NM_033376	potassium channel, subfamily K, member 3	Kcnk3	0.923	0.749	0.880	0.284	0.678	0.574	0.618	0.010
1387264_at	NM_053806	potassium channel, subfamily K, member 6 /// hypothetical gene supported by NM_053806	Kcnk6 /// LOC497732	0.477	0.853	2.346	0.021	0.346	0.181	2.177	0.066
1391381_at	BF410362	Potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	Kcnn2	0.901	0.650	0.880	0.328	0.897	0.724	0.705	0.923
1370111_at	NM_019314	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	Kcnn2	1.008	0.966	0.424	0.004	1.015	0.247	0.556	0.008
1368626_at	NM_019315	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3	Kcnn3	5.193	0.066	3.436	0.002	0.998	0.697	2.666	0.006
1391007_s_at	BE113377	potassium inwardly rectifying channel, subfamily J, member 11	Kcnj11	0.867	0.035	0.600	0.002	0.407	0.011	0.540	0.021
1387698_at	AB043638	potassium inwardly rectifying channel, subfamily J, member 11	Kcnj11	0.632	0.141	0.533	0.011	0.315	0.013	0.400	0.006
1369261_at	NM_053608	potassium inwardly-rectifying channel, subfamily J, member 13	Kcnj13	0.972	0.948	0.930	0.450	1.182	0.170	1.001	0.994

1370970_at	AI717104	potassium inwardly-rectifying channel, subfamily J, member 14	Kcnj14	1.187	0.304	1.666	0.208	1.180	0.987	2.163	0.518
1369741_at	U09243	potassium inwardly-rectifying channel, subfamily J, member 3	Kcnj3	1.204	0.494	0.892	0.768	1.886	0.125	1.110	0.562
1368560_at	NM_017297	potassium inwardly-rectifying channel, subfamily J, member 5	Kcnj5	1.925	0.025	0.996	0.894	1.003	0.916	0.924	0.270
1370704_at	AB073756	potassium inwardly-rectifying channel, subfamily J, member 6	Kcnj6	1.007	0.909	0.852	0.108	1.164	0.253	0.771	0.111
1369035_a_at	AB073753	potassium inwardly-rectifying channel, subfamily J, member 6	Kcnj6	1.011	0.944	1.002	0.964	1.052	0.942	1.544	0.022
1369334_at	NM_031828	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	Kcnma1	0.826	0.041	0.472	0.002	0.885	0.354	0.501	0.015
1372929_at	AI010839	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	Kcnma1	0.699	0.258	0.751	0.005	0.607	0.013	0.742	0.034
1379863_at	AW528891	potassium voltage gated channel, Shal-related family, member 2	Kcnd2	1.508	0.517	1.364	0.172	1.134	0.203	1.112	0.881
1369144_a_at	NM_031739	potassium voltage gated channel, Shal-related family, member 3	Kcnd3	1.918	0.252	0.964	0.896	1.085	0.874	0.896	0.724
1368524_at	NM_012856	potassium voltage gated channel, Shaw-related subfamily, member 1	Kcnc1	1.375	0.130	1.084	0.448	1.698	0.030	1.048	0.443
1378738_at	BE097574	potassium voltage-gated channel, shaker-related subfamily, beta member 1	Kcnab1	2.045	0.059	0.556	0.184	1.543	0.128	0.473	0.011
1391963_at	BF396103	Potassium voltage-gated channel, shaker-related subfamily, beta member 1	Kcnab1	2.037	0.998	1.282	0.461	1.085	0.827	1.429	0.811
1369043_at	NM_012971	potassium voltage-gated channel, shaker-related subfamily, member 4	Kcna4	1.837	0.018	0.791	0.128	1.592	0.224	1.362	0.174
1368343_at	NM_053949	potassium voltage-gated channel, subfamily H (eag-related), member 2	Kcnh2	1.304	0.369	1.387	0.720	0.802	0.117	1.180	0.220
1369017_at	NM_053937	potassium voltage-gated channel, subfamily H (eag-related), member 6	Kcnh6	0.653	0.051	0.255	0.003	0.204	0.038	0.243	0.013
1397599_at	BF394205	Potassium voltage-gated channel, subfamily Q, member 3	Kcnq3	3.074	0.072	2.638	0.082	1.192	0.138	2.817	0.019
1379836_at	BF400850	Potassium voltage-gated channel, subfamily Q, member 3	Kcnq3	2.330	0.080	1.586	0.179	2.399	0.133	2.440	0.006
1382902_at	AA943147	potential ubiquitin ligase	Herc6	19.632	0.002	6.640	0.022	35.983	0.004	22.115	0.003
1370995_at	AW528459	POU domain, class 2, transcription factor 1	Pou2f1	3.390	0.017	1.289	0.073	1.912	0.019	0.973	0.212
1370432_at	M72711	POU domain, class 3, transcription factor 1	Pou3f1	2.572	0.749	0.938	0.786	3.224	0.068	2.530	0.013
1371043_a_at	BE107327	POU domain, class 3, transcription factor 3	Pou3f3	1.479	0.137	0.999	0.904	0.956	0.970	1.082	0.850
1380211_at	BE109046	POU domain, class 4, transcription factor 1	Pou4f1	1.022	0.940	0.907	0.976	0.995	0.808	0.950	0.912
1373573_at	H31907	PP3111 protein	Pp3111	0.691	0.025	0.708	0.074	0.665	0.050	0.760	0.139
1373465_at	AI228284	PQ loop repeat containing 1	Pqlc1	0.814	0.547	0.824	0.102	1.255	0.094	0.592	0.057
1377179_at	BI283849	PQ loop repeat containing 2 (predicted)	Pqlc2_predicted	0.901	0.460	0.999	0.486	0.903	0.463	1.000	0.623
1390839_at	AW915795	PQ loop repeat containing 3	Pqlc3	0.968	0.719	1.038	0.390	0.380	0.095	1.247	0.256
1390165_at	BI288756	PR domain containing 15 (predicted)	Prdm15_predicted	1.306	0.133	0.739	0.058	1.066	0.946	0.869	0.064
1373712_at	BI282710	PR domain containing 2, with ZNF domain (mapped)	Prdm2_mapped	0.860	0.356	1.004	0.469	1.777	0.935	1.023	0.961
1389104_s_at	BF388420	PR domain containing 2, with ZNF domain (mapped)	Prdm2_mapped	0.938	0.518	1.202	0.362	1.188	0.229	1.189	0.816
1370639_at	U17837	PR domain containing 2, with ZNF domain (mapped)	Prdm2_mapped	0.984	0.532	1.461	0.036	1.376	0.158	1.201	0.934
1390202_at	BI289584	PR domain containing 2, with ZNF domain (mapped)	Prdm2_mapped	0.935	0.544	0.785	0.979	0.927	0.583	1.004	0.999
1397553_s_at	AI101637	PR domain containing 2, with ZNF domain (mapped)	Prdm2_mapped	3.066	0.971	1.679	0.920	1.341	0.404	1.111	0.230
1369236_at	NM_133312	PR domain containing 4	Prdm4	1.014	0.231	1.008	0.853	0.930	0.072	0.999	0.916
1372931_at	AI178741	PRA1 domain family 2 (predicted)	Praf2_predicted	0.413	0.252	1.216	0.171	0.378	0.053	1.226	0.645
1387903_at	D32249	praja 2, RING-H2 motif containing	Pja2	0.754	0.697	0.623	0.001	0.793	0.234	0.578	0.004
1375421_a_at	AI600019	praja 2, RING-H2 motif containing	Pja2	0.958	0.934	1.309	0.002	0.641	0.176	1.267	0.049
1374503_at	AI709810	pre B-cell leukemia transcription factor 3 (predicted)	Pbx3_predicted	0.834	0.108	0.894	0.735	0.675	0.044	0.703	0.036
1389014_at	BI297612	pre-B-cell colony enhancing factor 1	Pbef1	3.439	0.006	3.801	0.000	3.490	0.001	3.798	0.002
1396262_at	BM384211	pre-B-cell colony enhancing factor 1	Pbef1	3.950	0.022	3.051	0.126	2.926	0.014	3.317	0.028
1378458_at	BI281745	Pre-B-cell leukemia transcription factor 1 (predicted)	Pbx1_predicted	0.725	0.183	0.993	0.700	0.589	0.164	1.053	0.795
1380747_at	BE098757	Pre-B-cell leukemia transcription factor 1 (predicted)	Pbx1_predicted	0.840	0.328	0.799	0.027	1.154	0.974	0.648	0.036
1398487_at	BF419639	pre-B-cell leukemia transcription factor 1 (predicted)	Pbx1_predicted	0.831	0.593	0.910	0.188	0.928	0.743	0.998	0.195
1389432_at	BE101096	pre-B-cell leukemia transcription factor 2	Pbx2	0.908	0.928	0.734	0.256	0.977	0.714	0.606	0.010
1381262_at	BG374101	Pre-B-cell leukemia transcription factor interacting protein 1	Pbxip1	1.363	0.970	0.930	0.270	1.104	0.994	0.859	0.731
1398926_at	AI410456	prefoldin 1 (predicted)	Pfdn1_predicted	0.553	0.007	0.815	0.021	0.558	0.082	0.733	0.070
1398884_at	BM384924	prefoldin 5 (predicted)	Pfdn5_predicted	0.960	0.925	1.294	0.106	0.781	0.137	1.350	0.024
1370413_at	L26398	pregnancy specific beta-1-glycoprotein 4	Psg4	1.001	0.987	0.996	0.937	1.003	0.969	0.992	0.959
1370547_at	M84000	pregnancy-zone protein	Pzp	1.011	0.999	1.000	0.987	0.998	0.988	1.002	0.997
1387089_at	NM_133528	preimplantation protein 3	Prei3	0.903	0.637	0.544	0.021	0.641	0.012	0.715	0.021
1384792_at	BE107114	pre-mRNA processing factor 40 homolog A (yeast) (predicted)	Prpf40a_predicted	1.543	0.302	1.187	0.414	0.740	0.714	0.890	0.665
1367466_at	AI406518	pre-mRNA processing factor 8	Prpf8	0.663	0.748	0.775	0.631	0.620	0.080	0.965	0.879
1387836_at	NM_031692	prenylated SNARE protein	Ykt6	1.003	0.594	1.620	0.054	0.404	0.172	1.228	0.424
1372505_at	BM391393	Prenylated SNARE protein	Ykt6	0.988	0.690	0.729	0.008	0.825	0.074	0.782	0.019
1370407_at	AF332142	prenylcysteine oxidase 1	Pcyox1	0.406	0.002	0.613	0.002	0.428	0.004	0.568	0.025
1388165_at	X53232	preoptic regulatory factor-2	PORF-2	1.191	0.626	1.594	0.064	0.969	0.934	1.130	0.196
1371092_at	X15679	preprotrypsinogen IV	LOC286960	1.070	0.457	0.116	0.000	0.983	0.793	0.095	0.033
1376075_at	BM385544	presenilin 1	Psen1	1.842	0.073	1.726	0.025	1.624	0.047	2.651	0.008
1368792_at	NM_019163	presenilin 1	Psen1	0.950	0.726	1.334	0.174	0.816	0.318	0.905	0.153
1370064_at	AB004454	presenilin 2	Psen2	1.002	0.949	1.113	0.082	1.115	0.993	1.116	0.102
1372645_at	AI233095	presenilin associated, rhomboid-like	Psarl	0.676	0.186	0.874	0.336	0.728	0.025	1.023	0.952
1371338_at	AI232272	presenilin enhancer 2 homolog (C. elegans)	Psenen	0.751	0.770	0.886	0.089	0.696	0.009	0.869	0.076

1379369_at	AI171526	Prickle-like 1 (Drosophila)	Prickle1	0.658	0.489	2.647	0.032	0.531	0.024	1.617	0.100
1370156_at	BI278802	prion protein	Prnp	0.856	0.340	0.516	0.000	0.785	0.081	0.626	0.001
1368702_at	U05989	PRKC, apoptosis, WT1, regulator	Pawr	3.070	0.014	3.385	0.000	2.402	0.058	2.841	0.001
1371845_at	BF287209	processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae)	Pop4	0.381	0.367	0.901	0.585	0.342	0.102	0.693	0.266
1389336_at	BM390893	processing of precursor 5, ribonuclease P/MRP family (S. cerevisiae) (predicted)	Pop5_predicted	0.395	0.001	0.733	0.082	0.610	0.090	0.663	0.408
1373597_at	AI102689	processing of precursor 7, ribonuclease P family, (S. cerevisiae) (predicted)	Pop7_predicted	0.866	0.639	1.000	0.976	0.841	0.614	1.048	0.609
1386912_at	NM_019237	procollagen C-endopeptidase enhancer protein	Pcolce	0.796	0.121	0.507	0.001	1.008	0.546	0.612	0.005
1387854_at	BI282748	procollagen, type I, alpha 2	Col1a2	1.482	0.630	0.728	0.025	1.139	0.246	0.643	0.170
1388973_at	BM388861	procollagen, type IX, alpha 1	Col9a1	0.373	0.001	0.062	0.000	0.555	0.048	0.142	0.004
1370895_at	AI179399	procollagen, type V, alpha 2	Col5a2	1.266	0.119	0.697	0.203	1.105	0.147	0.853	0.819
1389966_at	AI176126	procollagen, type VI, alpha 3 (predicted)	Col6a3_predicted	1.001	0.982	1.002	1.000	0.983	0.840	0.948	0.818
1392915_at	BM389291	procollagen, type XI, alpha 1	Col11a1	0.999	0.995	0.757	0.261	2.125	0.305	1.000	0.998
1389891_at	BM391350	procollagen, type XI, alpha 2 (mapped)	Col11a2_mapped	1.295	0.188	0.792	0.528	2.545	0.025	1.029	0.925
1390846_at	BG380309	procollagen, type XVI, alpha 1	Col16a1	0.507	0.104	0.188	0.003	0.522	0.304	0.294	0.001
1388459_at	AI101782	procollagen, type XVIII, alpha 1	Col18a1	0.394	0.018	0.697	0.523	0.877	0.784	0.483	0.062
1398394_at	BE108058	Procollagen, type XVIII, alpha 1	Col18a1	0.824	0.750	1.310	0.641	0.592	0.999	2.388	0.790
1381431_at	AW252296	Procollagen, type XVIII, alpha 1	Col18a1	0.999	0.992	1.450	0.080	1.001	0.991	1.022	0.989
1374870_at	BF286402	Procollagen, type XXVII, alpha 1	Col27a1	1.155	0.598	0.562	0.005	1.589	0.274	0.680	0.112
1367807_at	NM_053827	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	Plod1	0.726	0.159	1.963	0.000	0.857	0.682	1.233	0.190
1372877_at	BI304070	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	Plod3	1.005	0.231	0.629	0.002	1.182	0.045	0.932	0.188
1370954_at	BI274401	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	P4ha1	0.382	0.383	2.175	0.069	0.547	0.025	1.707	0.071
1372610_at	BI274349	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide (predicted)	P4ha2_predicted	0.776	0.232	1.135	0.135	1.002	0.274	1.025	0.360
1367605_at	NM_022511	profilin 1	Pfn1	1.065	0.632	1.508	0.229	1.118	0.778	1.083	0.321
1387015_at	NM_030873	profilin 2	Pfn2	0.437	0.143	1.184	0.268	0.384	0.007	0.992	0.672
1398961_at	AI232296	Profilin 2	Pfn2	0.737	0.516	1.306	0.161	0.597	0.165	1.142	0.055
1367970_at	AF228737	profilin 2	Pfn2	0.991	0.803	1.078	0.289	0.756	0.714	0.897	0.028
1389701_at	AI599419	Progesterone receptor	Pgr	1.096	0.932	0.342	0.035	0.836	0.501	0.714	0.786
1387563_at	NM_022847	progesterone receptor	Pgr	1.002	0.994	0.991	0.916	0.981	0.994	0.986	0.090
1367619_at	NM_021766	progesterone receptor membrane component 1	Pgrmc1	0.713	0.046	0.718	0.000	0.761	0.013	0.744	0.047
1378515_at	BE116005	Progesterone receptor membrane component 1	Pgrmc1	0.434	0.096	1.064	0.847	0.402	0.042	0.667	0.227
1379427_at	AI137488	progesterone receptor membrane component 2	Pgrmc2	0.433	0.219	1.133	0.519	0.406	0.029	0.579	0.141
1388531_at	BF283382	progesterone receptor membrane component 2	Pgrmc2	0.796	0.249	1.150	0.076	0.527	0.014	0.951	0.445
1389169_at	AA944158	progesterone receptor membrane component 2	Pgrmc2	0.688	0.450	0.599	0.017	0.482	0.058	0.569	0.012
1392927_at	BG381724	progestin and adipoQ receptor family member IV	Paqr4	2.561	0.033	1.181	0.049	1.219	0.515	1.004	0.959
1367719_at	NM_053989	progestin induced protein	Dd5	1.138	0.258	1.426	0.003	0.811	0.022	1.399	0.024
1382603_at	AW521319	Programmed cell death 1 ligand 2 (predicted)	Pdcd1lg2_predicted	17.586	0.000	10.259	0.000	21.485	0.000	13.546	0.003
1371002_at	AI704628	programmed cell death 2	Pdcd2	1.325	0.218	2.101	0.010	1.128	0.327	1.903	0.033
1387521_at	NM_022265	programmed cell death 4	Pdcd4	0.581	0.091	0.185	0.004	0.626	0.090	0.179	0.009
1389454_at	BF408447	programmed cell death 5 (predicted)	Pdcd5_predicted	0.753	0.121	1.440	0.000	0.874	0.508	1.277	0.125
1388767_at	BI296393	programmed cell death 6 (predicted)	Pdcd6_predicted	1.020	0.964	1.483	0.039	1.067	0.570	1.441	0.075
1388120_at	BE328942	programmed cell death 6 interacting protein	Pdcd6ip	1.139	0.510	2.246	0.000	1.191	0.644	1.656	0.010
1370321_at	AF262320	programmed cell death 8	Pdcd8	1.171	0.273	1.117	0.132	1.145	0.164	1.186	0.028
1379317_a_at	BI280308	programmed cell death protein 11 (predicted)	Pdcd11_predicted	0.753	0.298	1.614	0.049	0.806	0.422	1.322	0.400
1389322_at	AI013847	programmed cell death protein 7 (predicted)	Pdcd7_predicted	0.696	0.017	0.756	0.155	0.883	0.385	0.734	0.146
1385709_x_at	AW529028	Progressive ankylosis homolog (mouse)	Ank	0.236	0.008	0.173	0.001	0.206	0.001	0.236	0.009
1394202_x_at	AI176117	Progressive ankylosis homolog (mouse)	Ank	0.570	0.012	0.821	0.055	0.524	0.008	0.824	0.048
1393439_a_at	AI045767	progressive ankylosis homolog (mouse)	Ank	0.278	0.019	0.208	0.000	0.286	0.000	0.275	0.018
1369249_at	NM_053714	progressive ankylosis homolog (mouse)	Ank	0.180	0.043	0.226	0.024	0.129	0.018	0.260	0.010
1386344_at	BG662519	Progressive ankylosis homolog (mouse)	Ank	0.298	0.163	0.365	0.003	0.215	0.004	0.403	0.008
1375815_at	BF391129	Progressive ankylosis homolog (mouse)	Ank	0.867	0.169	0.271	0.000	0.821	0.098	0.321	0.006
1367926_at	NM_031851	prohibitin	Phb	0.633	0.088	0.358	0.022	0.656	0.001	0.654	0.020
1367927_at	BI282863	prohibitin	Phb	0.556	0.292	0.776	0.115	0.470	0.058	0.775	0.032
1367463_at	AI235510	prohibitin 2	Phb2	0.566	0.053	1.251	0.003	0.477	0.003	1.083	0.328
1370789_a_at	L48060	prolactin receptor	Prlr	0.146	0.023	0.214	0.000	0.380	0.038	0.214	0.006
1376944_at	AI407163	Prolactin receptor	Prlr	0.407	0.041	0.168	0.002	0.491	0.071	0.346	0.009
1392612_at	AW142962	Prolactin receptor	Prlr	0.366	0.067	0.134	0.008	0.496	0.138	0.138	0.027
1370384_a_at	M57668	prolactin receptor	Prlr	0.361	0.321	0.174	0.005	0.378	0.022	0.230	0.031
1370300_at	AF061817	prolactin regulatory element binding	Preb	0.398	0.005	1.057	0.989	0.369	0.058	0.659	0.180
1368107_at	NM_031316	prolactin-like protein 1	Prlpi	1.048	0.319	0.983	0.969	0.903	0.286	1.009	0.937
1398302_at	AI013501	prolactin-like protein F	Prlpf	0.999	0.567	1.001	0.961	0.987	0.879	1.069	0.794
1367671_at	NM_022381	proliferating cell nuclear antigen	Pcna	0.541	0.022	1.338	0.002	0.543	0.000	1.151	0.340

1383421_at	BM386110	Proliferating cell nuclear antigen	Pcna	1.077	0.560	6.311	0.002	0.660	0.018	4.730	0.000
1371593_at	BI296121	Proliferating cell nuclear antigen	Pcna	0.686	0.614	0.634	0.013	0.506	0.006	0.565	0.017
1388353_at	BI296168	proliferation-associated 2G4	Pa2g4	0.560	0.329	2.312	0.003	0.404	0.001	1.552	0.096
1370381_at	U61729	proline rich 2	Pnrc1	1.913	0.000	1.801	0.000	2.412	0.001	1.911	0.001
1389549_at	AI172262	proline synthetase co-transcribed (predicted)	Prosc_predicted	0.690	0.005	0.630	0.032	0.632	0.044	0.885	0.119
1383722_at	H33436	proline synthetase co-transcribed (predicted)	Prosc_predicted	0.984	0.046	0.275	0.021	0.959	0.648	0.203	0.018
1376131_a_at	AW535500	proline, glutamic acid and leucine rich protein 1	Pelp1	0.989	0.482	0.975	0.796	0.941	0.619	1.064	0.716
1374567_at	AI408443	proline/serine-rich coiled-coil 2	Psrc2	1.135	0.887	0.693	0.013	1.547	0.029	0.966	0.666
1371603_at	BI291379	proline-rich polypeptide 3	Prr3	1.054	0.180	0.846	0.074	0.998	0.850	0.852	0.089
1372702_at	BI284972	proline-rich protein	PRP-2	0.673	0.185	0.275	0.001	0.681	0.003	0.253	0.006
1367635_at	NM_012998	prolyl 4-hydroxylase, beta polypeptide	P4hb	0.938	0.682	1.041	0.097	0.923	0.677	0.951	0.232
1368234_at	NM_031324	prolyl endopeptidase	Prep	0.448	0.024	1.151	0.324	0.610	0.004	1.057	0.507
1379248_at	AA926318	Prolylcarboxypeptidase (angiotensinase C) (predicted)	Prcp_predicted	1.009	0.975	1.075	0.737	0.893	0.997	0.877	0.041
1389527_at	BM384073	promethin	LOC378467	0.999	0.578	1.355	0.157	0.998	0.984	1.404	0.109
1368008_at	NM_021751	prominin 1	Prom1	0.999	0.992	0.354	0.000	0.193	0.065	0.284	0.033
1379019_at	AI639534	properdin factor, complement (mapped)	Pfc_mapped	3.472	0.060	1.994	0.018	3.617	0.036	1.555	0.545
1370187_at	AI502661	propionyl coenzyme A carboxylase, beta polypeptide	Pccb	0.954	0.506	0.729	0.177	0.994	0.982	1.007	0.909
1387247_at	M83745	proprotein convertase subtilisin/kexin type 1	Pcsk1	0.414	0.112	0.167	0.001	0.560	0.026	0.235	0.025
1368559_at	NM_017091	proprotein convertase subtilisin/kexin type 1	Pcsk1	0.481	0.575	0.179	0.000	0.480	0.123	0.271	0.007
1367835_at	NM_019279	proprotein convertase subtilisin/kexin type 1 inhibitor	Pcsk1n	0.731	0.518	0.288	0.000	0.703	0.020	0.405	0.004
1397662_at	BF395791	Proprotein convertase subtilisin/kexin type 2	Pcsk2	0.918	0.484	0.264	0.006	1.045	0.367	0.545	0.029
1387155_at	NM_012746	proprotein convertase subtilisin/kexin type 2	Pcsk2	0.782	0.884	0.451	0.001	0.762	0.924	0.585	0.000
1392773_at	AA859578	proprotein convertase subtilisin/kexin type 5	Pcsk5	0.873	0.192	1.007	0.970	0.422	0.135	0.980	0.261
1387812_at	NM_012999	proprotein convertase subtilisin/kexin type 6	Pcsk6	1.063	0.632	5.688	0.000	0.998	0.327	4.514	0.023
1385640_at	AI059511	proprotein convertase subtilisin/kexin type 9	Pcsk9	1.000	0.533	0.346	0.029	1.466	0.927	0.777	0.070
1369929_at	NM_013013	prosaposin	Psap	0.770	0.961	0.630	0.002	0.863	0.772	0.633	0.011
1367851_at	J04488	prostaglandin D2 synthase	Ptgds	1.014	0.137	0.898	0.015	1.136	0.179	0.942	0.045
1385434_at	AI705087	Prostaglandin E receptor 2, subtype EP2	Ptger2	0.998	0.989	0.802	0.286	1.899	0.051	1.018	0.202
1374532_at	AI704291	prostaglandin E synthase 2 (predicted)	Ptges2_predicted	0.816	0.661	2.000	0.008	0.598	0.008	2.183	0.012
1371372_at	AA944161	prostaglandin E synthase 3 (cytosolic) (predicted)	Ptges3_predicted	0.792	0.571	1.527	0.032	0.724	0.254	1.366	0.029
1367986_at	NM_019243	prostaglandin F2 receptor negative regulator	Ptgfrn	2.275	0.041	2.992	0.006	3.260	0.001	3.381	0.003
1368259_at	NM_017043	prostaglandin-endoperoxide synthase 1	Ptgs1	4.582	0.007	9.535	0.000	2.246	0.048	7.350	0.010
1368527_at	U03389	prostaglandin-endoperoxide synthase 2	Ptgs2	6.359	0.018	2.138	0.021	1.215	0.806	1.728	0.012
1382075_at	BF386499	Prostate tumor over expressed gene 1	Ptov1	0.424	0.045	0.519	0.039	1.000	0.073	0.492	0.039
1388430_at	BI280292	prostate tumor over expressed gene 1	Ptov1	0.474	0.271	0.442	0.042	0.517	0.037	0.521	0.003
1398247_at	NM_133404	protease, serine, 15	Prss15	1.211	0.239	6.044	0.005	0.950	0.659	3.708	0.001
1373152_at	AI177099	protease, serine, 23	Prss23	1.437	0.076	2.925	0.002	0.837	0.079	2.099	0.014
1367478_at	AI600136	protease, serine, 25	Prss25	1.306	0.016	1.174	0.240	2.415	0.003	2.250	0.007
1379747_at	AA866443	Protease, serine, 35	Prss35	1.865	0.117	2.229	0.039	0.671	0.144	2.537	0.082
1388582_at	BM392043	proteaseome (prosome, macropain) 28 subunit, 3	Psme3	0.721	0.906	1.018	0.740	0.950	0.846	0.793	0.296
1372506_at	AI233766	proteaseome (prosome, macropain) 28 subunit, 3	Psme3	0.719	0.977	1.777	0.057	0.507	0.068	1.187	0.327
1367711_at	NM_033236	proteasome (prosome, macropain) 26S subunit, ATPase 2	Psmc2	0.915	0.274	1.418	0.003	0.853	0.027	1.402	0.005
1387120_at	NM_031595	proteasome (prosome, macropain) 26S subunit, ATPase 3	Psmc3	0.852	0.639	1.074	0.565	0.501	0.000	0.995	0.950
1398869_at	BG378826	proteasome (prosome, macropain) 26S subunit, ATPase, 4	Psmc4	0.802	0.601	1.161	0.021	1.027	0.532	1.284	0.026
1382385_at	BE116344	proteasome (prosome, macropain) 26S subunit, ATPase, 6	Psmc6	0.473	0.048	0.600	0.044	0.583	0.206	0.885	0.089
1379850_at	BI296804	proteasome (prosome, macropain) 26S subunit, ATPase, 6	Psmc6	0.791	0.089	0.938	0.401	0.834	0.044	1.129	0.003
1384323_at	BF418369	proteasome (prosome, macropain) 26S subunit, ATPase, 6	Psmc6	0.646	0.134	1.262	0.018	0.624	0.003	1.232	0.058
1369992_at	NM_031978	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	Psmd1	0.962	0.636	0.889	0.112	0.771	0.081	0.739	0.031
1374712_at	AA946509	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (predicted)	Psmd11_predicted	0.899	0.111	2.185	0.000	0.762	0.259	1.560	0.038
1376069_at	BF414050	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (predicted)	Psmd11_predicted	0.732	0.290	1.011	0.353	0.766	0.003	1.141	0.015
1392983_at	BE103250	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	Psmd12	0.876	0.486	1.556	0.001	0.789	0.012	1.394	0.002
1371617_at	AI599711	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 (predicted)	Psmd13_predicted	0.856	0.491	1.459	0.010	0.626	0.041	1.037	0.262
1398858_at	D37934	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	Psmd2	0.740	0.059	1.085	0.272	0.756	0.033	1.141	0.050
1388466_at	BI285842	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	Psmd3	0.813	0.106	1.182	0.043	0.911	0.343	1.173	0.067
1392661_at	AI228227	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	Psmd4	1.177	0.267	0.783	0.616	1.253	0.334	1.305	0.260
1386930_at	NM_031331	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	Psmd4	0.819	0.617	2.033	0.006	0.728	0.064	1.574	0.090
1372267_at	AI233729	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 (predicted)	Psmd5_predicted	0.665	0.170	1.389	0.138	0.516	0.061	1.497	0.045
1371851_at	BM383811	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	Psmd6	0.713	0.225	0.790	0.017	0.685	0.025	0.895	0.079
1389245_at	BF542903	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (predicted)	Psmd7_predicted	1.208	0.807	1.332	0.009	1.238	0.034	1.304	0.004
1379322_at	BI289174	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (predicted)	Psmd7_predicted	0.961	0.855	1.321	0.091	1.055	0.785	1.234	0.366
1389519_at	BI275955	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	Psmd8	0.497	0.367	0.867	0.365	0.390	0.147	0.878	0.450

1368184_at	NM_130430	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	Psmd9	0.560	0.169	2.308	0.088	0.626	0.510	2.029	0.024
1367663_at	NM_017264	proteasome (prosome, macropain) 28 subunit, alpha	Psme1	2.982	0.005	3.756	0.005	3.860	0.001	4.976	0.000
1367710_at	NM_017257	proteasome (prosome, macropain) 28 subunit, beta	Psme2	4.772	0.000	6.032	0.000	5.999	0.001	8.536	0.001
1368817_at	AI180458	proteasome (prosome, macropain) activator subunit 4	Psme4	0.750	0.018	0.677	0.001	0.785	0.132	0.746	0.059
1368818_at	AW531920	proteasome (prosome, macropain) activator subunit 4	Psme4	0.540	0.165	0.200	0.000	0.541	0.012	0.606	0.101
1398778_at	NM_017278	proteasome (prosome, macropain) subunit, alpha type 1	Psma1	0.895	0.643	0.928	0.455	1.164	0.063	1.414	0.031
1398856_at	AA801204	proteasome (prosome, macropain) subunit, alpha type 2	Psma2	1.108	0.390	0.926	0.423	1.024	0.300	1.270	0.173
1368508_at	BI294912	proteasome (prosome, macropain) subunit, alpha type 3 /// proteasome subunit alpha type 3-like	Psma3 /// Psma3l	1.055	0.178	0.866	0.086	1.117	0.159	1.081	0.119
1368507_at	NM_017280	proteasome (prosome, macropain) subunit, alpha type 3 /// proteasome subunit alpha type 3-like	Psma3 /// Psma3l	0.978	0.420	1.693	0.032	0.992	0.247	2.158	0.017
1367837_at	NM_017281	proteasome (prosome, macropain) subunit, alpha type 4	Psma4	1.162	0.191	1.216	0.554	1.295	0.034	1.628	0.010
1387884_at	AI011191	proteasome (prosome, macropain) subunit, alpha type 5	Psma5	1.227	0.239	1.371	0.183	1.328	0.304	1.713	0.012
1369930_at	NM_017283	proteasome (prosome, macropain) subunit, alpha type 6	Psma6	1.286	0.102	1.659	0.012	1.209	0.045	1.815	0.007
1371869_at	BF282262	proteasome (prosome, macropain) subunit, alpha type 7	Psma7	2.171	0.099	2.519	0.004	2.143	0.001	2.715	0.011
1398812_at	NM_053590	proteasome (prosome, macropain) subunit, beta type 1	Psmb1	1.210	0.219	1.251	0.124	1.145	0.283	1.240	0.080
1374033_at	BG373505	proteasome (prosome, macropain) subunit, beta type 10	Psmb10	8.196	0.008	20.520	0.001	14.306	0.011	36.210	0.000
1398786_at	NM_017284	proteasome (prosome, macropain) subunit, beta type 2	Psmb2	1.387	0.481	0.790	0.240	1.694	0.296	1.548	0.058
1398853_at	AI169273	proteasome (prosome, macropain) subunit, beta type 3	Psmb3	0.670	0.309	0.810	0.098	0.635	0.150	1.033	0.661
1398831_at	NM_031629	proteasome (prosome, macropain) subunit, beta type 4	Psmb4	0.987	0.869	1.114	0.667	0.813	0.223	1.056	0.133
1371348_at	BI285627	proteasome (prosome, macropain) subunit, beta type 5	Psmb5	0.745	0.960	0.798	0.054	0.731	0.043	0.785	0.070
1398777_at	NM_057099	proteasome (prosome, macropain) subunit, beta type 6	Psmb6	0.693	0.293	1.444	0.119	0.623	0.021	1.201	0.301
1367656_at	NM_053532	proteasome (prosome, macropain) subunit, beta type 7	Psmb7	0.661	0.802	1.312	0.228	0.612	0.132	1.231	0.289
1371325_at	BM389083	protective protein for beta-galactosidase	Ppgb	0.849	0.815	1.202	0.023	1.207	0.190	1.164	0.645
1371449_at	BM388765	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 (predicted)	Pin1_predicted	0.570	0.021	1.072	0.875	0.678	0.146	1.096	0.692
1399048_at	BI274121	protein arginine N-methyltransferase 4	Prmt4	0.450	0.316	1.175	0.041	0.595	0.049	0.808	0.045
1374424_at	BE112720	protein arginine N-methyltransferase 5 (predicted)	Prmt5_predicted	0.584	0.000	0.864	0.381	0.651	0.009	0.921	0.534
1375388_at	BF400832	Protein disulfide isomerase associated 3	Pdia3	1.648	0.098	2.422	0.036	1.447	0.025	1.738	0.148
1398788_at	NM_017319	protein disulfide isomerase associated 3	Pdia3	1.033	0.843	0.984	0.755	1.119	0.792	1.087	0.793
1370007_at	NM_053849	protein disulfide isomerase associated 4	Pdia4	0.995	0.736	0.860	0.040	1.753	0.947	0.618	0.059
1378532_at	AI407172	Protein disulfide isomerase associated 4	Pdia4	1.004	0.744	12.428	0.000	0.734	0.003	2.095	0.170
1370859_at	BI284965	protein disulfide isomerase associated 6	Pdia6	0.672	0.170	0.782	0.024	0.769	0.256	0.810	0.042
1374828_at	AI045590	protein disulfide isomerase-associated 5	Pdia5	0.948	0.291	1.689	0.157	1.073	0.688	1.248	0.088
1369285_at	NM_031082	protein geranylgeranyltransferase type I, beta subunit	Pggt1b	1.412	0.278	1.892	0.132	0.995	0.145	2.960	0.157
1382191_at	AI228848	protein inhibitor of activated STAT 1 (predicted)	Pias1_predicted	1.783	0.019	1.579	0.020	1.203	0.018	1.493	0.160
1370196_at	AW532051	protein inhibitor of activated STAT 3	Pias3	0.962	0.929	2.454	0.000	1.020	0.436	1.253	0.148
1372857_at	AI407930	protein kinase C and casein kinase substrate in neurons 2	Pacsin2	1.195	0.629	1.481	0.151	0.733	0.101	1.372	0.163
1368068_a_at	NM_130740	protein kinase C and casein kinase substrate in neurons 2	Pacsin2	1.085	0.791	1.825	0.006	0.892	0.507	1.463	0.215
1390305_at	AI599263	protein kinase C binding protein 1	Prkcbp1	1.193	0.259	0.604	0.041	1.077	0.866	1.034	0.844
1396148_at	BE106782	Protein kinase C binding protein 1	Prkcbp1	0.810	0.364	0.464	0.025	0.753	0.043	0.498	0.149
1388371_at	AI008784	Protein kinase C substrate 80K-H (predicted)	Prkcsh_predicted	0.704	0.109	0.895	0.277	0.813	0.591	0.961	0.823
1372176_at	BF415343	protein kinase C, alpha	Prkca	0.962	0.912	7.665	0.014	0.470	0.020	3.726	0.046
1370585_a_at	X04440	protein kinase C, beta 1	Prkcb1	0.685	0.259	0.301	0.009	0.526	0.154	0.252	0.013
1397006_at	BF401586	Protein kinase C, beta 1	Prkcb1	1.001	0.979	0.997	0.290	1.670	0.050	0.974	0.840
1387114_at	NM_133307	protein kinase C, delta	Prkcd	2.136	0.035	2.865	0.011	4.330	0.012	2.357	0.008
1367691_at	NM_134449	protein kinase C, delta binding protein	Prkcdbp	1.469	0.038	0.997	0.989	1.004	0.961	0.967	0.547
1378644_at	BI301465	Protein kinase C, epsilon	Prkce	1.178	0.663	0.872	0.480	0.986	0.820	1.037	0.495
1374593_at	AA799421	protein kinase C, epsilon	Prkce	1.055	0.947	1.024	0.815	1.095	0.741	1.008	0.372
1378385_at	AI548474	Protein kinase C, eta	Prkch	2.329	0.485	0.529	0.369	1.587	0.247	0.432	0.145
1369089_at	NM_012628	protein kinase C, gamma	Prkcc	1.075	0.481	1.019	0.855	1.037	0.969	0.989	0.367
1373047_at	BF284699	Protein kinase C, iota	Prkci	1.206	0.608	1.404	0.064	1.161	0.639	1.225	0.158
1371203_at	AB020615	protein kinase C, iota	Prkci	0.999	0.650	1.156	0.461	0.926	0.792	0.759	0.690
1370197_a_at	AW533298	protein kinase C, zeta	Prkcz	0.441	0.316	1.220	0.989	1.041	0.328	1.066	0.994
1396906_at	BE105377	Protein kinase C, zeta	Prkcz	1.080	0.373	0.995	0.643	0.500	0.248	1.205	0.999
1386966_a_at	NM_021764	protein kinase C-binding protein Beta15	Pkcbpb15	1.171	0.173	1.051	0.515	1.387	0.829	1.045	0.614
1372995_at	AI703715	protein kinase D2	Prkd2	1.339	0.482	1.757	0.239	1.867	0.112	1.518	0.214
1387398_at	AA996685	protein kinase inhibitor, alpha	Pkia	2.533	0.015	1.963	0.015	1.317	0.351	1.704	0.134
1378510_at	BF386239	Protein kinase inhibitor, gamma	Pkig	1.594	0.075	1.631	0.228	1.780	0.008	2.181	0.223
1371600_at	AA943815	protein kinase inhibitor, gamma	Pkig	1.394	0.146	1.768	0.000	1.759	0.081	1.808	0.010
1398400_at	AW433595	protein kinase LYK5	Lyk5	0.671	0.358	0.447	0.004	0.528	0.226	0.890	0.837
1386992_at	NM_017175	protein kinase N1	Pkn1	1.251	0.323	2.347	0.029	1.021	0.423	1.945	0.019
1393055_at	BF525244	protein kinase N2	Pkn2	1.130	0.242	1.312	0.146	1.172	0.044	1.218	0.198
1369104_at	NM_019142	protein kinase, AMP-activated, alpha 1 catalytic subunit	Prkaa1	1.048	0.106	4.799	0.027	1.004	0.064	1.150	0.757

1386945_a_at	NM_031976	protein kinase, AMP-activated, beta 1 non-catalytic subunit	Prkab1	1.003	0.672	1.534	0.006	1.040	0.781	1.113	0.366
1369271_at	NM_022627	protein kinase, AMP-activated, beta 2 non-catalytic subunit	Prkab2	1.005	0.920	1.200	0.095	1.002	0.968	0.996	0.107
1376724_at	AI170671	Protein kinase, AMP-activated, beta 2 non-catalytic subunit	Prkab2	0.995	0.975	1.484	0.470	0.906	0.619	1.397	0.870
1367947_at	U42413	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	Prkag1	0.556	0.024	0.701	0.002	0.725	0.362	0.817	0.211
1373952_at	AI409841	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	Prkag2	1.119	0.538	1.564	0.082	1.226	0.424	1.487	0.077
1373951_at	AI407792	Protein kinase, cAMP dependent regulatory, type I, alpha	Prkar1a	0.759	0.170	0.558	0.000	0.766	0.448	0.645	0.001
1388375_at	AI234096	Protein kinase, cAMP dependent regulatory, type I, alpha	Prkar1a	0.737	0.299	0.432	0.003	0.659	0.017	0.447	0.024
1386905_at	NM_013181	protein kinase, cAMP dependent regulatory, type I, alpha	Prkar1a	0.807	0.809	1.082	0.246	0.675	0.063	0.945	0.195
1389463_at	BG375376	protein kinase, cAMP dependent regulatory, type I, beta	Prkar1b	0.741	0.158	1.144	0.200	0.461	0.001	0.833	0.187
1371133_a_at	M12492	protein kinase, cAMP dependent regulatory, type II beta	Prkar2b	0.913	0.593	0.807	0.034	0.584	0.014	0.933	0.267
1371835_at	AI411907	protein kinase, cAMP dependent, catalytic, beta (predicted)	Prkacb_predicted	0.594	0.111	0.520	0.002	0.497	0.000	0.504	0.003
1384772_at	BF400907	protein kinase, cAMP dependent, catalytic, beta (predicted)	Prkacb_predicted	0.546	0.167	0.928	0.737	0.397	0.077	0.895	0.388
1371578_at	AW915101	protein kinase, cAMP-dependent, catalytic, alpha	Prkaca	0.510	0.396	0.423	0.007	0.387	0.022	0.392	0.002
1395246_at	AI104783	Protein kinase, cAMP-dependent, regulatory, type 2, alpha	Prkar2a	1.478	0.018	1.143	0.285	0.728	0.070	0.721	0.324
1373400_at	AW918535	Protein kinase, cAMP-dependent, regulatory, type 2, alpha	Prkar2a	0.955	0.400	0.930	0.626	0.825	0.085	1.040	0.688
1378415_at	BM386879	Protein kinase, cAMP-dependent, regulatory, type 2, alpha	Prkar2a	1.610	0.723	1.082	0.442	1.004	0.982	1.000	0.971
1397018_at	BF399590	Protein kinase, cGMP-dependent, type 1 (mapped)	Prkg1_mapped	1.048	0.739	0.957	0.245	1.218	0.259	1.086	0.796
1389431_at	BF400782	protein kinase, DNA activated, catalytic polypeptide (predicted)	Prkdc_predicted	0.603	0.017	0.689	0.050	0.632	0.013	0.794	0.388
1371899_at	AI102009	protein kinase, interferon inducible double stranded RNA dependent activator	Prkra	0.591	0.057	0.420	0.015	1.018	0.967	0.639	0.067
1387242_at	NM_019335	Protein kinase, interferon-inducible double stranded RNA dependent	Prkr	4.060	0.001	1.473	0.077	9.644	0.001	2.478	0.020
1396919_at	AI137384	protein kinase, lysine deficient 1	Prkwnk1	1.078	0.043	1.105	0.996	1.154	0.163	1.101	0.799
1378686_at	BF405626	Protein kinase, lysine deficient 1	Prkwnk1	0.871	0.320	1.118	0.998	0.617	0.167	0.880	0.992
1387072_at	NM_053794	protein kinase, lysine deficient 1	Prkwnk1	1.248	0.383	2.564	0.010	1.026	0.889	1.950	0.009
1372791_at	AI235474	Protein kinase, lysine deficient 1	Prkwnk1	0.896	0.542	0.436	0.001	0.682	0.102	0.509	0.005
1394729_at	AI714037	Protein kinase, lysine deficient 1	Prkwnk1	1.415	0.900	0.966	0.856	1.317	0.377	0.996	0.977
1392626_at	BE110801	protein kinase, membrane associated tyrosine/threonine 1 (predicted)	Pkmyt1_predicted	0.991	0.823	1.492	0.036	1.002	0.991	1.010	0.322
1389686_at	BF408898	protein kinase, X-linked	Prkx	1.053	0.233	0.841	0.151	1.092	0.628	1.173	0.101
1398143_at	BF414789	protein kinase, X-linked	Prkx	0.998	0.683	1.036	0.082	1.007	0.307	1.097	0.613
1388717_at	BM384163	protein O-fucosyltransferase 2 (predicted)	Pofut2_predicted	0.259	0.009	0.345	0.004	0.357	0.005	0.322	0.008
1374538_at	AW915001	protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase	Pomgnt1	0.569	0.093	0.624	0.002	0.627	0.102	0.686	0.078
1380239_at	BE106083	Protein phosphatase 1 (formerly 2C)-like (predicted)	Ppm1l_predicted	1.364	0.018	0.968	0.901	1.427	0.027	0.971	0.945
1386863_at	NM_031527	protein phosphatase 1, catalytic subunit, alpha isoform	Ppp1ca	0.702	0.231	0.840	0.027	0.548	0.006	0.790	0.001
1386950_at	NM_013065	protein phosphatase 1, catalytic subunit, beta isoform	Ppp1cb	0.729	0.102	0.928	0.259	0.728	0.333	0.933	0.963
1392730_at	AI144948	Protein phosphatase 1, catalytic subunit, beta isoform	Ppp1cb	1.195	0.824	1.264	0.328	1.166	0.706	1.279	0.246
1367637_a_at	NM_022498	protein phosphatase 1, catalytic subunit, gamma isoform	Ppp1cc	1.016	0.732	0.621	0.000	1.211	0.058	0.873	0.155
1382307_at	BF406594	protein phosphatase 1, regulatory (inhibitor) subunit 12A	Ppp1r12a	1.120	0.191	1.981	0.098	0.678	0.544	1.138	0.644
1380311_at	AI535528	Protein phosphatase 1, regulatory (inhibitor) subunit 12A	Ppp1r12a	1.100	0.820	0.987	0.871	0.972	0.766	0.980	0.661
1389815_at	BF547738	protein phosphatase 1, regulatory (inhibitor) subunit 14B	Ppp1r14b	0.643	0.219	1.341	0.086	0.387	0.009	1.000	0.140
1375104_at	AI408517	Protein phosphatase 1, regulatory (inhibitor) subunit 14B	Ppp1r14b	0.702	0.617	1.316	0.057	0.452	0.008	1.010	0.423
1393082_at	AI044747	protein phosphatase 1, regulatory (inhibitor) subunit 14c	Ppp1r14c	3.029	0.009	1.571	0.057	4.369	0.004	2.121	0.013
1368716_at	NM_133425	protein phosphatase 1, regulatory (inhibitor) subunit 14c	Ppp1r14c	2.509	0.043	2.996	0.010	2.561	0.014	2.267	0.009
1384729_at	BI280301	protein phosphatase 1, regulatory (inhibitor) subunit 15b (predicted)	Ppp1r15b_predicted	1.001	0.831	1.109	0.362	0.977	0.747	1.030	0.603
1386968_at	NM_022676	protein phosphatase 1, regulatory (inhibitor) subunit 1A	Ppp1r1a	0.286	0.000	0.214	0.000	0.271	0.000	0.257	0.008
1383191_at	BE097583	protein phosphatase 1, regulatory (inhibitor) subunit 1A	Ppp1r1a	0.290	0.001	0.112	0.000	0.243	0.002	0.216	0.009
1383180_at	BF288097	protein phosphatase 1, regulatory (inhibitor) subunit 2	Ppp1r2	0.637	0.571	0.910	0.066	1.006	0.967	0.919	0.761
1372446_at	AI172276	protein phosphatase 1, regulatory (inhibitor) subunit 2	Ppp1r2	0.768	0.607	0.776	0.025	0.879	0.907	0.985	0.463
1393480_at	AW919998	protein phosphatase 1, regulatory (inhibitor) subunit 2	Ppp1r2	0.795	0.990	0.927	0.473	0.761	0.059	1.151	0.380
1384262_at	BI274037	protein phosphatase 1, regulatory (inhibitor) subunit 3B	Ppp1r3b	1.557	0.143	2.270	0.022	0.880	0.495	1.320	0.291
1373108_at	BM390827	protein phosphatase 1, regulatory (inhibitor) subunit 3C	Ppp1r3c	1.002	0.959	3.188	0.042	1.191	0.782	2.093	0.011
1374510_at	BI296300	Protein phosphatase 1, regulatory (inhibitor) subunit 3F (predicted)	Ppp1r3f_predicted	1.277	0.207	1.492	0.333	1.190	0.041	1.264	0.289
1383277_at	H32309	protein phosphatase 1, regulatory (inhibitor) subunit 7	Ppp1r7	0.576	0.171	1.063	0.155	0.473	0.116	0.938	0.496
1376566_at	BE109552	Protein phosphatase 1, regulatory (inhibitor) subunit 7	Ppp1r7	1.023	0.183	0.975	0.969	1.004	0.978	1.003	0.992
1373073_at	BF282816	protein phosphatase 1, regulatory (inhibitor) subunit 7	Ppp1r7	1.003	0.511	1.225	0.516	1.002	0.986	1.213	0.275
1373437_at	BI286565	Protein phosphatase 1, regulatory (inhibitor) subunit 8 (predicted)	Ppp1r8_predicted	1.226	0.979	1.444	0.052	0.306	0.087	1.413	0.167
1386971_at	NM_022951	protein phosphatase 1, regulatory subunit 10	Ppp1r10	0.592	0.017	0.258	0.002	0.835	0.018	0.497	0.019
1387143_at	NM_053474	protein phosphatase 1, regulatory subunit 9B	Ppp1r9b	1.165	0.199	0.809	0.194	1.256	0.337	0.752	0.088
1383475_at	AW521250	Protein phosphatase 1A, magnesium dependent, alpha isoform	Ppm1a	1.135	0.335	1.724	0.001	0.736	0.109	1.326	0.047
1368859_at	NM_017038	protein phosphatase 1A, magnesium dependent, alpha isoform	Ppm1a	1.002	0.466	1.282	0.459	1.058	0.866	1.165	0.406
1371136_at	AJ271834	protein phosphatase 1B, magnesium dependent, beta isoform	Ppm1b	0.838	0.014	1.823	0.021	0.765	0.050	1.387	0.002
1398807_at	NM_033096	protein phosphatase 1B, magnesium dependent, beta isoform	Ppm1b	0.498	0.222	0.585	0.004	0.479	0.001	0.717	0.007
1378124_at	AI501282	protein phosphatase 1B, magnesium dependent, beta isoform	Ppm1b	1.385	0.276	2.122	0.005	1.625	0.099	1.569	0.038

1388514_at	BI285247	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	Ppm1g	0.752	0.271	1.427	0.006	0.698	0.043	1.304	0.114
1390954_at	AI548159	protein phosphatase 1H (PP2C domain containing)	Ppm1h	0.961	0.955	2.078	0.006	0.520	0.045	1.799	0.270
1388805_at	BF408792	Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	Ppp2ca	0.940	0.194	2.532	0.003	0.773	0.227	1.600	0.005
1398790_at	NM_017039	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	Ppp2ca	1.017	0.881	1.588	0.004	0.882	0.938	1.526	0.014
1367827_at	NM_017040	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	Ppp2cb	0.923	0.926	1.390	0.071	0.965	0.925	1.551	0.015
1375245_at	AA800669	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	Ppp2r1a	0.701	0.503	1.070	0.523	0.461	0.075	0.953	0.612
1397689_at	BF288445	Protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	Ppp2r1a	1.034	0.937	1.333	0.811	1.686	0.369	1.091	0.808
1373959_at	AI411788	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	Ppp2r1b	1.149	0.546	1.388	0.031	0.883	0.501	1.185	0.016
1392741_at	AI145364	Protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	Ppp2r2a	1.501	0.088	1.816	0.854	1.131	0.161	0.993	0.261
1376938_at	AI717081	Protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	Ppp2r2a	1.074	0.107	1.587	0.110	1.034	0.884	0.904	0.756
1387485_a_at	M83297	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	Ppp2r2a	1.266	0.570	1.500	0.064	1.048	0.818	1.170	0.529
1395410_at	AI717707	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	Ppp2r3a	1.311	0.246	1.104	0.874	1.217	0.032	1.289	0.288
1399005_at	BG673380	protein phosphatase 2, regulatory subunit B (B56), alpha isoform (predicted)	Ppp2r5a_predicted	0.625	0.000	1.044	0.773	0.622	0.117	0.950	0.727
1392241_at	AW252634	Protein phosphatase 2, regulatory subunit B (B56), alpha isoform (predicted)	Ppp2r5a_predicted	0.987	0.338	0.998	0.921	0.942	0.347	1.026	0.997
1377235_a_at	BI281643	protein phosphatase 2, regulatory subunit B (B56), beta isoform	Ppp2r5b	1.842	0.031	1.314	0.201	3.224	0.006	1.045	0.580
1372609_at	AI236198	protein phosphatase 2, regulatory subunit B (B56), delta isoform	Ppp2r5d	0.591	0.181	1.657	0.193	0.856	0.035	1.140	0.642
1395502_at	BF557865	protein phosphatase 2, regulatory subunit B (B56), delta isoform	Ppp2r5d	0.999	0.613	1.259	0.150	0.938	0.796	1.050	0.214
1395826_at	BG664036	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (predicted)	Ppp2r5e_predicted	0.676	0.081	0.801	0.424	0.679	0.080	0.521	0.270
1388965_at	AI144583	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (predicted)	Ppp2r5e_predicted	0.840	0.729	0.823	0.280	0.528	0.024	0.670	0.007
1388107_at	BF282131	protein phosphatase 2, regulatory subunit B, delta isoform	Ppp2r2d	1.132	0.443	1.422	0.008	0.812	0.116	1.032	0.305
1368910_at	NM_019372	protein phosphatase 2C, magnesium dependent, catalytic subunit	Ppm2c	1.171	0.499	1.007	0.506	1.274	0.295	0.996	0.488
1379175_at	BF388224	Protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca	0.628	0.027	1.094	0.675	2.552	0.208	1.003	0.070
1384815_at	AI145507	Protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca	0.997	0.281	2.123	0.047	0.945	0.438	1.063	0.101
1373479_at	BE113127	Protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca	0.916	0.586	0.843	0.026	0.885	0.557	0.840	0.046
1368277_at	NM_017041	protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca	0.965	0.593	0.916	0.145	0.890	0.305	1.087	0.003
1383415_at	AW531415	Protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca	0.932	0.840	0.723	0.060	0.949	0.885	0.665	0.074
1387261_at	NM_017042	protein phosphatase 3, catalytic subunit, beta isoform	Ppp3cb	2.012	0.139	0.530	0.128	1.185	0.815	0.842	0.285
1375882_at	BG380745	protein phosphatase 3, catalytic subunit, beta isoform	Ppp3cb	1.284	0.231	0.731	0.018	1.142	0.296	0.820	0.076
1398469_at	BG372864	protein phosphatase 3, catalytic subunit, gamma isoform	Ppp3cc	1.022	0.218	1.551	0.132	0.990	0.525	1.337	0.244
1372982_at	BF387153	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	Ppp3r1	0.984	0.404	1.125	0.154	1.037	0.755	1.214	0.063
1390333_at	AA957050	protein phosphatase 4, catalytic subunit	Ppp4c	1.396	0.962	1.683	0.109	0.948	0.580	1.229	0.394
1370162_at	BI285346	protein phosphatase 4, regulatory subunit 1	Ppp4r1	1.323	0.017	1.122	0.399	1.149	0.291	1.000	0.992
1387858_at	AI535053	protein phosphatase 4, regulatory subunit 1	Ppp4r1	1.036	0.125	0.998	0.983	1.000	0.996	1.000	0.865
1388865_at	BG378896	protein phosphatase 4, regulatory subunit 2 (predicted)	Ppp4r2_predicted	1.318	0.244	1.602	0.029	0.950	0.520	1.207	0.663
1392997_at	BF556742	protein phosphatase 4, regulatory subunit 2 (predicted)	Ppp4r2_predicted	1.168	0.495	1.257	0.026	0.975	0.497	1.022	0.868
1393231_at	BM386467	protein phosphatase 4, regulatory subunit 2 (predicted)	Ppp4r2_predicted	1.181	0.856	0.481	0.001	0.947	0.783	0.689	0.002
1387801_at	NM_133589	protein phosphatase 6, catalytic subunit	Ppp6c	0.641	0.118	1.701	0.012	0.728	0.005	1.520	0.042
1373844_at	BE103921	protein phosphatase methylesterase 1	Ppme1	0.629	0.164	1.017	0.364	0.929	0.768	0.867	0.352
1371037_at	U06230	protein S (alpha)	Pros1	1.514	0.128	1.306	0.145	1.385	0.125	0.973	0.263
1390288_at	AI013362	protein serine kinase H1 (predicted)	Pskh1_predicted	0.881	0.652	0.327	0.017	0.684	0.027	0.575	0.042
1369688_s_at	U69109	protein tyrosine kinase 2 beta	Ptk2b	2.107	0.016	0.673	0.048	2.137	0.063	0.501	0.020
1371644_at	BF283086	protein tyrosine kinase 9	Ptk9	1.138	0.659	1.022	0.630	1.150	0.989	0.827	0.515
1370193_at	AI172261	protein tyrosine phosphatase 4a1	Ptp4a1	1.329	0.023	3.904	0.000	0.776	0.505	2.674	0.000
1367971_at	NM_053475	protein tyrosine phosphatase 4a2	Ptp4a2	1.336	0.100	1.577	0.010	1.020	0.745	1.455	0.031
1372084_at	AI104546	protein tyrosine phosphatase 4a3 (predicted)	Ptp4a3_predicted	0.623	0.188	0.343	0.001	0.320	0.050	0.263	0.000
1368516_at	NM_012763	protein tyrosine phosphatase alpha	LOC360370	0.630	0.693	0.719	0.083	0.947	0.238	0.704	0.017
1392940_at	BE095915	Protein tyrosine phosphatase domain containing 1 (predicted)	Ptpdc1_predicted	0.581	0.133	0.746	0.324	0.604	0.151	2.094	0.948
1388379_at	AI172465	Protein tyrosine phosphatase, non-receptor type 11	Ptpn11	1.446	0.257	1.724	0.006	1.052	0.644	1.690	0.006
1373065_at	AW916153	protein tyrosine phosphatase, non-receptor type 18	Ptpn18	1.001	0.553	1.000	0.889	1.410	0.272	1.045	0.485
1368361_a_at	NM_053990	protein tyrosine phosphatase, non-receptor type 2	Ptpn2	1.618	0.053	2.425	0.003	2.160	0.002	2.261	0.005
1368087_a_at	NM_133545	protein tyrosine phosphatase, non-receptor type 21	Ptpn21	4.219	0.000	3.252	0.007	3.919	0.003	4.694	0.010
1370473_a_at	AF077000	protein tyrosine phosphatase, non-receptor type 23	Ptpn23	2.054	0.056	4.438	0.003	2.026	0.071	2.767	0.003
1389362_at	AI317821	protein tyrosine phosphatase, non-receptor type 3	Ptpn3	3.623	0.006	4.472	0.002	1.802	0.030	2.646	0.009
1368010_at	NM_053908	protein tyrosine phosphatase, non-receptor type 6	Ptpn6	0.999	0.967	0.918	0.250	0.965	0.764	1.084	0.448
1367881_at	NM_013016	protein tyrosine phosphatase, non-receptor type substrate 1	Ptpns1	0.890	0.632	0.802	0.091	0.630	0.077	0.524	0.009
1387901_at	L19180	protein tyrosine phosphatase, receptor type, D	Ptprd	0.677	0.004	0.366	0.012	0.547	0.002	0.404	0.044
1380738_at	BM392254	Protein tyrosine phosphatase, receptor type, D	Ptprd	1.033	0.965	0.996	0.729	0.999	0.998	1.010	0.935
1368035_a_at	X83505	protein tyrosine phosphatase, receptor type, F	Ptprf	1.330	0.408	0.850	0.737	1.231	0.518	0.920	0.392
1368036_at	M60103	protein tyrosine phosphatase, receptor type, F	Ptprf	1.043	0.462	0.917	0.283	0.881	0.046	0.865	0.061
1396793_at	BE121129	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 (predicted)	Ppfia2_predicted	0.976	0.850	0.977	0.944	0.968	0.911	1.088	0.741

1387444_at	NM_133592	protein tyrosine phosphatase, receptor type, H	Ptprh	0.953	0.192	0.941	0.354	1.411	0.082	1.084	0.533
1368589_at	NM_017269	protein tyrosine phosphatase, receptor type, J	Ptprj	1.762	0.133	0.887	0.455	5.760	0.102	1.012	0.890
1370362_at	D45414	protein tyrosine phosphatase, receptor type, N	Ptprn	0.809	0.072	0.654	0.003	0.836	0.021	0.651	0.001
1370182_at	AI574884	protein tyrosine phosphatase, receptor type, N polypeptide 2	Ptprn2	0.675	0.979	0.253	0.000	0.739	0.503	0.305	0.009
1368412_a_at	D45412	protein tyrosine phosphatase, receptor type, O	Ptpro	1.468	0.058	0.950	0.921	1.334	0.178	1.013	0.497
1391605_at	BG666431	Protein tyrosine phosphatase, receptor type, T (predicted)	Ptprt_predicted	1.008	0.909	1.187	0.049	1.012	0.929	1.378	0.122
1368350_at	NM_013080	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	Ptprz1	1.138	0.251	1.388	0.006	1.226	0.638	1.586	0.008
1388015_at	U04998	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	Ptprz1	1.059	0.332	1.388	0.147	1.110	0.227	0.987	0.804
1374393_at	AI169080	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b (predicted)	Ptplb_predicted	1.133	0.382	1.406	0.262	0.997	0.512	1.404	0.001
1389136_at	AI406280	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor) (predicted)	Prkrir_predicted	0.933	0.411	1.450	0.046	0.810	0.180	1.000	0.997
1371966_at	BM392375	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	Pcmt1	0.916	0.579	0.770	0.014	0.764	0.594	0.930	0.950
1387258_a_at	D11475	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	Pcmt1	0.919	0.869	2.333	0.061	0.840	0.729	1.574	0.123
1374454_at	BM388557	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2 (predicted)	Pcmtd2_predicted	0.596	0.002	0.204	0.003	0.529	0.029	0.466	0.037
1375916_at	AA955163	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2 (predicted)	Pcmtd2_predicted	0.535	0.015	0.317	0.029	0.626	0.032	0.241	0.035
1368267_at	NM_053406	protein-O-mannosyltransferase 1	Pomt1	0.720	0.144	0.788	0.153	0.718	0.130	0.751	0.138
1374457_at	AI180194	protein-O-mannosyltransferase 2	Pomt2	1.824	0.004	3.730	0.002	1.371	0.084	2.256	0.002
1388393_at	BM385031	proteolipid protein 2 (mapped)	Plp2_mapped	1.289	0.062	3.745	0.000	0.856	0.134	2.269	0.015
1367786_at	NM_080767	proteosome (prosome, macropain) subunit, beta type 8	Psmb8	115.606	0.004	182.625	0.001	211.001	0.008	229.126	0.001
1370186_at	AI599350	proteosome (prosome, macropain) subunit, beta type 9	Psmb9	158.445	0.001	314.537	0.000	286.063	0.000	395.862	0.000
1370243_a_at	AI178772	prothymosin alpha	Ptma	0.655	0.193	1.222	0.585	0.587	0.278	0.793	0.656
1374266_at	AA955773	Protocadherin 1 (cadherin-like 1) (predicted)	Pcdh1_predicted	1.100	0.733	2.687	0.072	1.342	0.113	1.674	0.139
1393454_at	BF558981	Protocadherin 17 (predicted)	Pcdh17_predicted	1.806	0.261	0.903	0.739	0.942	0.711	1.436	0.795
1378486_at	BF409825	Protocadherin 17 (predicted)	Pcdh17_predicted	1.192	0.425	0.997	0.912	0.980	0.999	1.004	0.960
1391013_at	AW523567	Protocadherin 8	Pcdh8	3.391	0.022	5.074	0.000	2.103	0.074	1.788	0.017
1378665_at	BF415436	Protocadherin 9 (predicted)	Pcdh9_predicted	0.236	0.001	0.173	0.008	0.230	0.034	0.457	0.010
1383783_at	AW521192	protocadherin 9 (predicted)	Pcdh9_predicted	0.988	0.112	0.201	0.002	0.338	0.007	0.351	0.007
1397688_at	BG667330	protocadherin 9 (predicted)	Pcdh9_predicted	0.988	0.290	0.962	0.152	0.945	0.161	1.475	0.062
1397139_at	BF413644	Protocadherin alpha 4	Pcdha4	1.306	0.846	0.861	0.459	1.645	0.180	0.795	0.050
1390821_at	AI103156	protocadherin alpha 4 /// protocadherin alpha 13 /// protocadherin alpha 10 /// protocadherin alpha 11 /// protocadherin alpha 3 /// protocadherin alpha 8 /// protocadherin alpha 1 /// protocadherin alpha 2 /// protocadherin alpha 5 /// protocadherin alpha 6 /// protocadherin alpha 7 /// protocadherin alpha 9 /// protocadherin alpha subfamily C, 1 /// protocadherin alpha subfamily C, 2 /// protocadherin alpha 11	Pcdha4 /// Pcdha13 /// Pcdha10 /// Pcdha11 /// Pcdha3 /// Pcdha8 /// Pcdha1 /// Pcdha2 /// Pcdha5 /// Pcdha6 /// Pcdha7 /// Pcdha9 /// Pcdhac1 /// Pcdhac2	1.465	0.105	0.515	0.016	2.024	0.003	0.740	0.024
1393149_at	BG663483	protocadherin alpha 4 /// protocadherin alpha 13 /// protocadherin alpha 10 /// protocadherin alpha 11 /// protocadherin alpha 3 /// protocadherin alpha 8 /// protocadherin alpha 1 /// protocadherin alpha 2 /// protocadherin alpha 5 /// protocadherin alpha 6 /// protocadherin alpha 7 /// protocadherin alpha 9 /// protocadherin alpha subfamily C, 1 /// protocadherin alpha subfamily C, 2 /// protocadherin alpha 11	Pcdha4 /// Pcdha13 /// Pcdha10 /// Pcdha11 /// Pcdha3 /// Pcdha8 /// Pcdha1 /// Pcdha2 /// Pcdha5 /// Pcdha6 /// Pcdha7 /// Pcdha9 /// Pcdhac1 /// Pcdhac2	1.064	0.704	0.849	0.297	1.244	0.114	0.796	0.407
1388551_at	AW434022	protocadherin gamma subfamily C, 3 /// protocadherin gamma subfamily A, 9 /// protocadherin gamma subfamily A, 11 /// protocadherin gamma subfamily A, 7 /// protocadherin gamma subfamily A, 5 /// protocadherin gamma subfamily A, 8 /// protocadherin gamma b7 /// protocadherin gamma subfamily B, 5 /// protocadherin gamma a2 /// protocadherin gamma A3 /// protocadherin gamma subfamily A, 10 /// protocadherin gamma subfamily A, 12 /// protocadherin gamma a1	Pcdhgc3 /// Pcdhga9 /// Pcdhga11 /// Pcdhga7 /// Pcdhga5 /// Pcdhga8 /// Pcdhgb7 /// Pcdhgb5 /// Pcdhga2 /// Pcdhga3 /// Pcdhga10 /// Pcdhga12 /// Pcdhga1	0.685	0.025	0.512	0.007	0.778	0.054	0.699	0.148
1377079_a_at	BF386283	protoporphyrinogen oxidase (predicted)	Ppox_predicted	0.423	0.081	0.437	0.016	0.649	0.150	0.486	0.005
1399021_at	BI291269	PRP18 pre-mRNA processing factor 18 homolog (yeast)	Pprf18	1.103	0.944	0.810	0.811	0.978	0.123	0.729	0.083
1388005_at	AF244920	PRP18 pre-mRNA processing factor 18 homolog (yeast)	Pprf18	1.010	0.996	0.962	0.499	0.957	0.993	0.938	0.485
1398867_at	AB020022	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	Prpf19	0.844	0.212	1.299	0.043	1.060	0.409	1.263	0.024
1372432_at	BF395125	PRP3 pre-mRNA processing factor 3 homolog (yeast) (predicted)	Prpf3_predicted	0.743	0.127	2.021	0.065	1.134	0.859	1.813	0.532
1373273_at	BM384975	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A (predicted)	Prpf38a_predicted	0.636	0.175	1.123	0.443	0.594	0.014	1.169	0.480
1389684_at	AA850679	PRP39 pre-mRNA processing factor 39 homolog (yeast) (predicted)	Prpf39_predicted	1.373	0.052	1.407	0.010	1.187	0.078	1.325	0.008
1392461_at	BI291012	PRP4 pre-mRNA processing factor 4 homolog (yeast)	Prpf4	0.909	0.052	1.006	0.466	0.513	0.017	0.997	0.794
1382646_at	AI145475	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	Prpf4b	0.356	0.003	0.244	0.091	0.322	0.006	0.466	0.134
1397203_at	BE105398	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	Prpf4b	0.650	0.108	0.718	0.070	0.970	0.287	0.577	0.082
1376010_at	BM384201	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	Prpf4b	1.142	0.386	1.020	0.257	1.057	0.723	1.027	0.329

1373741_at	BM386451	pseudouridine synthase 1	Pus1	0.983	0.750	3.413	0.006	0.508	0.055	2.396	0.032
1372485_at	BF281220	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 1	Pcbd1	0.507	0.180	0.279	0.007	0.391	0.020	0.296	0.006
1394338_x_at	BF290004	PTK2 protein tyrosine kinase 2	Ptk2	2.263	0.062	1.426	0.082	3.092	0.005	1.300	0.158
1387875_at	BI294798	PTK2 protein tyrosine kinase 2	Ptk2	1.851	0.081	1.026	0.318	2.066	0.001	1.102	0.272
1383602_at	BE112428	Pumilio 1 (Drosophila) (predicted)	Pum1_predicted	1.132	0.055	1.160	0.017	1.220	0.264	1.136	0.071
1375396_at	BI282129	pumilio 1 (Drosophila) (predicted)	Pum1_predicted	1.239	0.188	1.232	0.087	0.970	0.609	1.000	0.444
1375534_at	BE118698	pumilio 2 (Drosophila)	Pum2	1.061	0.172	1.404	0.040	1.172	0.139	1.339	0.239
1398947_at	BE107358	pumilio 2 (Drosophila)	Pum2	1.060	0.514	1.046	0.826	1.103	0.075	1.055	0.091
1382198_at	AI233267	pumilio 2 (Drosophila)	Pum2	1.307	0.546	1.336	0.092	1.245	0.932	1.384	0.475
1375682_at	BM382879	Purine rich element binding protein A (predicted)	Pura_predicted	0.892	0.968	0.751	0.942	0.905	0.614	1.054	0.767
1369743_a_at	U32497	purinergic receptor P2X, ligand-gated ion channel 4	P2rx4	0.824	0.566	1.046	0.590	0.938	0.681	1.061	0.662
1387718_at	NM_019256	purinergic receptor P2X, ligand-gated ion channel, 7	P2rx7	0.997	0.984	0.998	0.936	1.003	0.880	1.000	0.976
1370606_at	U22830	purinergic receptor P2Y, G-protein coupled 1	P2ry1	0.404	0.078	0.103	0.002	0.414	0.063	0.153	0.002
1368145_at	NM_013002	Purkinje cell protein 4	Pcp4	0.785	0.796	0.434	0.011	0.516	0.021	0.250	0.011
1391415_at	AI043694	putatative 28 kDa protein	LOC289809	0.713	0.268	2.407	0.021	0.601	0.016	2.373	0.013
1388889_at	AI598417	putative aminopeptidase Fxna	Fxna	1.424	0.611	1.411	0.066	1.797	0.259	1.804	0.003
1384975_at	BM387447	putative aminopeptidase Fxna	Fxna	0.940	0.837	0.540	0.056	1.330	0.742	0.873	0.423
1399093_at	BM392394	putative GTP-binding protein	LOC293589	0.603	0.125	0.539	0.012	0.503	0.071	0.523	0.016
1376653_at	BE106772	putative homeodomain transcription factor 1	Phtf1	0.726	0.017	0.702	0.004	0.716	0.012	0.690	0.019
1390647_at	AI410924	Putative homeodomain transcription factor 2 (predicted)	Phtf2_predicted	0.347	0.009	0.169	0.001	0.493	0.010	0.254	0.009
1387770_at	NM_130743	putative ISG12(a) protein	isg12(a)	3.133	0.028	2.266	0.017	3.812	0.000	3.546	0.001
1376845_at	AA819034	putative ISG12(b) protein	isg12(b)	1.415	0.045	3.288	0.002	1.383	0.009	3.641	0.001
1370664_a_at	AF016185	putative pheromone receptor (Go-VN13B) /// putative pheromone receptor Go-VN13C	LOC286980 /// LOC286986	0.823	0.306	1.160	0.540	1.951	0.506	1.341	0.425
1370659_at	AF016179	putative pheromone receptor (Go-VN2)	LOC286981	1.225	0.874	0.923	0.852	1.246	0.363	0.872	0.151
1383343_at	BI300511	Putative pheromone receptor V2R4	LOC292498	0.613	0.121	0.738	0.429	1.030	0.912	1.014	0.953
1369543_s_at	NM_138856	putative regulation protein GS3	Gs3	0.930	0.380	1.126	0.582	0.925	0.044	1.340	0.233
1370565_at	AF057564	putative retrovirus-related gag protein	LOC286991	1.175	0.795	0.898	0.426	1.072	0.459	1.020	0.255
1370408_at	AF313411	putative small membrane protein NID67	Nid67	4.233	0.000	1.257	0.487	4.908	0.006	1.268	0.095
1373546_at	AI409922	Putative UA20 protein	Ua20	1.171	0.345	1.658	0.025	1.322	0.065	1.948	0.011
1397380_at	BG376947	PX domain containing serine/threonine kinase	Pxk	1.814	0.048	1.113	0.617	1.902	0.180	0.629	0.044
1390422_at	AW920759	PX domain containing serine/threonine kinase	Pxk	1.133	0.868	0.889	0.984	0.868	0.139	0.981	0.453
1395279_at	BI297004	PX domain containing serine/threonine kinase	Pxk	0.975	0.952	0.793	0.028	0.999	0.794	0.598	0.068
1389873_at	BI282953	PYD and CARD domain containing	Pycard	1.060	0.690	0.951	0.974	1.024	0.713	1.150	0.053
1369989_at	NM_022601	pyridoxine 5'-phosphate oxidase	Pnpo	0.324	0.031	0.496	0.001	0.348	0.060	0.584	0.004
1375215_x_at	BE109558	pyroglutamyl-peptidase I	Pgpep1	0.882	0.213	1.982	0.012	0.754	0.302	1.820	0.048
1377576_at	AA891800	pyrophosphatase (inorganic) 2 (predicted)	Ppa2_predicted	0.098	0.022	0.342	0.000	0.081	0.000	0.491	0.011
1388960_at	AI412958	pyrophosphatase (mapped)	Pyp_mapped	0.483	0.072	1.579	0.008	0.552	0.010	1.428	0.004
1373640_at	AW525211	pyrroline-5-carboxylate reductase family, member 2	Pycr2	0.346	0.032	0.705	0.004	0.342	0.063	0.710	0.025
1392535_at	AI169002	pyrroline-5-carboxylate reductase-like	Pycrl	0.599	0.050	0.759	0.236	0.521	0.413	0.556	0.225
1388521_at	BG380693	pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase) (predicted)	Pycs_predicted	0.747	0.102	0.625	0.001	0.621	0.027	0.752	0.029
1386917_at	NM_012744	Pyruvate carboxylase	Pc	0.375	0.397	0.469	0.005	0.751	0.209	0.606	0.124
1371388_at	BM389223	pyruvate dehydrogenase (lipoamide) beta	Pdhb	0.583	0.037	0.743	0.003	0.518	0.010	0.727	0.077
1383698_at	BF561717	pyruvate dehydrogenase E1 alpha 1	Pdha1	1.824	0.098	1.345	0.194	2.332	0.031	1.733	0.030
1371380_at	AI411413	pyruvate dehydrogenase E1 alpha 1	Pdha1	0.909	0.598	1.151	0.168	1.098	0.026	1.367	0.007
1368079_at	NM_053826	pyruvate dehydrogenase kinase, isoenzyme 1	Pdk1	0.929	0.812	15.713	0.051	0.974	0.754	9.334	0.041
1384315_at	BM389330	pyruvate dehydrogenase kinase, isoenzyme 3 (mapped)	Pdk3_mapped	0.956	0.210	0.606	0.067	0.927	0.116	0.673	0.082
1369150_at	NM_053551	pyruvate dehydrogenase kinase, isoenzyme 4	Pdk4	1.094	0.112	1.811	0.230	1.010	0.447	2.104	0.130
1370509_at	AF062741	pyruvate dehydrogenase phosphatase isoenzyme 2	Pdp2	0.895	0.164	1.626	0.069	0.797	0.304	1.063	0.361
1380045_at	AI411446	pyruvate dehydrogenase phosphatase isoenzyme 2	Pdp2	1.294	0.652	0.980	0.701	0.830	0.615	0.835	0.458
1368651_at	M17685	pyruvate kinase, liver and red blood cell	Pklr	0.507	0.018	0.201	0.000	0.525	0.020	0.223	0.025
1387263_at	NM_012624	pyruvate kinase, liver and red blood cell	Pklr	0.511	0.067	0.150	0.001	0.318	0.049	0.275	0.008
1397851_at	BE102226	Quaking homolog, KH domain RNA binding (mouse)	Qki	0.991	0.858	1.066	0.489	1.209	0.247	0.950	0.686
1372542_at	BE113281	Quaking homolog, KH domain RNA binding (mouse)	Qki	1.051	0.874	1.033	0.446	1.011	0.835	1.069	0.755
1383238_at	AI060136	queuine tRNA-ribosyltransferase 1	Qtrt1	1.001	0.993	3.364	0.023	0.999	0.961	1.757	0.010
1367695_at	NM_022390	quinoid dihydropteridine reductase	Qdpr	0.534	0.173	1.217	0.806	0.511	0.023	1.103	0.274
1372672_at	AI407095	quinolinate phosphoribosyltransferase	Qprt	1.068	0.783	0.858	0.478	1.519	0.225	1.086	0.507
1373481_at	AI227908	R3H domain containing 1	R3hdm1	0.941	0.031	1.791	0.001	1.042	0.636	1.519	0.003
1398780_at	NM_031774	Rab acceptor 1 (prenylated)	Rabac1	0.814	0.765	0.693	0.105	0.625	0.020	0.810	0.103
1396303_at	BI291790	Rab acceptor 1 (prenylated)	Rabac1	0.944	0.850	1.069	0.283	1.186	0.252	0.868	0.399
1387911_at	L10416	RAB geranylgeranyl transferase, b subunit	Rabggtb	1.250	0.138	2.404	0.008	0.984	0.680	1.683	0.021
1384089_at	AI575052	RAB guanine nucleotide exchange factor (GEF) 1 (predicted)	Rabgef1_predicted	1.673	0.091	1.759	0.009	1.175	0.820	1.395	0.412

1382039_at	AA944201	RAB, member of RAS oncogene family-like 2A	Rabl2a	1.420	0.069	1.013	0.727	1.915	0.224	0.888	0.740
1376807_at	BF417476	RAB, member of RAS oncogene family-like 3 (predicted)	Rabl3_predicted	0.600	0.467	0.790	0.006	0.918	0.150	0.866	0.206
1379349_a_at	AI406710	RAB, member of RAS oncogene family-like 5	Rabl5	1.034	0.995	0.932	0.579	1.044	0.953	0.881	0.108
1398841_at	AI411122	RAB1, member RAS oncogene family	Rab1	0.676	0.241	1.005	0.916	0.841	0.642	0.943	0.074
1373022_at	AI231860	RAB1, member RAS oncogene family	Rab1	0.627	0.559	0.688	0.001	0.640	0.228	0.672	0.007
1375338_at	AA945841	RAB10, member RAS oncogene family	Rab10	0.829	0.362	0.575	0.008	0.845	0.065	0.698	0.005
1368847_at	NM_017359	RAB10, member RAS oncogene family	Rab10	1.058	0.776	1.811	0.004	0.871	0.314	1.633	0.016
1398814_at	NM_031152	RAB11a, member RAS oncogene family	Rab11a	1.279	0.349	1.380	0.011	1.323	0.124	1.206	0.011
1374069_at	BE118560	RAB11a, member RAS oncogene family	Rab11a	1.167	0.434	0.461	0.007	1.584	0.328	0.591	0.013
1375163_at	BI275870	RAB11B, member RAS oncogene family	Rab11b	0.707	0.220	1.015	0.037	0.796	0.076	1.102	0.106
1398825_at	D01046	RAB11B, member RAS oncogene family	Rab11b	0.977	0.900	1.393	0.141	0.678	0.037	0.979	0.348
1388140_at	AW253722	RAB13, member RAS oncogene family	Rab13	2.513	0.078	1.703	0.238	1.781	0.078	4.196	0.026
1367884_at	NM_053589	RAB14, member RAS oncogene family	Rab14	0.780	0.192	1.393	0.057	0.736	0.065	0.958	0.561
1376796_at	BG372452	RAB14, member RAS oncogene family	Rab14	1.014	0.752	1.908	0.080	0.770	0.354	1.254	0.346
1373646_at	BM384841	RAB15, member RAS onocogene family	Rab15	9.374	0.034	6.952	0.032	2.521	0.071	1.755	0.093
1389292_at	AI411439	RAB18, member RAS oncogene family /// similar to Rab18 (predicted)	Rab18 /// RGD1563713_predicted	0.769	0.753	0.982	0.758	0.776	0.859	0.803	0.052
1392681_at	AW522578	RAB2, member RAS oncogene family	Rab2	0.873	0.399	0.710	0.001	0.676	0.050	0.657	0.022
1370087_at	NM_031718	RAB2, member RAS oncogene family	Rab2	0.803	0.969	1.597	0.010	0.603	0.229	1.261	0.148
1376029_at	BI295991	RAB2, member RAS oncogene family-like	Rab2l	10.942	0.000	11.710	0.001	19.723	0.000	19.133	0.000
1388839_at	AI233143	RAB2, member RAS oncogene family-like	Rab2l	0.933	0.913	0.798	0.499	1.406	0.932	1.693	0.839
1383089_at	BM386264	RAB21, member RAS oncogene family	Rab21	1.589	0.001	2.308	0.000	1.598	0.000	2.546	0.002
1376705_a_at	BF289020	RAB24, member RAS oncogene family	Rab24	1.120	0.361	1.779	0.000	0.866	0.385	1.392	0.001
1377363_at	AA945861	RAB25, member RAS oncogene family (predicted)	Rab25_predicted	0.579	0.650	1.101	0.536	0.426	0.037	0.942	0.469
1369004_at	NM_133580	RAB26, member RAS oncogene family	Rab26	0.937	0.878	0.801	0.035	0.981	0.892	0.802	0.073
1377669_at	BM389524	RAB27A, member RAS oncogene family	Rab27a	0.568	0.374	0.306	0.006	0.582	0.036	0.346	0.018
1384852_at	AI043615	RAB27A, member RAS oncogene family	Rab27a	0.908	0.986	0.827	0.531	0.921	0.353	0.796	0.593
1368216_at	NM_053978	RAB28, member RAS oncogene family	Rab28	0.803	0.077	1.024	0.238	0.889	0.131	1.229	0.032
1375985_at	BF282984	RAB2B, member RAS oncogene family	Rab2b	0.404	0.213	0.464	0.005	0.756	0.194	0.569	0.003
1388892_at	BF395178	RAB2B, member RAS oncogene family	Rab2b	1.016	0.394	0.898	0.380	1.243	0.720	0.899	0.120
1374502_at	AI180286	RAB3 GTPase activating protein subunit 2	Rab3gap2	1.580	0.058	1.786	0.010	1.417	0.097	1.574	0.087
1373894_at	BF410946	RAB31, member RAS oncogene family	Rab31	2.347	0.057	1.328	0.249	1.260	0.308	0.999	0.997
1394665_at	AI408761	RAB33B, member of RAS oncogene family (predicted)	Rab33b_predicted	0.975	0.523	1.080	0.261	1.086	0.775	1.209	0.830
1376573_at	BM391604	RAB34, member of RAS oncogene family	Rab34	0.819	0.206	1.497	0.009	0.510	0.071	1.126	0.691
1390268_at	AI013484	RAB35, member RAS oncogene family /// similar to RAB35, member RAS oncogene family	Rab35 /// LOC498191	1.540	0.283	1.833	0.043	1.362	0.006	1.798	0.086
1380132_at	BI291804	RAB3A interacting protein	Rab3ip	1.513	0.083	1.056	0.764	0.973	0.839	1.453	0.182
1387821_at	NM_017313	RAB3A interacting protein	Rab3ip	1.223	0.589	1.741	0.014	0.791	0.371	1.202	0.670
1391434_at	BF389910	RAB3A, member RAS oncogene family	Rab3a	0.148	0.029	0.608	0.034	0.062	0.002	0.483	0.048
1369816_at	NM_013018	RAB3A, member RAS oncogene family	Rab3a	0.369	0.032	0.583	0.241	0.379	0.040	0.297	0.023
1370061_at	NM_031091	RAB3B, member RAS oncogene family	Rab3b	0.927	0.887	0.337	0.001	1.030	0.782	0.386	0.031
1387147_at	NM_133536	RAB3C, member RAS oncogene family	Rab3c	0.969	0.527	1.006	0.657	0.731	0.080	1.530	0.048
1370055_at	M83681	RAB3D, member RAS oncogene family	Rab3d	0.402	0.257	0.539	0.000	0.322	0.004	0.501	0.004
1383826_at	AA924620	Rab40b, member RAS oncogene family (predicted)	Rab40b_predicted	0.459	0.383	0.372	0.022	0.223	0.030	0.375	0.024
1370181_at	BF281403	RAB4A, member RAS oncogene family	Rab4a	0.435	0.007	0.460	0.003	0.417	0.046	0.545	0.127
1367955_at	NM_017355	RAB4B, member RAS oncogene family	Rab4b	0.644	0.564	0.937	0.090	0.521	0.677	0.612	0.090
1388800_at	AI406667	RAB5A, member RAS oncogene family	Rab5a	1.276	0.056	2.001	0.002	1.278	0.023	1.616	0.005
1387641_at	NM_022692	RAB5A, member RAS oncogene family	Rab5a	0.972	0.804	1.285	0.040	1.262	0.486	1.509	0.694
1388823_at	BI274642	RAB5B, member RAS oncogene family (predicted)	Rab5b_predicted	1.652	0.061	1.405	0.003	2.384	0.002	1.961	0.009
1399153_at	AA996576	RAB5B, member RAS oncogene family (predicted)	Rab5b_predicted	1.033	0.750	0.961	0.222	1.040	0.719	0.644	0.186
1393288_at	BF560790	RAB5B, member RAS oncogene family (predicted)	Rab5b_predicted	1.051	0.821	1.013	0.961	1.034	0.619	0.944	0.113
1371836_at	H35233	RAB5C, member RAS oncogene family (predicted)	Rab5c_predicted	0.921	0.823	1.497	0.071	1.303	0.093	1.567	0.425
1373375_at	BI275835	Rab6 interacting protein 1 (predicted)	Rab6ip1_predicted	0.827	0.511	0.885	0.144	0.993	0.935	0.779	0.156
1397229_at	BF565781	RAB6A, member RAS oncogene family	Rab6a	1.487	0.297	1.125	0.123	1.223	0.095	1.054	0.877
1372707_at	AI412961	RAB6A, member RAS oncogene family	Rab6a	0.696	0.351	1.007	0.464	0.602	0.157	0.966	0.261
1371103_at	AA686757	RAB6A, member RAS oncogene family	Rab6a	1.057	0.962	3.824	0.017	0.679	0.000	1.208	0.021
1387797_at	AA946057	RAB7, member RAS oncogene family	Rab7	1.102	0.067	0.960	0.636	1.670	0.007	0.982	0.508
1398838_at	NM_023950	RAB7, member RAS oncogene family	Rab7	1.686	0.168	1.457	0.118	2.023	0.233	1.328	0.062
1368096_at	NM_133590	RAB7, member RAS oncogene family-like 1	Rab7l1	0.964	0.845	0.423	0.016	1.022	0.967	0.578	0.096
1370001_at	NM_053998	RAB8A, member RAS oncogene family	Rab8a	0.699	0.049	0.915	0.307	0.705	0.009	0.853	0.037
1391347_at	BF398743	RAB8B, member RAS oncogene family	Rab8b	7.178	0.005	1.672	0.124	5.615	0.013	2.340	0.085
1370539_at	U53475	RAB8B, member RAS oncogene family	Rab8b	1.249	0.118	1.241	0.090	1.054	0.721	1.007	0.954

1387186_at	NM_053458	RAB9, member RAS oncogene family	Rab9	1.959	0.081	2.097	0.003	1.986	0.023	2.608	0.001
1367980_at	NM_019124	rabaptin, RAB GTPase binding effector protein 1	Rabep1	1.123	0.784	1.336	0.010	0.847	0.117	1.242	0.154
1367981_at	U70777	rabaptin, RAB GTPase binding effector protein 1	Rabep1	1.021	0.881	1.417	0.069	0.719	0.284	1.909	0.127
1395843_at	AW143625	Rabaptin, RAB GTPase binding effector protein 1	Rabep1	0.761	0.905	0.899	0.150	1.075	0.058	0.862	0.169
1387176_at	NM_133591	rabphilin 3A-like (without C2 domains)	Rph3al	1.224	0.171	1.455	0.106	0.889	0.746	0.929	0.691
1373658_at	AI409259	Rac GTPase-activating protein 1 (predicted)	Racgap1_predicted	0.927	0.636	0.433	0.048	0.678	0.747	0.694	0.064
1377338_at	BF395193	RAD1 homolog (S. pombe) (predicted)	Rad1_predicted	1.122	0.928	1.454	0.021	1.024	0.991	1.119	0.278
1385090_at	BF389852	RAD17 homolog (S. pombe)	Rad17	0.878	0.983	1.809	0.013	0.755	0.303	1.874	0.023
1392449_at	BI282152	RAD18 homolog (S. cerevisiae) (predicted)	Rad18_predicted	1.032	0.921	1.223	0.064	0.811	0.288	1.352	0.383
1391491_a_at	BG377084	RAD23b homolog (S. cerevisiae)	Rad23b	0.749	0.279	2.236	0.028	0.627	0.176	1.214	0.398
1388550_at	BI295122	RAD23b homolog (S. cerevisiae)	Rad23b	0.692	0.609	1.842	0.008	0.560	0.026	1.496	0.001
1385565_at	BF564080	RAD50 homolog (S. cerevisiae)	Rad50	0.963	0.167	1.035	0.931	1.072	0.696	1.357	0.710
1390588_at	AI549091	RAD51-like 3 (S. cerevisiae) (predicted)	Rad51l3_predicted	1.015	0.979	0.973	0.541	1.035	0.884	0.998	0.990
1377902_a_at	AA893822	RAD52 homolog (S. cerevisiae) (predicted)	Rad52_predicted	0.592	0.025	1.131	0.184	0.610	0.012	1.433	0.235
1389453_at	AA818364	RAD52 motif 1 (predicted)	Rdm1_predicted	0.609	0.131	2.664	0.003	0.487	0.797	1.545	0.112
1397576_at	AI576144	Rad54 like 2 (S. cerevisiae) (predicted)	Rad54l2_predicted	1.001	0.897	0.993	0.101	1.251	0.058	1.006	0.923
1396511_at	AI763815	RAD9 homolog B (S. cerevisiae)	Rad9b	1.176	0.565	0.986	0.885	1.012	0.028	1.042	0.957
1387622_at	NM_021849	radical fringe gene homolog (Drosophila)	Rfng	0.997	0.988	1.000	0.984	0.998	0.994	0.994	0.967
1378902_at	BF413695	radical S-adenosyl methionine and flavodoxin domains 1 (predicted)	Rsafd1_predicted	1.617	0.226	0.860	0.096	1.384	0.147	1.092	0.386
1383825_at	AW527313	radixin	Rdx	0.473	0.006	1.024	0.471	0.924	0.089	0.817	0.464
1396207_at	BF565167	radixin	Rdx	0.607	0.016	1.341	0.340	0.669	0.601	0.838	0.860
1375542_at	AI407092	Radixin	Rdx	0.662	0.308	0.994	0.456	0.430	0.181	0.825	0.167
1388619_at	AW535398	radixin	Rdx	0.629	0.541	0.909	0.995	0.377	0.088	0.833	0.431
1378287_at	BI297296	radixin	Rdx	0.956	0.982	0.637	0.226	0.998	0.977	0.942	0.813
1395465_at	BF419215	RAE1 RNA export 1 homolog (S. pombe)	Rae1	1.290	0.323	1.093	0.669	1.204	0.365	1.095	0.972
1392464_at	BM392372	RAE1 RNA export 1 homolog (S. pombe)	Rae1	0.930	0.721	1.537	0.058	1.430	0.372	1.594	0.000
1368217_at	NM_032067	ralA binding protein 1	Ralbp1	1.535	0.007	1.131	0.182	1.182	0.016	1.118	0.092
1368218_at	U28830	ralA binding protein 1	Ralbp1	1.000	0.799	0.997	0.980	1.001	0.838	0.996	0.966
1389233_at	BI289596	RalBP1 associated Eps domain containing protein (predicted)	Reps1_predicted	0.460	0.421	0.683	0.018	0.782	0.238	0.828	0.032
1375427_at	AI411580	RAN binding protein 1 (predicted)	Ranbp1_predicted	0.880	0.303	1.382	0.551	0.819	0.641	0.819	0.746
1390577_at	BF396940	RAN binding protein 10 (predicted)	Ranbp10_predicted	1.156	0.693	1.041	0.735	1.142	0.937	1.312	0.169
1373955_at	BI280339	RAN binding protein 5 (predicted)	Ranbp5_predicted	1.316	0.190	4.321	0.000	0.852	0.228	3.249	0.004
1384551_at	AI578134	RAN binding protein 6 (predicted)	Ranbp6_predicted	0.627	0.039	0.898	0.074	0.613	0.215	0.827	0.265
1388341_at	BI285671	RAN GTPase activating protein 1	Rangap1	0.799	0.292	1.551	0.025	0.829	0.081	1.134	0.261
1367590_at	NM_053439	RAN, member RAS oncogene family	Ran	0.890	0.601	2.531	0.000	0.738	0.005	2.173	0.000
1373933_at	BF407276	Rap guanine nucleotide exchange factor (GEF) 2 (predicted)	Rapgef2_predicted	0.957	0.680	0.964	0.476	0.804	0.886	0.927	0.112
1368660_at	NM_021690	Rap guanine nucleotide exchange factor (GEF) 3	Rapgef3	3.007	0.070	1.020	0.453	1.243	0.642	1.017	0.046
1371081_at	U78517	Rap guanine nucleotide exchange factor (GEF) 4	Rapgef4	1.436	0.073	0.385	0.016	0.719	0.206	0.411	0.072
1377529_at	BF404045	Rap guanine nucleotide exchange factor (GEF) 4	Rapgef4	1.255	0.548	0.678	0.329	1.159	0.619	0.696	0.243
1389181_at	BM389650	Rap guanine nucleotide exchange factor (GEF) 6 (predicted)	Rapgef6_predicted	0.786	0.278	0.711	0.033	0.757	0.009	0.708	0.048
1378835_at	AI145398	Rap guanine nucleotide exchange factor (GEF) 6 (predicted)	Rapgef6_predicted	0.715	0.769	0.977	0.951	1.685	0.168	0.977	0.828
1387928_at	AF288611	Rap2 interacting protein	Rap2ip	1.138	0.033	0.498	0.024	1.116	0.089	0.484	0.026
1379552_s_at	AI535169	Rap2 interacting protein	Rap2ip	1.536	0.162	0.954	0.255	1.566	0.512	0.670	0.011
1373237_at	BI281233	Rap2 interacting protein x	Ripx	0.796	0.629	0.520	0.033	0.548	0.003	0.778	0.121
1378194_a_at	BG671338	rap2 interacting protein x	Ripx	1.053	0.992	0.975	0.130	0.699	0.038	1.264	0.505
1392922_at	BE116619	RAP2B, member of RAS oncogene family	Rap2b	1.650	0.005	1.068	0.824	1.812	0.021	1.238	0.605
1379397_at	BE106199	RAR-related orphan receptor alpha (predicted)	Rora_predicted	3.475	0.001	5.636	0.013	2.535	0.051	3.746	0.077
1377029_at	AI235414	RAR-related orphan receptor alpha (predicted)	Rora_predicted	1.346	0.019	1.702	0.083	2.594	0.004	1.640	0.258
1371257_at	BF386897	RAR-related orphan receptor beta (predicted)	Rorb_predicted	1.002	0.979	2.010	0.064	0.985	0.988	2.014	0.066
1376949_at	BE099848	Ras and a-factor-converting enzyme 1 homolog (S. cerevisiae)	Rce1	1.054	0.895	2.175	0.009	0.701	0.073	1.803	0.016
1372365_at	BM392293	Ras and Rab interactor 2 (predicted)	Rin2_predicted	1.589	0.048	0.522	0.014	2.434	0.007	0.780	0.056
1374525_at	BF284017	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1 (predicted)	Raph1_predicted	5.607	0.001	1.814	0.005	2.821	0.030	1.640	0.073
1376658_at	BF391087	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1 (predicted)	Raph1_predicted	10.028	0.013	7.152	0.015	3.219	0.025	4.161	0.040
1385987_at	BE098157	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1 (predicted)	Raph1_predicted	0.860	0.599	1.034	0.467	0.909	0.607	0.723	0.437
1373989_at	AI103943	Ras association (RalGDS/AF-6) domain family 1	Rassf1	1.996	0.041	2.707	0.003	1.815	0.100	2.294	0.004
1392688_at	AI113186	Ras association (RalGDS/AF-6) domain family 1	Rassf1	1.000	0.978	1.006	0.797	1.272	0.200	1.005	0.974
1391823_at	AA956842	Ras association (RalGDS/AF-6) domain family 3 (predicted)	Rassf3_predicted	2.218	0.048	1.057	0.786	2.038	0.040	0.681	0.488
1370415_at	AF002251	Ras association (RalGDS/AF-6) domain family 5	Rassf5	1.066	0.541	1.003	0.824	1.005	0.522	1.000	0.529
1379315_at	BM385768	Ras association (RalGDS/AF-6) domain family 7 (predicted)	Rassf7_predicted	1.006	0.969	2.458	0.043	0.849	0.881	1.947	0.099
1373624_at	AA945713	Ras association (RalGDS/AF-6) domain family 8 (predicted)	Rassf8_predicted	1.192	0.274	1.582	0.016	0.622	0.365	1.190	0.281
1398787_at	NM_013216	Ras homolog enriched in brain	Rheb	0.852	0.504	1.282	0.100	0.878	0.358	1.364	0.029

1399027_at	AI408053	ras homolog gene family, member A	Rhoa	0.930	0.770	1.584	0.015	0.761	0.389	1.344	0.020
1370130_at	NM_057132	ras homolog gene family, member A	Rhoa	0.898	0.978	1.684	0.298	0.900	0.353	1.177	0.749
1369958_at	NM_022542	ras homolog gene family, member B	Rhob	2.315	0.289	0.547	0.102	3.064	0.208	0.422	0.017
1393287_at	AW915147	Ras homolog gene family, member C (predicted)	Rhoc_predicted	1.921	0.001	1.050	0.338	5.224	0.003	1.097	0.576
1371659_at	AA891940	ras homolog gene family, member C (predicted)	Rhoc_predicted	2.849	0.003	1.761	0.083	3.075	0.001	1.450	0.053
1382197_at	AA955648	ras homolog gene family, member D (predicted)	Rhod_predicted	1.402	0.041	2.616	0.019	2.096	0.108	2.580	0.021
1389227_at	BG375902	Ras homolog gene family, member G	Rhog	2.126	0.067	1.776	0.038	1.675	0.013	1.733	0.049
1367874_at	AA849961	ras homolog gene family, member Q	Rhoq	2.963	0.028	1.720	0.032	2.010	0.063	1.285	0.335
1386967_at	NM_053522	ras homolog gene family, member Q	Rhoq	1.146	0.636	1.606	0.016	1.010	0.873	1.179	0.018
1372731_at	AI228628	ras homolog gene family, member T1 (predicted)	Rhot1_predicted	0.719	0.422	1.452	0.024	0.612	0.003	0.996	0.387
1374534_at	AI233243	ras homolog gene family, member T2	Rhot2	0.818	0.210	1.135	0.916	0.759	0.347	0.842	0.900
1397581_at	BF416022	ras homolog gene family, member V	Rhov	4.135	0.063	2.862	0.031	3.307	0.003	2.384	0.020
1370627_at	AF097887	ras homolog gene family, member V	Rhov	1.269	0.577	1.069	0.203	0.999	0.994	0.998	0.965
1370085_at	NM_013135	RAS p21 protein activator 1	Rasa1	0.904	0.874	0.960	0.893	0.997	0.991	0.870	0.694
1378740_at	AI577567	RAS protein activator like 2 (predicted)	Rasal2_predicted	1.555	0.135	1.928	0.046	0.855	0.651	1.356	0.083
1387806_at	NM_134346	RAS related protein 1b	Rap1b	1.319	0.359	0.821	0.025	1.307	0.213	0.923	0.056
1387908_at	AF239157	RAS, dexamethasone-induced 1	Rasd1	8.685	0.004	2.229	0.013	3.715	0.007	1.750	0.073
1370976_at	BE118966	Ras-GTPase-activating protein SH3-domain binding protein	G3bp	1.457	0.108	1.904	0.001	1.512	0.022	1.896	0.004
1389821_at	AA800815	Ras-induced senescence 1	Ris1	1.115	0.252	1.129	0.577	0.898	0.212	0.929	0.299
1389037_at	BM986252	Ras-like without CAAX 1 (predicted)	Rit1_predicted	1.004	0.509	1.000	0.912	0.913	0.654	0.950	0.911
1373774_at	AI412619	Ras-like without CAAX 2	Rit2	0.336	0.118	0.144	0.000	0.425	0.007	0.145	0.000
1383699_at	BG673521	Ras-like without CAAX 2	Rit2	0.933	0.993	0.536	0.010	1.070	0.994	0.538	0.016
1388332_at	AA799542	Ras-related C3 botulinum toxin substrate 1	Rac1	1.096	0.330	0.654	0.001	1.113	0.076	0.832	0.020
1372513_at	AI103616	ras-related C3 botulinum toxin substrate 1	Rac1	1.402	0.461	3.112	0.002	1.104	0.835	2.078	0.024
1367736_at	NM_053973	Ras-related GTP binding A	Rraga	0.782	0.369	0.591	0.005	0.774	0.162	0.708	0.121
1369696_at	NM_053972	Ras-related GTP binding B	RragB	0.341	0.009	0.268	0.006	0.334	0.000	0.311	0.026
1376881_at	AW528057	Ras-related GTP binding B	RragB	0.203	0.009	0.090	0.003	0.127	0.038	0.103	0.042
1377791_at	BI299500	Ras-related GTP binding B	RragB	0.256	0.031	0.070	0.003	0.158	0.002	0.205	0.019
1371723_at	BE110635	Ras-related GTP binding C (predicted)	Rragc_predicted	1.816	0.045	3.039	0.000	1.402	0.024	3.303	0.007
1382537_at	AA899991	Ras-related GTP binding C (predicted)	Rragc_predicted	1.075	0.159	2.463	0.025	0.682	0.288	2.367	0.048
1373427_at	BI288816	Ras-related GTP binding D (predicted)	Rragd_predicted	1.456	0.129	6.298	0.000	1.135	0.308	4.247	0.001
1388615_at	AI410112	RAS-related protein 1a	Rap1a	0.962	0.724	1.313	0.010	0.833	0.239	1.273	0.003
1387915_at	AF367467	Ratsg2	Ratsg2	1.002	0.690	1.621	0.009	1.117	0.386	1.391	0.023
1372427_at	AI170542	RAVER1 homolog (human)	Raver1h	0.767	0.889	0.618	0.082	1.007	0.896	0.680	0.012
1385194_at	BG671668	RB1-inducible coiled-coil 1 (predicted)	Rb1cc1_predicted	1.482	0.113	1.596	0.080	1.976	0.114	1.638	0.056
1379449_at	BG670920	RB1-inducible coiled-coil 1 (predicted)	Rb1cc1_predicted	1.241	0.385	0.831	0.052	1.702	0.102	0.893	0.082
1374331_at	AI178068	rcd1 (required for cell differentiation) homolog 1 (S. pombe)	Rqcd1	1.045	0.387	0.587	0.014	1.101	0.036	0.879	0.190
1392544_at	AI044879	rcd1 (required for cell differentiation) homolog 1 (S. pombe)	Rqcd1	0.812	0.799	0.616	0.125	0.886	0.199	0.641	0.095
1372290_at	BI275979	RD RNA-binding protein	Rdbp	0.623	0.056	1.352	0.034	0.763	0.016	1.298	0.356
1375173_at	BM392302	RDCR-0918-3 protein	LOC246120	1.511	0.037	1.421	0.013	1.266	0.042	1.516	0.002
1369922_at	NM_139255	RDCR-0918-3 protein	LOC246120	1.409	0.079	0.680	0.322	1.163	0.845	1.952	0.920
1382400_at	BE104395	rearranged L-myc fusion sequence (predicted)	Rlf_predicted	1.121	0.233	3.130	0.005	0.490	0.029	2.926	0.004
1367701_at	NM_031646	receptor (calcitonin) activity modifying protein 2	Ramp2	0.880	0.963	1.808	0.008	0.978	0.511	0.513	0.058
1381279_at	BF412519	receptor (TNFRSF)-interacting serine-threonine kinase 2	Ripk2	48.629	0.005	32.074	0.000	35.594	0.002	10.350	0.001
1371481_at	BI274372	receptor accessory protein 5 (predicted)	Reep5_predicted	0.791	0.502	1.545	0.002	0.933	0.334	1.250	0.017
1372841_at	BG376982	receptor accessory protein 6	Reep6	0.766	0.058	0.975	0.307	0.762	0.058	0.991	0.098
1380938_at	BE106206	receptor interacting protein kinase 5	Ripk5	0.670	0.066	0.494	0.000	0.838	0.024	0.492	0.003
1395736_at	BG666455	receptor interacting protein kinase 5	Ripk5	0.719	0.200	0.568	0.011	0.465	0.160	0.396	0.037
1392588_at	BG664535	receptor interacting protein kinase 5	Ripk5	0.769	0.382	0.508	0.053	0.479	0.003	0.431	0.008
1379285_at	AA819788	receptor transporter protein 4 (predicted)	Rtp4_predicted	17.228	0.003	11.762	0.000	35.566	0.000	30.234	0.000
1373028_at	BE113287	receptor-like tyrosine kinase	Ryk	0.693	0.475	0.474	0.061	0.677	0.568	0.509	0.045
1379973_at	AW530847	Receptor-like tyrosine kinase	Ryk	0.917	0.755	1.046	0.358	1.373	0.941	0.943	0.067
1371101_at	AB073721	receptor-like tyrosine kinase	Ryk	0.659	0.958	0.647	0.779	0.668	0.909	0.390	0.590
1389705_at	AI138061	recombination activating gene 1 activating protein 1 (predicted)	Rag1ap1_predicted	1.185	0.545	0.961	0.525	1.032	0.850	1.153	0.080
1374517_at	AA891612	RecQ protein-like	Recql	0.603	0.379	0.836	0.140	0.561	0.034	0.697	0.010
1393087_at	BI277503	RecQ protein-like 5 (predicted)	Recql5_predicted	1.068	0.449	0.817	0.066	1.214	0.285	0.824	0.437
1370938_at	AI535144	reg I binding protein I	Rbp1	0.578	0.047	0.423	0.040	0.524	0.029	0.503	0.048
1368629_at	NM_012641	regenerating islet-derived 1	Reg1	0.829	0.942	1.592	0.447	0.999	0.956	1.293	0.947
1367904_at	NM_019278	regulated endocrine-specific protein 18	Resp18	0.920	0.684	0.514	0.006	0.842	0.104	0.680	0.000
1369333_a_at	NM_053945	regulating synaptic membrane exocytosis 2	Rims2	0.579	0.155	3.132	0.008	0.804	0.385	1.315	0.300
1383279_at	BE119554	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	Rcbtb2	0.655	0.084	0.476	0.087	0.774	0.133	0.560	0.201

1386610_at	BG665272	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	Rcbtb2	0.596	0.362	0.934	0.915	0.724	0.477	0.929	0.997
1371563_at	BE109154	regulator of chromosome condensation 2 (predicted)	Rcc2_predicted	0.857	0.098	1.547	0.056	1.035	0.083	1.860	0.003
1373777_at	BF391820	Regulator of G-protein signaling 16	Rgs16	0.303	0.003	0.170	0.002	0.365	0.000	0.213	0.024
1394280_at	AW140991	regulator of G-protein signaling 17 (predicted)	Rgs17_predicted	0.485	0.038	3.010	0.004	0.582	0.076	3.245	0.009
1398483_at	AI229118	Regulator of G-protein signaling 17 (predicted)	Rgs17_predicted	0.673	0.111	1.605	0.060	0.691	0.118	1.589	0.020
1391075_at	AI179271	regulator of G-protein signaling 17 (predicted)	Rgs17_predicted	0.764	0.912	3.664	0.001	0.718	0.361	2.773	0.006
1387074_at	AY043246	regulator of G-protein signaling 2	Rgs2	1.492	0.166	1.093	0.289	2.224	0.089	0.867	0.799
1368505_at	NM_017214	regulator of G-protein signaling 4	Rgs4	1.360	0.128	1.385	0.061	1.042	0.458	1.446	0.104
1368506_at	U27767	regulator of G-protein signaling 4	Rgs4	1.815	0.303	2.127	0.066	0.665	0.169	1.742	0.058
1368373_at	NM_019343	regulator of G-protein signaling 7	Rgs7	0.606	0.004	1.438	0.058	0.763	0.191	1.402	0.042
1368500_a_at	NM_019224	regulator of G-protein signaling 9	Rgs9	2.038	0.000	1.356	0.142	1.170	0.161	0.849	0.139
1382090_at	AI070376	Regulator of G-protein signaling 9	Rgs9	2.475	0.017	1.320	0.282	1.206	0.905	0.504	0.146
1376443_at	BF419009	Regulator of G-protein signalling 3	Rgs3	1.007	0.981	0.934	0.257	0.954	0.312	0.784	0.246
1392036_at	BE102087	Regulator of nonsense transcripts 1 (predicted)	Rent1_predicted	0.884	0.234	1.067	0.659	0.881	0.181	0.695	0.034
1377152_at	AI111991	regulatory factor X, 1 (influences HLA class II expression) (predicted)	Rfx1_predicted	2.027	0.542	1.968	0.023	1.240	0.695	1.590	0.165
1382553_at	AI137120	Regulatory factor X, 3 (influences HLA class II expression)	Rfx3	1.498	0.317	0.710	0.364	1.664	0.243	0.681	0.056
1389515_at	AW251269	regulatory factor X-associated ankyrin-containing protein	Rfxank	0.616	0.242	1.222	0.517	0.481	0.004	1.086	0.085
1372133_at	AA955287	related RAS viral (r-ras) oncogene homolog 2	Rras2	1.835	0.176	3.031	0.003	2.519	0.003	2.677	0.010
1382058_at	BI292115	related RAS viral (r-ras) oncogene homolog 2	Rras2	1.185	0.354	2.932	0.011	1.304	0.291	2.815	0.009
1380655_at	AI317878	renal tumor antigen	Rage	1.086	0.993	2.429	0.159	1.106	0.923	1.552	0.444
1370910_at	BF283113	replication factor C (activator 1) 2	Rfc2	0.331	0.007	0.697	0.005	0.422	0.001	0.779	0.081
1388458_at	BI291451	replication factor C (activator 1) 4 (predicted)	Rfc4_predicted	0.892	0.695	4.179	0.003	0.750	0.502	2.750	0.043
1374919_at	BE103543	Replication factor C 1	Recc1	1.427	0.129	1.623	0.072	2.299	0.110	1.428	0.011
1388135_at	BM385924	replication protein A2	Rpa2	1.511	0.068	1.016	0.981	0.999	0.982	0.997	0.989
1398308_at	BM383451	replication protein A3 (predicted)	Rpa3_predicted	0.702	0.026	0.604	0.015	0.682	0.018	0.894	0.945
1368080_at	NM_054008	response gene to complement 32	Rgc32	1.002	0.353	15.849	0.006	1.020	0.228	5.615	0.045
1389972_at	AA943681	Response gene to complement 32	Rgc32	1.001	0.985	15.347	0.002	0.926	0.025	9.890	0.014
1367993_at	NM_031745	restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)	Rsn	0.794	0.105	1.036	0.643	0.343	0.054	1.315	0.349
1394241_at	BF401902	restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)	Rsn	0.965	0.916	1.340	0.065	0.659	0.111	0.976	0.427
1388208_a_at	AJ299017	ret proto-oncogene	Ret	0.629	0.097	0.947	0.929	0.715	0.185	0.375	0.017
1371112_at	AJ299017	ret proto-oncogene	Ret	0.740	0.287	1.064	0.523	0.379	0.225	0.891	0.462
1370989_at	AI639318	ret proto-oncogene	Ret	0.666	0.620	0.269	0.000	0.395	0.025	0.290	0.010
1390011_at	BI296601	Retbindin (predicted)	Rtbnd_predicted	1.016	0.969	0.999	0.851	1.000	0.576	0.956	0.699
1375921_at	BF281577	Reticulocalbin 1 (predicted)	Rcn1_predicted	0.794	0.015	0.970	0.755	0.685	0.014	0.779	0.303
1382767_at	AI175752	Reticulocalbin 1 (predicted)	Rcn1_predicted	0.635	0.044	1.235	0.751	1.549	0.292	1.506	0.340
1393643_at	AI112962	reticulocalbin 1 (predicted)	Rcn1_predicted	0.832	0.061	0.997	0.983	0.764	0.125	0.924	0.628
1387081_at	NM_017132	reticulocalbin 2	Rcn2	2.076	0.007	4.435	0.001	1.865	0.460	4.875	0.001
1377512_at	BI291272	Reticulocalbin 2	Rcn2	1.572	0.856	1.218	0.568	2.294	0.364	1.276	0.202
1368097_a_at	NM_053865	reticulon 1	Rtn1	0.421	0.015	0.320	0.001	0.638	0.002	0.424	0.002
1372527_at	BG380684	reticulon 2 (Z-band associated protein)	Rtn2	0.933	0.684	0.580	0.008	1.022	0.506	0.624	0.036
1373571_at	AI170276	reticulon 3	Rtn3	0.879	0.098	0.682	0.007	0.790	0.270	0.656	0.019
1387340_at	AI409824	reticulon 3	Rtn3	0.696	0.343	1.086	0.056	0.921	0.653	0.927	0.550
1368807_at	NM_080909	reticulon 3	Rtn3	1.116	0.824	1.155	0.612	1.124	0.573	0.899	0.109
1388027_a_at	AF051335	reticulon 4	Rtn4	0.903	0.789	0.605	0.085	1.495	0.592	1.163	0.509
1368888_a_at	AJ242963	reticulon 4	Rtn4	0.946	0.817	0.959	0.645	1.122	0.440	1.499	0.014
1373008_x_at	BF386649	reticulon 4 receptor	Rtn4r	0.602	0.061	1.087	0.304	0.593	0.061	1.005	0.812
1378306_at	AW529689	Retinal S-antigen	Sag	0.920	0.760	0.519	0.126	0.937	0.579	0.503	0.126
1391091_at	AI406286	retinitis pigmentosa 1 homolog (human) /// similar to cylindromatosis (turban tumor syndrome) (predicted)	Rp1h /// RGD1565647_predicted	2.465	0.024	1.941	0.048	2.359	0.004	2.097	0.010
1379287_at	BF391639	retinitis pigmentosa 1 homolog (human) /// similar to cylindromatosis (turban tumor syndrome) (predicted) /// similar to cylindromatosis (turban tumor syndrome)	Rp1h /// RGD1565647_predicted /// LOC498035	1.195	0.066	1.005	0.908	1.073	0.911	1.000	0.996
1385806_at	AA996771	retinitis pigmentosa 9 homolog (human) (predicted)	Rp9h_predicted	1.000	1.000	1.036	0.508	1.001	1.000	1.014	0.799
1377702_at	BG380173	Retinoblastoma 1	Rb1	0.677	0.289	0.188	0.000	1.970	0.012	0.418	0.007
1388185_at	AI178012	retinoblastoma 1	Rb1	1.515	0.426	0.456	0.052	1.158	0.297	0.579	0.029
1381323_at	BG381396	retinoblastoma binding protein 5 (predicted)	Rbbp5_predicted	1.168	0.316	1.331	0.032	1.009	0.945	0.918	0.170
1376947_at	AI178158	retinoblastoma binding protein 6	Rbbp6	1.152	0.184	1.457	0.056	2.061	0.004	1.476	0.025
1378544_at	BE117471	retinoblastoma binding protein 6	Rbbp6	1.303	0.220	1.147	0.257	1.677	0.125	1.033	0.497
1395965_at	BI298589	Retinoblastoma binding protein 6	Rbbp6	0.746	0.240	0.269	0.015	0.823	0.070	0.523	0.030
1375541_at	AA900525	Retinoblastoma binding protein 6	Rbbp6	1.000	0.435	0.990	0.593	0.999	0.851	0.912	0.533
1390941_at	BI277540	retinoblastoma binding protein 6	Rbbp6	1.520	0.699	1.275	0.274	1.589	0.555	1.091	0.354

1398768_at	NM_031816	retinoblastoma binding protein 7	Rbbp7	0.856	0.070	1.035	0.667	0.688	0.021	0.887	0.676
1394033_at	AA956258	retinoblastoma binding protein 9	Rbbp9	0.462	0.161	0.504	0.025	0.789	0.582	0.881	0.117
1368403_at	NM_031094	retinoblastoma-like 2	Rbl2	0.357	0.007	0.537	0.065	0.490	0.005	0.543	0.108
1378190_at	AA945871	Retinoblastoma-like 2	Rbl2	0.999	0.875	1.003	0.994	0.997	0.792	1.322	0.984
1373966_at	BF406242	Retinoic acid induced 1 (predicted)	Rai1_predicted	0.761	0.039	1.091	0.059	0.735	0.044	1.004	0.510
1389263_at	AI234852	retinoic acid induced 14	Rai14	2.276	0.165	1.021	0.651	1.311	0.790	1.223	0.773
1373369_at	AI406500	Retinoic acid induced 17 (predicted)	Rai17_predicted	1.999	0.003	0.965	0.518	1.356	0.031	0.946	0.303
1389927_at	BI303536	Retinoic acid induced 17 (predicted)	Rai17_predicted	1.455	0.049	2.481	0.021	1.293	0.101	1.622	0.030
1384557_at	AI136444	Retinoic acid induced 17 (predicted)	Rai17_predicted	1.122	0.653	2.135	0.683	1.628	0.028	2.780	0.115
1376755_at	BF419646	retinoic acid receptor, beta	Rarb	0.993	0.982	1.582	0.152	0.996	0.933	1.445	0.043
1371668_at	BI285959	Retinoid X receptor alpha	Rxra	0.576	0.023	0.915	0.826	0.392	0.003	0.662	0.132
1389051_at	BI274189	retinoid X receptor beta	Rxrb	1.108	0.230	1.173	0.636	1.329	0.074	1.013	0.661
1367939_at	NM_012733	retinol binding protein 1, cellular	Rbp1	2.038	0.093	4.154	0.001	2.150	0.017	3.536	0.003
1387766_a_at	NM_012640	retinol binding protein 2, cellular	Rbp2	1.225	0.207	0.997	0.656	0.830	0.915	1.024	0.971
1373918_at	BG374035	retinol dehydrogenase 11	Rdh11	0.614	0.457	0.561	0.016	0.444	0.008	0.702	0.019
1382949_at	BM386727	Retinol dehydrogenase 12 (predicted)	Rdh12_predicted	1.000	0.981	0.991	0.068	0.999	0.984	1.066	0.301
1370986_s_at	AW535280	Retroviral-like ovarian specific transcript 30-1 mRNA	---	1.297	0.937	0.880	0.587	1.347	0.129	0.940	0.055
1388247_at	U48828	Retroviral-like ovarian specific transcript 30-1 mRNA	---	1.066	0.948	1.124	0.432	1.109	0.114	0.953	0.588
1371197_at	U48828	Retroviral-like ovarian specific transcript 30-1 mRNA	---	1.109	0.995	0.634	0.205	0.999	0.984	1.025	0.206
1398494_at	BF404279	REV1-like (S. cerevisiae) (predicted)	Rev1l_predicted	1.913	0.008	3.741	0.009	1.017	0.673	2.022	0.349
1383347_at	BM384011	REV1-like (S. cerevisiae) (predicted)	Rev1l_predicted	0.942	0.609	0.965	0.636	1.269	0.207	0.996	0.636
1372266_at	BI281607	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae)	Rev3l	1.321	0.039	0.827	0.126	1.424	0.109	1.017	0.571
1378618_at	BF392356	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae)	Rev3l	1.054	0.821	0.794	0.198	1.043	0.035	1.158	0.899
1374448_at	AW523759	reversion-inducing-cysteine-rich protein with kazal motifs (predicted)	Reck_predicted	0.913	0.145	1.027	0.851	0.995	0.867	1.199	0.073
1372738_at	BE109600	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	Rexo1	0.813	0.110	1.487	0.276	0.981	0.174	1.298	0.282
1398679_at	AI639098	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	Rexo2	1.146	0.143	1.099	0.932	1.017	0.447	1.140	0.099
1371724_at	AA799631	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	Rexo2	0.844	0.190	0.929	0.089	0.878	0.062	0.875	0.156
1388912_at	AI237143	REX4, RNA exonuclease 4 homolog (S. cerevisiae)	Rexo4	1.001	0.702	1.140	0.124	0.791	0.253	1.012	0.949
1392244_at	AA818153	RGD1559433 (predicted)	RGD1559433_predicted	0.338	0.037	0.636	0.231	0.720	0.311	1.424	0.189
1397611_at	AW525619	RGD1559591 (predicted)	RGD1559591_predicted	111.128	0.000	19.798	0.008	246.483	0.000	32.460	0.004
1397518_at	BG372421	RGD1559665 (predicted)	RGD1559665_predicted	1.244	0.065	0.853	0.443	1.042	0.070	1.039	0.889
1398708_at	BI297590	RGD1559718 (predicted)	RGD1559718_predicted	1.129	0.064	1.158	0.290	0.702	0.099	1.192	0.217
1398341_at	BI295767	RGD1559720 (predicted)	RGD1559720_predicted	0.988	0.403	1.198	0.772	0.865	0.771	1.391	0.021
1373030_at	AJ225654	RGD1559728 (predicted)	RGD1559728_predicted	1.028	0.901	0.632	0.002	0.786	0.134	0.846	0.006
1389489_at	BE109900	RGD1559738 (predicted)	RGD1559738_predicted	1.761	0.127	0.889	0.491	1.569	0.090	1.275	0.136
1389243_at	AI599794	RGD1559893 (predicted)	RGD1559893_predicted	0.753	0.345	0.830	0.239	0.892	0.610	0.931	0.405
1374852_at	AI407613	RGD1559909 (predicted)	RGD1559909_predicted	0.511	0.009	0.688	0.021	0.516	0.008	0.632	0.014
1372751_at	BM390320	RGD1560018 (predicted)	RGD1560018_predicted	0.999	0.916	0.886	0.160	1.003	0.502	0.833	0.047
1381947_at	AI169006	RGD1560210 (predicted)	RGD1560210_predicted	1.055	0.392	1.096	0.142	1.045	0.801	0.880	0.647
1392779_at	BF551105	RGD1560223 (predicted)	RGD1560223_predicted	1.008	0.701	0.991	0.119	1.002	0.350	0.998	0.896
1389416_at	BI296051	RGD1560398 (predicted)	RGD1560398_predicted	0.720	0.093	1.986	0.025	0.726	0.075	1.491	0.088
1380478_at	AW533633	RGD1560472 (predicted)	RGD1560472_predicted	0.496	0.051	0.889	0.249	0.497	0.041	0.791	0.312
1379539_at	AI137339	RGD1560524 (predicted)	RGD1560524_predicted	0.991	0.985	0.996	0.952	1.001	0.995	1.001	0.640
1383674_at	BF419619	RGD1560566 (predicted)	RGD1560566_predicted	0.518	0.273	0.617	0.011	0.779	0.097	0.529	0.009
1383874_at	BG670036	RGD1560812 (predicted)	RGD1560812_predicted	1.803	0.098	1.086	0.375	1.763	0.568	2.403	0.006
1374003_at	BM389589	RGD1560835 (predicted)	RGD1560835_predicted	1.497	0.058	1.163	0.526	1.385	0.127	0.906	0.356
1392526_at	AA901274	RGD1560866 (predicted)	RGD1560866_predicted	0.836	0.620	0.281	0.003	0.561	0.280	0.262	0.001
1376784_at	BI274481	RGD1560869 (predicted)	RGD1560869_predicted	1.275	0.940	1.024	0.858	2.705	0.056	1.490	0.452
1372460_at	AI172405	RGD1561000 (predicted)	RGD1561000_predicted	0.759	0.052	0.792	0.050	0.600	0.008	0.782	0.043
1383227_at	BI288882	RGD1561072 (predicted)	RGD1561072_predicted	0.807	0.425	0.895	0.604	0.722	0.203	1.035	0.162
1385061_at	AI145445	RGD1561097 (predicted)	RGD1561097_predicted	1.002	0.861	0.485	0.016	0.996	0.905	0.594	0.012
1371504_at	BF281215	RGD1561181 (predicted)	RGD1561181_predicted	0.968	0.798	1.265	0.097	0.835	0.021	1.162	0.098
1383136_a_at	AI764288	RGD1561438 (predicted)	RGD1561438_predicted	1.077	0.727	0.951	0.975	1.506	0.403	1.374	0.044
1386120_at	BF393607	RGD1561595 (predicted)	RGD1561595_predicted	0.625	0.120	0.647	0.020	0.546	0.273	0.518	0.028
1389580_at	BM384827	RGD1561695 (predicted)	RGD1561695_predicted	0.731	0.413	0.428	0.006	0.964	0.637	0.907	0.407
1385463_at	AI043627	RGD1561717 (predicted)	RGD1561717_predicted	1.123	0.437	5.930	0.010	0.987	0.789	1.914	0.023
1389744_at	AW527194	RGD1561752 (predicted)	RGD1561752_predicted	0.499	0.014	0.462	0.077	0.484	0.018	0.668	0.042
1371480_at	AI407985	RGD1561797 (predicted)	RGD1561797_predicted	0.919	0.281	1.694	0.069	0.708	0.107	1.849	0.057
1380323_at	BE105023	RGD1561936 (predicted)	RGD1561936_predicted	2.939	0.056	3.319	0.000	1.938	0.083	2.222	0.001
1394205_at	AA955942	RGD1561936 (predicted)	RGD1561936_predicted	1.250	0.226	0.878	0.055	0.956	0.441	1.028	0.337
1373616_at	BM386276	RGD1561936 (predicted)	RGD1561936_predicted	0.880	0.855	0.974	0.731	0.743	0.026	0.858	0.006

1377461_at	AI409983	RGD1561952 (predicted)	RGD1561952_predicted	1.409	0.182	11.073	0.002	0.999	0.063	7.515	0.002
1395214_at	BM391078	RGD1562012 (predicted)	RGD1562012_predicted	0.470	0.277	1.279	0.955	0.385	0.043	0.771	0.914
1371488_at	AW915978	RGD1562079 (predicted)	RGD1562079_predicted	1.442	0.042	1.986	0.002	1.428	0.083	2.041	0.004
1390527_at	BE099470	RGD1562114 (predicted)	RGD1562114_predicted	0.751	0.507	1.392	0.018	0.597	0.081	1.577	0.024
1383534_at	AA997058	RGD1562237 (predicted)	RGD1562237_predicted	0.442	0.241	0.454	0.004	0.441	0.347	0.510	0.003
1383099_at	BG670905	RGD1562241 (predicted)	RGD1562241_predicted	1.246	0.343	1.434	0.188	0.868	0.526	1.072	0.541
1384809_at	AW526563	RGD1562481 (predicted)	RGD1562481_predicted	0.416	0.295	1.612	0.411	0.287	0.005	0.579	0.101
1394662_at	BI295646	RGD1562481 (predicted)	RGD1562481_predicted	1.201	0.362	0.940	0.634	0.863	0.972	0.977	0.771
1381307_at	AI412008	RGD1562538 (predicted)	RGD1562538_predicted	0.631	0.989	1.405	0.394	0.990	0.992	1.447	0.739
1392462_at	AA817891	RGD1562568 (predicted)	RGD1562568_predicted	1.425	0.576	0.935	0.080	1.854	0.560	1.061	0.279
1374536_at	BG671506	RGD1562568 (predicted)	RGD1562568_predicted	1.091	0.811	0.671	0.108	1.014	0.943	0.782	0.043
1397790_at	BF394731	RGD1562574 (predicted)	RGD1562574_predicted	1.001	0.959	0.671	0.275	0.927	0.804	0.862	0.283
1378661_x_at	BM389983	RGD1562704 (predicted)	RGD1562704_predicted	1.188	0.529	1.028	0.999	1.103	0.355	1.143	0.228
1373934_at	AI178214	RGD1563075 (predicted)	RGD1563075_predicted	1.256	0.066	0.920	0.550	0.998	0.978	0.869	0.421
1372262_at	BI285626	RGD1563087 (predicted)	RGD1563087_predicted	0.707	0.142	0.684	0.014	0.625	0.006	0.755	0.023
1375662_at	BI291391	RGD1563087 (predicted)	RGD1563087_predicted	0.696	0.721	1.181	0.376	0.809	0.324	0.826	0.071
1388452_at	AI716904	RGD1563308 (predicted)	RGD1563308_predicted	0.573	0.133	0.276	0.007	0.601	0.003	0.212	0.021
1396815_at	AW251438	RGD1563361 (predicted)	RGD1563361_predicted	1.002	0.845	1.476	0.104	0.953	0.745	1.206	0.049
1379418_at	AW916753	RGD1563361 (predicted)	RGD1563361_predicted	0.994	0.909	0.901	0.534	0.890	0.998	0.919	0.169
1383449_at	AA801218	RGD1563374 (predicted)	RGD1563374_predicted	1.023	0.835	0.869	0.983	1.102	0.509	1.272	0.500
1389716_at	BI295883	RGD1563479 (predicted)	RGD1563479_predicted	1.617	0.747	0.673	0.026	1.259	0.049	0.697	0.078
1373586_at	AI411113	RGD1563515 (predicted)	RGD1563515_predicted	0.748	0.876	0.485	0.004	0.658	0.269	0.515	0.000
1383221_at	BG378463	RGD1563547 (predicted)	RGD1563547_predicted	0.934	0.816	1.622	0.001	0.855	0.610	1.036	0.365
1375136_at	AA946053	RGD1563661 (predicted)	RGD1563661_predicted	1.016	0.621	1.527	0.076	0.635	0.234	1.278	0.045
1396810_at	AI578423	RGD1563714 (predicted)	RGD1563714_predicted	0.751	0.226	0.747	0.578	0.478	0.775	0.512	0.534
1395249_at	BF400750	RGD1563912 (predicted)	RGD1563912_predicted	0.313	0.002	0.228	0.006	0.444	0.131	0.173	0.032
1375305_at	BI282028	RGD1563912 (predicted)	RGD1563912_predicted	0.425	0.002	0.258	0.000	0.510	0.031	0.226	0.015
1393263_at	AW522530	RGD1563912 (predicted)	RGD1563912_predicted	0.466	0.010	0.174	0.000	0.906	0.213	0.189	0.028
1392823_at	AI146105	RGD1563912 (predicted)	RGD1563912_predicted	0.579	0.038	0.143	0.004	0.304	0.112	0.255	0.010
1375191_at	AI230379	RGD1564011 (predicted)	RGD1564011_predicted	1.830	0.003	2.601	0.002	1.653	0.006	1.893	0.000
1376801_at	AW915035	RGD1564450 (predicted)	RGD1564450_predicted	1.003	0.405	1.429	0.027	1.458	0.385	1.347	0.026
1398332_at	BM386294	RGD1564468 (predicted)	RGD1564468_predicted	0.548	0.205	0.400	0.011	0.545	0.190	0.268	0.012
1391037_at	BF412161	RGD1564491 (predicted)	RGD1564491_predicted	0.398	0.002	0.310	0.001	0.360	0.074	0.374	0.051
1383409_at	BM383714	RGD1564737 (predicted)	RGD1564737_predicted	2.143	0.284	1.452	0.035	2.168	0.040	1.343	0.085
1397838_at	BF522792	RGD1564792 (predicted)	RGD1564792_predicted	0.943	0.831	0.997	0.945	1.004	0.997	1.009	0.063
1396118_at	AI410171	RGD1564942 (predicted)	RGD1564942_predicted	1.001	0.561	1.000	0.994	0.981	0.814	1.000	0.737
1372928_at	AI169749	RGD1564965 (predicted)	RGD1564965_predicted	0.510	0.037	0.476	0.001	0.735	0.130	0.793	0.413
1371513_at	BG378743	RGD1564971 (predicted)	RGD1564971_predicted	0.629	0.056	0.766	0.196	0.735	0.058	0.912	0.263
1375464_at	BI290815	RGD1564982 (predicted)	RGD1564982_predicted	0.776	0.335	1.179	0.033	0.919	0.504	0.857	0.375
1372548_at	AI412018	RGD1565050 (predicted)	RGD1565050_predicted	0.461	0.047	0.840	0.282	0.360	0.090	0.589	0.086
1398366_at	BF282644	RGD1565074 (predicted)	RGD1565074_predicted	0.511	0.037	1.467	0.165	0.582	0.044	1.080	0.517
1392558_at	AI101600	RGD1565142 (predicted)	RGD1565142_predicted	0.993	0.843	0.598	0.050	0.979	0.806	0.597	0.055
1386337_at	AI548910	RGD1565210 (predicted)	RGD1565210_predicted	0.468	0.416	0.986	0.462	0.671	0.127	0.897	0.198
1393880_at	AI030169	RGD1565240 (predicted)	RGD1565240_predicted	1.316	0.807	0.601	0.496	0.821	0.678	0.642	0.104
1395603_at	BI300879	RGD1565487 (predicted)	RGD1565487_predicted	0.964	0.951	1.309	0.959	1.894	0.042	0.987	0.491
1374294_at	AW534851	RGD1565594 (predicted)	RGD1565594_predicted	1.832	0.031	0.835	0.031	1.555	0.259	0.950	0.396
1396677_at	BF406365	RGD1565612 (predicted)	RGD1565612_predicted	0.882	0.605	0.660	0.939	1.035	0.783	1.015	0.917
1392929_at	BF416678	RGD1565616 (predicted)	RGD1565616_predicted	0.756	1.000	0.706	0.200	0.881	0.681	0.589	0.040
1377728_at	BI280802	RGD1565641 (predicted)	RGD1565641_predicted	0.783	0.354	1.700	0.011	0.774	0.025	1.711	0.005
1393800_at	AW526472	RGD1565777 (predicted)	RGD1565777_predicted	0.877	0.245	0.512	0.002	0.637	0.072	0.788	0.395
1367508_at	BI281225	RGD1565784 (predicted)	RGD1565784_predicted	0.517	0.044	1.419	0.068	0.383	0.003	1.240	0.679
1392484_at	AA892339	RGD1565814 (predicted)	RGD1565814_predicted	0.808	0.137	2.520	0.005	0.719	0.026	2.035	0.003
1381775_at	BF391321	RGD1566102 (predicted)	RGD1566102_predicted	0.867	0.075	0.362	0.011	1.244	0.621	0.785	0.114
1388900_at	BG381414	RGD1566118 (predicted)	RGD1566118_predicted	1.759	0.015	7.071	0.004	0.945	0.686	3.950	0.004
1372585_at	BM388445	RGD1566254 (predicted)	RGD1566254_predicted	975.780	0.006	547.221	0.014	1259.582	0.006	612.973	0.013
1388316_at	BG668062	RGD1566320 (predicted)	RGD1566320_predicted	0.773	0.060	1.235	0.122	0.685	0.098	1.366	0.037
1380946_at	AW251808	RGD1566367 (predicted)	RGD1566367_predicted	0.588	0.279	0.727	0.115	0.319	0.060	0.476	0.100
1392973_at	AI073173	RGD1566412 (predicted)	RGD1566412_predicted	1.088	0.144	0.355	0.002	1.338	0.021	0.500	0.061
1371704_at	BI274402	Rho family GTPase 1	Rnd1	0.916	0.733	1.213	0.185	0.844	0.195	1.101	0.233
1386062_at	AI060227	Rho family GTPase 3	Rnd3	7.596	0.000	4.762	0.009	7.460	0.001	2.725	0.000
1394077_at	BF548080	Rho family GTPase 3	Rnd3	1.989	0.023	2.261	0.052	2.798	0.006	1.597	0.093

1377663_at	AI598323	Rho family GTPase 3	Rnd3	1.761	0.096	1.253	0.292	1.953	0.008	1.440	0.008
1371366_at	AI408677	Rho GDP dissociation inhibitor (GDI) alpha	Arhgdia	0.918	0.777	3.634	0.009	0.827	0.079	2.288	0.004
1398108_at	AW532298	Rho GDP dissociation inhibitor (GDI) alpha	Arhgdia	0.436	0.930	4.901	0.119	0.591	0.112	2.846	0.450
1397356_at	AI234957	Rho GTPase activating protein 1 (predicted)	Arhgap1_predicted	2.056	0.180	2.465	0.166	4.598	0.037	1.088	0.853
1391101_at	AI407134	Rho GTPase activating protein 12 (predicted)	Arhgap12_predicted	2.083	0.416	2.283	0.083	1.399	0.105	1.744	0.036
1387035_a_at	NM_022244	Rho GTPase activating protein 17	Arhgap17	2.860	0.016	2.068	0.007	4.308	0.000	2.518	0.006
1396575_at	AI576265	Rho GTPase activating protein 20 /// hypothetical gene supported by NM_213629	Arhgap20 /// LOC497830	0.561	0.010	0.757	0.038	0.616	0.027	0.707	0.398
1374086_at	BF282296	Rho GTPase activating protein 21 (predicted)	Arhgap21_predicted	1.869	0.106	2.083	0.001	1.270	0.126	2.168	0.002
1392590_at	BG377201	Rho GTPase activating protein 24	Arhgap24	0.299	0.077	0.189	0.008	0.194	0.019	0.308	0.038
1393677_at	BI275079	Rho GTPase activating protein 26 (predicted)	Arhgap26_predicted	1.310	0.097	1.856	0.091	0.982	0.887	1.256	0.639
1396139_at	BE120196	Rho GTPase activating protein 26 (predicted)	Arhgap26_predicted	0.997	0.993	1.000	0.972	1.749	0.008	0.831	0.064
1391581_at	BE104302	Rho GTPase activating protein 5	Arhgap5	1.268	0.024	1.528	0.051	1.225	0.055	1.888	0.057
1392864_at	BM384008	Rho GTPase activating protein 5	Arhgap5	1.135	0.124	1.298	0.025	1.005	0.682	1.099	0.494
1395776_at	BF396580	Rho GTPase activating protein 5	Arhgap5	1.001	0.709	0.815	0.485	1.233	0.321	1.014	0.483
1376501_at	AA945062	Rho GTPase activating protein 8	Arhgap8	6.837	0.000	6.065	0.002	12.247	0.002	10.622	0.001
1378800_at	BI291526	Rho GTPase activating protein 8	Arhgap8	4.369	0.073	3.725	0.001	3.613	0.018	5.209	0.000
1370002_at	NM_021694	Rho guanine nucleotide exchange factor (GEF) 1	Arhgef1	1.011	0.936	1.313	0.066	0.762	0.798	0.937	0.990
1374486_at	AI412491	Rho guanine nucleotide exchange factor (GEF) 11	Arhgef11	1.319	0.036	0.862	0.125	1.035	0.444	0.786	0.070
1398299_at	NM_023982	Rho guanine nucleotide exchange factor (GEF) 11	Arhgef11	1.002	0.955	0.969	0.820	0.963	0.981	0.972	0.210
1395229_at	BG375118	Rho guanine nucleotide exchange factor (GEF) 12	Arhgef12	2.518	0.047	3.373	0.001	2.022	0.104	3.381	0.001
1378062_at	BF398677	Rho guanine nucleotide exchange factor (GEF) 12	Arhgef12	1.608	0.540	2.001	0.005	1.585	0.295	1.241	0.060
1394348_at	BF545496	Rho guanine nucleotide exchange factor (GEF) 12	Arhgef12	1.000	0.985	1.660	0.132	1.001	0.865	1.025	0.884
1394494_at	AA963519	Rho guanine nucleotide exchange factor (GEF) 19 (predicted)	Arhgef19_predicted	1.001	0.963	0.994	0.991	1.004	0.997	0.995	0.980
1381297_at	BI292668	Rho guanine nucleotide exchange factor (GEF) 5	Arhgef5	12.951	0.000	7.007	0.001	10.144	0.001	5.975	0.002
1382389_at	AI179755	Rho guanine nucleotide exchange factor (GEF) 5	Arhgef5	3.519	0.002	3.200	0.009	4.422	0.001	3.245	0.002
1394015_at	AA965157	Rho guanine nucleotide exchange factor 7	Arhgef7	0.997	0.865	0.988	0.845	0.986	0.933	1.001	0.938
1390786_at	BE099756	rho/rac guanine nucleotide exchange factor (GEF) 2	Arhgef2	1.508	0.170	2.915	0.000	0.933	0.864	2.259	0.012
1373878_at	AI104213	Rho-associated coiled-coil forming kinase 1	Rock1	1.299	0.182	1.044	0.077	1.065	0.665	1.077	0.118
1377061_at	BE097238	RhoGAP involved in beta-catenin-N-cadherin and NMDA receptor signaling (predicted)	RICS_predicted	0.672	0.239	1.056	0.829	0.571	0.168	0.607	0.393
1374376_at	BM386483	Rho-guanine nucleotide exchange factor (predicted)	Rgnef_predicted	0.475	0.051	3.925	0.001	0.356	0.360	3.123	0.012
1382258_at	AW521384	Rho-guanine nucleotide exchange factor (predicted)	Rgnef_predicted	0.847	0.368	1.019	0.177	1.177	0.248	1.101	0.675
1379026_at	AI072008	Rhomboid, veinlet-like 4 (Drosophila) (predicted)	Rhbdl4_predicted	1.009	0.744	0.354	0.109	0.616	0.098	0.148	0.092
1372051_at	BI294778	Rhomboid, veinlet-like 7 (Drosophila) (predicted)	Rhbdl7_predicted	0.641	0.146	1.194	0.110	0.691	0.101	0.966	0.985
1382055_at	BE096213	rhotekin	Rtkn	0.822	0.189	0.847	0.126	0.998	0.362	1.025	0.842
1372671_at	BI284293	riboflavin kinase	Rfk	0.782	0.501	0.923	0.469	0.683	0.055	1.007	0.349
1375093_at	AI236089	ribokinase (predicted)	Rbks_predicted	0.618	0.295	0.908	0.478	0.532	0.013	1.092	0.925
1371451_at	AI010940	ribonuclease H2, large subunit	Rnaseh2a	1.255	0.217	1.189	0.223	1.662	0.023	1.500	0.029
1376273_at	BI285089	ribonuclease III, nuclear	Rnasen	0.738	0.321	1.087	0.253	1.265	0.761	1.182	0.810
1398437_at	BF412792	Ribonuclease III, nuclear	Rnasen	1.091	0.681	0.519	0.050	1.126	0.710	0.991	0.483
1380425_at	AI012859	Ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)	Rnasel	14.850	0.057	0.568	0.019	9.401	0.000	1.095	0.739
1377116_at	BI301478	Ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)	Rnasel	1.394	0.065	1.414	0.073	2.811	0.023	1.681	0.027
1377815_at	BE102535	ribonuclease P 14 subunit homolog (human) (predicted)	Rpp14_predicted	0.748	0.003	1.087	0.083	0.757	0.001	0.854	0.975
1372845_at	BG380782	ribonuclease P 21 subunit (human)	Rpp21	1.785	0.265	1.622	0.331	2.225	0.007	1.634	0.300
1378181_at	BI279714	ribonuclease P 40 subunit (human)	Rpp40	1.283	0.294	2.451	0.080	1.672	0.068	1.987	0.005
1375211_at	BM391506	ribonuclease T2 (predicted)	Rnaset2_predicted	0.723	0.805	1.213	0.041	1.496	0.049	1.602	0.001
1370880_at	X62528	ribonuclease/angiogenin inhibitor 1	Rnh1	2.204	0.021	3.787	0.000	1.799	0.080	2.783	0.010
1371596_at	AI008971	ribonucleic acid binding protein S1	Rnps1	1.008	0.678	1.836	0.001	0.897	0.359	1.536	0.006
1371862_at	AI412015	ribonucleotide reductase M1 (mapped)	Rrm1_mapped	0.753	0.670	0.834	0.562	0.913	0.507	0.856	0.477
1398766_at	NM_013067	ribophorin I	Rpn1	0.729	0.076	0.804	0.007	0.840	0.407	0.769	0.014
1381319_at	BF407155	Ribophorin II	Rpn2	0.954	0.525	1.018	0.962	0.734	0.103	1.000	0.996
1398776_at	NM_031698	ribophorin II	Rpn2	0.891	0.626	0.588	0.002	0.779	0.139	0.625	0.002
1389468_at	BF393902	ribose 5-phosphate isomerase A (predicted)	Rpia_predicted	1.021	0.778	0.799	0.171	1.092	0.146	0.874	0.393
1386394_at	AA956971	Ribose-phosphate pyrophosphokinase I -like	LOC314140	0.616	0.068	1.569	0.079	0.644	0.452	1.511	0.032
1394196_at	AA956971	Ribose-phosphate pyrophosphokinase I -like	LOC314140	0.557	0.130	1.306	0.160	0.536	0.109	1.369	0.122
1390769_at	AI535312	Ribose-phosphate pyrophosphokinase I -like	LOC314140	0.866	0.704	1.362	0.055	0.840	0.543	1.660	0.000
1367625_at	NM_031100	ribosomal protein L10	Rpl10	0.889	0.966	1.017	0.743	0.740	0.264	0.975	0.645
1367580_at	NM_031065	ribosomal protein L10A	Rpl10a	0.849	0.507	1.311	0.093	0.592	0.023	1.069	0.523
1371330_at	BI284252	ribosomal protein L11	Rpl11	0.953	0.816	1.270	0.118	0.776	0.054	1.240	0.057
1386858_at	NM_031101	ribosomal protein L13	Rpl13	0.823	0.268	1.064	0.215	0.689	0.002	1.008	0.560
1367588_a_at	NM_022179	ribosomal protein L13A	Rpl13a	0.957	0.512	1.334	0.023	0.893	0.248	1.128	0.197
1375375_at	AI059414	Ribosomal protein L14	Rpl14	1.126	0.669	1.205	0.044	0.906	0.005	0.990	0.875

1387887_at	AA874811	ribosomal protein L14	Rpl14	0.763	0.949	1.049	0.778	0.663	0.137	1.155	0.967
1398315_at	AA800007	ribosomal protein L15	Rpl15	0.960	0.939	1.201	0.146	0.803	0.211	1.102	0.023
1398871_at	BG671311	ribosomal protein L17	Rpl17	0.841	0.216	1.152	0.286	0.716	0.043	1.179	0.144
1367623_at	NM_031102	ribosomal protein L18	Rpl18	0.704	0.255	1.102	0.260	0.664	0.010	0.999	0.783
1367610_at	NM_031103	ribosomal protein L19	Rpl19	0.957	0.797	1.107	0.328	0.840	0.243	1.042	0.438
1398764_at	NM_053330	ribosomal protein L21	Rpl21	1.008	0.402	1.249	0.000	0.962	0.456	1.109	0.077
1370253_at	AI228150	ribosomal protein L22	Rpl22	0.775	0.307	1.188	0.225	0.709	0.003	1.167	0.297
1388989_at	BI302675	ribosomal protein L22 like 1 (predicted)	Rpl22l1_predicted	0.705	0.074	1.069	0.510	0.701	0.046	1.069	0.159
1398885_at	AA925327	ribosomal protein L23	Rpl23	0.852	0.623	1.343	0.035	0.739	0.141	1.198	0.039
1396812_at	BF547253	Ribosomal protein L24	Rpl24	1.360	0.204	1.099	0.093	1.002	0.949	0.966	0.802
1398854_at	BI297634	ribosomal protein L24	Rpl24	0.976	0.406	1.158	0.241	0.793	0.891	1.191	0.015
1388303_at	AI598536	ribosomal protein L26	Rpl26	0.886	0.650	1.191	0.073	0.724	0.052	1.057	0.049
1367561_at	NM_022514	ribosomal protein L27	Rpl27	0.825	0.432	1.110	0.069	0.747	0.038	1.167	0.125
1371344_at	AI177054	ribosomal protein L27a (predicted)	Rpl27a_predicted	0.897	0.486	1.129	0.532	0.793	0.032	0.997	0.969
1398830_at	NM_022697	ribosomal protein L28	Rpl28	0.859	0.523	1.294	0.036	0.685	0.004	1.078	0.107
1367582_at	NM_017150	ribosomal protein L29	Rpl29	0.887	0.512	1.211	0.208	0.737	0.144	1.112	0.293
1396049_x_at	BG057530	ribosomal protein L3	Rpl3	0.940	0.383	0.984	0.770	0.972	0.107	0.982	0.923
1371300_at	AA892367	ribosomal protein L3	Rpl3	0.948	0.958	0.954	0.902	0.843	0.059	0.792	0.138
1398774_at	NM_022699	ribosomal protein L30	Rpl30	0.961	0.936	1.265	0.030	0.773	0.069	1.214	0.024
1367634_at	NM_022506	ribosomal protein L31	Rpl31	0.878	0.800	1.184	0.058	0.761	0.090	1.069	0.138
1384548_at	BM388159	ribosomal protein L32	Rpl32	0.842	0.226	1.097	0.066	0.754	0.003	1.001	0.044
1398216_at	BF399439	Ribosomal protein L32	Rpl32	1.055	0.890	0.931	0.138	1.181	0.508	0.627	0.056
1371761_at	AI013910	ribosomal protein L34 (predicted)	Rpl34_predicted	0.951	0.887	1.619	0.012	0.815	0.159	1.484	0.009
1388372_at	AW914118	ribosomal protein L35	Rpl35	0.865	0.823	1.563	0.025	0.763	0.050	1.242	0.075
1398760_at	NM_021264	ribosomal protein L35a	Rpl35a	1.014	0.899	1.267	0.052	0.955	0.244	1.141	0.043
1371573_at	AW142090	ribosomal protein L36a (predicted)	Rpl36a_predicted	0.958	0.752	1.187	0.004	0.870	0.189	1.010	0.383
1398789_at	NM_031106	ribosomal protein L37	Rpl37	0.957	0.936	1.377	0.006	0.846	0.117	1.363	0.002
1367934_at	NM_012875	ribosomal protein L39	Rpl39	1.219	0.746	1.454	0.004	0.937	0.740	1.481	0.007
1371916_at	AI409380	Ribosomal protein L3-like (predicted)	Rpl3l_predicted	0.637	0.047	0.827	0.555	0.738	0.004	0.995	0.680
1398749_at	NM_022510	ribosomal protein L4	Rpl4	0.899	0.469	1.171	0.067	0.728	0.012	1.009	0.923
1370866_at	AA944073	ribosomal protein L41	Rpl41	0.890	0.326	1.094	0.154	0.790	0.005	1.085	0.412
1398761_at	NM_031099	ribosomal protein L5	Rpl5	0.779	0.305	0.910	0.160	0.814	0.040	0.819	0.066
1367567_at	NM_053971	ribosomal protein L6	Rpl6	0.897	0.527	1.174	0.087	0.784	0.016	1.076	0.220
1394867_at	AA944444	Ribosomal protein L7	Rpl7	1.312	0.890	1.068	0.532	0.846	0.101	0.833	0.139
1398917_at	BF281221	ribosomal protein L7	Rpl7	0.941	0.899	1.070	0.725	0.643	0.086	0.947	0.543
1375788_at	BM388719	Ribosomal protein L7	Rpl7	0.904	0.914	1.005	1.000	0.612	0.139	0.970	0.824
1371297_at	BI281697	ribosomal protein L7a (predicted)	Rpl7a_predicted	0.914	0.101	1.168	0.118	0.789	0.068	1.048	0.531
1371305_at	AI409193	ribosomal protein L8	Rpl8	0.795	0.806	1.328	0.111	0.630	0.125	1.098	0.257
1384714_x_at	BI850152	ribosomal protein L8 /// similar to 60S ribosomal protein L8 (predicted)	Rpl8 /// RGD1561333_predicted	0.983	0.975	1.484	0.081	0.825	0.223	1.047	0.326
1371301_at	BG666892	ribosomal protein L9	Rpl9	0.849	0.323	1.028	0.745	0.792	0.039	0.989	0.809
1386868_at	NM_031109	ribosomal protein S10	Rps10	0.874	0.577	1.253	0.139	0.742	0.042	1.179	0.051
1367630_at	NM_031110	ribosomal protein S11	Rps11	0.869	0.711	0.987	0.364	0.722	0.040	0.962	0.808
1367640_at	NM_031709	ribosomal protein S12	Rps12	1.056	0.661	1.311	0.059	0.849	0.256	1.228	0.023
1392232_at	AI030983	ribosomal protein S13	Rps13	0.619	0.082	1.344	0.167	0.810	0.953	1.398	0.019
1398872_at	BE107613	ribosomal protein S13	Rps13	0.881	0.553	1.336	0.025	0.723	0.016	1.248	0.053
1368211_at	NM_022672	ribosomal protein S14	Rps14	0.825	0.804	1.176	0.325	0.653	0.084	1.069	0.534
1386874_at	NM_017151	ribosomal protein S15	Rps15	0.848	0.692	1.017	0.898	0.719	0.013	1.046	0.658
1398775_at	NM_053982	ribosomal protein S15a	Rps15a	0.945	0.848	1.550	0.023	0.789	0.270	1.377	0.005
1371318_at	BG666872	ribosomal protein S16	Rps16	1.057	0.579	1.393	0.027	0.779	0.264	1.256	0.019
1367645_at	NM_017152	ribosomal protein S17	Rps17	0.867	0.432	1.368	0.052	0.714	0.023	1.113	0.036
1388296_at	BF281388	ribosomal protein S18	Rps18	1.000	0.894	1.270	0.097	0.812	0.295	1.173	0.037
1371377_at	BG668512	ribosomal protein S19	Rps19	0.943	0.842	1.560	0.035	0.761	0.033	1.496	0.030
1367639_a_at	U92700	ribosomal protein S2	Rps2	0.696	0.585	1.290	0.131	0.726	0.045	1.062	0.595
1375219_a_at	AA944861	ribosomal protein S2 /// similar to 40S ribosomal protein S2 (predicted) /// similar to ribosomal protein S2 (predicted) /// similar to ribosomal protein S2 (predicted)	Rps2 /// RGD1561077_predicted /// RGD1559516_predicted /// RGD1559900_predicted	0.844	0.323	1.495	0.022	0.882	0.064	1.267	0.110
1371295_at	AW914097	ribosomal protein S20	Rps20	1.064	0.366	1.525	0.012	1.019	0.252	1.518	0.009
1398852_at	BF410811	ribosomal protein S21	Rps21	0.935	0.331	1.056	0.093	0.905	0.021	0.943	0.814
1370242_at	AA848284	ribosomal protein S23	Rps23	1.057	0.734	1.315	0.063	0.877	0.069	1.298	0.027

1390494_at	AI177484	ribosomal protein S24	Rps24	0.810	0.207	1.385	0.286	0.642	0.169	0.977	0.908
1398546_at	BF396217	Ribosomal protein S24	Rps24	1.039	0.871	0.992	0.850	0.964	0.860	0.998	0.884
1369966_a_at	BG375811	ribosomal protein S24	Rps24	0.936	0.911	0.997	0.817	0.771	0.017	1.007	0.943
1388313_at	BM389289	ribosomal protein s25	Rps25	0.818	0.529	1.066	0.508	0.746	0.061	1.024	0.735
1367596_at	NM_013224	ribosomal protein S26	Rps26	0.954	0.601	1.186	0.170	0.771	0.130	0.963	0.537
1367717_at	NM_053597	ribosomal protein S27	Rps27	0.964	0.848	1.312	0.019	0.806	0.074	1.290	0.086
1367685_at	NM_031113	ribosomal protein S27a	Rps27a	0.870	0.899	1.008	0.705	0.764	0.112	0.978	0.844
1387890_at	AI229633	ribosomal protein S29	Rps29	0.832	0.059	1.134	0.649	0.751	0.016	1.010	0.883
1371299_at	BG665124	ribosomal protein S3	Rps3	0.775	0.708	1.127	0.382	0.617	0.129	1.034	0.787
1367606_at	NM_017153	ribosomal protein S3a	Rps3a	0.819	0.594	1.034	0.410	0.681	0.125	0.941	0.249
1371308_at	AA799501	ribosomal protein S4, X-linked	Rps4x	0.821	0.763	1.080	0.642	0.657	0.165	0.989	0.561
1377843_at	BF548385	Ribosomal protein S5	Rps5	0.825	0.858	1.662	0.005	0.734	0.999	1.212	0.095
1398882_at	BI282255	ribosomal protein S5	Rps5	0.804	0.975	1.323	0.073	0.588	0.129	1.126	0.114
1367573_at	NM_017160	ribosomal protein S6	Rps6	0.872	0.343	1.155	0.150	0.721	0.005	1.068	0.353
1383454_a_at	BM389456	ribosomal protein S6 kinase, polypeptide 1	Rps6kc1	1.167	0.144	0.990	0.388	1.099	0.266	0.485	0.007
1390689_at	BF401605	ribosomal protein S6 kinase, polypeptide 1	Rps6kc1	1.249	0.168	0.980	0.141	0.547	0.051	1.166	0.242
1368116_a_at	M57428	ribosomal protein S6 kinase, polypeptide 1	Rps6kb1	1.029	0.697	1.239	0.783	1.107	0.079	1.080	0.991
1389494_at	BM388595	ribosomal protein S6 kinase, polypeptide 4 (predicted)	Rps6ka4_predicted	0.756	0.055	0.518	0.074	1.040	0.605	0.642	0.102
1382271_at	AA955815	Ribosomal protein S6 kinase, polypeptide 5 (predicted)	Rps6ka5_predicted	0.381	0.089	1.059	0.516	0.479	0.049	0.852	0.921
1398582_at	AI045780	Ribosomal protein S6 kinase, polypeptide 5 (predicted)	Rps6ka5_predicted	1.371	0.554	1.222	0.807	1.420	0.309	1.257	0.842
1367597_at	NM_031706	ribosomal protein S8	Rps8	0.972	0.590	1.478	0.002	0.762	0.010	1.456	0.004
1387888_at	AA799768	ribosomal protein S9	Rps9	0.828	0.675	1.071	0.194	0.654	0.092	0.921	0.518
1388244_s_at	BG153272	ribosomal protein SA	Rpsa	0.827	0.143	1.098	0.365	0.799	0.020	0.997	0.939
1367569_at	NM_017138	ribosomal protein SA	Rpsa	0.720	0.587	0.970	0.844	0.656	0.065	0.889	0.261
1371189_x_at	BG153272	ribosomal protein SA /// similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (predicted) /// similar to Ribosomal protein SA (predicted)	Rpsa /// RGD1563757_predicted /// RGD1566037_predicted	0.881	0.135	1.044	0.422	0.805	0.259	1.004	0.819
1371340_at	AW919054	ribosomal protein, large P2 /// similar to 60S acidic ribosomal protein P2 (predicted)	Rplp2 /// RGD1566221_predicted	0.898	0.761	1.165	0.036	0.924	0.080	1.071	0.050
1371307_at	AW914090	ribosomal protein, large, P1	Rplp1	0.948	0.819	1.067	0.314	0.820	0.058	0.994	0.569
1372431_at	AI575434	ribosomal protein, mitochondrial, L12	Mrpl12	0.324	0.115	1.499	0.001	0.483	0.021	1.413	0.060
1373477_at	BM390306	ribosomal protein, mitochondrial, L15	Mrpl19	0.509	0.096	2.155	0.019	0.333	0.077	1.980	0.008
1367686_at	NM_030835	ribosome associated membrane protein 4	RAMP4	0.574	0.196	0.762	0.001	0.673	0.197	0.743	0.002
1386900_at	AI103695	ribosome associated membrane protein 4	RAMP4	0.615	0.456	1.490	0.152	0.632	0.043	1.314	0.318
1388413_at	BI282760	ribosome binding protein 1 homolog 180kDa (dog) (predicted)	Rrbp1_predicted	1.144	0.002	1.741	0.010	1.065	0.804	1.460	0.043
1383500_at	BI279795	ribosome binding protein 1 homolog 180kDa (dog) (predicted)	Rrbp1_predicted	0.885	0.199	1.137	0.263	0.839	0.208	1.056	0.190
1378709_at	BI300330	Ribulose-5-phosphate-3-epimerase (predicted)	Rpe_predicted	1.001	0.116	1.020	0.622	1.002	0.984	0.997	0.086
1371020_at	BE102826	RIM binding protein 2	Rimbp2	0.755	0.103	0.477	0.015	0.681	0.069	0.681	0.149
1377623_at	AA925355	ring finger (C3HC4 type) and KH domain containing 1 (predicted)	Rkhd1_predicted	1.219	0.054	1.976	0.003	1.026	0.231	1.616	0.031
1388651_at	AA800053	ring finger and CHY zinc finger domain containing 1	Rchy1	0.717	0.182	0.917	0.213	0.908	0.317	0.980	0.686
1377590_at	BF420493	Ring finger and FYVE like domain containing protein	Rffl	1.329	0.045	0.999	0.990	1.061	0.023	1.005	0.825
1385504_at	AW524664	ring finger and FYVE like domain containing protein	Rffl	1.087	0.580	1.207	0.106	1.120	0.550	1.229	0.192
1374545_at	AA945202	ring finger and KH domain containing 2 (predicted)	Rkhd2_predicted	1.425	0.003	1.508	0.020	1.352	0.030	1.399	0.007
1380682_at	BF396302	Ring finger and KH domain containing 3 (predicted)	Rkhd3_predicted	1.019	0.343	0.874	0.177	0.523	0.004	0.903	0.059
1388937_at	BF283351	ring finger protein (C3HC4 type) 19 (predicted)	Rnf19_predicted	1.258	0.055	1.085	0.041	1.234	0.174	1.286	0.039
1378524_at	AW533310	ring finger protein (C3HC4 type) 19 (predicted)	Rnf19_predicted	1.352	0.186	0.622	0.104	0.509	0.071	0.498	0.025
1375891_at	BG379665	ring finger protein 1	Ring1	0.633	0.176	1.012	0.458	0.901	0.556	0.760	0.015
1371526_at	BG371468	ring finger protein 10	Rnf10	0.800	0.232	1.181	0.092	0.872	0.200	0.988	0.058
1368122_at	NM_053438	ring finger protein 103	Rnf103	0.521	0.066	0.629	0.020	0.359	0.001	0.579	0.020
1373015_at	BI280348	ring finger protein 11 (predicted)	Rnf11_predicted	0.943	0.695	0.880	0.088	0.823	0.245	0.916	0.127
1373456_at	BI300764	ring finger protein 111 (predicted)	Rnf111_predicted	1.075	0.642	0.891	0.228	0.969	0.859	0.948	0.606
1367544_at	BE120556	ring finger protein 111 (predicted)	Rnf111_predicted	1.063	0.769	0.854	0.025	0.894	0.452	0.945	0.181
1390524_at	BM392295	ring finger protein 12	Rnf12	0.895	0.681	4.592	0.000	0.804	0.095	3.053	0.033
1385403_at	AI071834	ring finger protein 121 (predicted)	Rnf121_predicted	1.755	0.113	1.715	0.278	1.475	0.118	1.348	0.153
1386639_at	BF549828	ring finger protein 121 (predicted)	Rnf121_predicted	1.152	0.191	0.743	0.472	0.929	0.444	0.966	0.265
1385644_at	AI058291	ring finger protein 121 (predicted)	Rnf121_predicted	1.010	0.762	1.664	0.186	0.888	0.364	0.857	0.613
1384098_at	AA925710	ring finger protein 125 (predicted)	Rnf125_predicted	1.401	0.499	1.307	0.078	1.011	0.780	1.304	0.439
1381764_s_at	AA819792	ring finger protein 126	Rnf126	0.990	0.285	1.393	0.115	0.703	0.017	1.215	0.496
1376639_at	AW252111	ring finger protein 126	Rnf126	1.001	0.968	1.008	0.986	0.999	0.926	1.008	0.967
1387201_at	NM_053588	ring finger protein 138	Rnf138	1.765	0.155	5.225	0.003	2.682	0.024	4.304	0.004
1389258_at	AI317840	ring finger protein 138	Rnf138	1.379	0.277	0.867	0.748	1.632	0.010	0.918	0.899

1377564_at	AI549166	Ring finger protein 138	Rnf138	1.370	0.445	1.548	0.599	1.373	0.239	0.911	0.459
1382379_at	AW529177	ring finger protein 138	Rnf138	1.408	0.468	1.856	0.015	3.034	0.020	1.565	0.010
1376440_at	BF391522	ring finger protein 139 (predicted)	Rnf139_predicted	2.628	0.019	2.160	0.026	4.517	0.004	2.893	0.011
1388995_at	BF407666	ring finger protein 14	Rnf14	0.921	0.502	1.217	0.032	1.020	0.269	1.286	0.014
1394698_at	AI535431	Ring finger protein 146	Rnf146	0.800	0.227	0.874	0.771	0.611	0.128	0.542	0.095
1371778_at	BI296773	ring finger protein 146	Rnf146	1.237	0.361	1.232	0.026	0.870	0.979	1.133	0.325
1389525_at	AI171788	ring finger protein 149	Rnf149	0.838	0.500	1.257	0.007	0.712	0.177	1.121	0.428
1373471_at	AI548624	ring finger protein 166	Rnf166	0.843	0.059	0.635	0.019	0.586	0.095	0.623	0.021
1388636_at	BI280272	ring finger protein 167	Rnf167	0.901	0.930	0.775	0.135	0.886	0.083	0.872	0.302
1371597_at	BI281621	ring finger protein 187 (predicted)	Rnf187_predicted	0.533	0.061	0.472	0.013	0.521	0.001	0.466	0.013
1383269_at	BF556833	ring finger protein 2	Rnf2	0.925	0.036	1.323	0.163	1.108	0.290	0.882	0.328
1376805_at	BF559331	Ring finger protein 2	Rnf2	0.682	0.128	1.457	0.041	0.856	0.361	1.251	0.021
1378022_at	BE113167	ring finger protein 20 (predicted)	Rnf20_predicted	1.011	0.275	1.220	0.055	0.942	0.501	1.060	0.553
1372088_at	AI012434	ring finger protein 25	Rnf25	2.775	0.017	2.598	0.005	2.332	0.020	1.794	0.024
1398336_at	AI012577	ring finger protein 25	Rnf25	1.261	0.776	0.974	0.488	1.738	0.045	0.810	0.942
1395571_at	BF557189	ring finger protein 3 (predicted)	Rnf3_predicted	0.961	0.917	1.120	0.833	0.796	0.072	1.038	0.493
1383679_at	BF411972	ring finger protein 31 (predicted)	Rnf31_predicted	1.758	0.158	2.410	0.001	2.621	0.001	2.646	0.001
1388993_at	AI179991	ring finger protein 34	Rnf34	1.451	0.209	1.461	0.138	1.057	0.740	1.089	0.063
1387329_at	NM_134467	ring finger protein 38	Rnf38	1.013	0.849	1.018	0.751	1.001	0.995	0.862	0.486
1368662_at	NM_134374	ring finger protein 39	Rnf39	1.113	0.332	0.915	0.904	2.337	0.125	1.002	0.985
1371489_at	AI011748	Ring finger protein 4	Rnf4	0.743	0.429	1.246	0.026	0.972	0.420	1.274	0.093
1388089_a_at	AY050655	ring finger protein 4	Rnf4	0.841	0.745	2.171	0.037	0.837	0.661	1.236	0.195
1387458_at	NM_019182	ring finger protein 4	Rnf4	1.029	0.944	1.094	0.672	0.633	0.194	0.795	0.174
1384374_at	BF523755	Ring finger protein 41	Rnf41	1.022	0.714	0.890	0.232	0.989	0.676	0.882	0.261
1391252_at	BI290717	ring finger protein 41	Rnf41	1.193	0.756	1.133	0.790	0.825	0.114	1.296	0.633
1395276_at	AA899483	Ring finger protein 7 (predicted)	Rnf7_predicted	1.729	0.036	1.458	0.869	1.079	0.298	0.955	0.552
1371638_at	AA858518	ring finger protein 7 (predicted)	Rnf7_predicted	0.775	0.610	0.772	0.314	0.639	0.058	0.984	0.348
1389069_at	BM384061	ring finger protein 8	Rnf8	1.225	0.124	1.079	0.313	2.025	0.205	1.180	0.120
1383034_at	AA998572	RING1 and YY1 binding protein (predicted)	Rybp_predicted	1.154	0.251	5.245	0.000	1.136	0.240	2.780	0.025
1372674_at	BE107155	RING1 and YY1 binding protein (predicted)	Rybp_predicted	0.981	0.898	0.915	0.445	0.795	0.072	0.899	0.372
1393406_at	AI576602	Ring-box 1	Rbx1	0.908	0.173	0.772	0.213	0.724	0.285	0.884	0.230
1388333_at	BF291171	ring-box 1	Rbx1	0.721	0.914	1.295	0.214	0.688	0.270	1.434	0.005
1388538_at	AI179646	ring-box 1	Rbx1	0.766	0.954	0.356	0.002	1.110	0.436	0.666	0.023
1385856_at	BE096718	RIO kinase 1 (yeast)	Riok1	1.061	0.855	1.310	0.354	1.148	0.695	1.003	0.614
1377503_at	BG371773	RIO kinase 2 (yeast)	Riok2	0.743	0.028	1.248	0.159	0.991	0.122	1.205	0.086
1390047_at	BG378174	RIO kinase 3 (yeast) (predicted)	Riok3_predicted	1.520	0.069	3.297	0.002	1.461	0.027	1.903	0.020
1394363_at	H34775	RIO kinase 3 (yeast) (predicted)	Riok3_predicted	1.955	0.142	17.162	0.000	1.669	0.560	11.791	0.000
1395699_at	BE126478	RIO kinase 3 (yeast) (predicted)	Riok3_predicted	1.025	0.396	3.824	0.008	0.890	0.440	2.213	0.039
1372867_at	AI177333	RNA (guanine-7-) methyltransferase	Rnmt	1.484	0.044	1.098	0.131	2.401	0.042	1.702	0.083
1382998_at	AI044778	RNA (guanine-7-) methyltransferase	Rnmt	2.647	0.053	3.291	0.028	1.440	0.052	2.040	0.010
1398572_at	BI294251	RNA (guanine-7-) methyltransferase	Rnmt	1.370	0.408	1.209	0.344	1.647	0.020	1.303	0.015
1393088_at	BF554013	RNA (guanine-9-) methyltransferase domain containing 1	Rg9mtd1	0.825	0.764	2.077	0.034	0.610	0.095	2.148	0.060
1390933_a_at	BF283097	RNA (guanine-9-) methyltransferase domain containing 3	Rg9mtd3	0.819	0.403	1.281	0.209	0.707	0.091	1.088	0.223
1370356_at	D83948	RNA binding motif protein 10	Rbm10	0.947	0.892	1.443	0.185	0.753	0.325	1.182	0.019
1377656_at	BG375054	RNA binding motif protein 13	Rbm13	0.559	0.464	1.216	0.058	0.519	0.185	1.421	0.061
1389664_at	BM387379	RNA binding motif protein 15B (predicted)	Rbm15b_predicted	1.773	0.023	1.123	0.414	1.801	0.011	1.144	0.106
1369896_s_at	NM_139094	RNA binding motif protein 16	Rbm16	0.901	0.440	1.076	0.280	0.759	0.028	1.021	0.431
1388355_at	BF396644	RNA binding motif protein 17	Rbm17	0.743	0.104	1.109	0.843	0.749	0.034	0.922	0.704
1371952_at	AI010954	RNA binding motif protein 18 (predicted)	Rbm18_predicted	0.832	0.777	0.982	0.481	0.899	0.955	0.781	0.131
1392503_at	BE100371	RNA binding motif protein 22	Rbm22	0.946	0.678	1.279	0.009	0.784	0.489	1.204	0.066
1382013_at	AI071118	RNA binding motif protein 24 (predicted)	Rbm24_predicted	0.554	0.148	0.419	0.080	0.464	0.034	0.498	0.011
1388751_at	AW433787	RNA binding motif protein 24 (predicted)	Rbm24_predicted	0.519	0.167	0.467	0.005	0.484	0.001	0.557	0.004
1388886_at	BM392240	RNA binding motif protein 25 (predicted)	Rbm25_predicted	1.227	0.390	0.822	0.020	0.963	0.659	0.627	0.065
1391848_at	BG376780	RNA binding motif protein 27 (predicted)	Rbm27_predicted	0.924	0.556	1.016	0.670	1.076	0.605	0.998	0.355
1389981_at	BE116889	RNA binding motif protein 27 (predicted)	Rbm27_predicted	0.938	0.618	0.805	0.077	0.770	0.014	0.841	0.127
1395520_at	AW530017	RNA binding motif protein 28 (predicted)	Rbm28_predicted	0.847	0.961	1.441	0.502	0.943	0.313	1.171	0.620
1371583_at	AI598399	RNA binding motif protein 3	Rbm3	1.108	0.394	1.324	0.145	1.029	0.444	1.262	0.199
1389065_at	BM392304	RNA binding motif protein 34	Rbm34	0.937	0.149	0.998	0.369	0.972	0.852	1.040	0.869
1385199_a_at	AI073196	RNA binding motif protein 34	Rbm34	1.098	0.298	2.154	0.015	1.346	0.415	1.986	0.025
1374844_at	BF284573	RNA binding motif protein 4 (predicted)	Rbm4_predicted	0.411	0.003	1.221	0.166	0.659	0.091	1.302	0.219
1384091_at	AA899909	RNA binding motif protein 4 (predicted)	Rbm4_predicted	0.534	0.293	0.946	0.721	0.481	0.107	0.735	0.128

1395762_at	BG670091	RNA binding motif protein 4 (predicted)	Rbm4_predicted	1.343	0.445	1.450	0.011	1.480	0.160	1.254	0.180
1372251_at	BI282892	RNA binding motif protein 5	Rbm5	0.801	0.148	0.802	0.285	0.689	0.012	0.867	0.343
1382749_at	BI293987	RNA binding motif protein 5	Rbm5	1.178	0.807	0.807	0.865	1.044	0.607	1.187	0.667
1394155_at	AI010943	RNA binding motif protein 7 (predicted)	Rbm7_predicted	2.860	0.017	1.973	0.048	2.131	0.042	1.224	0.477
1376503_a_at	BE104991	RNA binding motif protein 7 (predicted)	Rbm7_predicted	1.496	0.203	1.376	0.120	1.380	0.128	1.163	0.584
1372829_at	BE113079	RNA binding motif protein 8 (predicted)	Rbm8_predicted	0.856	0.534	1.255	0.108	0.618	0.038	1.105	0.458
1396310_at	BF545380	RNA binding motif protein 9 (predicted)	Rbm9_predicted	1.723	0.014	1.002	0.962	1.270	0.668	0.925	0.638
1385281_at	BF388412	RNA binding motif protein 9 (predicted)	Rbm9_predicted	0.937	0.354	1.222	0.735	0.486	0.393	1.538	0.455
1388794_at	BE107489	RNA binding motif protein, X chromosome retrogene (predicted)	Rbmxrt_predicted	0.666	0.304	1.132	0.295	0.731	0.121	1.231	0.033
1375870_a_at	BF420140	RNA binding motif, single stranded interacting protein 1	Rbms1	6.171	0.002	1.506	0.015	7.708	0.002	2.896	0.002
1394888_at	AW920350	RNA binding motif, single stranded interacting protein 1	Rbms1	0.863	0.668	1.113	0.850	0.971	0.520	1.229	0.945
1390032_at	BG374052	RNA binding motif, single stranded interacting protein 2	Rbms2	0.510	0.036	0.932	0.420	0.515	0.001	0.919	0.155
1391921_at	AW530941	RNA guanylyltransferase and 5'-phosphatase (predicted)	Rngtt_predicted	1.221	0.068	1.059	0.072	1.538	0.027	1.000	0.999
1396373_at	BF416860	RNA guanylyltransferase and 5'-phosphatase (predicted)	Rngtt_predicted	1.537	0.563	1.231	0.451	1.097	0.817	1.505	0.169
1374289_at	AA818183	RNA polymerase 1-1	Rpo1-1	0.800	0.711	1.387	0.023	0.394	0.018	1.236	0.111
1387268_at	NM_031773	RNA polymerase 1-2	Rpo1-2	0.436	0.064	2.330	0.028	0.421	0.002	1.794	0.010
1387098_at	NM_031772	RNA polymerase 1-4	Rpo1-4	1.001	0.827	0.999	0.265	1.007	0.852	0.998	0.586
1391815_at	BG664098	RNA pseudouridylate synthase domain containing 3 (predicted)	Rpusd3_predicted	1.032	0.716	0.541	0.074	0.949	0.591	0.553	0.061
1372370_at	AI233741	RNA pseudouridylate synthase domain containing 4	Rpusd4	1.046	0.660	0.841	0.250	0.998	0.602	1.117	0.576
1388529_at	AI237372	RNA terminal phosphate cyclase domain 1	Rtcd1	0.710	0.045	1.489	0.054	0.489	0.017	1.508	0.253
1373452_at	AI232273	RNA terminal phosphate cyclase-like 1	Rcl1	1.192	0.859	3.344	0.019	1.346	0.338	1.930	0.052
1378639_at	BM389576	RNA, U transporter 1	Rnut1	0.692	0.015	0.828	0.060	0.669	0.027	0.832	0.300
1374836_at	AA964554	RNA, U3 small nucleolar interacting protein 2 (predicted)	Rnu3ip2_predicted	0.983	0.644	1.420	0.145	0.617	0.919	1.317	0.152
1377746_at	AI010418	RNA-binding protein 12	Rbm12	0.446	0.012	0.973	0.115	0.468	0.005	1.027	0.719
1395092_at	BM388276	RNA-binding region (RNP1, RRM) containing 2	Rnpc2	2.779	0.024	1.027	0.145	1.872	0.772	1.170	0.799
1398993_at	AI045458	RNA-binding region (RNP1, RRM) containing 2	Rnpc2	1.483	0.070	1.937	0.008	1.594	0.017	1.527	0.033
1379737_a_at	BG372903	RNA-binding region (RNP1, RRM) containing 2	Rnpc2	1.362	0.101	1.467	0.010	1.539	0.031	1.559	0.033
1381967_at	BE114972	RNA-binding region (RNP1, RRM) containing 2	Rnpc2	1.303	0.301	1.581	0.012	1.264	0.084	1.624	0.004
1399101_at	AA849715	RNA-binding region (RNP1, RRM) containing 2	Rnpc2	1.093	0.691	0.569	0.013	1.332	0.574	0.847	0.277
1389666_at	AA892855	rod outer segment membrane protein 1	Rom1	0.867	0.853	0.965	0.502	0.982	0.961	0.903	0.380
1374647_at	BI299718	rosbin, round spermatid basic protein 1 (predicted)	Rsbn1_predicted	1.736	0.014	1.225	0.264	1.427	0.060	1.085	0.611
1396963_at	BF404522	Roundabout homolog 1 (Drosophila)	Robo1	1.002	0.734	1.259	0.158	1.021	0.724	0.947	0.249
1379693_at	AI409154	Roundabout homolog 2 (Drosophila)	Robo2	0.763	0.662	0.149	0.004	1.051	0.816	0.438	0.024
1379750_at	BE119799	roundabout homolog 2 (Drosophila)	Robo2	0.701	0.682	0.431	0.230	0.399	0.066	0.583	0.196
1389030_a_at	BI282912	Rous sarcoma oncogene	Src	0.975	0.558	1.192	0.749	0.767	0.540	0.999	0.988
1370751_at	U77931	rRNA promoter binding protein	LOC257642	1.534	0.708	4.444	0.059	2.885	0.507	1.430	0.352
1371213_at	AJ005023	RT1 class I, A3	RT1-A3	1.282	0.014	1.110	0.019	1.190	0.174	1.489	0.055
1388236_x_at	M24026	RT1 class I, CE12	RT1-CE12	2.755	0.143	5.825	0.013	2.986	0.131	8.071	0.009
1370463_x_at	U50449	RT1 class I, CE16	RT1-CE16	1.942	0.052	2.693	0.004	2.465	0.003	3.670	0.001
1370972_x_at	BI300597	RT1 class I, CE5	RT1-CE5	3.708	0.015	7.419	0.001	6.395	0.001	17.701	0.000
1388255_x_at	AJ243338	RT1 class I, CE5	RT1-CE5	1.960	0.164	9.571	0.000	6.106	0.030	23.167	0.000
1371209_at	AJ243338	RT1 class I, CE5	RT1-CE5	1.611	0.320	4.437	0.090	5.149	0.038	12.557	0.027
1389089_at	BM389027	RT1 class I, locus Ke4	RT1-Ke4	0.752	0.150	1.184	0.039	0.676	0.024	1.114	0.009
1388071_x_at	M24024	RT1 class Ib, locus Aw2	RT1-Aw2	3.920	0.000	3.802	0.001	4.417	0.000	4.902	0.000
1371078_at	AI500830	RT1 class Ib, locus Aw2	RT1-Aw2	15.491	0.000	16.381	0.000	19.220	0.000	23.461	0.000
1379818_at	BF288109	RT1 class Ib, locus Aw2	RT1-Aw2	35.192	0.000	16.652	0.000	37.729	0.000	17.872	0.000
1369110_x_at	NM_012645	RT1 class Ib, locus Aw2	RT1-Aw2	5.368	0.000	12.971	0.004	10.622	0.000	22.869	0.002
1396304_at	BI292055	RT1 class Ib, locus Aw2	RT1-Aw2	4.650	0.001	1.906	0.020	5.238	0.020	3.786	0.006
1371171_at	M10094	RT1 class Ib, locus Aw2	RT1-Aw2	5.948	0.001	5.547	0.000	7.672	0.000	8.082	0.002
1392954_at	AI029637	RT1 class Ib, locus Aw2	RT1-Aw2	7.213	0.002	9.520	0.002	19.491	0.001	13.455	0.000
1379496_at	AI029460	RT1 class Ib, locus Aw2	RT1-Aw2	6.453	0.002	7.100	0.010	7.619	0.004	10.019	0.018
1380415_at	AI233027	RT1 class Ib, locus Aw2	RT1-Aw2	6.498	0.006	2.578	0.007	12.400	0.001	6.480	0.002
1393108_at	BM387813	RT1 class Ib, locus Aw2	RT1-Aw2	7.377	0.006	5.645	0.001	10.230	0.002	6.680	0.001
1390562_s_at	BE102350	RT1 class Ib, locus Aw2	RT1-Aw2	6.529	0.008	4.611	0.011	7.855	0.000	7.141	0.000
1377036_at	BE102350	RT1 class Ib, locus Aw2	RT1-Aw2	3.090	0.013	3.230	0.021	7.126	0.005	2.554	0.007
1379357_at	AI408767	RT1 class Ib, locus Aw2	RT1-Aw2	5.609	0.018	5.542	0.009	7.964	0.013	7.955	0.005
1370429_at	L40362	RT1 class Ib, locus Aw2	RT1-Aw2	6.651	0.022	5.583	0.054	11.450	0.014	12.556	0.010
1382437_at	BM383464	RT1 class Ib, locus Aw2	RT1-Aw2	2.515	0.054	2.036	0.000	7.440	0.011	3.699	0.006
1379436_a_at	AA945875	RT1 class Ib, locus Aw2	RT1-Aw2	1.852	0.120	1.008	0.242	2.055	0.051	0.998	0.988
1388202_at	BI395698	RT1 class Ib, locus Aw2	RT1-Aw2	3.240	0.132	5.289	0.013	4.167	0.090	8.948	0.009
1391266_at	AI072881	RT1 class Ib, locus Aw2	RT1-Aw2	1.696	0.133	1.247	0.982	3.420	0.005	1.289	0.203

1371111_at	X82669	RT1 class Ib, locus Aw2	RT1-Aw2	1.104	0.370	1.478	0.021	1.867	0.050	1.497	0.047
1377851_at	AI012250	RT1 class Ib, locus Aw2	RT1-Aw2	1.910	0.509	4.935	0.046	12.896	0.058	4.068	0.112
1398027_at	BF405186	RT1 class Ib, locus Aw2	RT1-Aw2	0.815	0.684	0.825	0.235	1.266	0.250	1.050	0.376
1375850_at	BG371810	RT1 class Ib, locus Aw2	RT1-Aw2	0.719	0.704	1.216	0.077	1.122	0.097	0.880	0.455
1390100_s_at	BG371810	RT1 class Ib, locus Aw2	RT1-Aw2	0.792	0.864	1.077	0.347	1.001	0.701	0.674	0.227
1388203_x_at	BI395698	RT1 class Ib, locus Aw2 /// histocompatibility 2, T region locus 24 /// RT1 class I, CE2 /// RT1-149 protein /// RT1 class I, CE15 /// RT1 class I, CE10	RT1-Aw2 /// RT1-T24-1 /// RT1-CE2 /// RT1-149 /// RT1-CE15 /// RT1-CE10	2.871	0.125	5.987	0.019	3.448	0.080	8.639	0.012
1371267_at	M64795	RT1 class Ib, locus Aw2 /// RT1 class I, CE12 /// RT1 class I, CE1 /// RT1 class I, CE2 /// RT1 class I, CE15	RT1-Aw2 /// RT1-CE12 /// RT1-CE1 /// RT1-CE2 /// RT1-CE15	1.849	0.124	1.849	0.010	2.021	0.037	1.577	0.056
1370428_x_at	AJ249701	RT1 class Ib, locus Aw2 /// RT1 class Ia, locus A2 /// RT1 class I, A3	RT1-Aw2 /// RT1-A2 /// RT1-A3	5.062	0.000	6.736	0.002	6.395	0.001	8.298	0.001
1387205_at	NM_022921	RT1 class Ib, locus M3	RT1-M3	6.082	0.004	6.846	0.000	11.496	0.000	10.822	0.003
1388212_a_at	AJ243974	RT1 class Ib, locus S3	RT1-S3	25.695	0.000	34.998	0.000	54.931	0.000	62.584	0.000
1388164_at	AF029241	RT1 class Ib, locus S3	RT1-S3	47.084	0.003	36.960	0.000	79.404	0.000	96.716	0.001
1371123_x_at	AJ243973	RT1 class Ib, locus S3	RT1-S3	28.968	0.009	49.820	0.000	51.747	0.000	107.001	0.000
1388213_a_at	AJ243973	RT1 class Ib, locus S3	RT1-S3	65.124	0.012	78.726	0.000	126.888	0.000	174.671	0.000
1377334_at	BG378249	RT1 class II, locus Ba	RT1-Ba	1.345	0.008	2.760	0.029	3.438	0.034	15.930	0.039
1370822_at	AF307302	RT1 class II, locus Ba	RT1-Ba	1.046	0.896	5.563	0.067	1.022	0.906	73.020	0.003
1371033_at	AI715202	RT1 class II, locus Bb	RT1-Bb	0.909	0.788	3.316	0.023	1.172	0.249	12.441	0.001
1370883_at	Y00480	RT1 class II, locus Da	RT1-Da	2.328	0.112	10.003	0.004	6.397	0.006	77.562	0.004
1370383_s_at	BI279526	RT1 class II, locus Db1	RT1-Db1	1.031	0.197	4.312	0.048	1.123	0.642	23.180	0.007
1370382_at	BI279526	RT1 class II, locus Db1	RT1-Db1	1.201	0.505	1.291	0.373	1.031	0.926	8.248	0.038
1389734_x_at	BI282965	RT1-149 protein	RT1-149	2.898	0.449	8.405	0.119	7.759	0.128	10.138	0.076
1374050_at	BE100918	RUN and FYVE domain containing 1	Rufy1	1.226	0.080	2.180	0.025	1.200	0.092	1.233	0.171
1381841_at	BF411958	RUN and FYVE domain containing 1	Rufy1	1.015	0.992	1.409	0.087	0.799	0.439	0.912	0.897
1373687_at	BI284968	RUN and TBC1 domain containing 3	Rutbc3	0.937	0.435	1.241	0.837	0.631	0.061	1.027	0.851
1398114_at	BF564763	Runt related transcription factor 1	Runx1	1.044	0.173	1.004	0.899	0.741	0.289	0.881	0.078
1396592_at	BF405096	Runt related transcription factor 2	Runx2	1.265	0.997	1.694	0.133	1.238	0.795	0.755	0.089
1373280_at	AA848324	RuvB-like 2 (E. coli)	Ruvbl2	0.714	0.325	3.041	0.025	0.903	0.212	2.506	0.037
1375715_at	BE112777	RWD domain containing 1	Rwdd1	0.969	0.236	0.631	0.320	0.908	0.676	1.399	0.167
1388192_at	AI711028	RWD domain containing 3	Rwdd3	1.179	0.345	0.880	0.355	1.239	0.308	0.904	0.230
1392170_at	BE121336	RWD domain containing 3	Rwdd3	1.050	0.987	1.010	0.945	1.007	0.985	0.783	0.595
1376879_at	AI716916	RWD domain containing 4A	Rwdd4a	0.464	0.016	1.132	0.958	0.510	0.267	1.061	0.832
1389480_at	AI598462	RWD domain containing 4A	Rwdd4a	0.481	0.052	0.448	0.001	0.623	0.120	0.395	0.003
1382088_at	AI548753	Ryanodine receptor 2, cardiac	Ryr2	5.948	0.024	0.364	0.146	13.046	0.003	0.537	0.059
1386890_at	NM_031114	S100 calcium binding protein A10 (calpactin)	S100a10	3.076	0.005	2.705	0.006	3.876	0.006	1.996	0.011
1375170_at	BG378926	S100 calcium binding protein A11 (calizzarin)	S100a11	6.108	0.004	16.799	0.000	3.893	0.124	9.324	0.000
1367661_at	AF140232	S100 calcium binding protein A6 (calcyclin)	S100a6	13.129	0.055	7.371	0.001	1.920	0.195	2.581	0.002
1381252_at	BE098160	SA rat hypertension-associated gene	Sah	0.900	0.246	0.334	0.017	0.570	0.133	0.322	0.038
1394458_at	BF291026	SA rat hypertension-associated gene	Sah	0.757	0.501	0.971	0.590	0.625	0.313	0.844	0.272
1383303_at	BI282211	SA rat hypertension-associated gene	Sah	1.024	0.663	0.231	0.001	1.309	0.069	0.277	0.000
1368433_at	NM_053798	SAC1 (suppressor of actin mutations 1, homolog)-like (S. cerevisiae)	Sacm1l	0.725	0.105	0.927	0.037	0.826	0.121	0.831	0.043
1372741_at	AI412013	saccharopine dehydrogenase (putative)	Sccpdh	0.506	0.012	0.519	0.000	0.404	0.001	0.473	0.007
1367798_at	NM_017201	S-adenosylhomocysteine hydrolase	Ahcy	0.532	0.049	1.516	0.026	0.530	0.013	0.938	0.576
1395273_at	BE115782	S-adenosylhomocysteine hydrolase-like 1 (predicted)	Ahcyl1_predicted	0.972	0.830	1.513	0.099	0.978	0.950	1.022	0.474
1367933_at	NM_031011	S-adenosylmethionine decarboxylase 1	Amd1	0.518	0.000	0.482	0.001	0.502	0.011	0.630	0.012
1373284_at	AI176607	salvador homolog 1 (Drosophila) (predicted)	Sav1_predicted	1.152	0.230	1.692	0.001	1.316	0.048	1.898	0.021
1393453_at	BI290287	salvador homolog 1 (Drosophila) (predicted)	Sav1_predicted	1.038	0.761	1.275	0.128	1.047	0.442	1.027	0.055
1373973_at	AI169082	SAP30 binding protein (predicted)	Sap30bp_predicted	0.942	0.834	1.362	0.230	0.897	0.808	1.118	0.417
1388815_at	BE329438	SAPS domain family, member 1 (predicted)	Saps1_predicted	1.825	0.186	1.620	0.007	2.393	0.004	2.248	0.000
1385758_at	BF399333	SAPS domain family, member 1 (predicted)	Saps1_predicted	0.930	0.996	1.108	0.228	0.981	0.819	1.442	0.014
1375037_at	AI176244	SAPS domain family, member 3 (predicted)	Saps3_predicted	0.834	0.429	0.607	0.008	1.068	0.977	0.577	0.026
1367470_at	AA851321	SAR1 gene homolog A (S. cerevisiae)	Sar1a	0.585	0.236	0.598	0.001	0.587	0.017	0.482	0.001
1398353_at	AI236260	SAR1 gene homolog A (S. cerevisiae)	Sar1a	0.883	0.572	3.204	0.003	0.815	0.004	2.329	0.003
1388681_at	AI105294	SAR1 gene homolog B (S. cerevisiae)	Sar1b	1.655	0.022	1.043	0.545	1.718	0.028	1.134	0.169
1368058_at	NM_022394	scaffold attachment factor B	Safb	0.971	0.863	0.940	0.808	0.806	0.486	0.889	0.642
1386956_at	NM_031541	scavenger receptor class B, member 1	Scarb1	1.980	0.043	1.447	0.218	2.398	0.065	1.695	0.038
1368379_at	NM_054001	scavenger receptor class B, member 2	Scarb2	0.612	0.522	2.205	0.023	0.554	0.056	2.118	0.018
1372250_at	BI294932	SCF apoptosis response protein 1	LOC499941	1.003	0.168	1.374	0.298	0.813	0.505	1.051	0.540

1377916_at	AW915529	schlafen 2 (predicted)	Slfn2_predicted	2.213	0.050	1.032	0.799	1.333	0.233	0.800	0.227
1392842_at	AI072951	Schlafen 5 (predicted)	Slfn5_predicted	1.398	0.351	0.999	0.649	0.969	0.164	1.005	0.291
1379957_at	BE107457	schlafen 8	Slfn8	22.595	0.000	10.398	0.000	33.708	0.000	23.785	0.001
1389367_at	AI409747	schwannomin interacting protein 1	Schip1	1.024	0.140	0.517	0.017	0.763	0.139	0.752	0.018
1379281_at	AA892798	sclerostin domain containing 1	Sostdc1	1.001	0.992	1.532	0.135	1.436	0.185	0.989	0.917
1390685_at	BF395810	Scm-like with four mbt domains 1	Sfmbt1	1.599	0.005	0.821	0.774	3.169	0.002	3.637	0.024
1368129_at	NM_031647	Scm-like with four mbt domains 1	Sfmbt1	8.842	0.014	6.803	0.003	8.567	0.017	6.984	0.001
1388776_at	AI169176	scotin	MGC94600	1.386	0.170	1.142	0.050	2.725	0.006	1.490	0.011
1368978_at	NM_033499	scrapie responsive gene 1	Scrg1	0.999	0.995	0.974	0.783	1.002	0.987	0.974	0.772
1399024_at	AI180441	SCY1-like 1 (S. cerevisiae)	Scyl1	0.767	0.198	1.083	0.971	0.899	0.285	0.939	0.035
1382635_at	BF289119	SCY1-like 1 (S. cerevisiae)	Scyl1	1.206	0.684	0.997	0.197	0.494	0.153	0.745	0.224
1382921_at	AA997613	SDA1 domain containing 1	Sdad1	0.679	0.100	5.125	0.001	0.611	0.163	3.452	0.019
1390704_at	BF394953	SDA1 domain containing 1	Sdad1	0.978	0.198	1.019	0.816	0.858	0.283	1.119	0.673
1368158_at	NM_019364	sec1 family domain containing 1	Scfd1	0.802	0.524	1.041	0.436	0.942	0.221	0.957	0.226
1369991_at	NM_031723	Sec11-like 1 (S. cerevisiae)	Sec11l1	0.987	0.993	1.423	0.028	1.017	0.936	1.444	0.014
1370817_at	AB022714	Sec11-like 3 (S. cerevisiae)	Sec11l3	0.993	0.978	0.934	0.057	0.960	0.326	0.966	0.441
1371437_at	BM986228	SEC13-like 1 (S. cerevisiae)	Sec13l1	0.703	0.284	0.949	0.017	0.704	0.084	0.929	0.070
1369092_at	NM_057147	sec22 homolog	Sec22l2	0.708	0.112	1.661	0.018	0.836	0.946	1.500	0.047
1377691_at	AI599376	SEC22 vesicle trafficking protein-like 1 (S. cerevisiae)	Sec22l1	0.815	0.885	1.960	0.197	0.705	0.058	1.250	0.119
1380163_at	BI302685	SEC23 interacting protein	Sec23ip	1.158	0.538	0.714	0.053	0.919	0.327	0.866	0.039
1388755_at	AI179139	SEC23A (S. cerevisiae) (predicted)	Sec23a_predicted	0.562	0.132	0.942	0.554	0.747	0.029	1.168	0.352
1388857_at	BF289044	SEC23B (S. cerevisiae) (predicted)	Sec23b_predicted	0.700	0.520	1.144	0.940	0.775	0.187	1.161	0.094
1392211_at	BF408070	SEC24 related gene family, member B (S. cerevisiae) (predicted)	Sec24b_predicted	0.862	0.334	0.901	0.573	0.917	0.627	0.891	0.205
1389455_at	BG380421	SEC24 related gene family, member B (S. cerevisiae) (predicted)	Sec24b_predicted	1.003	0.969	1.004	0.116	0.951	0.988	0.969	0.776
1367753_at	NM_033021	SEC31-like 1 (S. cerevisiae)	Sec31l1	0.887	0.574	1.071	0.709	1.426	0.062	1.094	0.529
1375749_at	BF404853	SEC3-like 1 (S. cerevisiae)	Sec3l1	1.087	0.757	1.007	0.952	0.997	0.233	0.993	0.960
1371368_at	BI279499	Sec61 alpha 1 subunit (S. cerevisiae)	Sec61a1	0.495	0.328	0.649	0.011	0.771	0.099	0.673	0.030
1382615_at	BI284366	Sec61 alpha 1 subunit (S. cerevisiae)	Sec61a1	0.765	0.619	0.753	0.217	0.968	0.293	0.541	0.002
1388519_at	BI281906	Sec61 beta subunit (predicted)	Sec61b_predicted	0.814	0.541	0.935	0.215	0.761	0.160	0.782	0.138
1375659_at	BG381529	Sec61, alpha subunit 2 (S. cerevisiae) (predicted)	Sec61a2_predicted	0.768	0.022	0.711	0.004	0.838	0.003	0.813	0.025
1384519_at	BG377412	SEC63-like (S. cerevisiae) (predicted)	Sec63_predicted	0.547	0.036	0.859	0.573	0.704	0.018	1.087	0.631
1397964_at	AI406662	SEC63-like (S. cerevisiae) (predicted)	Sec63_predicted	0.459	0.143	0.912	0.454	0.484	0.160	0.338	0.079
1374917_at	AI548571	SEC63-like (S. cerevisiae) (predicted)	Sec63_predicted	0.598	0.259	0.482	0.015	0.860	0.511	0.686	0.018
1390501_at	BE101157	Secernin 3	Scrn3	0.717	0.584	0.699	0.018	0.366	0.058	0.764	0.034
1382644_at	AA875527	Secernin 3	Scrn3	0.750	0.772	0.707	0.018	1.123	0.960	0.765	0.047
1368094_at	NM_024002	SECIS binding protein 2	Secisbp2	1.364	0.371	1.724	0.012	1.124	0.595	1.625	0.001
1368044_at	NM_022669	secretogranin 2	Scg2	0.796	0.622	0.455	0.001	0.856	0.452	0.524	0.004
1368656_at	NM_053856	secretogranin III	Scg3	0.944	0.211	0.695	0.002	0.869	0.061	0.710	0.010
1396375_at	BF417934	Secretogranin III	Scg3	1.921	0.424	0.925	0.847	1.574	0.508	0.996	0.992
1370978_at	BM387205	secretory carrier membrane protein 1	Scamp1	2.546	0.035	1.465	0.008	1.368	0.110	1.201	0.029
1388819_at	BM386698	secretory carrier membrane protein 1	Scamp1	2.334	0.035	0.565	0.003	1.271	0.157	0.670	0.007
1371769_at	BI279666	secretory carrier membrane protein 2	Scamp2	0.879	0.603	0.798	0.214	0.634	0.716	0.634	0.005
1371090_at	BM387006	secretory carrier membrane protein 2	Scamp2	1.091	0.729	0.947	0.264	0.936	0.980	0.750	0.031
1370921_at	BI281156	secretory carrier membrane protein 3	Scamp3	0.557	0.542	0.868	0.280	0.596	0.030	0.616	0.075
1367688_at	NM_031725	secretory carrier membrane protein 4	Scamp4	0.656	0.171	1.277	0.014	1.003	0.227	1.373	0.052
1367992_at	NM_013175	secretory granule neuroendocrine protein 1	Sgne1	0.847	0.681	0.563	0.000	0.878	0.248	0.581	0.010
1367998_at	NM_053372	secretory leukocyte peptidase inhibitor /// similar to secretory leukocyte protease inhibitor (predicted)	Slpi /// RGD1563818_predicted	1.128	0.122	1.232	0.662	1.064	0.809	1.036	0.397
1374825_at	BG380338	seizure related 6 homolog (mouse)-like 2 (predicted)	Sez6l2_predicted	0.700	0.011	0.397	0.004	0.748	0.169	0.535	0.029
1376073_at	BI285936	Sel1 (suppressor of lin-12) 1 homolog (C. elegans)	Sel1h	0.793	0.755	3.065	0.001	0.846	0.319	2.473	0.000
1382935_at	BE113823	SEL1 domain containing protein RGD735029	RGD735029	0.659	0.110	1.742	0.041	0.822	0.288	1.933	0.030
1381174_at	BG381120	SEL1 domain containing protein RGD735029	RGD735029	0.901	0.637	2.663	0.008	0.548	0.154	2.347	0.001
1387046_at	NM_053792	selective LIM binding factor, rat homolog	Slb	0.715	0.062	0.491	0.001	0.752	0.260	0.460	0.000
1374524_at	BM384384	selenocysteine lyase	Scly	4.520	0.007	4.270	0.009	7.567	0.000	6.375	0.001
1393256_at	AI137711	selenophosphate synthetase 1	Sephs1	0.448	0.018	0.644	0.171	0.637	0.112	0.630	0.004
1381650_at	BM389433	Selenophosphate synthetase 1	Sephs1	0.734	0.091	0.931	0.761	0.766	0.759	0.755	0.454
1389215_at	AI407424	selenophosphate synthetase 1	Sephs1	0.833	0.380	1.228	0.762	1.311	0.989	1.451	0.243
1372876_at	AA799700	selenophosphate synthetase 2	Sephs2	0.674	0.172	0.785	0.225	0.472	0.067	0.911	0.201
1398752_at	NM_133297	selenoprotein	42248	0.727	0.958	0.615	0.024	0.778	0.843	0.586	0.006
1368806_at	AA799627	selenoprotein P, plasma, 1	Sepp1	0.472	0.012	0.132	0.001	0.519	0.002	0.222	0.006
1367593_at	NM_013027	selenoprotein W, muscle 1	Sepw1	1.550	0.027	1.544	0.165	3.212	0.001	1.880	0.011

1388745_at	AI228417	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	Sema4a	20.562	0.006	4.867	0.001	7.947	0.002	2.129	0.015
1395864_at	AA945715	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	Sema4a	6.871	0.034	1.013	0.944	3.588	0.062	1.272	0.896
1374678_at	BE109578	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	Sema4b	6.191	0.024	1.612	0.055	6.155	0.018	1.533	0.068
1380248_at	AA819138	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G (predicted)	Sema4g_predicted	0.997	0.963	0.574	0.203	1.004	0.979	0.582	0.204
1392795_at	AA963069	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (predicted)	Sema6a_predicted	1.622	0.457	0.765	0.154	1.604	0.097	0.741	0.104
1387322_at	NM_053471	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	Sema6b	1.221	0.477	0.332	0.047	1.119	0.622	0.432	0.045
1368984_at	NM_057148	septin 2	37500	1.821	0.156	9.086	0.022	0.985	0.801	1.690	0.030
1388389_at	BF282620	septin 2	37500	1.017	0.909	0.738	0.038	0.971	0.347	0.752	0.020
1396135_at	BF567887	Septin 4	38231	1.017	0.894	0.879	0.194	1.158	0.514	0.751	0.553
1386955_at	BM387903	septin 5	38596	1.318	0.284	2.001	0.052	1.058	0.859	1.204	0.208
1396145_at	AW142500	Septin 6 (predicted)	Sept6_predicted	0.759	0.014	1.274	0.743	0.759	0.326	1.324	0.220
1372949_at	BG663067	Septin 6 (predicted)	Sept6_predicted	0.786	0.557	1.840	0.026	0.650	0.115	1.623	0.060
1387436_at	NM_022616	septin 7	39326	1.419	0.943	1.656	0.317	1.005	0.949	0.951	0.999
1386296_at	AI639205	septin 8 (predicted)	Sept8_predicted	0.942	0.206	0.520	0.039	1.214	0.405	0.601	0.022
1386906_a_at	AF180526	septin 9	40057	0.748	0.672	0.763	0.819	0.481	0.268	0.807	0.398
1367698_a_at	NM_031837	septin 9	40057	0.791	0.741	1.262	0.089	0.632	0.113	1.165	0.825
1375374_at	BF400606	Sequestosome 1	Sqstm1	2.402	0.001	2.383	0.006	1.815	0.009	2.484	0.001
1389381_at	AI411586	sequestosome 1	Sqstm1	6.956	0.007	23.579	0.000	2.040	0.151	12.735	0.001
1371353_at	BG663093	sequestosome 1	Sqstm1	1.140	0.288	3.071	0.000	0.852	0.143	3.202	0.002
1371943_at	BF420075	Ser/Thr-like protein kinase lyk4 /// serine/threonine kinase 40 (predicted)	Lyk4 /// Stk40_predicted	1.396	0.138	1.430	0.021	1.966	0.000	1.840	0.003
1368790_at	NM_133617	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10	Serpina10	1.722	0.064	0.596	0.009	5.012	0.005	0.712	0.500
1368224_at	NM_031531	serine (or cysteine) peptidase inhibitor, clade A, member 3N	Serpina3n	3.296	0.001	2.642	0.032	3.674	0.006	1.000	0.075
1369972_at	NM_057108	serine (or cysteine) peptidase inhibitor, clade B, member 5	Serpinb5	0.491	0.042	0.490	0.036	0.419	0.021	0.543	0.106
1375003_at	AA997359	serine (or cysteine) peptidase inhibitor, clade B, member 6a	Serpinb6a	1.150	0.665	1.021	0.530	0.806	0.825	0.908	0.558
1376918_at	AI029930	Serine (or cysteine) peptidase inhibitor, clade C (antithrombin), member 1	Serpinc1	1.691	0.314	0.600	0.137	0.982	0.567	0.587	0.119
1388569_at	AI179984	serine (or cysteine) peptidase inhibitor, clade F, member 1	Serpinf1	0.868	0.040	1.000	0.999	0.878	0.045	0.999	0.998
1372254_at	AW915763	serine (or cysteine) peptidase inhibitor, clade G, member 1	Serping1	19.176	0.002	16.403	0.000	24.445	0.001	19.680	0.001
1368256_at	NM_053779	serine (or cysteine) peptidase inhibitor, clade I, member 1	Serpini1	0.691	0.131	0.186	0.000	1.197	0.662	0.423	0.020
1387131_at	AF193015	serine (or cysteine) peptidase inhibitor, clade I, member 1	Serpini1	0.882	0.799	0.385	0.014	0.979	0.912	0.600	0.005
1391850_at	BE116159	Serine (or cysteine) peptidase inhibitor, clade I, member 1	Serpini1	0.875	0.800	0.821	0.619	1.210	0.081	0.863	0.221
1369748_at	NM_133612	serine (or cysteine) peptidase inhibitor, clade I, member 2	Serpini2	1.023	0.230	0.969	0.163	1.026	0.674	0.962	0.692
1367647_at	NM_022519	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	Serpina1	1.271	0.037	0.418	0.149	1.048	0.845	0.466	0.150
1373686_at	AA893495	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 6 (mapped)	Serpina6_mapped	0.772	0.310	4.393	0.017	0.996	0.991	2.141	0.032
1377034_at	BF411331	serine (or cysteine) proteinase inhibitor, clade B, member 1a	Serpinb1a	0.909	0.241	0.571	0.080	0.910	0.830	0.596	0.079
1380346_at	BE100150	serine (or cysteine) proteinase inhibitor, clade B, member 1a	Serpinb1a	1.311	0.481	1.107	0.443	0.740	0.746	0.985	0.912
1372440_at	BI275818	serine (or cysteine) proteinase inhibitor, clade E, member 2	Serpine2	1.407	0.240	0.951	0.188	1.177	0.099	0.953	0.018
1370220_at	BI283159	serine carboxypeptidase 1	Scpep1	0.902	0.940	1.176	0.712	0.845	0.027	1.045	0.116
1385670_at	BF521655	serine dehydratase-like (predicted)	Sdsl_predicted	0.958	0.324	0.840	0.090	0.857	0.416	0.755	0.342
1374748_at	AI010087	serine hydroxymethyl transferase 1 (soluble)	Shmt1	1.009	0.871	0.986	0.984	0.988	0.996	1.014	0.618
1388695_at	BF285150	serine hydroxymethyl transferase 2 (mitochondrial)	Shmt2	1.104	0.220	1.671	0.085	1.109	0.256	1.555	0.169
1388307_at	BG671458	serine incorporator 1	Serinc1	0.825	0.851	0.746	0.029	0.919	0.363	0.808	0.057
1375084_at	BF419780	serine incorporator 2	Serinc2	1.545	0.057	0.863	0.393	1.164	0.088	1.261	0.583
1398986_at	AA944455	serine incorporator 3	Serinc3	1.308	0.318	0.947	0.765	1.184	0.104	0.845	0.088
1397197_at	BE120228	Serine incorporator 3	Serinc3	1.144	0.809	0.862	0.266	3.080	0.021	0.868	0.130
1373203_at	AI236953	serine palmitoyltransferase, long chain base subunit 1 (predicted)	Sptlc1_predicted	0.755	0.002	0.738	0.011	0.818	0.052	0.807	0.027
1383290_at	BI280343	serine peptidase inhibitor, Kunitz type 1	Spint1	2.199	0.001	2.845	0.003	2.461	0.000	2.603	0.005
1388320_at	AI412117	serine protease inhibitor, Kunitz type 2	Spint2	0.878	0.240	0.734	0.001	0.993	0.900	0.853	0.025
1390131_at	BE112936	serine racemase	Srr	0.947	0.929	0.689	0.037	1.466	0.463	0.900	0.873
1377914_at	AI059437	serine/arginine repetitive matrix 1 (predicted)	Srrm1_predicted	2.009	0.017	2.374	0.011	1.409	0.093	1.476	0.643
1371425_at	BF396399	Serine/arginine repetitive matrix 1 (predicted)	Srrm1_predicted	1.291	0.028	1.402	0.001	1.203	0.497	1.369	0.005
1390048_at	BF408990	serine/arginine repetitive matrix 2 (predicted)	Srrm2_predicted	0.549	0.030	0.617	0.015	0.777	0.562	0.790	0.366
1398940_at	AW532525	serine/arginine repetitive matrix 2 (predicted)	Srrm2_predicted	0.791	0.114	0.572	0.021	1.077	0.311	0.717	0.007
1371714_at	BG378760	Serine/arginine-rich protein specific kinase 1	Srpk1	0.830	0.757	0.407	0.003	0.606	0.079	0.485	0.010
1383182_at	AW144184	serine/arginine-rich protein specific kinase 1	Srpk1	1.132	0.819	1.930	0.030	0.871	0.084	2.770	0.042
1375459_at	BE113419	serine/arginine-rich protein specific kinase 2 (predicted)	Srpk2_predicted	0.542	0.168	1.049	0.219	0.604	0.170	1.083	0.706
1370920_at	AI102055	serine/arginine-rich protein specific kinase 2 (predicted)	Srpk2_predicted	0.986	0.391	1.413	0.004	0.746	0.047	1.149	0.049
1367936_at	NM_019206	serine/threonine kinase 10	Stk10	1.075	0.997	1.255	0.230	1.659	0.135	0.886	0.585

1370322_at	D86220	serine/threonine kinase 16	Stk16	0.612	0.137	0.367	0.053	0.680	0.035	0.662	0.074
1376751_at	AI044250	serine/threonine kinase 19	Stk19	1.001	0.638	0.909	0.938	0.941	0.811	1.030	0.934
1369037_at	NM_019349	serine/threonine kinase 2	Slk	0.900	0.456	0.696	0.143	0.902	0.463	0.693	0.146
1388396_at	BI275932	serine/threonine kinase 25 (STE20 homolog, yeast)	Stk25	1.232	0.246	0.929	0.061	1.223	0.246	0.688	0.025
1369712_at	NM_031735	serine/threonine kinase 3 (STE20 homolog, yeast)	Stk3	1.219	0.242	0.998	0.989	2.611	0.012	1.135	0.354
1396707_at	BF404674	Serine/threonine kinase 32A (predicted)	Stk32a_predicted	1.006	0.930	1.021	0.047	1.000	0.990	1.033	0.104
1377534_at	BE097305	serine/threonine kinase 32C (predicted)	Stk32c_predicted	0.948	0.996	0.269	0.046	1.005	0.985	0.284	0.017
1390488_a_at	AI176077	serine/threonine kinase 38	Stk38	1.228	0.115	1.032	0.494	0.996	0.813	1.031	0.377
1393520_at	AA850272	Serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	Stk39	1.393	0.616	1.076	0.844	1.084	0.715	1.686	0.082
1372077_at	AI009198	serine/threonine kinase receptor associated protein	Strap	0.838	0.475	2.237	0.000	0.988	0.351	1.674	0.010
1367725_at	NM_022602	serine/threonine-protein kinase pim-3	Pim3	0.596	0.812	3.059	0.008	0.953	0.771	2.542	0.019
1396116_at	BG669152	serologically defined colon cancer antigen 1	Sdccag1	0.924	0.421	0.772	0.009	1.116	0.633	0.668	0.034
1374738_at	BF416387	serologically defined colon cancer antigen 10	Sdccag10	1.116	0.179	2.621	0.058	1.019	0.453	1.275	0.060
1371706_at	AI101371	serologically defined colon cancer antigen 3	Sdccag3	0.941	0.467	0.879	0.173	0.896	0.596	1.059	0.988
1383573_at	BE117444	Serologically defined colon cancer antigen 33 (predicted)	Sdccag33_predicted	0.484	0.005	0.301	0.000	0.593	0.004	0.444	0.003
1380283_at	BF411100	Serologically defined colon cancer antigen 33 (predicted)	Sdccag33_predicted	0.429	0.019	0.258	0.000	0.429	0.011	0.304	0.000
1392611_at	BE117629	Serologically defined colon cancer antigen 33 (predicted)	Sdccag33_predicted	0.355	0.095	0.162	0.003	0.323	0.097	0.209	0.007
1372874_at	BI299261	Serologically defined colon cancer antigen 8	Sdccag8	0.521	0.032	0.349	0.004	0.541	0.042	0.409	0.012
1388076_at	AF388527	Serpine1 mRNA binding protein 1	Serbp1	0.779	0.174	1.527	0.033	0.675	0.009	1.151	0.127
1389153_at	BI296087	Serpine1 mRNA binding protein 1	Serbp1	0.659	0.330	0.572	0.001	0.812	0.035	0.651	0.009
1387632_at	NM_022271	sertolin	LOC64038	0.768	0.814	0.761	0.194	0.601	0.029	1.003	0.964
1382452_at	AI603408	serum deprivation response protein	Sdpr	4.027	0.095	1.299	0.180	2.697	0.124	1.217	0.151
1375638_at	AI009714	serum deprivation response protein	Sdpr	0.866	0.740	1.233	0.530	0.923	0.519	0.869	0.471
1377827_at	AA851587	serum response factor binding protein 1	Srfbp1	0.973	0.416	3.876	0.049	1.042	0.779	4.059	0.085
1385368_at	AA998786	Serum response factor binding protein 1	Srfbp1	1.109	0.718	1.257	0.501	1.724	0.210	1.507	0.037
1367802_at	NM_019232	serum/glucocorticoid regulated kinase	Sgk	2.877	0.002	2.277	0.000	2.060	0.151	1.908	0.002
1392262_at	BF402235	Seryl-aminoacyl-tRNA synthetase 1	Sars1	1.961	0.087	7.656	0.001	1.058	0.511	2.838	0.018
1375441_at	BI278468	seryl-aminoacyl-tRNA synthetase 1	Sars1	0.874	0.511	2.597	0.004	0.705	0.023	2.396	0.002
1397578_at	BE099423	SET and MYND domain containing 1 (predicted)	Smyd1_predicted	1.010	0.990	1.007	0.973	1.003	0.989	1.004	0.944
1371904_at	BI294698	SET and MYND domain containing 2	Smyd2	0.640	0.222	1.299	0.001	0.805	0.046	1.109	0.498
1393116_at	BI286804	SET and MYND domain containing 4 (predicted)	Smyd4_predicted	0.594	0.101	0.561	0.042	0.634	0.101	0.665	0.061
1393493_at	BE117956	SET binding protein 1 (predicted)	Setbp1_predicted	1.053	0.068	0.883	0.675	1.415	0.652	0.966	0.801
1389562_at	BF396686	SET binding protein 1 (predicted)	Setbp1_predicted	1.309	0.113	0.804	0.420	0.736	0.158	1.070	0.358
1378678_at	BF417886	SET binding protein 1 (predicted)	Setbp1_predicted	0.993	0.403	0.559	0.062	1.015	0.897	0.700	0.050
1378434_at	BF400808	SET binding protein 1 (predicted)	Setbp1_predicted	1.435	0.530	1.243	0.892	1.176	0.677	1.757	0.150
1396768_at	BF404627	SET binding protein 1 (predicted)	Setbp1_predicted	1.078	0.870	0.803	0.476	1.034	0.855	1.409	0.217
1374603_at	AA943793	SET domain and mariner transposase fusion gene	Setmar	1.003	0.956	0.663	0.539	0.998	0.938	0.911	0.480
1382141_at	BI291928	SET domain, bifurcated 1 (predicted)	Setdb1_predicted	1.209	0.170	1.447	0.092	0.621	0.865	1.641	0.210
1372461_at	BG381708	SET translocation (predicted) /// RGD1561000 (predicted)	Set_predicted /// RGD1561000_predicted	0.840	0.061	1.948	0.019	0.650	0.004	1.509	0.027
1387266_at	NM_080905	seven in absentia 1A	Siah1a	1.377	0.043	2.539	0.000	0.993	0.577	2.181	0.001
1377647_at	AA924088	sex comb on midleg homolog 1 (predicted)	Scmh1_predicted	1.223	0.145	1.701	0.017	0.719	0.515	1.107	0.713
1389249_at	BE114850	SH2 domain binding protein 1 (tetratricopeptide repeat containing)	Sh2bp1	0.716	0.007	0.575	0.002	0.782	0.061	0.604	0.016
1385970_at	BF289079	SH2 domain binding protein 1 (tetratricopeptide repeat containing)	Sh2bp1	0.993	0.360	0.670	0.410	1.117	0.225	0.696	0.161
1371882_a_at	AI104139	SH2-B PH domain containing signaling mediator 1	Sh2bpsm1	0.998	0.971	1.747	0.008	1.001	0.988	1.388	0.014
1378926_at	BF415792	SH3 and multiple ankyrin repeat domains 1	Shank1	0.958	0.451	0.959	0.958	0.996	0.474	0.842	0.012
1371487_at	BG666075	SH3 domain binding glutamic acid-rich protein-like 3 (predicted)	Sh3bgrl3_predicted	0.717	0.813	0.852	0.289	0.343	0.008	0.735	0.299
1373267_at	AW527403	Sh3 domain YSC-like 1 (predicted)	Sh3yl1_predicted	0.557	0.793	0.951	0.081	1.374	0.412	1.618	0.272
1369777_a_at	NM_133440	SH3/ankyrin domain gene 2	Shank2	1.363	0.187	1.718	0.006	1.201	0.325	1.969	0.039
1388462_at	AI407506	SH3-binding kinase 1	Sbk1	2.044	0.019	0.846	0.458	1.376	0.089	0.451	0.049
1387294_at	NM_054011	SH3-domain binding protein 5 (BTK-associated)	Sh3bp5	1.242	0.162	2.198	0.000	0.929	0.727	2.982	0.073
1367699_at	AB008161	SH3-domain GRB2-like 1	Sh3gl1	1.173	0.201	1.835	0.007	1.157	0.212	1.031	0.804
1389550_at	BM385941	SH3-domain GRB2-like 2	Sh3gl2	0.965	0.441	0.390	0.017	0.996	0.917	0.684	0.022
1381203_at	AA819246	SH3-domain GRB2-like B1 (endophilin)	Sh3glb1	2.585	0.000	1.961	0.013	4.243	0.006	2.605	0.002
1390096_at	BF284481	SH3-domain GRB2-like B1 (endophilin)	Sh3glb1	1.677	0.001	0.315	0.005	2.160	0.002	0.502	0.012
1382007_at	AA964563	SH3-domain GRB2-like B1 (endophilin)	Sh3glb1	1.893	0.043	2.173	0.005	1.847	0.028	2.370	0.006
1391759_at	BF283873	SH3-domain GRB2-like B1 (endophilin)	Sh3glb1	1.760	0.103	0.997	0.931	1.457	0.014	0.994	0.964
1376486_at	BG381092	SH3-domain GRB2-like endophilin B2	Sh3glb2	0.529	0.012	0.518	0.019	0.607	0.028	0.711	0.106
1370419_a_at	AF230520	SH3-domain kinase binding protein 1	Sh3kbp1	1.041	0.894	0.789	0.790	1.002	0.864	1.113	0.152
1387957_a_at	AF255888	SH3-domain kinase binding protein 1	Sh3kbp1	1.072	0.942	0.813	0.069	1.512	0.626	0.872	0.137
1372970_at	BM389664	Sh3kbp1 binding protein 1 (predicted)	Shkbp1_predicted	0.778	0.030	0.894	0.605	0.871	0.428	0.895	0.472

1368069_at	NM_031153	SHANK-associated RH domain interacting protein	Sharpin	0.583	0.118	0.942	0.138	1.174	0.460	1.112	0.890
1377986_at	AI029749	short coiled-coil protein /// similar to short coiled-coil protein	Scoc /// LOC498931	1.433	0.010	0.828	0.050	1.183	0.092	0.776	0.035
1388822_at	AI409077	short coiled-coil protein /// similar to short coiled-coil protein	Scoc /// LOC498931	1.006	0.984	0.662	0.006	1.425	0.032	0.912	0.207
1387349_at	NM_013028	short stature homeobox 2	Shox2	0.953	0.728	1.023	0.205	1.239	0.015	0.831	0.077
1378940_at	AI170278	SHQ1 homolog (S. cerevisiae) (predicted)	Shq1_predicted	1.191	0.368	1.127	0.139	1.060	0.648	1.055	0.779
1384363_at	AI070597	Shwachman-Bodian-Diamond syndrome homolog (human)	Sbds	0.616	0.072	1.003	0.997	0.962	0.349	1.003	0.979
1374436_at	AI070122	Shwachman-Bodian-Diamond syndrome homolog (human)	Sbds	1.393	0.320	1.052	0.347	1.268	0.139	1.038	0.670
1392012_at	BE100353	Siah binding protein 1; FBP interacting repressor; pyrimidine tract binding splicing factor; Ro ribonucleoprotein-binding protein 1	Siahbp1	13.309	0.014	1.233	0.053	8.218	0.019	1.290	0.187
1367464_at	AI598391	siah binding protein 1; FBP interacting repressor; pyrimidine tract binding splicing factor; Ro ribonucleoprotein-binding protein 1	Siahbp1	0.943	0.504	1.655	0.004	0.907	0.274	1.405	0.157
1388828_at	AI579643	SID1 transmembrane family, member 2 (predicted)	Sidt2_predicted	1.282	0.076	0.950	0.651	1.037	0.050	1.022	0.380
1372715_at	AA819349	sideroflexin 1	Sfxn1	0.394	0.011	0.846	0.112	0.379	0.000	0.809	0.136
1387008_at	NM_022948	sideroflexin 3	Sfxn3	0.351	0.112	0.145	0.000	0.384	0.007	0.515	0.081
1393204_at	AI711190	sideroflexin 4 (predicted)	Sfxn4_predicted	0.703	0.170	1.556	0.040	1.344	0.593	1.569	0.036
1371427_at	BG380709	signal peptidase complex subunit 1 homolog (S. cerevisiae) (predicted)	Spcs1_predicted	0.906	0.754	0.813	0.075	1.090	0.526	0.985	0.226
1389140_at	AI172437	signal peptidase complex subunit 2 homolog (S. cerevisiae) (predicted)	Spcs2_predicted	0.728	0.795	2.033	0.005	0.705	0.323	1.856	0.016
1367476_at	AA799994	signal recognition particle 14 (predicted)	Srp14_predicted	0.785	0.455	0.730	0.025	0.801	0.183	0.953	0.044
1388974_at	AI101527	signal recognition particle 19 (predicted)	Srp19_predicted	0.615	0.289	1.473	0.014	0.560	0.031	1.314	0.142
1383410_at	BI290777	signal recognition particle 54	Srp54	0.910	0.267	1.503	0.019	0.877	0.284	1.212	0.000
1385680_at	BG667707	signal recognition particle 54	Srp54	0.644	0.909	1.240	0.110	0.873	0.718	1.042	0.941
1371626_at	BI296671	signal recognition particle 68 (predicted)	Srp68_predicted	0.716	0.381	1.251	0.006	0.724	0.152	1.016	0.407
1371343_at	BM391232	signal recognition particle receptor ('docking protein')	Srpr	0.822	0.329	0.734	0.010	0.846	0.182	0.743	0.003
1382166_at	BF407425	signal recognition particle receptor, B subunit	Srprb	0.404	0.620	1.369	0.235	0.632	0.176	1.015	0.347
1378932_at	AI103196	Signal recognition particle receptor, B subunit	Srprb	0.584	0.814	1.064	0.575	0.600	0.044	1.116	0.570
1367690_at	NM_017199	signal sequence receptor 4	Ssr4	0.727	0.707	0.592	0.007	0.732	0.220	0.592	0.006
1373090_at	AI230697	signal sequence receptor, alpha	Ssr1	0.663	0.501	1.270	0.473	0.781	0.357	0.939	0.825
1381987_at	AI175803	Signal sequence receptor, alpha	Ssr1	0.947	0.703	0.827	0.060	0.936	0.802	0.571	0.013
1391283_at	AI713146	Signal sequence receptor, alpha	Ssr1	1.000	0.945	1.000	0.978	1.462	0.121	0.998	0.156
1390767_at	BF391148	signal sequence receptor, alpha	Ssr1	0.725	0.985	1.090	0.057	0.752	0.589	0.992	0.865
1382738_at	BF282918	Signal sequence receptor, beta (predicted)	Ssr2_predicted	0.628	0.111	1.040	0.855	0.700	0.295	0.930	0.656
1373185_at	BE329347	signal sequence receptor, beta (predicted)	Ssr2_predicted	0.640	0.239	0.914	0.122	0.603	0.024	0.915	0.021
1375652_at	BI285910	signal sequence receptor, gamma	Ssr3	1.032	0.482	1.234	0.551	1.188	0.338	1.304	0.383
1369718_at	NM_031120	signal sequence receptor, gamma	Ssr3	1.006	0.852	1.306	0.699	0.336	0.211	1.391	0.439
1388777_at	BE113224	signal sequence receptor, gamma	Ssr3	1.061	0.880	0.973	0.435	1.081	0.667	1.136	0.387
1387354_at	NM_032612	signal transducer and activator of transcription 1	Stat1	28.134	0.000	9.902	0.002	23.797	0.000	13.394	0.002
1368835_at	AW434718	signal transducer and activator of transcription 1	Stat1	14.504	0.000	5.499	0.000	19.507	0.000	8.666	0.001
1372757_at	BM386875	signal transducer and activator of transcription 1	Stat1	7.381	0.001	4.737	0.000	8.266	0.000	7.279	0.002
1373670_at	AA799569	Signal transducer and activator of transcription 2	Stat2	10.314	0.000	4.284	0.011	22.175	0.001	4.592	0.003
1389571_at	BG666368	signal transducer and activator of transcription 2	Stat2	17.983	0.007	32.826	0.007	25.498	0.000	49.365	0.001
1370224_at	BE113920	signal transducer and activator of transcription 3	Stat3	2.662	0.002	2.924	0.056	2.863	0.001	1.905	0.094
1371781_at	BI285863	signal transducer and activator of transcription 3	Stat3	2.016	0.003	1.616	0.031	2.963	0.005	1.658	0.013
1368231_at	NM_017064	signal transducer and activator of transcription 5A	Stat5a	1.010	0.869	1.313	0.632	0.824	0.869	1.209	0.303
1387876_at	AI177626	signal transducer and activator of transcription 5B	Stat5b	1.332	0.100	3.244	0.002	1.227	0.121	1.415	0.296
1391527_at	BE109296	Signal transducer and activator of transcription 6 (predicted)	Stat6_predicted	1.477	0.047	1.815	0.164	2.219	0.018	1.437	0.095
1367533_at	BG663097	signal transducer and activator of transcription interacting protein 1	Statip1	0.614	0.024	0.797	0.012	0.786	0.053	0.941	0.233
1392017_at	BF397766	Signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	Stam2	2.324	0.008	1.251	0.253	1.819	0.134	1.168	0.431
1370330_at	AF026504	signal-induced proliferation-associated 1 like 1	Sipa1l1	0.932	0.889	0.834	0.143	0.812	0.034	0.673	0.138
1376040_at	BI290044	signal-induced proliferation-associated 1 like 2	Sipa1l2	1.291	0.068	0.875	0.044	0.905	0.506	0.670	0.054
1377690_at	AA818651	signal-induced proliferation-associated 1 like 3	Sipa1l3	1.040	0.503	0.949	0.615	1.036	0.511	0.761	0.613
1394538_at	BF404879	Signal-induced proliferation-associated gene 1	Sipa1	0.923	0.588	0.984	0.856	0.998	0.553	0.996	0.762
1389420_at	BI279446	signal-transducing adaptor protein-2	Stap2	1.725	0.038	1.551	0.089	20.298	0.003	8.760	0.012
1376465_at	BI295240	Sim ilar to glucocorticoid induced gene 1 (predicted)	RGD1563869_predicted	0.862	0.302	0.641	0.066	0.394	0.055	0.576	0.031
1381670_at	BF412681	Similar to [Ascaris lumbricoides mRNA sequence.], gene product (predicted)	RGD1561753_predicted	1.144	0.685	1.694	0.338	0.987	0.960	1.529	0.198
1388773_at	BI278479	similar to [Mouse primary response gene B94 mRNA, 3end.], gene product	LOC299339	201.549	0.000	70.732	0.000	35.437	0.013	6.162	0.003
1381376_at	AI103284	Similar to [Mouse primary response gene B94 mRNA, 3end.], gene product	LOC299339	6.883	0.011	4.389	0.016	1.943	0.478	1.027	0.780
1371905_at	BM384949	similar to 0610007L01Rik protein	MGC94190	0.640	0.024	1.208	0.035	0.715	0.041	1.085	0.074
1379064_at	BI296614	Similar to 0610007L01Rik protein	MGC94190	1.224	0.773	1.866	0.435	1.051	0.843	1.497	0.080
1398927_at	BF406225	similar to 0610010K06Rik protein	RGD1307161	0.806	0.224	0.935	0.053	0.845	0.624	0.776	0.068
1372303_at	BE110633	similar to 0910001A06Rik protein (predicted)	RGD1307697_predicted	1.097	0.834	1.041	0.350	1.033	0.934	0.740	0.053
1374822_at	BE118465	Similar to 106 kDa O-GlcNAc transferase-interacting protein (predicted)	RGD1307844_predicted	1.650	0.418	2.614	0.001	1.171	0.925	1.854	0.001

1373605_at	AI176540	similar to 106 kDa O-GlcNAc transferase-interacting protein (predicted)	RGD1307844_predicted	1.248	0.545	1.273	0.075	1.120	0.053	1.259	0.270
1373174_at	AW915592	similar to 1110001K21Rik protein	LOC497867	0.840	0.067	0.679	0.014	0.622	0.180	0.705	0.066
1390042_at	AI071166	similar to 1110007F12Rik protein	MGC109491	24.900	0.000	5.697	0.008	52.784	0.001	13.685	0.008
1393100_at	AI071493	similar to 1110008L16Rik protein (predicted)	RGD1305089_predicted	0.806	0.550	0.560	0.045	0.930	0.993	1.016	0.305
1390448_at	AA800699	similar to 1110065L07Rik protein (predicted)	RGD1308317_predicted	0.998	0.935	0.991	0.794	0.999	0.995	1.001	0.990
1376476_at	BI279598	similar to 1200003M09Rik protein (predicted)	RGD1305553_predicted	0.864	0.991	0.867	0.320	1.067	0.762	0.857	0.277
1380735_at	BM385424	Similar to 1500019C06Rik protein (predicted)	RGD1560433_predicted	1.308	0.046	0.768	0.254	0.977	0.822	0.606	0.118
1380694_at	BM390450	Similar to 1500019C06Rik protein (predicted)	RGD1560433_predicted	1.097	0.185	0.902	0.095	0.973	0.769	0.792	0.040
1382797_at	AW526331	similar to 1500019C06Rik protein (predicted)	RGD1560433_predicted	0.619	0.517	1.788	0.016	0.490	0.087	1.586	0.039
1374756_at	BI295129	similar to 1500031N24Rik protein (predicted) /// similar to 1500031N24Rik protein (predicted)	RGD1311188_predicted /// RGD1562665_predicted	1.467	0.317	1.101	0.534	1.014	0.890	1.026	0.700
1372934_at	AI104146	similar to 1700019E19Rik protein (predicted)	RGD1307392_predicted	1.823	0.022	0.671	0.154	1.250	0.043	0.997	0.945
1374701_at	BG378096	similar to 1700022N24Rik protein	MGC109455	0.757	0.599	1.832	0.003	0.723	0.078	1.461	0.041
1374245_at	BI282085	similar to 1700029B21Rik protein	LOC363251	0.982	0.885	1.751	0.003	0.987	0.909	1.111	0.354
1379972_at	AI070438	similar to 1700060H10Rik protein	RGD1308699	0.482	0.096	0.569	0.012	0.439	0.037	0.928	0.331
1371891_at	BG371476	similar to 1700123O20Rik protein (predicted)	RGD1308430_predicted	0.562	0.436	0.738	0.082	0.736	0.091	0.738	0.208
1390730_at	BM383911	similar to 1810009O10Rik protein	RGD1305651	0.372	0.044	0.299	0.000	0.436	0.056	0.348	0.008
1371631_at	BF420639	similar to 2010003J03Rik protein	RGD1304686	0.908	0.458	2.921	0.009	0.907	0.413	1.832	0.030
1372154_at	AW521019	similar to 2010321M09Rik protein	RGD1359616	0.730	0.061	0.988	0.834	0.659	0.006	1.080	0.131
1371749_at	AI169439	similar to 2210021J22Rik protein (predicted)	RGD1306001_predicted	0.530	0.116	1.242	0.060	0.532	0.198	1.092	0.063
1377598_at	AJ225648	similar to 2310002F18Rik protein	MGC124824	0.420	0.091	0.443	0.003	0.422	0.003	0.464	0.047
1376455_at	BI296172	similar to 2310010G13Rik protein	MGC114471	0.480	0.060	0.835	0.144	0.497	0.044	1.000	0.180
1380072_at	AI233871	similar to 2310044H10Rik protein	MGC93975	0.742	0.981	0.928	0.334	0.999	0.988	0.929	0.298
1398890_at	AI410096	similar to 2310044H10Rik protein	MGC93975	0.985	0.981	0.803	0.001	0.913	0.572	0.767	0.006
1372396_at	BE113316	Similar to 2310047B19Rik protein (predicted)	RGD1308026_predicted	0.479	0.082	0.739	0.047	0.508	0.014	0.695	0.575
1373115_at	BI281909	similar to 2310061I09Rik protein (predicted)	RGD1304653_predicted	1.060	0.773	1.281	0.360	1.236	0.704	1.104	0.596
1398949_at	BM392094	similar to 2410001C21Rik protein	RGD1311072	0.528	0.001	0.805	0.043	0.779	0.105	0.898	0.170
1388402_at	AI175019	similar to 2410001H17Rik protein (predicted)	RGD1305824_predicted	1.038	0.669	0.864	0.179	1.094	0.621	0.937	0.439
1388923_at	BG381657	similar to 2410004L22Rik protein	RGD1311565	2.526	0.023	1.085	0.285	3.421	0.058	0.504	0.016
1393218_at	AI176155	Similar to 2410024A21Rik protein	RGD1304878	1.142	0.062	0.770	0.415	1.141	0.191	1.006	0.897
1372429_at	BF419113	similar to 24432 protein	LOC307798	0.439	0.001	0.578	0.010	0.460	0.036	0.631	0.125
1383955_at	BF554586	Similar to 2510002A14Rik protein (predicted)	RGD1311309_predicted	1.348	0.690	1.054	0.134	1.060	0.788	1.123	0.043
1374764_at	BG378053	similar to 2610033H07Rik protein (predicted)	RGD1305605_predicted	0.615	0.482	1.041	0.840	0.924	0.256	1.099	0.715
1384786_at	AI073019	Similar to 2610034M16Rik protein (predicted)	RGD1560925_predicted	1.171	0.889	1.180	0.320	1.286	0.983	0.972	0.096
1389361_at	AI012506	similar to 2610111M03Rik protein	LOC363544	0.273	0.010	0.854	0.184	0.405	0.007	0.666	0.032
1374707_at	BM384854	similar to 2610301G19Rik protein (predicted)	RGD1309922_predicted	1.591	0.198	0.808	0.347	1.180	0.659	0.857	0.222
1377010_at	BI274499	similar to 2610317D23Rik protein (predicted)	RGD1565411_predicted	0.945	0.779	0.797	0.385	0.793	0.313	0.942	0.323
1393158_at	BI298434	similar to 2610528M18Rik protein	LOC363198	2.455	0.028	0.971	0.615	2.243	0.032	1.265	0.239
1375763_at	BF407879	similar to 2700008B19Rik protein (predicted)	RGD1566204_predicted	0.944	0.480	1.064	0.016	1.010	0.178	1.090	0.172
1389652_at	AI171655	Similar to 2700029M09Rik protein (predicted)	RGD1311747_predicted	0.699	0.249	0.687	0.006	0.697	0.063	0.832	0.007
1378638_a_at	BM384709	similar to 2700029M09Rik protein (predicted)	RGD1311747_predicted	0.444	0.670	0.868	0.123	0.608	0.289	0.620	0.012
1374067_at	AA852011	similar to 2700078E11Rik protein	RGD1308127	0.815	0.608	1.201	0.149	0.761	0.006	1.094	0.071
1389298_at	AI412864	Similar to 2700078E11Rik protein	RGD1308127	0.966	0.939	1.034	0.427	1.065	0.704	1.105	0.720
1388791_at	BI275911	similar to 2810022L02Rik protein	RGD1309930	1.829	0.033	1.718	0.026	2.721	0.007	2.557	0.027
1367541_at	BE113965	similar to 2810410A08Rik protein (predicted)	RGD1566062_predicted	0.630	0.017	1.115	0.091	0.309	0.125	1.060	0.398
1372891_at	BF408856	similar to 2810437L13Rik protein (predicted)	RGD1305631_predicted	0.749	0.072	1.079	0.351	0.899	0.253	1.088	0.287
1376498_at	BI282766	similar to 2900002H16Rik protein (predicted)	RGD1307973_predicted	0.287	0.063	2.014	0.011	0.356	0.048	1.326	0.125
1374981_at	BF399062	similar to 2-aminoadipic 6-semialdehyde dehydrogenase (predicted)	RGD1311135_predicted	1.011	0.900	0.570	0.230	0.950	0.852	1.367	0.745
1377187_at	BI291427	similar to 3000004N20Rik protein (predicted) /// similar to RIKEN cDNA 3000004N20 (predicted)	RGD1307658_predicted /// RGD1564940_predicted	0.821	0.080	0.964	0.686	0.708	0.065	0.861	0.928
1379537_at	AW251543	similar to 3222401M22Rik protein (predicted)	RGD1307304_predicted	1.001	0.947	0.997	0.980	0.995	0.945	0.999	0.972
1375052_at	AI229218	similar to 3300001A09Rik protein	LOC501015	1.406	0.176	4.033	0.037	1.009	0.966	4.061	0.028
1379894_at	AI501165	similar to 3632451O06Rik protein (predicted)	RGD1310110_predicted	0.802	0.897	1.008	0.634	1.051	0.995	1.327	0.342
1397580_at	AI500809	Similar to 40S ribosomal protein S16 (predicted)	RGD1564574_predicted	1.270	0.135	0.995	0.966	0.946	0.841	1.165	0.073
1392131_at	AI012870	similar to 40S ribosomal protein S2 (predicted)	RGD1566024_predicted	0.516	0.009	0.700	0.081	0.528	0.010	0.693	0.107
1393051_at	BF551457	similar to 40S ribosomal protein S29	LOC501619	0.937	0.885	1.016	0.749	0.757	0.247	0.924	0.352
1389638_at	BG380701	similar to 4632419K20Rik protein	MGC94288	1.548	0.105	2.759	0.012	1.437	0.139	1.689	0.363
1371507_at	BM384151	Similar to 4921517L17Rik protein	RGD1311678	0.541	0.000	0.461	0.002	0.659	0.001	0.670	0.010
1391224_at	AI169436	similar to 4921517L17Rik protein	RGD1311678	0.886	0.293	1.677	0.051	0.977	0.934	3.721	0.012
1394427_at	AW524670	Similar to 4921517L17Rik protein	RGD1311678	0.940	0.380	0.483	0.029	0.899	0.459	0.488	0.027
1395064_at	BE118876	similar to 4930429A08Rik protein (predicted)	RGD1564943_predicted	0.800	0.445	0.408	0.030	0.962	0.741	0.500	0.015

1382907_at	BI289723	similar to 4930431B09Rik protein	LOC310721	0.909	0.734	0.371	0.000	0.602	0.027	0.423	0.000
1389883_at	BF284719	Similar to 4930438D12Rik protein (predicted)	RGD1563224_predicted	0.659	0.310	0.650	0.019	0.738	0.026	0.566	0.006
1373961_at	AI170410	similar to 4930453N24Rik protein	MGC95208	5.128	0.004	6.848	0.005	8.191	0.000	9.156	0.004
1382630_at	BI302656	Similar to 4930506M07Rik protein (predicted)	RGD1311558_predicted	1.676	0.206	1.547	0.014	1.000	0.885	1.339	0.036
1374362_at	BF412970	similar to 4930566A11Rik protein (predicted)	RGD1306674_predicted	1.432	0.068	0.860	0.692	2.435	0.179	0.970	0.438
1375657_at	BE107438	Similar to 4933407C03Rik protein (predicted)	RGD1306101_predicted	0.750	0.048	0.940	0.449	0.829	0.207	0.969	0.274
1382064_at	BE095778	similar to 4933407C03Rik protein (predicted)	RGD1306101_predicted	0.613	0.449	1.150	0.251	0.485	0.144	0.917	0.341
1397096_at	BF413218	Similar to 4933407C03Rik protein (predicted)	RGD1306101_predicted	1.256	0.890	0.974	0.454	0.876	0.215	1.439	0.197
1373988_at	BM387458	similar to 4933425L03Rik protein (predicted)	RGD1559481_predicted	1.381	0.682	1.728	0.085	2.606	0.158	1.802	0.098
1393354_at	BE097947	Similar to 4933427D14Rik protein (predicted)	RGD1304728_predicted	0.708	0.031	0.888	0.727	1.217	0.335	1.002	0.953
1381558_at	BG374759	Similar to 4933427D14Rik protein (predicted)	RGD1304728_predicted	1.846	0.091	0.960	0.835	1.128	0.740	1.089	0.358
1393057_at	BF404098	similar to 5730403M16Rik protein	LOC308320	1.868	0.035	0.699	0.878	2.169	0.011	1.274	0.047
1374220_at	AI599176	similar to 5730405I09Rik protein (predicted)	RGD1565969_predicted	0.362	0.498	0.369	0.026	0.518	0.168	0.394	0.036
1392579_at	BI295501	similar to 5830411E10Rik protein	RGD1306658	0.534	0.155	0.566	0.012	0.847	0.622	0.882	0.845
1376701_a_at	BE109436	similar to 5930416I19Rik protein	MGC94282	0.968	0.580	1.167	0.049	1.000	0.998	1.246	0.606
1378180_at	BI284767	similar to 6030466N05Rik protein	LOC290741	1.328	0.351	1.431	0.230	0.919	0.904	1.154	0.989
1375181_at	AI170643	similar to 60S ribosomal protein L12	LOC499782	1.052	0.331	1.609	0.005	0.852	0.844	1.476	0.001
1398324_at	BI279866	similar to 60S ribosomal protein L18a	MGC72957	0.847	0.631	1.281	0.111	0.686	0.023	1.147	0.191
1371313_at	AI172199	similar to 60S ribosomal protein L23a (predicted)	RGD1565656_predicted	0.954	0.811	1.293	0.079	0.832	0.200	1.114	0.046
1375632_at	H35210	similar to 60S ribosomal protein L38 (predicted)	RGD1561636_predicted	0.940	0.251	1.094	0.879	0.961	0.211	1.021	0.365
1373976_at	BF396534	similar to 8430411H09Rik protein (predicted)	RGD1563990_predicted	1.001	0.986	1.063	0.647	1.151	0.348	1.048	0.822
1384117_at	BF555676	similar to 9130011E15Rik protein (predicted)	RGD1564887_predicted	0.736	0.039	0.969	0.300	0.511	0.031	1.677	0.135
1372112_at	AA945761	similar to 9230105E10Rik protein	RGD1304579	4.981	0.000	1.366	0.037	6.842	0.000	2.779	0.011
1393225_at	BE115446	Similar to a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 10	LOC314655	1.001	0.965	0.956	0.868	1.004	0.998	0.986	0.488
1389655_at	AA892330	similar to A230072I16Rik protein	RGD1306819	0.512	0.024	3.366	0.008	0.620	0.008	3.298	0.012
1372917_at	AI111992	similar to A230072I16Rik protein	RGD1306819	0.651	0.100	0.652	0.034	0.580	0.100	0.659	0.035
1379544_at	AI146108	Similar to A530083I02Rik protein (predicted)	RGD1311357_predicted	1.290	0.590	0.862	0.388	1.425	0.030	0.726	0.090
1377407_at	BI290154	similar to Aa2-174	RGD1309578	0.866	0.763	1.002	0.981	0.990	0.949	1.000	0.992
1375044_at	AI073208	Similar to Ab1-133	RGD1306344	2.240	0.045	1.001	0.649	2.226	0.043	1.005	0.965
1396265_at	BE097728	Similar to Ab1-133	RGD1306344	0.845	0.589	0.358	0.003	1.084	0.095	0.641	0.086
1382354_at	BE099884	Similar to Ab2-008	RGD1305133	1.312	0.007	1.032	0.886	1.264	0.384	1.010	0.920
1376676_a_at	BI296154	similar to Ab2-008	RGD1305133	0.888	0.181	0.960	0.513	0.856	0.334	0.877	0.879
1395616_at	BE116128	similar to Ab2-008	RGD1305133	0.848	0.299	1.106	0.111	0.772	0.411	0.957	0.838
1398522_at	BM386512	similar to Ab2-034	RGD1310191	0.851	0.166	0.899	0.040	0.868	0.289	0.733	0.059
1392087_at	AI227607	Similar to Ab2-034	RGD1310191	1.197	0.373	1.312	0.699	0.791	0.495	1.008	0.250
1393450_at	BI292896	Similar to Ab2-034	RGD1310191	0.974	0.437	0.876	0.152	0.896	0.128	0.866	0.353
1389199_at	AI407536	Similar to Ab2-095	RGD1309079	0.840	0.316	1.831	0.038	0.924	0.792	1.861	0.001
1371394_x_at	BG664827	similar to Ab2-143 (predicted)	RGD1561927_predicted	0.939	0.752	1.085	0.142	1.154	0.160	1.151	0.194
1372372_at	BG372437	similar to Ab2-225	RGD1306952	0.419	0.069	0.675	0.013	0.422	0.013	0.632	0.002
1396103_at	BF556107	similar to Ab2-225	RGD1306952	0.763	0.583	0.309	0.042	0.918	0.858	0.375	0.028
1373144_at	BM388977	similar to Ac2-125 (predicted)	RGD1563733_predicted	1.281	0.417	1.286	0.923	0.693	0.485	1.374	0.030
1392482_at	BF409567	similar to actin filament associated protein; actin filament-associated protein, 110 kDa (predicted)	RGD1311580_predicted	3.751	0.003	1.558	0.019	1.408	0.448	1.358	0.282
1398206_at	BE109223	Similar to actin filament associated protein; actin filament-associated protein, 110 kDa (predicted)	RGD1311580_predicted	2.214	0.004	1.177	0.569	1.246	0.049	0.970	0.613
1373181_at	BE101285	Similar to actin filament associated protein; actin filament-associated protein, 110 kDa (predicted)	RGD1311580_predicted	1.001	0.982	0.999	0.984	1.008	0.955	1.049	0.959
1385315_at	AI145941	Similar to actin monomer-binding protein (predicted)	RGD1309731_predicted	0.995	0.927	1.641	0.082	1.002	0.975	0.967	0.983
1375641_at	BI296526	similar to actin related protein 2/3 complex, subunit 5-like (predicted)	RGD1560362_predicted	0.821	0.366	2.723	0.020	0.625	0.062	2.790	0.007
1383704_at	BF410844	similar to actin-related protein 3-beta (predicted)	RGD1565759_predicted	0.980	0.830	0.983	0.953	1.002	0.947	1.017	0.336
1391421_at	AI599819	similar to Acyl-CoA dehydrogenase family member 8, mitochondrial precursor (ACAD-8) (predicted)	RGD1564209_predicted	1.363	0.081	0.930	0.710	1.349	0.215	1.264	0.840
1379262_at	AW525769	similar to acyl-CoA thioesterase	LOC302640	1.907	0.156	1.549	0.288	1.423	0.140	1.790	0.689
1386571_at	BF567145	similar to adaptor molecule SRCASM (predicted)	RGD1562626_predicted	2.042	0.101	1.872	0.138	1.963	0.077	1.584	0.039
1398474_at	BI300593	Similar to Adenosine deaminase CG11994-PA	LOC311352	0.400	0.046	0.293	0.000	0.548	0.022	0.384	0.040
1377498_at	BE100752	similar to adenosine monophosphate deaminase 2 (isoform L)	LOC362015	0.173	0.014	0.353	0.086	0.854	0.498	0.419	0.021
1372782_a_at	BE111787	similar to adenosine monophosphate deaminase 2 (isoform L)	LOC362015	0.604	0.029	0.444	0.002	0.678	0.260	0.501	0.001
1399003_at	BE116554	similar to adipocyte-specific protein 4	RGD1308813	0.887	0.277	0.823	0.138	0.831	0.747	0.733	0.048
1388981_at	AI104127	similar to ADP-ribosylation factor GTPase-activating protein 3 (ARF GAP 3)	LOC503165	1.022	0.611	1.610	0.001	0.947	0.644	1.174	0.023
1371733_at	BG667965	similar to ADP-ribosylation factor-like 10B (predicted)	RGD1565940_predicted	1.075	0.722	1.526	0.030	1.231	0.067	1.719	0.024
1397815_at	BG671292	similar to ADP-ribosylation factor-like 10C	LOC500282	1.721	0.746	3.316	0.014	1.387	0.722	2.216	0.077
1384157_at	AW916872	similar to ADP-ribosylation factor-like 10C	LOC500282	0.615	0.820	2.436	0.042	0.629	0.395	2.038	0.082
1373133_at	BF410786	similar to ADP-ribosylation factor-like 10C	LOC500282	0.971	0.885	1.437	0.010	0.903	0.687	1.352	0.011
1377110_at	BF420720	similar to ADP-ribosylation-like factor 12 protein (predicted)	RGD1563128_predicted	1.004	0.994	1.010	0.400	3.565	0.035	0.993	0.488
1379005_at	AI555974	similar to ADP-ribosylation-like factor 6-interacting protein 6	LOC499798	0.906	0.524	0.970	0.749	1.163	0.756	1.019	0.413

1397607_at	AI176987	similar to adult retina protein (predicted)	RGD1310862_predicted	1.082	0.691	1.372	0.074	1.009	0.874	0.996	0.991
1372316_at	BM384131	similar to AI115348 protein (predicted)	RGD1311939_predicted	3.243	0.000	0.743	0.039	3.039	0.000	1.124	0.888
1389208_at	AA944562	similar to AI448196 protein (predicted)	RGD1561477_predicted	1.196	0.561	0.424	0.004	1.086	0.256	0.558	0.189
1380156_at	BF396185	Similar to AI661453 protein (predicted)	RGD1561662_predicted	0.692	0.020	0.352	0.013	0.408	0.004	0.385	0.036
1376304_at	AI716243	Similar to AI661453 protein (predicted)	RGD1561662_predicted	0.404	0.339	0.824	0.467	0.405	0.009	0.859	0.413
1391298_at	BF416081	Similar to Aig1 protein (predicted)	RGD1562920_predicted	0.908	0.617	0.973	0.753	0.911	0.615	0.974	0.782
1375845_at	BI290029	similar to Aig1 protein (predicted)	RGD1562920_predicted	0.902	0.878	0.770	0.010	1.018	0.900	0.765	0.037
1381824_at	AI602689	Similar to Aig1 protein (predicted)	RGD1562920_predicted	1.013	0.884	0.956	0.831	0.973	0.961	0.872	0.502
1380022_at	BE119114	similar to AL023001 protein (predicted)	RGD1305001_predicted	1.094	0.568	1.251	0.077	0.618	0.206	1.312	0.378
1382179_at	AW534743	similar to alcohol dehydrogenase PAN2 (predicted)	RGD1565196_predicted	0.672	0.163	0.924	0.382	0.967	0.298	1.039	0.342
1386718_at	BF566188	similar to aldo-keto reductase family 1, member C12 (predicted)	RGD1562954_predicted	0.913	0.144	0.568	0.096	0.537	0.191	0.705	0.091
1373958_at	AA943149	similar to ALEX3 protein	LOC367902	0.772	0.587	1.347	0.175	0.714	0.010	1.390	0.302
1392799_at	AI013895	similar to Alkaline phytoceramidase (aPHC) (Alkaline ceramidase) (predicted)	RGD1561254_predicted	1.214	0.331	0.669	0.035	1.307	0.136	0.774	0.189
1395587_at	BF389646	Similar to Alkaline phytoceramidase (aPHC) (Alkaline ceramidase) (predicted)	RGD1561254_predicted	1.036	0.952	1.159	0.242	1.003	0.901	0.998	0.767
1393701_at	BF397095	similar to Alpha-1,4-N-acetylglucosaminyltransferase (Alpha4GnT) (predicted)	RGD1310265_predicted	1.186	0.345	1.378	0.136	0.972	0.906	1.106	0.146
1392184_at	BI298049	Similar to ALS2CR12 gene product	LOC316413	2.198	0.010	0.923	0.685	1.710	0.011	1.278	0.019
1376678_at	BF283712	similar to amyloid beta (A4) precursor protein-binding, family B, member 2 (predicted)	RGD1562438_predicted	0.467	0.067	0.860	0.303	0.423	0.033	0.707	0.048
1378248_at	BE110453	Similar to amyloid beta (A4) precursor protein-binding, family B, member 2 (predicted)	RGD1562438_predicted	0.936	0.479	0.369	0.011	0.717	0.017	0.510	0.103
1395717_at	BF394620	Similar to amyloid beta (A4) precursor protein-binding, family B, member 2 (predicted)	RGD1562438_predicted	1.016	0.641	0.315	0.013	2.187	0.114	0.792	0.113
1377697_at	BI275738	Similar to amyloid beta (A4) precursor protein-binding, family B, member 2 (predicted)	RGD1562438_predicted	1.259	0.855	0.294	0.000	0.988	0.917	0.462	0.007
1389307_at	AW435479	similar to Amyloid beta (A4) precursor-like protein 1 (predicted)	RGD1561211_predicted	0.639	0.666	0.370	0.005	0.758	0.109	0.353	0.012
1367482_at	AI172459	similar to anaphase promoting complex subunit 11 homolog (predicted)	RGD1561880_predicted	0.949	0.318	1.802	0.061	0.651	0.096	1.425	0.483
1389281_at	BE116601	Similar to ankyrin repeat domain 25 (predicted)	RGD1563532_predicted	1.072	0.560	0.291	0.008	1.043	0.675	0.463	0.018
1367488_at	BM386411	similar to ankyrin repeat domain protein 17 isoform b (predicted)	RGD1562348_predicted	1.316	0.006	1.148	0.045	1.146	0.104	1.153	0.431
1392723_at	BF388065	Similar to ankyrin repeat domain protein 17 isoform b (predicted)	RGD1562348_predicted	1.033	0.166	1.054	0.469	0.797	0.234	1.002	0.994
1399008_at	AW434064	similar to ankyrin repeat domain protein 17 isoform b (predicted)	RGD1562348_predicted	0.887	0.715	0.763	0.060	0.830	0.482	0.871	0.185
1391416_at	BE117929	similar to ankyrin repeat domain protein 17 isoform b (predicted)	RGD1562348_predicted	0.930	0.956	1.081	0.822	1.030	0.493	1.166	0.032
1398432_at	AI236704	similar to Ankyrin repeat domain protein 28 (predicted)	RGD1559931_predicted	0.971	0.903	1.710	0.030	0.719	0.028	1.623	0.268
1381223_at	BG372869	similar to Annexin A9 (Annexin 31) (Annexin XXXI) (predicted)	RGD1560197_predicted	0.958	0.071	0.859	0.485	0.955	0.800	0.862	0.452
1372007_at	BE099064	similar to AOF2 protein (predicted)	RGD1562975_predicted	1.026	0.828	1.058	0.428	0.685	0.148	0.861	0.762
1372348_at	AI104502	Similar to AP2 associated kinase 1 (predicted)	RGD1563580_predicted	0.729	0.134	0.469	0.010	0.666	0.041	0.570	0.022
1379948_at	BM392001	Similar to AP2 associated kinase 1 (predicted)	RGD1563580_predicted	0.668	0.395	0.687	0.863	0.824	0.345	0.820	0.231
1377939_at	AW527217	Similar to APG4 autophagy 4 homolog C	LOC313391	1.008	0.141	1.117	0.722	1.358	0.147	0.973	0.520
1378968_at	BI289975	similar to Apoptosis facilitator Bcl-2-like protein 14	LOC500348	1.001	0.448	1.001	0.992	1.046	0.587	0.999	0.893
1371807_at	BE110607	similar to apoptosis related protein APR-3; p18 protein (predicted)	RGD1311605_predicted	0.432	0.183	0.293	0.003	0.545	0.002	0.342	0.011
1394727_at	AI407942	Similar to ARG99 homolog (predicted)	RGD1564868_predicted	1.313	0.857	1.859	0.416	1.077	0.569	1.707	0.242
1382461_at	AI101582	similar to arginine N-methyltransferase p82 isoform (predicted)	RGD1304869_predicted	0.989	0.838	2.361	0.108	0.958	0.030	1.111	0.568
1374018_at	AA851212	similar to ASC-1 complex subunit P100 (predicted)	RGD1561422_predicted	0.840	0.050	2.584	0.165	0.781	0.158	1.674	0.161
1391959_at	BM387121	Similar to AT motif-binding factor (predicted)	RGD1560268_predicted	1.894	0.229	0.914	0.359	1.149	0.458	0.838	0.320
1377961_at	AI072467	similar to AT motif-binding factor (predicted)	RGD1560268_predicted	0.991	0.479	2.555	0.072	1.656	0.394	1.012	0.941
1390118_at	BI274651	similar to ATP/GTP-binding protein	RGD1307679	1.739	0.317	1.124	0.771	1.058	0.114	0.877	0.947
1379717_at	BM385804	similar to ATP-binding cassette transporter ABCG3 /// similar to ATP-binding cassette, sub-family G (WHITE), member 3 /// similar to ATP-binding cassette, subfamily G, member 3	LOC360910 /// LOC360997 /// LOC498435	13.559	0.000	6.371	0.000	20.037	0.000	11.525	0.000
1388864_at	BI276976	similar to ATP-dependent RNA-helicase (predicted)	RGD1562539_predicted	1.078	0.565	2.268	0.005	1.079	0.899	2.049	0.025
1388829_at	AA946348	similar to autoantigen	LOC361399	1.271	0.086	1.563	0.023	1.013	0.132	1.158	0.025
1396878_at	AW528235	similar to autophagy 5-like	LOC365601	0.576	0.316	1.074	0.154	1.557	0.241	0.919	0.382
1373526_at	AI105153	similar to autophagy 5-like	LOC365601	1.001	0.407	1.245	0.166	1.006	0.886	1.091	0.146
1385526_at	AA956721	similar to autophagy 5-like	LOC365601	0.999	0.798	2.100	0.015	0.810	0.203	1.784	0.001
1376160_at	BF408850	similar to Avian reticuloendotheliosis viral (v-rel) oncogene related B	LOC365510	5.472	0.002	2.633	0.001	10.969	0.003	6.250	0.005
1377417_at	BE099931	similar to AW046014 protein	LOC363328	0.700	0.278	0.751	0.462	0.729	0.084	0.848	0.486
1386081_at	AA800678	similar to AW046014 protein	LOC363328	0.981	0.926	1.084	0.847	0.976	0.891	1.001	0.991
1374455_at	AI599343	similar to AYP1 (predicted)	RGD1310634_predicted	0.992	0.348	0.811	0.287	0.918	0.124	0.818	0.296
1395519_at	BG670960	similar to B230212L03Rik protein	MGC95152	1.055	0.459	0.421	0.041	0.917	0.971	0.423	0.042
1374558_at	AI010316	Similar to B7-like protein GL50-B (predicted)	RGD1562791_predicted	1.142	0.362	1.364	0.188	1.141	0.986	0.419	0.020
1381804_at	BI293313	Similar to BAZF (predicted)	RGD1563179_predicted	0.824	0.042	0.142	0.018	2.316	0.051	0.259	0.004
1394375_x_at	BF554138	Similar to BAZF (predicted)	RGD1563179_predicted	1.291	0.374	0.115	0.001	1.229	0.988	0.284	0.004
1386833_at	BF554138	Similar to BAZF (predicted)	RGD1563179_predicted	1.275	0.549	0.206	0.005	0.967	0.721	0.395	0.036
1386832_a_at	BF554138	Similar to BAZF (predicted)	RGD1563179_predicted	1.226	0.617	0.078	0.000	0.696	0.114	0.075	0.026
1396112_at	BF408519	similar to BB128963 protein	RGD1305958	0.995	0.431	0.750	0.053	0.970	0.938	0.595	0.067
1372117_at	BE329026	similar to BB128963 protein	RGD1305958	0.433	0.438	0.450	0.005	0.381	0.142	0.617	0.080
1391437_at	AA874995	similar to BC002216 protein	MGC94339	0.417	0.686	0.875	0.541	0.558	0.142	0.850	0.315

1383314_at	BE110098	Similar to BC003277 protein (predicted)	RGD1565452_predicted	1.113	0.764	0.902	0.537	0.756	0.710	0.678	0.147
1388407_at	AI008077	similar to BC003940 protein (predicted)	RGD1311925_predicted	1.122	0.646	2.929	0.003	1.105	0.963	2.801	0.008
1381556_at	BI303853	Similar to BC013672 protein	LOC498673	79.298	0.001	16.384	0.009	255.873	0.001	103.428	0.003
1381847_at	AI137632	Similar to BC021442 protein (predicted)	RGD1561413_predicted	1.194	0.586	1.273	0.031	1.819	0.626	1.076	0.932
1375854_at	AI175992	similar to beta-catenin-interacting protein ICAT	LOC503000	0.525	0.063	1.249	0.137	0.296	0.005	0.683	0.142
1373279_at	BI275726	similar to beta-catenin-interacting protein ICAT	LOC503000	0.726	0.234	0.309	0.009	0.670	0.175	0.369	0.003
1392670_at	BF291168	Similar to BH3-only member B protein (predicted)	RGD1559427_predicted	1.169	0.140	0.736	0.237	1.441	0.224	0.798	0.635
1385783_at	BF418697	similar to BH3-only member B protein (predicted)	RGD1559427_predicted	0.999	0.520	0.878	0.328	1.048	0.856	0.979	0.940
1374361_at	BI276503	Similar to bK1191B2.3.1 (PUTATIVE novel Acyl Transferase similar to C. elegans C50D2.7) (variant 1) (predicted)	RGD1306698_predicted	0.999	0.674	0.801	0.383	1.000	0.999	0.772	0.382
1377860_at	BM392227	similar to bM410K19.2.2 (novel protein similar to extra-cellular matrix proteins and chondroitin sulfate proteoglycans, variant 2) (predicted)	RGD1306981_predicted	5.105	0.013	5.877	0.002	8.295	0.020	4.351	0.002
1385445_at	BE119167	Similar to bM410K19.2.2 (novel protein similar to extra-cellular matrix proteins and chondroitin sulfate proteoglycans, variant 2) (predicted)	RGD1306981_predicted	4.060	0.038	2.486	0.001	6.282	0.023	2.163	0.002
1379659_at	BF284068	similar to BMP-2 inducible kinase	LOC289485	1.962	0.199	1.871	0.026	0.846	0.454	1.558	0.087
1388976_at	AI178272	similar to BolA domain-containing protein like (11.4 kD) (1P25) (predicted)	RGD1305975_predicted	0.438	0.226	0.371	0.025	0.482	0.025	0.438	0.062
1382467_at	C07140	similar to brain expressed X-linked protein 2	LOC363498	0.495	0.001	0.731	0.126	0.548	0.005	0.595	0.127
1394299_at	BG669326	similar to brain expressed X-linked protein 2	LOC363498	0.344	0.274	0.585	0.092	0.434	0.427	0.579	0.096
1371379_at	AI011738	similar to Brain protein 44 (predicted)	RGD1563422_predicted	0.573	0.570	0.709	0.063	0.553	0.174	0.812	0.269
1378825_a_at	AI011101	Similar to brain specific protein 4 (predicted)	RGD1560320_predicted	1.172	0.893	0.949	0.335	1.454	0.609	0.860	0.437
1394782_at	AI547795	similar to brain-muscle-ARNT-like protein 2c	LOC362464	1.023	0.486	1.010	0.763	1.043	0.626	1.009	0.225
1388639_at	BF284148	Similar to Breast carcinoma amplified sequence 3 homolog (K20D4) (predicted)	RGD1560788_predicted	0.993	0.653	0.517	0.027	0.998	0.941	0.461	0.011
1396110_at	BE107839	Similar to Breast carcinoma amplified sequence 3 homolog (K20D4) (predicted)	RGD1560788_predicted	0.999	0.737	0.838	0.370	1.104	0.737	0.921	0.633
1377801_at	AI237031	Similar to BTB (PO)Z domain containing 12 (predicted)	RGD1566009_predicted	1.330	0.607	0.859	0.668	1.234	0.977	1.268	0.747
1375177_at	AI454932	similar to BTEB3 protein (predicted)	RGD1565099_predicted	1.000	0.999	1.036	0.660	1.003	0.963	1.000	0.217
1376888_a_at	AI501092	similar to Btk-PH-domain binding protein	LOC301119	0.998	0.065	1.016	0.702	1.083	0.763	1.020	0.098
1392122_x_at	BF559040	similar to Btk-PH-domain binding protein	LOC301119	1.003	0.188	1.028	0.674	1.029	0.454	0.989	0.888
1383587_at	BF283779	similar to Butyrate-induced transcript 1 (predicted)	RGD1565496_predicted	0.258	0.017	0.508	0.017	0.222	0.006	0.631	0.108
1371547_at	BI282112	similar to C10 (predicted)	RGD1309695_predicted	0.705	0.310	0.763	0.504	0.501	0.026	0.713	0.672
1383175_a_at	BF561368	similar to C11orf17 protein (predicted)	RGD1306959_predicted	1.020	0.200	1.935	0.055	0.886	0.075	2.055	0.043
1385458_a_at	AA799992	similar to C11orf17 protein (predicted)	RGD1306959_predicted	1.055	0.523	1.518	0.067	0.684	0.125	1.604	0.056
1392938_s_at	BF561368	similar to C11orf17 protein (predicted)	RGD1306959_predicted	1.151	0.621	1.273	0.420	1.009	0.803	1.733	0.002
1383176_at	BF561368	similar to C11orf17 protein (predicted)	RGD1306959_predicted	0.908	0.883	2.188	0.011	0.884	0.142	1.914	0.169
1380827_at	AA819867	similar to C1orf25	RGD1307890	1.918	0.134	0.794	0.424	1.400	0.029	0.816	0.036
1377601_at	BM386514	similar to C21orf70 protein	RGD1311257	0.834	0.277	1.053	0.579	0.758	0.291	1.003	0.913
1380449_at	AI112513	Similar to C230080I20Rik protein (predicted)	RGD1560924_predicted	0.623	0.016	0.457	0.003	0.443	0.049	0.627	0.064
1395423_at	AW920217	Similar to C230080I20Rik protein (predicted)	RGD1560924_predicted	0.865	0.347	0.435	0.009	0.406	0.032	0.482	0.025
1379615_at	AI011501	similar to C230080I20Rik protein (predicted)	RGD1560924_predicted	1.184	0.632	0.808	0.987	0.517	0.789	1.116	0.930
1373924_at	AI712686	similar to C530044N13Rik protein	RGD1306568	0.389	0.005	0.358	0.001	0.245	0.001	0.563	0.046
1397277_at	AW920086	Similar to C630007L23Rik protein (predicted)	RGD1562190_predicted	0.592	0.062	1.243	0.603	1.012	0.076	1.004	0.983
1382340_at	AA924048	similar to C630007L23Rik protein (predicted)	RGD1562190_predicted	1.284	0.209	1.150	0.655	1.771	0.034	0.907	0.621
1390865_at	AW524822	similar to Ca2+-dependent activator for secretion protein 2 (predicted)	RGD1559440_predicted	2.193	0.474	2.322	0.027	3.826	0.013	2.554	0.009
1377030_at	BF390550	Similar to cajalin 2 isoform a (predicted)	RGD1565556_predicted	1.000	0.403	0.963	0.788	1.806	0.350	1.063	0.035
1378159_at	BF391007	Similar to cajalin 2 isoform a (predicted)	RGD1565556_predicted	1.239	0.909	0.931	0.068	1.499	0.312	0.722	0.078
1380198_at	BF564882	Similar to cajalin 2 isoform a (predicted)	RGD1565556_predicted	1.031	0.932	1.005	0.918	1.094	0.387	0.999	0.995
1381999_at	BE096370	similar to calmodulin regulated spectrin-associated protein 1 (predicted)	RGD1565022_predicted	0.695	0.482	1.731	0.039	1.064	0.153	1.076	0.120
1371622_at	AA943541	similar to candidate tumor suppressor OVCA2 (predicted)	RGD1564623_predicted	0.592	0.423	1.505	0.177	0.501	0.019	0.736	0.796
1377869_at	BI284261	similar to carbon catabolite repression 4 protein homolog	LOC310395	0.707	0.001	0.417	0.009	0.830	0.021	0.605	0.008
1376726_at	AI101117	similar to Carbonic anhydrase-related protein 10 (Carbonic anhydrase-related protein X) (predicted)	RGD1561624_predicted	0.489	0.110	0.175	0.003	0.591	0.138	0.172	0.009
1398668_at	BF290204	Similar to carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (predicted)	RGD1560536_predicted	0.997	0.985	0.893	0.113	1.003	0.935	0.899	0.122
1378049_at	AI603565	similar to Cas-associated zinc finger protein (predicted)	RGD1306498_predicted	0.306	0.016	0.616	0.233	0.399	0.016	0.998	0.704
1375968_at	AI556268	similar to Catna2 protein (predicted)	RGD1559632_predicted	0.970	0.099	0.308	0.114	1.131	0.625	0.458	0.041
1374408_at	AI410173	similar to CBF1 interacting corepressor	RGD1309199	1.138	0.085	0.755	0.028	1.388	0.031	0.951	0.090
1386229_at	AI101392	similar to CBF1 interacting corepressor	RGD1309199	1.285	0.122	0.632	0.002	1.484	0.130	0.676	0.027
1379603_at	BE116890	similar to CBL E3 ubiquitin protein ligase (Signal transduction protein CBL) (predicted)	RGD1561386_predicted	1.181	0.544	1.391	0.369	1.026	0.951	0.996	0.701
1378462_at	BE107396	Similar to Cc1-6	LOC500496	1.411	0.477	1.577	0.200	1.840	0.047	1.440	0.043
1383152_at	BF544427	similar to Cc1-9	RGD1308955	0.623	0.088	0.725	0.035	0.751	0.005	0.414	0.018
1382509_at	AA956256	similar to CCR4	RGD1310783	1.086	0.038	0.872	0.251	0.999	0.310	0.941	0.330
1371302_at	AI406651	Similar to Cdc2l1 protein	LOC502663	0.785	0.534	0.711	0.042	0.574	0.059	0.556	0.055
1374547_at	BI285509	Similar to Cdc2l1 protein	LOC502663	0.928	0.625	0.588	0.063	0.995	0.767	0.589	0.069
1388448_at	AI235065	Similar to CDC42 small effector 2 (predicted)	RGD1565337_predicted	1.917	0.141	2.609	0.005	2.382	0.158	2.663	0.007

1392542_at	AA944330	similar to CDC42 small effector 2 (predicted) /// similar to CDC42 small effector 2 (predicted)	RGD1565337_predicted /// RGD1563924_predicted	1.754	0.225	10.568	0.000	1.188	0.673	6.790	0.000
1379235_x_at	AI179539	similar to CDC45L	LOC287961	1.769	0.080	1.179	0.425	0.735	0.847	1.051	0.115
1379234_a_at	AI179539	similar to CDC45L	LOC287961	1.115	0.686	0.873	0.090	1.141	0.333	0.898	0.558
1373425_at	BF284224	similar to CDC-like kinase 2	LOC365842	1.230	0.069	1.508	0.017	0.908	0.987	1.264	0.041
1389983_at	AA848782	similar to cDNA sequence AF155546	RGD1309387	0.676	0.053	1.258	0.297	0.672	0.012	0.998	0.484
1377687_at	AI009660	Similar to cDNA sequence AK129302 (predicted)	RGD1561708_predicted	0.672	0.161	0.495	0.144	1.083	0.832	0.482	0.122
1389729_at	AI408907	similar to cDNA sequence BC003324	MGC94142	0.413	0.216	1.421	0.024	0.436	0.109	0.915	0.549
1372711_at	AI409292	similar to cDNA sequence BC005537	LOC498750	1.161	0.093	0.866	0.041	1.341	0.010	0.943	0.070
1382945_at	AI028809	Similar to cDNA sequence BC006662	RGD1304748	0.712	0.286	0.794	0.126	1.145	0.605	0.718	0.152
1373132_at	AI178689	similar to CDNA sequence BC006909 (predicted)	RGD1561284_predicted	1.093	0.481	0.972	0.128	1.029	0.861	0.720	0.084
1375874_at	AA799680	similar to cDNA sequence BC013529 (predicted)	RGD1309759_predicted	1.000	0.980	0.631	0.033	0.957	0.759	0.535	0.017
1376792_at	AW251313	Similar to CDNA sequence BC014699 (predicted)	RGD1559797_predicted	2.514	0.132	1.330	0.564	0.667	0.211	1.206	0.127
1379399_at	AI711484	similar to cDNA sequence BC016188	RGD1306108	1.283	0.074	0.993	0.987	1.451	0.422	0.992	0.976
1389330_at	AA894060	similar to cDNA sequence BC017158	RGD1310127	0.599	0.035	0.386	0.000	1.174	0.385	0.569	0.040
1394605_at	AI409909	similar to CDNA sequence BC017647 (predicted)	RGD1566149_predicted	2.068	0.039	0.999	0.997	1.676	0.003	1.141	0.338
1382029_at	BE104800	similar to CDNA sequence BC017647 (predicted)	RGD1566149_predicted	1.090	0.503	1.201	0.223	1.347	0.130	1.342	0.032
1379500_at	AA860044	similar to cDNA sequence BC018601	LOC498404	1.911	0.082	6.493	0.007	1.000	0.055	3.321	0.008
1391536_at	AA892645	similar to cDNA sequence BC020002 (predicted)	RGD1308432_predicted	1.049	0.120	0.891	0.584	1.100	0.763	1.078	0.855
1393922_at	BF567535	similar to CDNA sequence BC020077 (predicted)	RGD1561825_predicted	0.888	0.673	1.292	0.813	0.883	0.704	1.136	0.325
1394599_at	AA998165	similar to cDNA sequence BC022133 (predicted)	RGD1561296_predicted	1.739	0.075	4.891	0.002	1.047	0.547	2.477	0.005
1374028_at	AI412665	similar to CDNA sequence BC024479	LOC500974	1.326	0.260	1.158	0.118	1.754	0.026	1.133	0.089
1379646_at	AI229747	Similar to CDNA sequence BC024479	LOC500974	0.836	0.904	0.874	0.425	0.909	0.190	0.777	0.511
1396683_at	BE099973	Similar to CDNA sequence BC024479	LOC500974	0.996	0.985	0.996	0.978	1.004	0.808	0.998	0.905
1381282_at	BF416808	similar to cDNA sequence BC026432 (predicted)	RGD1308345_predicted	0.335	0.040	1.340	0.522	0.643	0.075	1.161	0.356
1383798_at	AI411061	similar to CDNA sequence BC026682	MGC94145	0.574	0.085	0.429	0.005	0.692	0.037	0.515	0.022
1383268_at	BG667725	Similar to cDNA sequence BC027127; 9330184N17Rik (predicted)	RGD1308957_predicted	1.027	0.997	0.442	0.086	1.236	0.946	0.640	0.086
1371409_at	AI231196	similar to cDNA sequence BC031181 (predicted)	RGD1562987_predicted	0.632	0.238	0.656	0.001	0.531	0.006	0.565	0.001
1383553_at	BE097591	similar to CDNA sequence BC034204	RGD1311293	0.870	0.277	1.002	0.951	0.861	0.124	0.999	0.988
1374597_at	BI275770	similar to CDNA sequence BC034664 (predicted)	RGD1560440_predicted	0.641	0.692	1.164	0.285	0.706	0.431	1.276	0.033
1372767_at	AI231284	similar to cDNA sequence BC043098 (predicted)	RGD1565461_predicted	1.129	0.079	1.522	0.003	1.092	0.439	1.290	0.002
1383969_at	BI294901	similar to CDNA sequence BC043301 (predicted)	RGD1561832_predicted	0.845	0.804	0.580	0.037	0.869	0.896	0.672	0.043
1371410_at	AI599071	similar to cDNA sequence BC056474 (predicted)	RGD1564058_predicted	0.774	0.701	1.153	0.385	0.715	0.477	0.897	0.465
1388516_at	AI104258	Similar to CDV-3B	LOC315970	1.432	0.093	3.883	0.000	1.214	0.043	3.049	0.001
1383028_at	BE120656	similar to CDV-3B	LOC315970	2.319	0.106	3.891	0.016	0.999	0.821	3.654	0.001
1385316_at	BF386882	similar to cell adhesion molecule nectin-3 gamma (predicted)	RGD1565805_predicted	1.089	0.047	1.167	0.016	0.997	0.872	1.330	0.201
1378739_at	AA818135	similar to cell death-inducing DFFA-like effector c	LOC500292	8.637	0.011	10.036	0.010	7.234	0.000	5.637	0.010
1398957_at	AA817907	similar to cell division cycle 2-like 1 (predicted)	RGD1566355_predicted	0.900	0.452	1.077	0.390	0.906	0.686	1.240	0.195
1390757_at	BE116564	similar to cell division cycle 2-like 1 (predicted)	RGD1566355_predicted	0.989	0.786	1.014	0.921	0.848	0.989	1.122	0.510
1376864_at	BF396386	similar to cell division cycle and apoptosis regulator 1 (predicted)	RGD1560358_predicted	1.411	0.046	0.509	0.009	1.143	0.319	0.520	0.004
1382238_at	AW534965	similar to cell division cycle and apoptosis regulator 1 (predicted)	RGD1560358_predicted	0.985	0.465	0.807	0.211	0.833	0.371	0.813	0.039
1377062_at	BE100468	similar to centrosomal Nek2-associated protein 1 (predicted)	RGD1562262_predicted	0.571	0.115	0.995	0.956	1.005	0.178	0.988	0.901
1379290_at	BI294016	similar to centrosome protein Cep63	LOC300963	1.005	0.812	0.754	0.102	1.168	0.037	0.675	0.156
1373339_at	AI599410	similar to cervical cancer receptor (predicted)	RGD1310591_predicted	1.271	0.010	1.915	0.001	1.054	0.475	1.657	0.021
1394756_at	AA955494	Similar to CG10084-PA	RGD1308297	1.538	0.084	1.224	0.979	0.873	0.881	0.938	0.197
1397396_at	BE109259	Similar to CG10084-PA	RGD1308297	0.994	0.266	1.113	0.565	0.940	0.510	0.999	0.971
1393678_at	BI275975	similar to CG10084-PA	RGD1308297	1.077	0.792	1.339	0.025	0.967	0.551	1.432	0.026
1392669_at	BE117193	similar to CG10084-PA	RGD1308297	0.896	0.801	0.863	0.170	0.850	0.992	0.913	0.520
1399056_at	AI716436	similar to CG10585-PA	LOC365592	1.471	0.074	0.945	0.537	1.123	0.662	0.971	0.832
1372433_at	AI104715	similar to CG11030-PA (predicted)	RGD1310211_predicted	1.392	0.518	2.964	0.001	1.195	0.138	1.874	0.005
1396017_at	BF415778	Similar to CG11206-PA	LOC313672	1.173	0.676	0.863	0.091	1.044	0.311	0.845	0.887
1378742_at	BM388241	Similar to CG12054-PA (predicted)	RGD1309692_predicted	0.660	0.202	0.401	0.044	0.997	0.306	0.492	0.057
1374953_at	AI599484	similar to CG12279-PA	LOC500420	0.582	0.141	0.551	0.000	0.489	0.002	0.600	0.049
1372882_at	BG379301	similar to CG12379-PA (predicted)	RGD1308635_predicted	0.550	0.185	1.073	0.866	0.297	0.010	0.912	0.630
1374358_at	BE098806	similar to CG13901-PA	RGD1307648	0.701	0.744	0.898	0.113	0.638	0.027	0.900	0.620
1375853_at	BF284358	Similar to CG13957-PA (predicted)	RGD1309995_predicted	2.355	0.001	1.719	0.004	2.639	0.001	2.032	0.009
1392838_at	BF398054	similar to CG13957-PA (predicted)	RGD1309995_predicted	2.767	0.006	2.405	0.001	2.384	0.010	2.193	0.019
1390887_at	AI105458	Similar to CG13957-PA (predicted)	RGD1309995_predicted	1.021	0.467	1.137	0.582	1.159	0.860	1.003	0.650
1398971_at	BI283725	similar to CG14967-PA	RGD1307929	0.772	0.914	0.764	0.080	0.773	0.245	0.536	0.009
1398915_at	BI278208	similar to CG14977-PA (predicted)	RGD1309735_predicted	0.626	0.337	1.358	0.157	0.614	0.040	1.285	0.300
1367551_a_at	AI406693	similar to CG14980-PB	RGD1306410	0.851	0.138	0.796	0.034	0.804	0.124	0.913	0.290

1382653_at	AI136405	similar to CG15929-PA (predicted)	RGD1306798_predicted	1.030	0.553	0.920	0.443	1.518	0.211	0.809	0.975
1378841_at	AA899057	Similar to CG16812-PA (predicted)	RGD1307554_predicted	1.146	0.280	0.883	0.218	0.783	0.067	1.014	0.934
1389644_at	BI289857	similar to CG16896-PA	LOC299949	0.330	0.001	0.964	0.865	0.359	0.017	0.678	0.038
1372636_at	AI007924	Similar to CG18661-PA	RGD1307155	1.327	0.246	2.373	0.000	0.973	0.618	1.372	0.058
1377524_at	AI044320	similar to CG18661-PA (predicted)	RGD1566003_predicted	0.429	0.026	0.643	0.160	0.391	0.005	0.791	0.384
1372698_at	BI275970	similar to CG2662-PA (predicted)	RGD1305094_predicted	0.598	0.084	0.951	0.484	0.710	0.071	0.745	0.079
1374840_at	BG377716	Similar to CG2919-PA (predicted)	RGD1305604_predicted	0.990	0.338	1.000	0.996	1.112	0.078	0.980	0.937
1372086_at	BM387251	similar to CG32384-PA (predicted)	RGD1311955_predicted	1.878	0.032	8.649	0.002	0.545	0.027	4.498	0.010
1398998_at	AI407273	similar to CG4768-PA (predicted)	RGD1309748_predicted	2.232	0.002	2.198	0.001	1.201	0.184	1.812	0.007
1391069_at	AI231713	Similar to CG4768-PA (predicted)	RGD1309748_predicted	1.509	0.005	2.269	0.003	1.508	0.107	2.786	0.052
1378098_at	AI406802	Similar to CG4768-PA (predicted)	RGD1309748_predicted	1.265	0.060	0.590	0.008	1.064	0.711	0.890	0.893
1385802_at	BF418288	Similar to CG4768-PA (predicted)	RGD1309748_predicted	0.975	0.686	0.907	0.346	1.035	0.409	1.134	0.998
1391325_at	BF397406	Similar to CG4768-PA (predicted)	RGD1309748_predicted	1.004	0.811	0.610	0.093	0.952	0.758	0.952	0.992
1397432_at	BE119690	similar to CG4854-PA (predicted)	RGD1307214_predicted	1.090	0.553	1.001	0.991	0.952	0.581	0.986	0.503
1371335_at	AA944393	similar to CG6105-PA	MGC72942	0.714	0.972	0.970	0.469	0.441	0.027	0.674	0.265
1392533_at	AI716888	similar to CG6796-PA	RGD1305145	0.549	0.123	0.667	0.458	0.999	0.649	0.405	0.054
1374418_at	BF289188	similar to CG8009-PA (predicted)	RGD1308816_predicted	1.148	0.594	0.874	0.608	0.870	0.559	1.049	0.153
1390403_at	BE108405	similar to CG8312-PA	RGD1304790	0.661	0.327	0.439	0.013	0.772	0.036	0.615	0.014
1382261_at	AW534331	similar to CG8841-PA (predicted)	RGD1311422_predicted	0.518	0.193	0.927	0.426	0.630	0.037	0.892	0.985
1374898_at	AW527473	similar to CG8841-PA (predicted)	RGD1311422_predicted	0.624	0.215	0.714	0.003	0.478	0.001	0.696	0.011
1376718_at	AI575121	similar to CG9117-PA	RGD1306932	0.696	0.104	0.452	0.006	0.506	0.003	0.575	0.190
1373964_at	AA818815	similar to CG9147-PB (predicted)	RGD1305487_predicted	0.878	0.176	0.574	0.005	0.848	0.089	0.657	0.026
1379715_at	BE115506	similar to CG9346-PA (predicted)	RGD1307882_predicted	0.780	0.013	1.468	0.061	0.827	0.023	0.732	0.498
1382135_at	AI012683	similar to CG9346-PA (predicted)	RGD1307882_predicted	1.319	0.040	1.656	0.016	1.150	0.078	1.492	0.053
1382290_at	AI717186	similar to CG9643-PA (predicted)	RGD1306300_predicted	0.556	0.087	0.800	0.230	0.694	0.058	1.264	0.077
1394737_at	BE108874	similar to CG9752-PA	RGD1311345	0.745	0.559	1.234	0.104	0.674	0.002	1.205	1.000
1382468_at	AW143385	similar to CG9752-PA	RGD1311345	0.775	0.676	0.793	0.328	0.943	0.140	1.055	0.841
1374136_at	BG665121	similar to CG9882-PA (predicted)	RGD1306157_predicted	0.694	0.042	2.439	0.032	0.659	0.096	2.078	0.105
1395577_at	AA800508	Similar to CG9882-PA (predicted)	RGD1306157_predicted	1.058	0.395	0.987	0.978	1.037	0.820	1.137	0.569
1373600_at	AI412518	Similar to CG9996-PA	LOC300173	1.207	0.411	1.548	0.009	1.250	0.365	1.325	0.024
1379649_at	BF394502	Similar to CG9996-PA	LOC300173	1.003	0.800	1.209	0.081	0.665	0.077	0.980	0.625
1381217_at	AI639158	similar to CGI-09 protein (predicted)	RGD1308877_predicted	0.714	0.052	2.016	0.033	0.454	0.216	1.165	0.240
1393443_a_at	AW434918	similar to CGI-112 protein	RGD1308113	0.177	0.001	0.565	0.151	0.261	0.007	0.790	0.258
1367494_at	AW523764	similar to CGI-35 protein (predicted)	RGD1310899_predicted	0.962	0.697	1.135	0.448	0.922	0.164	1.214	0.030
1392797_at	AI045916	similar to CGI-41 protein	RGD1311265	0.677	0.204	0.999	0.948	0.842	0.464	0.772	0.158
1375456_at	AI007882	Similar to Cgi67 serine protease precursor	RGD1305246	1.470	0.426	1.988	0.226	0.942	0.738	1.319	0.154
1373060_at	AI406281	similar to CGI-84 protein (predicted)	RGD1306781_predicted	0.915	0.330	1.352	0.941	0.689	0.325	1.478	0.670
1395013_at	AW531495	similar to CGI-94 protein (predicted)	RGD1559610_predicted	0.993	0.748	0.756	0.096	0.989	0.832	0.754	0.088
1371722_at	BI274676	similar to CGI-96 protein; gastric cancer antigen Zg14	RGD1311547	0.848	0.318	0.893	0.292	0.747	0.107	0.779	0.513
1373948_at	BG376678	similar to CGTHBA protein (-14 gene protein)	RGD1308665	1.032	0.445	0.692	0.033	0.939	0.860	0.813	0.295
1374743_at	BE115056	similar to channel-interacting PDZ domain protein isoform 1 (predicted)	RGD1564282_predicted	1.291	0.043	2.348	0.005	1.005	0.577	1.976	0.044
1372064_at	BI296385	similar to chemokine (C-X-C motif) ligand 16	Cxcl16	15.707	0.001	17.057	0.000	19.869	0.001	24.659	0.000
1381957_at	AW529176	Similar to chondroitin sulfate synthase 3 (predicted)	RGD1560819_predicted	1.124	0.779	1.060	0.153	1.096	0.246	1.063	0.252
1382460_at	AI229438	Similar to chr2 synaptotagmin (predicted)	RGD1565705_predicted	1.008	0.989	0.712	0.006	0.916	0.621	0.672	0.152
1381825_at	BM385475	similar to chromosome 1 open reading frame 172	RGD1303271	0.669	0.120	0.979	0.873	0.936	0.323	0.922	0.258
1398446_at	BG376030	similar to chromosome 1 open reading frame 2 (predicted)	RGD1306107_predicted	0.536	0.003	0.464	0.001	0.795	0.055	0.618	0.138
1397865_at	AI138056	Similar to chromosome 1 open reading frame 51 (predicted)	RGD1559569_predicted	1.010	0.607	0.932	0.894	2.018	0.069	1.833	0.517
1398364_at	BF555972	similar to chromosome 1 open reading frame 63	RGD1359529	0.599	0.002	0.788	0.007	0.776	0.119	0.932	0.050
1389204_at	AI009647	similar to chromosome 10 open reading frame 18 (predicted)	RGD1564456_predicted	1.876	0.024	1.006	0.973	1.799	0.110	1.232	0.600
1379623_at	AA874896	similar to chromosome 10 open reading frame 4; similar to putative acid phosphatase F26C11.1 /// similar to FRA10AC1 protein isoform FRA10AC1-1	RGD1309482 /// LOC499351	0.934	0.516	1.314	0.137	1.003	0.153	0.945	0.737
1378987_at	BE119446	Similar to chromosome 10 open reading frame 42	LOC294560	0.446	0.051	0.854	0.510	0.325	0.014	0.717	0.054
1386569_at	BF563922	Similar to chromosome 10 open reading frame 42	LOC294560	0.363	0.217	0.697	0.050	0.612	0.140	0.527	0.027
1383664_a_at	AI172176	similar to chromosome 11 open reading frame2 (predicted)	RGD1560544_predicted	1.226	0.119	1.132	0.448	0.997	0.655	0.774	0.099
1388351_at	BM384128	similar to chromosome 13 open reading frame 12 (predicted)	RGD1305831_predicted	0.967	0.182	1.349	0.242	1.069	0.061	1.278	0.135
1388739_at	BF398626	similar to chromosome 14 open reading frame 130	RGD1359144	0.700	0.012	1.377	0.006	0.438	0.008	1.058	0.066
1376441_at	AI102249	similar to chromosome 14 open reading frame 135 (predicted)	RGD1566114_predicted	0.768	0.825	0.356	0.003	0.983	0.918	0.596	0.098
1379406_at	AA925559	similar to chromosome 14 open reading frame 21 (predicted)	RGD1308396_predicted	0.376	0.071	1.273	0.125	0.364	0.028	1.436	0.949
1398452_at	BI298587	similar to chromosome 14 open reading frame 35 (predicted)	RGD1559923_predicted	1.198	0.090	5.845	0.000	0.801	0.948	4.794	0.018
1391443_at	BF289340	similar to chromosome 14 open reading frame 35 (predicted)	RGD1559923_predicted	0.721	0.672	0.827	0.501	0.897	0.320	0.824	0.154
1372206_at	AI412469	similar to chromosome 14 open reading frame 9	RGD1307475	0.935	0.741	1.915	0.009	1.198	0.213	1.343	0.028

1376492_at	AI548527	similar to chromosome 16 open reading frame 28 (predicted)	RGD1565247_predicted	1.082	0.608	0.960	0.750	0.958	0.909	0.687	0.106
1386622_at	BF542874	Similar to chromosome 16 open reading frame 28 (predicted)	RGD1565247_predicted	1.002	0.963	0.993	0.840	0.686	0.031	1.034	0.369
1393242_at	BE104107	similar to chromosome 16 open reading frame 33; minus -99 protein (predicted)	RGD1310922_predicted	0.781	0.692	1.084	0.623	0.865	0.019	1.081	0.415
1393361_at	H34199	similar to chromosome 16 open reading frame 33; minus -99 protein (predicted)	RGD1310922_predicted	0.996	0.842	1.402	0.211	1.009	0.876	1.813	0.146
1374217_at	BG375463	similar to chromosome 16 open reading frame 5	RGD1310686	0.577	0.152	0.719	0.242	0.555	0.047	0.863	0.362
1374169_at	AI236128	similar to chromosome 16 open reading frame 5	RGD1310686	0.621	0.175	0.853	0.492	0.495	0.002	0.935	0.647
1375674_at	BI294949	similar to chromosome 16 open reading frame 5	RGD1310686	0.937	0.230	1.147	0.335	0.933	0.112	0.996	0.931
1380456_at	AI044224	Similar to chromosome 16 open reading frame 7 (predicted)	RGD1565149_predicted	1.398	0.786	0.963	0.684	0.674	0.218	0.698	0.391
1373514_at	AA899109	similar to chromosome 17 open reading frame 27 (predicted)	RGD1308168_predicted	70.575	0.009	24.658	0.000	163.644	0.005	53.407	0.000
1379740_at	AW521797	Similar to chromosome 18 open reading frame 54	LOC361346	0.534	0.002	1.636	0.046	0.628	0.308	1.669	0.104
1379887_at	BI290897	similar to chromosome 2 open reading frame 3; transcription factor 9 (binds GC-rich sequences) (predicted)	RGD1304792_predicted	1.368	0.203	1.856	0.023	0.723	0.278	1.823	0.018
1388626_at	AI638949	similar to chromosome 20 open reading frame 116 (predicted)	RGD1309979_predicted	0.726	0.646	0.704	0.095	0.556	0.030	0.645	0.002
1379525_at	BF559514	similar to chromosome 20 open reading frame 155	RGD1311037	0.789	0.078	0.403	0.008	0.835	0.167	0.646	0.036
1390717_at	BM391963	similar to chromosome 20 open reading frame 155	RGD1311037	1.387	0.741	1.908	0.038	0.594	0.151	1.360	0.005
1390397_at	BF413152	similar to chromosome 20 open reading frame 39	RGD1310753	1.001	0.995	0.421	0.042	1.927	0.104	0.589	0.030
1394784_at	BF522436	similar to chromosome 20 open reading frame 6	RGD1306067	0.793	0.601	1.837	0.118	0.988	0.905	1.170	0.123
1392902_at	AW141642	similar to chromosome 20 open reading frame 6	RGD1306067	0.964	0.848	1.212	0.592	0.964	0.892	0.959	0.716
1371599_at	AI228587	similar to chromosome 6 open reading frame 106 isoform a	LOC294154	0.780	0.244	2.082	0.005	0.841	0.056	1.584	0.041
1391214_at	BI289378	similar to chromosome 6 open reading frame 188	RGD1304835	0.909	0.705	1.701	0.244	8.613	0.002	3.793	0.060
1399127_at	AA964600	similar to chromosome 6 open reading frame 70 (predicted)	RGD1562376_predicted	0.960	0.491	1.044	0.741	0.927	0.216	0.909	0.368
1373033_at	BI289505	similar to chromosome 6 open reading frame 83; similar to RIKEN cDNA 5630401J11	MGC105508	1.608	0.032	2.519	0.010	1.926	0.101	1.861	0.019
1377872_at	BM383822	similar to chromosome 7 open reading frame 30 (predicted)	RGD1306936_predicted	0.685	0.467	0.937	0.597	0.250	0.043	0.822	0.172
1392078_at	BE108128	Similar to chromosome 9 open reading frame 20 (predicted)	RGD1560865_predicted	2.743	0.236	0.932	0.891	3.887	0.026	1.055	0.885
1374202_at	BM389779	Similar to chromosome 9 open reading frame 7 (predicted)	RGD1311501_predicted	0.485	0.348	1.189	0.182	0.717	0.215	2.006	0.014
1378578_at	BE117291	similar to chromosome X open reading frame 23 (predicted)	RGD1562161_predicted	2.248	0.005	1.982	0.099	2.238	0.033	1.241	0.289
1391603_at	AW527410	Similar to chromosome X open reading frame 23 (predicted)	RGD1562161_predicted	1.016	0.922	0.818	0.383	1.036	0.859	0.796	0.267
1382072_at	AA944162	Similar to cis-Golgi matrix protein GM130 (predicted)	RGD1562587_predicted	1.139	0.524	1.372	0.558	1.016	0.965	1.178	0.315
1388861_at	BF555471	similar to cisplatin resistance related protein CRR9p (predicted)	RGD1307896_predicted	0.815	0.398	0.963	0.560	0.892	0.127	0.809	0.099
1399018_at	AI410301	similar to cisplatin resistance-associated overexpressed protein (predicted)	RGD1307981_predicted	0.702	0.011	0.714	0.001	0.851	0.738	0.805	0.003
1382957_at	BF408881	similar to cisplatin resistance-associated overexpressed protein (predicted)	RGD1307981_predicted	0.793	0.031	0.650	0.006	0.861	0.224	0.707	0.046
1377694_at	AI598976	Similar to cisplatin resistance-associated overexpressed protein (predicted)	RGD1307981_predicted	0.818	0.084	0.631	0.151	0.860	0.661	0.466	0.118
1389622_at	AI232643	similar to citrin (predicted)	RGD1565889_predicted	0.854	0.891	0.574	0.092	0.974	0.471	0.820	0.175
1383616_at	AA997562	similar to class II cytokine receptor 4 (predicted)	RGD1560373_predicted	4.752	0.004	2.255	0.002	14.722	0.007	3.223	0.002
1367537_at	AI012479	similar to Clast4 protein (predicted)	RGD1560908_predicted	1.693	0.008	1.598	0.017	1.696	0.000	1.502	0.019
1371789_at	AI411601	similar to ClpP protease	LOC301117	0.619	0.455	1.225	0.067	0.766	0.015	0.967	0.997
1395716_at	AW919386	Similar to c-myc promoter binding protein (predicted)	RGD1562639_predicted	0.924	0.818	1.857	0.181	0.695	0.543	0.754	0.337
1372399_at	BM392127	similar to cofactor of BRCA1; negative elongation factor protein B (predicted)	RGD1307832_predicted	0.884	0.640	1.147	0.036	0.873	0.381	0.918	0.199
1381552_at	BG380975	Similar to cofactor required for Sp1 transcriptional activation subunit 8 (predicted)	RGD1564993_predicted	1.301	0.153	1.025	0.621	1.119	0.288	0.927	0.247
1372014_at	BM392138	similar to cofactor required for Sp1 transcriptional activation subunit 8 (predicted)	RGD1564993_predicted	0.933	0.786	0.667	0.143	1.153	0.908	0.969	0.854
1391474_at	AA858511	Similar to cofactor required for Sp1 transcriptional activation, subunit 2, 150kDa (predicted)	RGD1560170_predicted	0.581	0.116	0.369	0.000	0.576	0.039	0.436	0.014
1382634_at	AI044343	similar to cofactor required for Sp1 transcriptional activation, subunit 2, 150kDa (predicted)	RGD1560170_predicted	0.773	0.171	1.024	0.832	0.616	0.103	1.005	0.796
1390138_at	BE107413	similar to coiled-coil domain containing 8	MGC72567	0.654	0.063	0.658	0.007	0.496	0.067	0.978	0.314
1384969_at	BE109107	Similar to collagen, type XXIV, alpha 1 (predicted)	RGD1565539_predicted	0.830	0.117	0.559	0.055	1.005	0.541	0.557	0.055
1375767_at	BI287681	similar to common-site lymphoma leukemia guanine nucleotide exchange factor like (5N754) (predicted)	RGD1308089_predicted	3.656	0.016	4.297	0.001	3.467	0.012	4.657	0.006
1373820_at	AI179107	similar to constitutive photomorphogenic protein 1	RGD1304773	0.991	0.238	1.159	0.082	1.059	0.144	1.287	0.263
1371248_at	BI286387	similar to Cornifin alpha (Small proline-rich protein 1) (SPRR1)	LOC499660	11.666	0.019	2.753	0.082	1.481	0.586	0.994	0.986
1371632_at	AI231166	Similar to Coronin, actin binding protein 1C (predicted)	RGD1564490_predicted	1.417	0.227	1.317	0.040	0.740	0.108	1.224	0.124
1396250_at	BF558291	Similar to Coronin, actin binding protein 1C (predicted)	RGD1564490_predicted	1.407	0.295	2.658	0.011	1.129	0.399	2.335	0.007
1398878_at	Y17326	similar to CPSF4 protein	MGC108785	1.217	0.473	2.103	0.001	0.792	0.584	1.884	0.002
1388503_at	BE107430	similar to CREBBP/EP300 inhibitory protein 1 (predicted)	RGD1562702_predicted	0.760	0.005	0.514	0.001	0.866	0.075	0.549	0.017
1388708_at	AI236927	similar to cross-immune reaction antigen PCIA1 (predicted)	RGD1565813_predicted	0.737	0.315	1.022	0.730	0.829	0.297	0.758	0.149
1385525_at	AI029991	similar to C-type lectin-like receptor 2 (predicted)	RGD1563517_predicted	1.002	0.987	0.995	0.860	1.061	0.756	0.968	0.727
1372400_at	AI180403	similar to cullin 4A (predicted)	RGD1563853_predicted	0.798	0.595	0.971	0.077	0.774	0.237	0.891	0.608
1377673_at	BF411339	Similar to cyclin K	LOC500715	1.102	0.541	1.286	0.049	1.040	0.956	1.164	0.143
1372062_at	BF394161	similar to cyclin-dependent kinase 2-interacting protein (predicted)	RGD1563395_predicted	0.497	0.016	1.048	0.361	0.344	0.000	1.275	0.205
1384488_at	BI290067	similar to cyclin-dependent kinase inhibitor 2D	Cdkn2d	1.005	0.718	0.586	0.042	1.000	0.965	0.587	0.062
1375495_at	BG376193	Similar to cyclin-dependent kinase-like 4	LOC503009	1.062	0.848	0.922	0.763	0.872	0.692	1.120	0.686
1373823_at	AA944180	similar to Cyclin-dependent kinases regulatory subunit 2 (CKS-2) (predicted)	RGD1562047_predicted	15.391	0.003	12.154	0.000	12.383	0.001	6.706	0.000
1392958_at	AI547426	similar to cylindromatosis (turban tumor syndrome)	LOC498035	2.817	0.000	1.320	0.051	3.350	0.000	1.645	0.009
1371321_at	AI230604	similar to Cytochrome c oxidase polypeptide VIb (Cytochrome c oxidase subunit AED) (predicted)	RGD1565270_predicted	0.838	0.526	0.931	0.424	0.602	0.038	0.810	0.381
1392720_at	BG376949	similar to Cytochrome P450 4F6 (CYPIVF6) (predicted)	RGD1561655_predicted	1.006	0.900	1.192	0.107	1.390	0.106	1.029	0.582

1370990_at	AI178339	similar to cytokine receptor related protein 4	Cytor4	0.968	0.888	1.166	0.206	1.088	0.650	1.173	0.198
1372288_at	BE109521	similar to D11Bwg0280e protein	RGD1309256	0.999	0.877	1.340	0.517	2.016	0.289	1.372	0.020
1398923_at	AI101122	similar to D11Bwg0434e protein (predicted)	RGD1305687_predicted	0.800	0.709	0.743	0.094	0.692	0.067	0.614	0.030
1390462_at	BI281732	similar to D11lgp1 (predicted)	RGD1308881_predicted	0.850	0.391	1.033	0.358	0.732	0.472	0.747	0.655
1388584_at	AI598881	Similar to D15Wsu75e protein	RGD1305776	0.931	0.355	1.588	0.030	1.116	0.641	1.201	0.056
1383700_at	AA965075	similar to D15Wsu75e protein	RGD1305776	1.224	0.993	2.639	0.010	0.962	0.894	1.926	0.154
1373049_at	AI169619	similar to D1Ertd622e protein (predicted)	RGD1562136_predicted	4.962	0.030	3.715	0.000	6.655	0.005	3.998	0.000
1396068_at	AA899954	Similar to D1Ertd622e protein (predicted)	RGD1562136_predicted	1.037	0.312	1.011	0.855	1.084	0.688	1.002	0.960
1372563_at	AA799488	similar to D330021B20 protein	RGD1308143	0.580	0.013	0.304	0.000	0.620	0.036	0.478	0.026
1398363_at	AI178206	similar to D3Mm3e (predicted)	RGD1561494_predicted	1.414	0.740	1.268	0.030	0.715	0.663	0.948	0.599
1382396_at	BE101337	similar to D7Wsu128e protein	RGD1306614	0.634	0.194	1.128	0.812	0.515	0.069	0.910	0.307
1388648_at	AA799764	Similar to D7Wsu128e protein	RGD1306614	0.616	0.236	0.452	0.017	0.616	0.083	0.646	0.037
1373228_at	BI288760	Similar to D8Ertd354e protein (predicted)	RGD1560755_predicted	0.298	0.016	0.492	0.002	0.351	0.014	0.352	0.053
1392550_at	BE111725	similar to dapper 1 (predicted)	RGD1564008_predicted	0.640	0.646	0.812	0.578	0.499	0.038	0.378	0.061
1390974_a_at	BI285675	Similar to deaminase domain containing 1	LOC502396	0.598	0.261	0.403	0.013	0.278	0.283	0.485	0.029
1377270_a_at	BF396493	similar to decapping enzyme Dcp1b (predicted)	RGD1562214_predicted	0.613	0.501	1.700	0.009	1.620	0.431	1.321	0.035
1377835_at	BM390876	similar to dedicator of cytokinesis 8	LOC499337	0.829	0.006	0.308	0.009	1.172	0.056	0.522	0.019
1379420_at	AI145019	similar to Dehydrogenase/reductase SDR family member 7 precursor (Retinal short-chain dehydrogenase/reductase 4) (predicted)	RGD1565002_predicted	0.429	0.085	0.462	0.003	0.463	0.003	0.457	0.005
1374718_at	AA945915	Similar to deltex 3-like (predicted)	RGD1565144_predicted	12.220	0.000	6.350	0.000	14.747	0.000	9.142	0.000
1389504_at	BI297929	Similar to Deltex3 (predicted)	RGD1566181_predicted	1.187	0.398	0.959	0.756	0.992	0.524	0.880	0.801
1383042_at	AA944383	Similar to Dendritic cell protein GA17 (predicted)	RGD1565840_predicted	1.606	0.328	1.208	0.143	2.184	0.361	1.038	0.772
1373044_at	BI285403	similar to Dendritic cell protein GA17 (predicted)	RGD1565840_predicted	0.801	0.827	1.245	0.843	0.695	0.645	1.083	0.542
1375563_at	AA944394	Similar to dendritic cell-derived ubiquitin-like protein (predicted)	RGD1305506_predicted	0.791	0.039	0.355	0.000	0.792	0.032	0.389	0.012
1384773_at	AI044323	similar to dendritic cell-derived ubiquitin-like protein (predicted)	RGD1305506_predicted	0.923	0.427	0.623	0.008	0.795	0.193	0.491	0.002
1372764_at	BI276261	similar to density regulated protein drp1	LOC498180	1.023	0.987	1.288	0.242	0.784	0.309	1.098	0.965
1375269_at	BM391516	similar to Deoxyribose-phosphate aldolase-like (predicted)	RGD1562330_predicted	0.510	0.389	0.860	0.120	0.348	0.067	0.924	0.045
1399054_at	BG375798	similar to deubiquitinating enzyme UBH1 (predicted)	RGD1563750_predicted	0.802	0.918	1.043	0.121	1.029	0.708	0.997	0.616
1397439_at	AI101639	similar to diacylglycerol kinase epsilon	LOC497978	0.449	0.012	0.770	0.333	0.571	0.332	0.652	0.200
1376377_at	BF398599	Similar to Diap3 protein (predicted)	RGD1565114_predicted	1.047	0.853	1.001	0.995	1.403	0.033	1.004	0.627
1379329_at	AI600082	Similar to dimerization cofactor of hepatocyte nuclear factor 1 (HNF1) from muscle (predicted)	RGD1563318_predicted	0.815	0.190	0.983	0.334	0.817	0.683	0.891	0.311
1379330_s_at	AI600082	Similar to dimerization cofactor of hepatocyte nuclear factor 1 (HNF1) from muscle (predicted)	RGD1563318_predicted	0.661	0.685	1.021	0.912	0.644	0.022	0.753	0.464
1397179_at	BF544981	similar to DIP13 alpha (predicted)	RGD1309388_predicted	2.032	0.023	0.782	0.141	1.510	0.204	0.586	0.202
1382556_a_at	AI412140	similar to DIP13 alpha (predicted)	RGD1309388_predicted	1.599	0.057	3.254	0.000	1.383	0.161	2.765	0.001
1389539_at	BG378248	similar to DIP13 alpha (predicted)	RGD1309388_predicted	1.158	0.754	1.218	0.067	0.739	0.227	1.417	0.063
1376729_at	AI231781	similar to DIP13 alpha (predicted)	RGD1309388_predicted	0.901	0.986	1.030	0.680	0.694	0.513	1.029	0.710
1375580_at	AI547421	Similar to dipeptidylpeptidase 9	LOC301130	0.974	0.853	0.806	0.109	0.897	0.506	0.777	0.230
1374199_at	BI282130	similar to Disco-interacting protein 2 homolog	LOC309692	0.839	0.979	0.745	0.978	0.694	0.099	0.746	0.388
1392495_at	BF408346	similar to dJ202D23.2 (novel protein similar to C21ORF5 (KIAA0933)) (predicted)	RGD1305534_predicted	1.082	0.722	0.855	0.279	0.776	0.228	0.919	0.012
1391282_at	AI029285	Similar to dJ55C23.6 gene product (predicted)	RGD1306962_predicted	0.599	0.020	0.650	0.003	0.661	0.516	0.562	0.027
1373899_at	BI275244	similar to dJ842G6.1.1 (novel protein) (predicted)	RGD1309829_predicted	0.513	0.029	1.797	0.012	0.656	0.045	1.008	0.116
1372075_at	AI177866	similar to dJ862K6.2.2 (splicing factor, arginine/serine-rich 6 (SRP55-2)(isoform 2))	LOC362264	0.619	0.062	0.599	0.015	0.986	0.736	0.812	0.033
1394392_at	BI289554	similar to dJ881L22.2 (novel protein) (predicted)	RGD1307696_predicted	0.869	0.490	1.036	0.825	0.621	0.009	0.910	0.553
1382093_at	AI178038	Similar to DKFZP434B168 protein (predicted)	RGD1308014_predicted	0.752	0.437	0.678	0.412	0.542	0.032	0.735	0.344
1379424_at	BE115825	Similar to DKFZP434B168 protein (predicted)	RGD1308014_predicted	0.721	0.917	0.774	0.081	0.798	0.085	0.682	0.051
1390249_at	BF558075	similar to DKFZP434H132 protein	RGD1305464	1.657	0.080	3.871	0.015	0.484	0.024	1.807	0.008
1390058_at	BI291197	similar to DKFZP547E1010 protein	LOC361990	0.941	0.855	0.952	0.900	0.823	0.007	1.052	0.592
1380848_at	AI102396	similar to DKFZP547E1010 protein /// similar to Protein HT031 homolog	LOC361990 /// LOC500378	1.002	0.854	1.163	0.300	0.999	0.991	0.904	0.527
1393718_at	BE117189	Similar to DKFZP564P1916 protein (predicted)	RGD1311704_predicted	1.388	0.171	1.503	0.081	1.024	0.878	1.553	0.080
1381713_at	BE106279	Similar to DKFZP564P1916 protein (predicted)	RGD1311704_predicted	1.304	0.207	2.162	0.010	1.277	0.830	2.137	0.011
1390719_at	BI294889	Similar to DKFZP564P1916 protein (predicted)	RGD1311704_predicted	0.976	0.434	1.769	0.065	0.722	0.707	1.491	0.214
1372584_at	BG672517	similar to DKFZP566K1924 protein	RGD1308373	0.505	0.003	0.263	0.000	0.638	0.011	0.385	0.011
1391184_at	BM390990	Similar to DNA binding protein RFX2	LOC301121	1.289	0.417	1.264	0.316	1.027	0.902	1.425	0.065
1389268_at	BI285816	similar to DNA polymerase lambda	LOC361767	0.862	0.029	1.001	0.934	1.008	0.996	1.179	0.410
1372353_at	BE096387	similar to DNA segment on chromosome X and Y (unique) 155 expressed sequence isoform 1	LOC288526	1.141	0.394	2.712	0.022	0.923	0.880	1.966	0.046
1383638_at	AW524125	Similar to DNA segment on chromosome X and Y (unique) 155 expressed sequence isoform 1 (predicted)	RGD1566363_predicted	0.900	0.233	0.351	0.016	1.364	0.063	0.750	0.005
1381143_at	AI029836	Similar to DNA segment, Chr 1, Brigham & Womens Genetics 0212 expressed (predicted)	RGD1560909_predicted	0.791	0.515	0.924	0.228	1.103	0.473	0.919	0.618
1392481_at	BG057566	similar to DNA segment, Chr 1, Brigham & Womens Genetics 0212 expressed (predicted)	RGD1560909_predicted	0.992	0.791	1.644	0.027	0.875	0.242	1.865	0.000
1388327_at	AI232357	similar to DNA segment, Chr 10, ERATO Doi 214, expressed (predicted)	RGD1309529_predicted	0.583	0.306	1.064	0.238	0.419	0.004	0.946	0.488
1394568_at	BE108086	similar to DNA segment, Chr 10, Wayne State University 102, expressed (predicted)	RGD1563365_predicted	0.785	0.444	1.341	0.268	0.931	0.978	1.170	0.201
1372019_at	AI231789	similar to DNA segment, Chr 13, Wayne State University 50, expressed (predicted)	RGD1310128_predicted	0.995	0.407	1.278	0.075	1.301	0.334	1.206	0.133

1372803_at	BF281969	similar to DNA segment, Chr 14, ERATO Doi 449, expressed	RGD1305689	0.467	0.059	0.946	0.269	0.569	0.298	0.947	0.092
1367493_at	AI599288	similar to DNA segment, Chr 18, Wayne State University 98, expressed (predicted)	RGD1560212_predicted	0.680	0.103	1.177	0.234	0.623	0.063	1.288	0.142
1385020_at	BM387790	similar to DNA segment, Chr 19, Brigham & Womens Genetics 1357 expressed (predicted) /// hypothetical protein LOC499339	RGD1308750_predicted /// LOC499339	0.505	0.032	2.539	0.029	0.522	0.050	1.209	0.992
1376408_at	BF418111	similar to DNA segment, Chr 19, Brigham & Womens Genetics 1357 expressed (predicted) /// similar to DNA segment, Chr 19, Brigham & Womens Genetics 1357 expressed (predicted) /// hypothetical protein LOC499339	RGD1308750_predicted /// RGD1560288_predicted /// LOC499339	1.033	0.103	6.758	0.043	1.303	0.311	3.246	0.011
1386725_at	BF566582	similar to DNA segment, Chr 19, ERATO Doi 386, expressed (predicted)	RGD1307934_predicted	1.214	0.158	2.004	0.056	1.006	0.947	0.822	0.064
1377414_at	BF400262	Similar to DNA segment, Chr 19, ERATO Doi 386, expressed (predicted)	RGD1307934_predicted	1.848	0.345	2.711	0.008	1.622	0.713	1.341	0.156
1374176_at	AI408727	similar to DNA segment, Chr 4, Brigham & Womens Genetics 0951 expressed	RGD1308059	1.381	0.274	1.128	0.538	1.023	0.439	1.058	0.822
1375645_at	AI408842	similar to DNA segment, Chr 4, ERATO Doi 22, expressed (predicted)	RGD1560286_predicted	1.588	0.346	3.007	0.011	1.576	0.072	2.375	0.060
1392816_at	BI304039	similar to DNA segment, Chr 6, Wayne State University 163, expressed (predicted)	RGD1311164_predicted	1.003	0.379	0.771	0.028	0.709	0.328	0.768	0.085
1399165_a_at	AA943500	similar to DNA segment, Chr 7, ERATO Doi 462, expressed (predicted)	RGD1309393_predicted	0.199	0.003	1.212	0.549	0.219	0.001	1.055	0.383
1376221_at	BG373555	similar to DNA segment, Chr 7, ERATO Doi 462, expressed (predicted)	RGD1309393_predicted	0.687	0.516	0.739	0.019	0.450	0.073	0.837	0.111
1374472_at	AI710526	similar to DNA segment, Chr 8, ERATO Doi 531, expressed	MGC116266	1.396	0.008	1.872	0.002	1.029	0.119	1.909	0.002
1388420_at	BM389730	similar to DNA topoisomerase (ATP-hydrolysing)	LOC361100	1.104	0.340	0.945	0.430	1.218	0.063	0.954	0.302
1374727_at	AF244895	similar to DnaJ (Hsp40) homolog, subfamily B, member 12	LOC294513	1.206	0.240	0.934	0.987	1.169	0.045	0.980	0.801
1389487_at	AA818949	similar to DnaJ (Hsp40) homolog, subfamily B, member 12 /// similar to DnaJ (Hsp40) homolog, subfamily B, member 12	LOC294513 /// LOC363376	1.884	0.133	2.533	0.018	1.091	0.216	1.604	0.014
1399039_at	BM383865	Similar to Dnajb10 protein (predicted)	RGD1560574_predicted	0.411	0.017	1.246	0.025	0.461	0.033	1.141	0.188
1389102_at	BG378147	similar to Dock1 protein (predicted)	RGD1566072_predicted	0.622	0.075	0.771	0.064	1.116	0.379	0.592	0.055
1383846_at	AI576094	similar to Docking protein 5 (Downstream of tyrosine kinase 5) (Protein dok-5) (predicted)	RGD1562846_predicted	1.934	0.007	1.088	0.133	1.514	0.710	0.961	0.860
1396206_at	BG665525	similar to Docking protein 5 (Downstream of tyrosine kinase 5) (Protein dok-5) (predicted)	RGD1562846_predicted	1.319	0.136	0.969	0.572	1.064	0.969	1.014	0.690
1372504_at	AI179780	similar to dolichyl-phosphate mannosyltransferase polypeptide 3 (Dolichol-phosphate mannose synthase subunit 3) (predicted) /// similar to dolichyl-phosphate mannosyltransferase polypeptide 3 (Dolichol-phosphate mannose synthase subunit 3) (predicted)	RGD1561807_predicted /// RGD1561645_predicted	0.710	0.197	0.976	0.924	0.889	0.148	1.106	0.392
1373997_at	AA925118	Similar to Drctnnb1a (predicted)	RGD1562906_predicted	0.923	0.582	1.604	0.223	0.828	0.449	1.024	0.917
1385499_at	AI029352	similar to DRE1 protein (predicted)	RGD1565895_predicted	0.999	0.997	0.793	0.038	1.001	0.999	0.742	0.075
1394359_at	BF553498	similar to DUF729 domain containing 1	LOC364500	1.455	0.009	1.000	0.948	1.916	0.020	0.987	0.882
1372650_at	BI296334	similar to Dynamin binding protein (Scaffold protein Tuba)	LOC309362	0.884	0.273	1.287	0.113	0.886	0.816	1.020	0.623
1392279_at	BI291154	similar to dynein, axonemal, intermediate chain 1	LOC500442	0.873	0.619	0.575	0.061	0.999	0.999	0.627	0.340
1396106_at	BF565241	Similar to dystrobrevin alpha isoform 1 (predicted)	RGD1561985_predicted	0.895	0.644	0.721	0.905	1.495	0.254	1.038	0.824
1374416_at	AI169330	similar to E2-induced gene 2 protein (predicted)	RGD1562228_predicted	0.757	0.153	1.121	0.426	0.702	0.038	1.119	0.341
1393466_at	BF411837	similar to EAPG6122 (predicted)	RGD1563673_predicted	0.903	0.057	0.709	0.115	0.972	0.077	0.713	0.117
1388600_at	AI011713	Similar to EF-hand domain (C-terminal) containing 1	LOC301295	3.291	0.031	0.759	0.348	9.038	0.000	2.054	0.133
1397772_at	BF390195	Similar to EF-hand domain (C-terminal) containing 1	LOC301295	1.005	0.948	0.947	0.412	1.607	0.068	0.998	0.967
1391163_at	BM385306	similar to Eftud1 protein (predicted)	RGD1566096_predicted	1.090	0.858	3.712	0.001	0.879	0.430	2.918	0.004
1396880_at	AI548656	similar to EG:49E4.1 (predicted)	RGD1563471_predicted	0.903	0.852	1.416	0.791	1.399	0.901	1.141	0.362
1382084_at	AA850264	Similar to EHM2 (predicted)	RGD1562988_predicted	0.769	0.747	0.805	0.055	0.644	0.101	0.774	0.180
1389975_at	BE116949	similar to ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D) (predicted)	RGD1561943_predicted	0.631	0.084	0.323	0.001	0.589	0.130	0.326	0.002
1391062_at	AA875129	similar to elongation protein 4 homolog (predicted)	RGD1566052_predicted	0.434	0.004	0.187	0.000	0.531	0.004	0.180	0.013
1391843_at	BF393134	Similar to elongation protein 4 homolog (predicted)	RGD1566052_predicted	1.394	0.232	0.789	0.386	1.195	0.521	0.838	0.422
1375530_at	BG374612	similar to EMeg32 protein (predicted)	RGD1563144_predicted	0.907	0.507	1.424	0.251	1.125	0.792	1.211	0.516
1384048_at	BI297740	Similar to EMSY protein (predicted)	RGD1310712_predicted	0.909	0.183	0.993	0.949	1.016	0.062	1.209	0.161
1394572_at	AI231560	Similar to EMSY protein (predicted)	RGD1310712_predicted	1.245	0.551	0.944	0.804	0.801	0.346	0.931	0.999
1378611_at	BE112744	Similar to encephalopsin	LOC498289	0.516	0.021	0.430	0.059	0.643	0.035	0.780	0.130
1393373_at	BI289640	similar to encephalopsin	LOC498289	0.339	0.026	0.860	0.754	0.481	0.062	0.923	0.484
1371544_at	BE109666	similar to Enhancer of rudimentary homolog (predicted)	RGD1561971_predicted	0.737	0.337	1.044	0.948	0.620	0.046	1.218	0.083
1382464_at	BF547020	similar to ENSANGP00000021391 (predicted)	RGD1309779_predicted	0.457	0.067	0.554	0.008	0.605	0.031	0.567	0.001
1393185_at	BF283249	Similar to envelope (predicted)	RGD1559689_predicted	1.001	0.487	1.011	0.247	1.005	0.937	0.962	0.628
1375714_at	BI289124	similar to Erbb2 interacting protein isoform 2 (predicted)	RGD1562952_predicted	1.205	0.074	1.142	0.384	1.214	0.164	1.377	0.003
1383346_at	BF387821	similar to ERCC4_MOUSE (predicted)	RGD1560340_predicted	0.750	0.883	0.803	0.044	0.913	0.993	0.658	0.013
1371439_at	AA894008	similar to erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked) isoform 1 (predicted)	RGD1564762_predicted	1.308	0.368	1.873	0.069	1.084	0.604	1.171	0.985
1392311_at	BF389762	Similar to erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked) isoform 1 (predicted)	RGD1564762_predicted	1.796	0.629	0.832	0.360	0.842	0.545	0.918	0.750
1388535_at	BF403698	Similar to erythroid differentiation-related factor 1 (predicted)	RGD1306820_predicted	1.145	0.851	2.116	0.052	1.116	0.656	1.262	0.377
1398999_at	BF283508	similar to es 64 /// similar to hypothetical protein (predicted)	LOC363675 /// RGD1563557_predicted	0.746	0.431	1.306	0.085	0.757	0.210	1.430	0.089
1398943_at	BI274583	similar to Eso3 protein (predicted)	RGD1562476_predicted	0.506	0.218	0.374	0.036	0.365	0.027	0.446	0.009
1389482_at	BI279701	similar to EST AA792894	RGD1306495	1.086	0.452	0.725	0.022	1.099	0.488	0.936	0.173
1395813_at	AW144176	similar to EST AA792894	RGD1306495	0.880	0.485	0.755	0.018	1.120	0.605	0.843	0.165
1377685_at	AW435161	similar to establishment of cohesion 1 homolog 1	LOC498820	1.230	0.023	1.216	0.049	0.979	0.849	1.204	0.077

1397712_at	BF290256	similar to establishment of cohesion 1 homolog 1	LOC498820	1.085	0.818	1.123	0.280	1.155	0.914	1.486	0.794
1372331_at	BM386033	similar to eukaryotic translation initiation factor 1A, Y-linked (predicted)	RGD1560198_predicted	1.034	0.287	1.293	0.040	1.003	0.977	1.346	0.028
1388328_at	BM392200	similar to Eukaryotic translation initiation factor 3 subunit 2 (eIF-3 beta) (predicted)	RGD1560498_predicted	0.678	0.578	1.179	0.211	0.582	0.107	1.072	0.584
1391935_at	AI575608	similar to eukaryotic translation initiation factor 4E member 3	LOC297481	1.248	0.101	1.024	0.708	1.232	0.317	0.918	0.587
1398197_at	BF390021	Similar to Exocyst complex component Sec15B (predicted)	RGD1560638_predicted	2.349	0.758	0.852	0.502	1.156	0.192	0.585	0.535
1381872_at	AI137061	Similar to expressed sequence AA408877	RGD1308513	0.994	0.150	0.897	0.142	0.639	0.067	0.845	0.404
1398991_at	BM389704	Similar to expressed sequence AA408877	RGD1308513	0.450	0.152	0.215	0.000	0.581	0.012	0.298	0.014
1399138_at	BG672805	similar to expressed sequence AA408877	RGD1308513	0.766	0.250	0.237	0.005	0.652	0.109	0.266	0.002
1374197_at	AI177275	Similar to expressed sequence AA415817 (predicted)	RGD1562597_predicted	0.763	0.307	0.373	0.007	0.748	0.030	0.548	0.011
1391968_at	BM389535	Similar to expressed sequence AA415817 (predicted)	RGD1562597_predicted	1.134	0.585	0.720	0.186	0.742	0.311	0.547	0.121
1374639_at	AA800800	similar to Expressed sequence AI317223	LOC287522	1.325	0.589	1.374	0.093	1.161	0.165	1.100	0.699
1395349_at	BF561061	Similar to expressed sequence AI317237 (predicted)	RGD1305671_predicted	2.072	0.040	2.491	0.012	1.425	0.000	1.970	0.028
1376419_at	BE116226	Similar to expressed sequence AI317237 (predicted)	RGD1305671_predicted	1.556	0.043	1.089	0.337	1.464	0.055	0.956	0.510
1396868_at	AI555860	Similar to expressed sequence AI317237 (predicted)	RGD1305671_predicted	1.170	0.050	1.002	0.338	1.012	0.972	1.008	0.531
1382113_at	BF398543	Similar to expressed sequence AI449175	MGC72612	0.732	0.038	0.946	0.056	0.942	0.817	1.034	0.838
1372202_at	BF284058	similar to expressed sequence AI597479	RGD1310553	0.814	0.535	0.617	0.090	0.567	0.006	0.737	0.061
1378812_at	BF412101	similar to expressed sequence AI854635 (predicted)	RGD1565881_predicted	1.230	0.124	1.446	0.092	0.755	0.354	1.080	0.077
1379062_at	BI291230	similar to Expressed sequence AU019823 (predicted)	RGD1560003_predicted	0.996	0.517	1.189	0.255	2.348	0.135	1.400	0.237
1378374_at	BE100748	similar to expressed sequence AU021034 (predicted)	RGD1560137_predicted	0.995	0.954	0.991	0.923	0.998	0.987	1.372	0.096
1398920_at	AI228651	Similar to expressed sequence AU040320 (predicted)	RGD1307489_predicted	0.683	0.003	0.350	0.001	0.667	0.022	0.472	0.009
1394478_at	BF388080	Similar to expressed sequence AU040320 (predicted)	RGD1307489_predicted	1.001	0.979	0.972	0.782	0.997	0.860	1.007	0.986
1399051_at	BE104409	similar to expressed sequence AV312086 (predicted)	RGD1305514_predicted	1.673	0.010	3.147	0.001	1.190	0.037	2.519	0.003
1380753_at	BF398036	similar to expressed sequence AV312086 (predicted)	RGD1305514_predicted	0.996	0.485	1.042	0.831	1.087	0.489	0.924	0.591
1390657_at	BI291389	Similar to expressed sequence AV312086 (predicted)	RGD1305514_predicted	1.034	0.914	1.019	0.937	1.307	0.586	0.853	0.163
1399108_at	BM383630	similar to expressed sequence AV340375	RGD1308959	1.360	0.144	0.994	0.983	3.073	0.057	1.467	0.088
1380513_at	BE095638	similar to Expressed sequence AW060207	RGD1309034	2.298	0.054	2.548	0.017	5.712	0.001	4.290	0.004
1390758_at	BF393473	Similar to Expressed sequence AW060207	RGD1309034	1.188	0.404	0.690	0.068	1.499	0.404	1.030	0.347
1388493_at	AI600030	Similar to Expressed sequence AW146242 (predicted)	RGD1306494_predicted	0.997	0.987	0.998	0.827	0.864	0.989	1.148	0.883
1373547_at	AA849782	similar to expressed sequence AW209491	RGD1308147	0.259	0.035	0.145	0.001	0.230	0.034	0.324	0.000
1376919_at	BG665267	Similar to expressed sequence AW212394 (predicted)	RGD1562317_predicted	0.704	0.616	1.471	0.045	0.678	0.070	1.448	0.043
1371970_at	AA799328	similar to expressed sequence AW413625 (predicted)	RGD1560913_predicted	0.550	0.606	0.795	0.865	0.895	0.870	0.668	0.765
1371663_at	AI232361	similar to expressed sequence AW556797 (predicted)	RGD1305138_predicted	1.515	0.044	2.298	0.058	1.252	0.074	1.290	0.181
1382942_at	BF397627	Similar to Ext1	LOC299907	2.561	0.031	0.953	0.827	3.847	0.002	1.571	0.013
1373393_at	BM384468	similar to Ext1	LOC299907	2.339	0.134	1.760	0.002	2.291	0.002	1.996	0.009
1392083_at	BF415852	Similar to Ext1	LOC299907	1.417	0.847	0.861	0.039	1.708	0.308	0.868	0.175
1373290_at	AI012781	similar to Ezh2 protein	LOC312299	0.995	0.841	1.112	0.646	1.280	0.105	1.787	0.098
1367522_at	AA894324	similar to Factor VIII associated protein (predicted)	RGD1566014_predicted	0.576	0.186	0.693	0.009	0.629	0.061	0.782	0.008
1399020_at	AI232979	similar to family with sequence similarity 40, member A	LOC362012	0.750	0.057	0.525	0.009	0.687	0.047	0.690	0.061
1394826_at	BF417759	Similar to Fanconi anemia, complementation group F (predicted)	RGD1561456_predicted	0.885	0.634	1.141	0.562	0.946	0.828	0.698	0.034
1386901_at	NM_031561	similar to fatty acid translocase/CD36 (predicted)	RGD1562323_predicted	1.122	0.696	0.665	0.039	0.937	0.683	0.685	0.042
1389320_at	BF419881	similar to F-box only protein 25	LOC364637	0.444	0.004	0.277	0.005	0.647	0.008	0.394	0.007
1375041_at	AI599362	Similar to F-box only protein 27 (predicted)	RGD1563982_predicted	9.994	0.022	6.968	0.000	16.757	0.000	12.598	0.004
1376714_at	AI236072	similar to F-box protein FBL2	RGD1308119	1.369	0.124	1.762	0.018	1.260	0.182	1.566	0.002
1379559_at	BF400293	Similar to F-box protein FBL2	RGD1308119	1.463	0.698	0.993	0.512	1.013	0.965	1.102	0.553
1380192_at	AI105297	similar to F-box protein FBL2	RGD1308119	1.497	0.946	1.222	0.304	1.553	0.442	0.972	0.899
1384457_at	AI030755	similar to Fbxw17 protein (predicted)	RGD1561663_predicted	7.005	0.001	7.067	0.003	24.708	0.000	6.195	0.007
1389783_s_at	BI280865	similar to Fc fragment of IgG binding protein; IgG Fc binding protein	RGD1311906	0.236	0.013	0.361	0.009	0.213	0.011	0.312	0.093
1392886_a_at	AI453967	similar to FCRL	RGD1306176	0.996	0.990	1.098	0.573	1.240	0.677	1.126	0.545
1374433_at	BI301532	Similar to Ferritin light chain (Ferritin L subunit) (predicted)	RGD1563902_predicted	2.576	0.009	4.770	0.000	1.701	0.050	4.644	0.005
1372420_at	AI408084	similar to FKSG24 (predicted)	RGD1308064_predicted	0.591	0.004	1.266	0.190	0.502	0.002	1.455	0.024
1392621_at	AI231159	similar to FKSG26 protein (predicted)	RGD1309054_predicted	0.688	0.839	0.931	0.147	0.269	0.075	0.839	0.634
1391346_at	BG373537	similar to FKSG26 protein (predicted)	RGD1309054_predicted	1.036	0.872	0.989	0.861	1.006	0.726	0.948	0.529
1389351_at	BM387864	similar to FLI-LRR associated protein-1	LOC367314	4.547	0.000	4.117	0.001	2.814	0.080	4.307	0.001
1381094_at	BG376156	Similar to FLJ00022 protein (predicted)	RGD1309709_predicted	1.224	0.124	1.005	0.974	0.860	0.832	0.810	0.080
1367548_at	BE118462	similar to FLJ00052 protein (predicted)	RGD1305986_predicted	0.926	0.522	1.206	0.157	1.070	0.193	1.210	0.555
1373954_at	BG381520	Similar to FLJ00052 protein (predicted)	RGD1305986_predicted	0.979	0.557	0.789	0.523	1.309	0.139	0.677	0.399
1380671_at	BF409069	Similar to FLJ00251 protein (predicted)	RGD1311619_predicted	1.591	0.277	2.052	0.167	1.623	0.016	1.660	0.599
1382660_at	AA923866	Similar to FLJ20298 protein isoform a (predicted)	RGD1563084_predicted	0.513	0.287	0.960	0.204	0.780	0.160	0.773	0.055
1376832_at	AA800763	similar to FLJ20689 (predicted)	RGD1308907_predicted	0.897	0.674	0.777	0.247	0.942	0.869	1.106	0.316
1378853_at	BG377853	similar to FLJ22405 protein (predicted)	RGD1304842_predicted	0.975	0.435	1.186	0.963	6.563	0.017	1.017	0.857
1379059_at	BG373522	similar to FLJ23471 protein (predicted)	RGD1307875_predicted	35.068	0.000	16.502	0.002	1.047	0.595	3.210	0.023

1371421_at	BM391873	Similar to FLJ40243 protein	RGD1305413	0.250	0.078	0.338	0.001	0.251	0.005	0.422	0.001
1379228_at	BF418531	similar to flt3 ligand (predicted)	RGD1560528_predicted	0.879	0.787	1.573	0.040	2.310	0.008	1.740	0.029
1372652_at	BM386443	similar to forkhead protein AFXH (predicted)	RGD1561201_predicted	0.657	0.836	0.212	0.000	0.922	0.239	0.358	0.015
1378477_a_at	BI281796	similar to Formin homology 2 domain containing 1	LOC291964	0.421	0.083	0.765	0.056	0.831	0.161	0.889	0.487
1395764_at	BF398145	Similar to formin-like 2 isoform B (predicted)	RGD1560248_predicted	2.580	0.405	1.382	0.058	3.335	0.033	1.437	0.113
1394141_at	AI638976	Similar to FoxB2 protein	LOC502382	1.124	0.305	0.747	0.972	1.117	0.289	1.007	0.994
1376580_at	BG375952	similar to frataxin (predicted)	RGD1565754_predicted	0.472	0.089	1.494	0.246	0.609	0.768	1.966	0.116
1383654_a_at	BE112523	similar to fructosamine-3-kinase (predicted)	Fnsk_predicted	0.162	0.012	0.154	0.021	0.084	0.003	0.339	0.109
1398342_at	BF549775	similar to Fus1 protein	LOC501052	0.561	0.150	1.302	0.326	0.509	0.001	0.974	0.384
1381882_at	AI072357	similar to FYVE, RhoGEF and PH domain containing 6 (predicted)	RGD1565609_predicted	17.944	0.018	23.730	0.000	10.149	0.025	8.838	0.008
1397223_at	AI231513	Similar to FYVE, RhoGEF and PH domain containing 6 (predicted)	RGD1565609_predicted	1.927	0.022	3.232	0.044	1.821	0.016	1.253	0.361
1375588_at	BF405893	similar to FYVE, RhoGEF and PH domain containing 6 (predicted)	RGD1565609_predicted	1.009	0.972	0.996	0.990	1.100	0.484	1.000	0.955
1396280_at	BI277872	similar to G patch domain and KOW motifs (predicted)	RGD1560419_predicted	2.074	0.049	2.038	0.077	1.380	0.072	3.084	0.004
1379827_at	BG376569	similar to G protein pathway suppressor 2	LOC497941	0.904	0.965	1.171	0.015	0.899	0.218	1.206	0.083
1389451_at	AI179502	similar to G protein-coupled receptor 172B (predicted)	RGD1560410_predicted	0.498	0.080	0.766	0.101	0.930	0.911	0.723	0.212
1389345_at	AI231218	Similar to G2 (predicted)	RGD1310754_predicted	0.851	0.496	0.621	0.004	1.153	0.844	0.757	0.020
1395633_at	BF391829	Similar to G2 (predicted)	RGD1310754_predicted	1.016	0.604	1.005	0.875	2.102	0.079	0.997	0.833
1374533_at	AI234190	similar to GA binding protein transcription factor, beta subunit 2 (GABPB2) (predicted)	RGD1560391_predicted	2.692	0.002	1.552	0.122	3.393	0.000	1.498	0.022
1394708_at	BF288532	Similar to GA binding protein transcription factor, beta subunit 2 (GABPB2) (predicted)	RGD1560391_predicted	1.016	0.995	0.975	0.988	0.978	0.925	0.982	0.918
1376633_at	AW529927	Similar to Gamma-parvin (predicted)	RGD1562984_predicted	0.905	0.800	0.253	0.001	1.001	0.863	0.300	0.010
1386226_at	AA893682	Similar to Gamma-tubulin complex component 4 (GCP-4) (predicted)	RGD1306924_predicted	0.970	0.590	0.857	0.111	1.070	0.051	0.889	0.118
1388429_at	BM384085	similar to gem (nuclear organelle) associated protein 7	LOC499391	1.755	0.344	1.344	0.439	1.064	0.515	1.257	0.326
1371376_at	AI072448	similar to Gene model 461 (predicted)	RGD1565596_predicted	0.981	0.334	0.976	0.748	0.972	0.307	0.979	0.768
1389990_at	BE329244	Similar to Gene model 609 (predicted)	RGD1563727_predicted	1.401	0.883	1.340	0.356	1.367	0.237	1.090	0.082
1367509_at	AI231812	Similar to general transcription factor IIH, polypeptide 5 (predicted)	RGD1560991_predicted	0.682	0.278	0.785	0.040	0.583	0.040	0.812	0.116
1372602_at	BI295979	Similar to genethonin 1	RGD1311800	1.681	0.196	13.726	0.000	1.887	0.044	11.316	0.006
1383337_at	AA963875	Similar to genetic suppressor element 1 (predicted)	RGD1562686_predicted	0.892	0.197	0.482	0.024	0.798	0.524	0.625	0.027
1389481_at	BI282891	similar to GI:13385412-like protein splice form I	RGD735065	0.798	0.738	0.748	0.110	0.647	0.000	0.853	0.254
1380410_at	AI043958	Similar to GLI pathogenesis-related 2	LOC502947	25.602	0.000	7.859	0.001	30.239	0.000	10.810	0.001
1375909_at	BI285792	similar to glutathione transferase GSTM7-7	MGC108896	0.582	0.038	1.098	0.665	0.832	0.050	1.118	0.695
1374412_at	BF557666	Similar to glyceraldehyde-3-phosphate dehydrogenase (predicted)	RGD1559570_predicted	1.394	0.272	1.318	0.220	1.893	0.078	1.154	0.379
1390755_at	BE105876	similar to Gnefr protein (predicted)	RGD1563497_predicted	1.738	0.064	5.094	0.007	1.614	0.055	4.486	0.003
1394347_at	BF568007	similar to golgi autoantigen golgin subtype a4; tGolgin-1	LOC501069	0.454	0.057	1.351	0.500	0.356	0.019	0.979	0.119
1398965_at	BF388772	similar to golgi autoantigen golgin subtype a4; tGolgin-1	LOC501069	1.003	0.868	1.335	0.004	1.002	0.422	1.275	0.019
1392517_at	AI102175	similar to Golgin 45 (Basic leucine zipper nuclear factor 1)	LOC498266	1.054	0.786	1.765	0.085	0.740	0.305	1.517	0.148
1385077_at	BE097285	similar to golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 (predicted)	RGD1307160_predicted	0.943	0.278	0.979	0.832	0.910	0.359	0.859	0.368
1389044_at	BF283388	similar to golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 (predicted)	RGD1307160_predicted	1.036	0.465	1.020	0.100	0.684	0.586	0.975	0.505
1390611_at	BF406297	similar to golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 (predicted)	RGD1307160_predicted	1.605	0.730	1.029	0.811	0.910	0.996	1.137	0.335
1379452_at	AI411492	similar to growth arrest-specific protein 2 - mouse (predicted)	RGD1563167_predicted	0.888	0.721	0.247	0.001	0.653	0.206	0.326	0.057
1374505_at	AI411031	similar to growth hormone-inducible soluble protein (predicted)	RGD1563076_predicted	1.052	0.785	0.886	0.038	1.577	0.004	1.100	0.787
1381025_at	BF410266	Similar to growth/differentiation factor GDF-3 precursor - mouse (predicted)	RGD1559624_predicted	1.167	0.681	0.876	0.449	2.556	0.043	1.029	0.154
1377008_at	BI296868	similar to GTL2, imprinted maternally expressed untranslated (predicted)	RGD1566401_predicted	1.004	0.986	0.843	0.746	1.321	0.793	0.802	0.013
1373572_at	BF282247	similar to GTP binding protein 5	LOC296462	0.315	0.016	0.666	0.155	0.534	0.019	0.767	0.118
1381791_at	AA818889	Similar to GTPase activating protein testicular GAP1 (predicted)	RGD1562031_predicted	1.222	0.490	0.986	0.729	5.073	0.109	0.945	0.196
1395899_at	AW921250	Similar to GTPase activating protein testicular GAP1 (predicted)	RGD1565009_predicted	0.925	0.632	0.772	0.074	1.238	0.985	0.797	0.103
1396765_at	BF390955	Similar to GTPase activating RANGAP domain-like 3 (predicted)	RGD1564019_predicted	0.577	0.040	1.087	0.715	0.435	0.030	1.018	0.420
1398492_at	BF395819	Similar to Guanine nucleotide-binding protein beta subunit 2-like 1 (Receptor of activated protein kinase C 1) (predicted)	RGD1562180_predicted	0.950	0.842	0.708	0.859	1.001	0.086	0.653	0.204
1376990_at	BE118704	Similar to HCDI protein (predicted)	RGD1309307_predicted	2.557	0.004	1.618	0.011	3.624	0.000	2.000	0.003
1393673_at	BE120005	similar to HCDI protein (predicted)	RGD1309307_predicted	1.297	0.027	0.971	0.726	1.896	0.019	0.996	0.982
1376222_at	AI710677	similar to HCDI protein (predicted)	RGD1309307_predicted	0.462	0.027	0.503	0.034	0.694	0.021	0.372	0.081
1389021_at	BF284746	similar to HCV NS3-transactivated protein 1 (predicted)	RGD1306332_predicted	0.703	0.079	1.352	0.003	0.564	0.005	1.284	0.014
1373811_at	AA942728	similar to heat shock protein 8 (predicted)	RGD1560590_predicted	2.440	0.057	1.042	0.181	3.097	0.043	0.974	0.901
1392259_at	AI574925	similar to HECT domain containing 1 (predicted)	RGD1561653_predicted	1.211	0.285	1.632	0.093	1.199	0.859	0.836	0.497
1383615_a_at	AI059295	similar to HECT domain containing 1 (predicted)	RGD1561653_predicted	1.117	0.489	1.046	0.771	1.001	0.997	1.247	0.991
1372394_at	AI175474	similar to HECT domain containing 1 (predicted)	RGD1561653_predicted	0.942	0.497	1.278	0.022	0.995	0.941	1.210	0.001
1393611_at	AA964538	similar to Hel308 protein	LOC289471	1.888	0.172	0.455	0.047	0.651	0.104	0.327	0.018
1374921_at	BI274548	similar to helicase-like protein NHL isoform 2	RGD1306721	0.373	0.001	0.612	0.402	0.655	0.018	0.564	0.028
1389158_at	BE329196	Similar to helicase-like protein NHL isoform 2	RGD1306721	0.910	0.088	1.002	0.732	0.891	0.361	1.025	0.682
1377532_at	AW434782	similar to Hepatocellular carcinoma-associated antigen 58 homolog (predicted)	RGD1305020_predicted	1.534	0.160	1.267	0.166	1.497	0.037	1.294	0.505
1376931_at	BG380736	similar to Hepatocellular carcinoma-associated antigen 58 homolog (predicted)	RGD1305020_predicted	1.236	0.313	2.074	0.042	1.167	0.242	1.699	0.171

1376270_at	AI059493	Similar to HESB like domain containing 1 (predicted)	RGD1563216_predicted	1.079	0.538	1.292	0.408	0.753	0.256	1.007	0.842
1388446_at	BF397834	similar to heterogeneous nuclear ribonucleoprotein A0 (predicted)	RGD1563684_predicted	0.724	0.278	0.714	0.008	0.451	0.005	0.709	0.023
1375772_at	BI296534	Similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein (Topoisomerase-inhibitor suppressed) (predicted)	RGD1559977_predicted	0.983	0.752	1.016	0.176	1.328	0.463	1.054	0.058
1374181_at	BF290678	similar to heterogeneous nuclear ribonucleoprotein G - human	LOC302855	0.369	0.015	0.517	0.016	0.428	0.154	0.631	0.141
1395523_at	AW523475	Similar to heterogeneous nuclear ribonucleoprotein G - human	LOC302855	0.894	0.784	0.491	0.076	0.626	0.604	1.212	0.257
1371887_at	BF398549	similar to high mobility group protein homolog HMG4 (predicted)	RGD1564407_predicted	0.431	0.001	0.717	0.099	0.898	0.268	0.345	0.049
1382316_at	BE118866	similar to histone cell cycle regulation defective homolog A isoform 1	LOC363849	0.812	0.256	1.026	0.156	1.650	0.306	0.825	0.994
1390384_at	AA875257	similar to Histone H2A.x (H2a/x) (predicted)	RGD1566119_predicted	0.508	0.071	0.916	0.393	0.373	0.026	0.698	0.649
1386059_at	BF284475	Similar to histone H2b-613 (predicted)	RGD1562346_predicted	1.014	0.205	0.591	0.012	0.746	0.338	0.729	0.046
1393488_at	AI103612	Similar to HIV-1 Rev binding protein	LOC363266	1.348	0.183	1.961	0.623	1.025	0.410	1.199	0.651
1396286_at	BG372956	Similar to HIV-1 Rev binding protein	LOC363266	0.592	0.207	0.671	0.590	0.974	0.247	0.661	0.891
1382533_at	AI012699	similar to HIV-1 Rev binding protein	LOC363266	1.247	0.798	1.266	0.777	0.919	0.643	0.894	0.474
1383158_at	AI575747	similar to HIV-1 Rev binding protein	LOC363266	0.936	0.877	1.042	0.651	0.742	0.136	1.041	0.542
1382245_at	BF397964	Similar to HMG-1 (predicted)	RGD1559799_predicted	1.257	0.348	1.294	0.578	1.036	0.883	1.167	0.973
1388929_at	AI011716	Similar to HMG-1 (predicted)	RGD1559799_predicted	0.972	0.787	0.815	0.314	0.895	0.174	0.831	0.068
1373447_at	BF281350	similar to HN1-like protein	RGD1305117	1.021	0.082	1.571	0.008	1.493	0.012	1.349	0.007
1394976_at	AI008980	Similar to HN1-like protein	RGD1305117	2.009	0.800	1.597	0.124	1.432	0.379	1.771	0.895
1388504_at	AI231313	similar to HR21spA	MGC116373	0.746	0.266	0.736	0.001	0.806	0.088	0.968	0.767
1382823_at	AI070008	Similar to HR21spA	MGC116373	1.691	0.447	15.496	0.000	1.222	0.473	12.913	0.000
1379700_at	AA956376	similar to HS1 binding protein 3 (predicted)	RGD1311331_predicted	0.971	0.242	1.063	0.642	0.706	0.115	1.004	0.300
1396499_at	BF403327	similar to HSD-29 (predicted)	RGD1559656_predicted	1.043	0.923	1.083	0.204	1.075	0.593	1.031	0.775
1379778_at	AI713278	similar to HSPC043 protein (predicted)	RGD1307983_predicted	0.988	0.507	2.935	0.000	1.456	0.057	2.910	0.023
1388346_at	BM386531	similar to HSPC171 protein (predicted)	RGD1560953_predicted	0.621	0.665	0.624	0.033	0.632	0.110	0.564	0.005
1377730_at	BF290890	similar to HSPC288 (predicted)	RGD1310769_predicted	0.589	0.209	0.769	0.000	0.829	0.017	0.929	0.216
1375354_at	BE098366	Similar to HT014 (predicted)	RGD1308048_predicted	0.607	0.091	1.219	0.286	0.549	0.064	0.980	0.076
1374554_at	BF281325	similar to HT014 (predicted)	RGD1308048_predicted	0.592	0.530	1.958	0.007	0.600	0.070	1.746	0.060
1374882_at	AW433860	similar to HT021 (predicted)	RGD1306063_predicted	0.598	0.066	0.597	0.056	0.896	0.553	0.865	0.784
1379939_a_at	AW526107	Similar to HT021 (predicted)	RGD1306063_predicted	0.778	0.465	1.911	0.031	1.000	0.524	3.340	0.002
1397448_at	BE108434	Similar to HT021 (predicted)	RGD1306063_predicted	1.260	0.567	1.001	0.880	1.003	0.968	0.992	0.624
1380407_at	AI179886	similar to HTGN29 protein; keratinocytes associated transmembrane protein 2	RGD1310352	0.608	0.037	0.418	0.073	0.589	0.059	0.331	0.020
1371619_at	BI296718	similar to HTGN29 protein; keratinocytes associated transmembrane protein 2	RGD1310352	0.521	0.359	0.423	0.002	0.521	0.188	0.387	0.001
1375899_at	BF283736	Similar to HTPAP protein (predicted)	RGD1559978_predicted	1.524	0.003	1.836	0.008	1.751	0.051	1.777	0.004
1373160_at	BM388961	similar to HTPAP protein (predicted)	RGD1559978_predicted	0.690	0.066	0.926	0.259	0.596	0.071	0.935	0.699
1385030_at	BE097270	Similar to HTPAP protein (predicted)	RGD1559978_predicted	0.937	0.299	1.021	0.466	1.174	0.430	1.025	0.903
1379540_at	BM383595	Similar to HTPAP protein (predicted)	RGD1559978_predicted	1.329	0.312	1.335	0.088	1.092	0.182	1.275	0.090
1390667_at	BF408543	similar to Hypothetical 55.1 kDa protein F09G8.5 in chromosome III (predicted)	RGD1565856_predicted	0.533	0.002	0.883	0.707	0.409	0.003	0.585	0.404
1395391_at	BF412774	similar to hypothetical gene supported by AK029636; BC048562	LOC498677	0.971	0.977	0.994	0.862	0.999	0.090	1.000	0.677
1382834_at	AI070996	Similar to hypothetical gene supported by AK044523 (predicted)	RGD1562175_predicted	1.002	0.900	0.992	0.970	1.012	0.803	0.988	0.935
1380118_at	BI275569	similar to hypothetical gene supported by AK085276 (predicted)	RGD1562252_predicted	0.904	0.445	0.956	0.792	1.197	0.716	1.041	0.431
1398608_at	BG371578	similar to hypothetical gene supported by BC007071	RGD1311868	1.010	0.887	1.468	0.117	1.061	0.577	1.408	0.009
1388946_at	AI233763	similar to hypothetical p38 protein (predicted)	RGD1311910_predicted	0.737	0.029	0.699	0.274	0.523	0.004	0.587	0.103
1382807_at	BE100287	similar to hypothetical protein	RGD1310450	0.683	0.001	0.720	0.051	1.109	0.841	0.805	0.054
1388532_at	AI599496	similar to hypothetical protein	RGD1310571	0.385	0.013	1.323	0.868	0.308	0.002	1.094	0.151
1393011_at	BE104363	similar to hypothetical protein	LOC361041	0.483	0.050	0.131	0.000	0.870	0.169	0.190	0.043
1377615_at	AI112395	similar to hypothetical protein	LOC304280	0.575	0.089	0.439	0.001	0.495	0.021	0.444	0.000
1373982_at	BM385377	similar to hypothetical protein	RGD1306595	0.485	0.206	1.121	0.556	0.433	0.007	1.056	0.979
1389788_at	AW522732	similar to hypothetical protein	RGD1307336	0.667	0.249	0.950	0.847	0.641	0.443	1.087	0.605
1380320_at	AI176284	similar to hypothetical protein	RGD1311361	0.943	0.433	3.409	0.005	0.665	0.276	2.966	0.042
1386733_at	BF544390	Similar to hypothetical protein (predicted)	RGD1306694_predicted	1.492	0.001	0.988	0.966	1.085	0.161	0.897	0.352
1383494_at	BF414338	similar to hypothetical protein (predicted)	RGD1562788_predicted	1.294	0.004	0.904	0.969	0.959	0.771	0.965	0.688
1375429_at	BI294768	Similar to hypothetical protein (predicted)	RGD1562784_predicted	0.647	0.030	0.670	0.013	0.607	0.003	0.614	0.007
1377232_at	BF406608	similar to hypothetical protein (predicted)	RGD1305269_predicted	0.517	0.033	0.290	0.005	0.455	0.160	0.224	0.001
1390414_at	BI296515	similar to hypothetical protein (predicted)	RGD1308489_predicted	1.677	0.038	2.276	0.087	2.803	0.084	2.226	0.106
1377868_at	AW530090	similar to hypothetical protein (predicted)	RGD1561019_predicted	0.540	0.043	0.631	0.104	0.564	0.007	0.684	0.026
1376546_at	BE120498	similar to hypothetical protein (predicted)	RGD1565432_predicted	0.442	0.044	0.577	0.004	0.494	0.013	0.435	0.052
1385083_at	BG378253	similar to hypothetical protein (predicted)	RGD1563056_predicted	0.509	0.086	0.948	0.849	0.565	0.106	0.910	0.867
1374328_at	BF403886	similar to hypothetical protein (predicted)	RGD1566393_predicted	1.467	0.136	1.602	0.062	1.270	0.184	1.704	0.029
1389194_at	AI406491	Similar to hypothetical protein (predicted)	RGD1565536_predicted	0.565	0.138	0.474	0.007	0.440	0.012	0.527	0.023
1381150_at	BF410638	Similar to hypothetical protein (predicted)	RGD1305239_predicted	0.799	0.173	0.967	0.084	0.858	0.986	0.791	0.425
1386061_at	BF523573	similar to hypothetical protein (predicted)	RGD1306694_predicted	1.101	0.231	0.677	0.029	1.016	0.224	0.783	0.252

1372110_at	BE113148	Similar to hypothetical protein (predicted)	RGD1305269_predicted	0.513	0.245	0.180	0.000	0.489	0.021	0.345	0.002
1391461_at	BF285149	similar to hypothetical protein (predicted)	RGD1306576_predicted	0.667	0.294	1.004	0.875	0.816	0.236	0.654	0.033
1373191_at	BG375890	similar to hypothetical protein (predicted)	RGD1560131_predicted	0.931	0.326	1.714	0.009	0.793	0.354	1.367	0.000
1381491_at	BE097634	Similar to hypothetical protein (predicted)	RGD1305269_predicted	1.209	0.333	0.791	0.272	1.430	0.317	0.659	0.283
1388983_at	BI296386	similar to hypothetical protein (predicted)	RGD1305045_predicted	0.642	0.367	0.942	0.482	0.618	0.064	1.060	0.416
1374031_at	BI295824	similar to hypothetical protein (predicted)	RGD1310937_predicted	1.140	0.423	1.769	0.006	1.309	0.760	2.001	0.007
1392987_at	AI136865	Similar to hypothetical protein (predicted)	RGD1561605_predicted	0.832	0.429	1.149	0.067	0.764	0.321	0.882	0.510
1380825_at	BE102406	Similar to hypothetical protein (predicted)	RGD1305269_predicted	1.359	0.493	0.911	0.594	1.358	0.332	0.419	0.351
1392911_at	AI548807	Similar to hypothetical protein (predicted)	RGD1562470_predicted	1.048	0.786	0.870	0.022	1.033	0.187	1.024	0.757
1390218_at	BI295950	similar to hypothetical protein (predicted)	RGD1310440_predicted	1.338	0.789	2.163	0.001	1.150	0.593	1.562	0.003
1395974_at	BE096056	Similar to hypothetical protein (predicted)	RGD1311334_predicted	1.139	0.925	1.420	0.113	1.444	0.999	1.229	0.007
1397456_at	BI293930	similar to hypothetical protein (predicted)	RGD1560620_predicted	1.006	0.952	1.081	0.508	0.999	0.916	1.002	0.417
1375508_at	BE095963	Similar to hypothetical protein (predicted)	RGD1559908_predicted	1.012	0.973	0.999	0.995	1.193	0.233	1.294	0.476
1376155_at	BE113295	similar to hypothetical protein 2BE2121 - Chinese hamster (fragment) (predicted)	RGD1561110_predicted	2.275	0.002	1.946	0.105	0.929	0.518	1.260	0.146
1380819_at	BF391871	Similar to hypothetical protein 2BE2121 - Chinese hamster (fragment) (predicted)	RGD1561110_predicted	1.026	0.993	0.986	0.457	0.998	0.724	0.902	0.084
1391857_at	AI044397	similar to hypothetical protein 4732467B22 (predicted)	RGD1561732_predicted	0.485	0.003	0.308	0.006	0.526	0.110	0.727	0.280
1398021_at	AI411984	similar to hypothetical protein 4930474N05 (predicted) /// similar to hypothetical protein 4930474N05 (predicted) /// similar to hypothetical protein 4930474N05 (predicted) /// similar to hypothetical protein 4930474N05 (predicted) /// similar to hypothetical protein 4930474N05 (predicted) /// similar to hypothetical protein 4930474N05 (predicted) /// similar to hypothetical protein 4930474N05 (predicted) /// similar to hypothetical protein 4930474N05 (predicted)	RGD1563218_predicted /// RGD1566067_predicted /// RGD1565329_predicted /// RGD1562098_predicted /// RGD1566353_predicted /// RGD1565349_predicted /// RGD1559554_predicted /// RGD1561935_predicted	0.991	0.510	1.002	0.890	1.204	0.096	1.012	0.895
1385383_at	AI145747	similar to hypothetical protein 4933409I22 (predicted)	RGD1565763_predicted	0.657	0.021	0.110	0.005	2.769	0.038	1.008	0.686
1396709_at	BE108621	Similar to Hypothetical protein 5031404N19 (predicted)	RGD1305628_predicted	1.444	0.559	0.992	0.117	1.271	0.530	0.562	0.094
1376903_at	BF400799	Similar to Hypothetical protein 6330514E13 (predicted)	RGD1559693_predicted	1.070	0.959	0.994	0.793	0.995	0.865	1.066	0.674
1393309_at	AI145786	Similar to Hypothetical protein 6720416P20 (predicted)	RGD1311412_predicted	1.231	0.526	0.660	0.024	1.070	0.826	0.827	0.047
1392551_at	AI104921	Similar to Hypothetical protein 6720416P20 (predicted)	RGD1311412_predicted	1.057	0.752	0.382	0.007	1.373	0.498	0.575	0.010
1395866_at	BF543899	Similar to Hypothetical protein 6720416P20 (predicted)	RGD1311412_predicted	1.529	0.846	0.490	0.003	1.108	0.276	0.679	0.022
1395404_at	BE110529	Similar to Hypothetical protein 9030012M21 (predicted)	RGD1304570_predicted	0.645	0.045	0.657	0.008	0.570	0.019	0.722	0.025
1393214_at	BG371744	Similar to hypothetical protein A230042K10 (predicted)	RGD1566144_predicted	1.204	0.228	1.079	0.191	1.968	0.036	1.132	0.453
1383639_at	AA924348	Similar to hypothetical protein A230042K10 (predicted)	RGD1566144_predicted	1.001	0.694	0.879	0.927	0.960	0.036	0.990	0.899
1373584_at	BE113205	similar to hypothetical protein A430031N04 (predicted)	RGD1559643_predicted	1.035	0.963	1.168	0.565	1.792	0.008	1.097	0.721
1390968_at	AI706441	Similar to hypothetical protein A430031N04 (predicted)	RGD1559643_predicted	0.988	0.995	1.000	0.997	0.999	0.953	1.127	0.991
1379668_at	BI296117	similar to hypothetical protein B230397C21 (predicted)	RGD1564725_predicted	0.551	0.098	0.881	0.533	0.496	0.023	0.891	0.259
1389209_at	BG666095	similar to hypothetical protein BC002942	RGD1306274	0.805	0.601	0.890	0.761	0.976	0.641	0.848	0.475
1393610_at	AI137173	similar to hypothetical protein BC008163 (predicted)	RGD1305162_predicted	2.766	0.038	1.186	0.336	1.050	0.879	1.886	0.051
1372184_at	BM392213	similar to hypothetical protein BC011833 (predicted)	RGD1309188_predicted	0.695	0.397	0.759	0.007	0.581	0.019	0.819	0.008
1385188_at	BG379787	Similar to hypothetical protein BC011833 (predicted)	RGD1309188_predicted	0.782	0.599	0.760	0.552	0.670	0.170	0.826	0.566
1389676_at	BI294925	similar to hypothetical protein BC011981 (predicted)	RGD1310609_predicted	0.851	0.090	0.778	0.529	0.444	0.048	1.445	0.333
1394502_at	BF284587	similar to hypothetical protein BC013035 (predicted)	RGD1560996_predicted	0.998	0.077	0.996	0.561	1.005	0.822	1.000	0.559
1375315_at	BE098345	similar to hypothetical protein BC013035 (predicted)	RGD1560996_predicted	0.799	0.395	0.479	0.003	0.617	0.099	0.486	0.050
1373965_at	BM385251	similar to hypothetical protein BC013949 (predicted)	RGD1310931_predicted	1.139	0.261	1.689	0.118	1.000	0.996	1.045	0.428
1375884_at	AW520742	similar to Hypothetical protein BC014729	MGC105560	0.927	0.555	1.023	0.448	0.973	0.191	1.115	0.374
1395125_at	BI301937	Similar to hypothetical protein BC015148 (predicted)	RGD1309095_predicted	0.784	0.339	1.829	0.043	0.914	0.788	1.501	0.105
1384252_at	AI603103	similar to hypothetical protein BC015148 (predicted)	RGD1309095_predicted	0.623	0.508	1.415	0.211	0.577	0.057	1.277	0.113
1393085_at	BI290341	similar to hypothetical protein BC018453	RGD1307700	3.135	0.019	1.821	0.040	6.520	0.004	2.663	0.005
1372699_at	AI112403	Similar to hypothetical protein C130032F08 (predicted)	RGD1304910_predicted	0.729	0.650	2.074	0.045	1.506	0.632	2.738	0.002
1380554_at	AI101463	Similar to hypothetical protein C530015C18 (predicted)	RGD1564396_predicted	0.962	0.645	0.563	0.042	0.879	0.089	0.564	0.038
1393547_at	BE101549	similar to hypothetical protein C630023L15 (predicted)	RGD1560399_predicted	0.223	0.010	0.288	0.046	0.277	0.008	0.489	0.026
1391944_at	BI296237	similar to Hypothetical protein C6orf60 (predicted)	RGD1311294_predicted	0.542	0.022	0.436	0.004	0.439	0.281	0.546	0.016
1377011_at	BF415061	Similar to hypothetical protein CG003 (predicted)	RGD1307034_predicted	0.362	0.079	0.529	0.003	0.423	0.005	0.413	0.011
1398919_at	BI296033	similar to Hypothetical protein CGI-99	RGD1304704	0.662	0.181	1.061	0.184	0.581	0.013	1.028	0.255
1373346_at	AI009492	similar to hypothetical protein CL25084 (predicted)	RGD1306508_predicted	0.749	0.039	0.499	0.000	0.698	0.012	0.532	0.024
1395331_at	BF548263	similar to hypothetical protein CL25084 (predicted)	RGD1306508_predicted	0.395	0.313	0.207	0.009	0.436	0.124	0.289	0.024
1392494_at	AI180300	similar to hypothetical protein D030056L22	LOC499331	1.151	0.024	0.883	0.541	1.053	0.732	1.099	0.186
1373620_at	AI102038	Similar to hypothetical protein D10Ertd438e (predicted)	RGD1307879_predicted	0.819	0.458	1.177	0.136	0.900	0.055	0.890	0.327
1392522_at	AA925790	similar to hypothetical protein D10Ertd438e (predicted)	RGD1307879_predicted	0.747	0.752	9.720	0.010	0.834	0.475	5.022	0.013
1388957_at	AA891790	Similar to hypothetical protein D10Ertd641e (predicted)	RGD1560152_predicted	1.280	0.536	1.375	0.012	1.066	0.666	1.299	0.008
1375540_at	BF400209	similar to hypothetical protein D11Ertd497e	RGD1308696	0.900	0.524	1.137	0.083	1.002	0.395	0.955	0.840

1373077_at	BI285902	similar to hypothetical protein D11Ertd497e	RGD1308696	0.866	0.737	0.907	0.384	0.571	0.041	0.917	0.103
1370298_at	AF052042	similar to hypothetical protein D11Ertd99e (predicted)	RGD1564337_predicted	0.874	0.654	1.154	0.566	0.440	0.026	1.124	0.316
1372713_at	BE109614	Similar to hypothetical protein D12Ertd771e	RGD1309550	1.336	0.121	0.972	0.541	1.199	0.051	1.148	0.095
1374913_at	BI295047	similar to hypothetical protein D12Ertd771e	RGD1309550	1.827	0.222	1.249	0.890	0.939	0.962	1.171	0.781
1397483_at	BE104832	Similar to hypothetical protein D12Ertd771e	RGD1309550	0.935	0.708	0.893	0.485	0.860	0.857	0.979	0.583
1372188_at	BM392171	Similar to hypothetical protein D15Ertd785e	MGC114417	1.352	0.554	1.396	0.342	0.943	0.078	1.326	0.302
1393609_at	AA964480	Similar to hypothetical protein D15Ertd785e	MGC114417	1.098	0.730	1.046	0.871	1.902	0.628	1.007	0.770
1388336_at	AI411514	Similar to hypothetical protein D2Ertd391e (predicted)	RGD1310685_predicted	0.627	0.297	0.514	0.033	0.799	0.151	0.719	0.058
1376719_at	AI172189	similar to hypothetical protein D4Ertd89e	RGD1305703	1.130	0.026	0.974	0.645	1.215	0.093	0.939	0.499
1383715_at	BI284371	similar to hypothetical protein D4Ertd89e	RGD1305703	0.894	0.981	1.215	0.359	0.782	0.313	1.014	0.144
1388790_at	BM384998	similar to hypothetical protein D5Ertd33e	RGD1310857	0.454	0.098	1.003	0.314	0.502	0.024	0.907	0.767
1382818_at	AI177067	similar to hypothetical protein D630010C10	RGD1309752	0.923	0.293	0.922	0.462	0.601	0.108	0.897	0.007
1397259_at	BF291133	similar to hypothetical protein D630010C10	RGD1309752	0.763	0.325	1.084	0.513	1.144	0.302	1.060	0.145
1385108_at	AW524173	Similar to hypothetical protein D630010C10	RGD1309752	1.334	0.508	0.733	0.082	1.258	0.125	0.685	0.027
1378860_at	AW525986	Similar to hypothetical protein D930020E02 (predicted)	RGD1562973_predicted	0.468	0.013	0.185	0.010	1.007	0.997	0.516	0.010
1385558_at	AW532330	Similar to hypothetical protein D930024E11 (predicted)	RGD1561304_predicted	1.036	0.289	0.206	0.038	0.938	0.025	0.393	0.033
1389386_at	AI170759	similar to hypothetical protein DKFZp313N0621 (predicted)	RGD1560717_predicted	0.812	0.093	0.904	0.340	0.408	0.252	0.559	0.000
1377365_at	BG372342	similar to hypothetical protein DKFZp434H2010 (predicted)	RGD1311019_predicted	2.563	0.034	1.644	0.048	2.753	0.054	1.443	0.072
1384989_at	BE107398	similar to hypothetical protein DKFZp434H2010 (predicted)	RGD1311019_predicted	1.004	0.974	1.036	0.509	1.143	0.489	1.018	0.043
1382399_at	AW530026	similar to hypothetical protein DKFZp434K1421	RGD1309863	1.058	0.242	0.989	0.943	1.073	0.134	1.264	0.974
1382904_at	BF397274	similar to hypothetical protein DKFZp434K1421	RGD1309863	0.955	0.647	1.091	0.036	1.156	0.504	1.056	0.054
1373715_at	BI274516	similar to hypothetical protein DKFZp434K1815	LOC304396	0.962	0.874	0.953	0.706	0.795	0.454	0.864	0.741
1375678_at	AI412430	similar to hypothetical protein DKFZp434P0316 (predicted)	RGD1562974_predicted	2.918	0.000	1.834	0.017	3.263	0.001	1.789	0.014
1397041_at	BF404629	Similar to hypothetical protein DKFZp564D0478 (predicted)	RGD1304793_predicted	1.017	0.619	1.362	0.166	1.073	0.069	0.765	0.150
1376833_at	AW525740	similar to hypothetical protein DKFZp564D0478 (predicted)	RGD1304793_predicted	1.539	0.783	1.388	0.071	1.246	0.578	1.247	0.189
1377995_at	AA799854	similar to hypothetical protein DKFZp761D0211	RGD1311484	0.800	0.009	1.257	0.022	0.463	0.035	1.012	0.156
1378744_at	AI412523	Similar to hypothetical protein DKFZp761D0211	RGD1311484	1.423	0.257	1.668	0.560	1.200	0.170	1.048	0.526
1382948_at	BI296929	similar to hypothetical protein E130310N06 (predicted)	RGD1559882_predicted	1.097	0.485	1.002	0.564	1.001	0.709	0.998	0.403
1391819_at	BM390584	similar to hypothetical protein ET (predicted)	RGD1307394_predicted	1.006	0.647	2.603	0.042	0.994	0.898	1.586	0.147
1382196_at	BI293505	Similar to hypothetical protein ET (predicted)	RGD1307394_predicted	0.977	0.883	0.675	0.535	0.644	0.362	0.525	0.345
1372222_at	BI285621	Similar to hypothetical protein F730001J03 (predicted)	RGD1311757_predicted	0.539	0.376	0.575	0.002	0.563	0.049	0.502	0.023
1391356_at	BI282688	similar to hypothetical protein FLJ10006	RGD1304762	1.494	0.018	2.288	0.060	1.775	0.153	2.049	0.075
1372522_at	AI556235	similar to hypothetical protein FLJ10154	RGD1310061	0.779	0.098	0.554	0.002	0.998	0.989	0.742	0.101
1395516_at	BG663870	similar to hypothetical protein FLJ10154	RGD1310061	1.001	0.997	1.198	0.033	1.730	1.000	1.129	0.072
1383461_at	AA946382	similar to hypothetical protein FLJ10204	RGD1311362	1.183	0.707	1.655	0.014	0.897	0.039	1.493	0.014
1374715_at	BE097245	similar to hypothetical protein FLJ10233	RGD1309487	1.152	0.554	2.812	0.008	1.137	0.812	2.864	0.006
1389192_at	AA800521	similar to hypothetical protein FLJ10241	MGC109149	0.920	0.255	1.008	0.873	0.924	0.280	0.997	0.633
1375461_at	BI285588	similar to hypothetical protein FLJ10241	MGC109149	0.810	0.441	0.545	0.063	0.991	0.994	0.853	0.231
1371738_at	BI287983	similar to hypothetical protein FLJ10375 (predicted)	RGD1308260_predicted	0.969	0.433	1.115	0.302	1.030	0.355	1.187	0.108
1372302_at	BF284897	similar to hypothetical protein FLJ10579	RGD1308697	4.108	0.011	2.856	0.010	5.080	0.003	4.604	0.012
1395297_at	AI556097	similar to hypothetical protein FLJ10652	RGD1309621	3.200	0.002	3.091	0.029	2.984	0.004	1.992	0.329
1373143_at	BM390131	similar to hypothetical protein FLJ10652	RGD1309621	3.956	0.015	4.236	0.000	6.715	0.005	2.688	0.001
1379278_at	BE103919	similar to hypothetical protein FLJ10871 (predicted)	RGD1311539_predicted	0.998	0.517	0.799	0.566	1.145	0.341	0.996	0.277
1395072_at	AW534686	Similar to hypothetical protein FLJ10901 (predicted)	RGD1311892_predicted	1.533	0.073	1.049	0.683	1.111	0.092	0.774	0.010
1377341_at	AA859545	similar to hypothetical protein FLJ10925	RGD1305455	0.903	0.192	0.829	0.512	0.900	0.355	0.926	0.733
1380546_at	AA926048	similar to hypothetical protein FLJ10986 /// similar to hypothetical protein FLJ10986	LOC298250 /// LOC298251	1.002	0.926	0.634	0.131	1.482	0.479	0.744	0.196
1381816_at	BE119617	similar to hypothetical protein FLJ11218	RGD1309804	1.283	0.365	1.034	0.968	1.068	0.221	0.999	0.989
1382008_at	AI044348	similar to hypothetical protein FLJ11218	RGD1309804	0.996	0.993	0.780	0.053	0.624	0.036	0.915	0.796
1385277_x_at	AA818849	similar to hypothetical protein FLJ11354 (predicted)	RGD1310093_predicted	6.503	0.002	1.849	0.004	16.826	0.004	5.776	0.025
1385276_a_at	AA818849	similar to hypothetical protein FLJ11354 (predicted)	RGD1310093_predicted	18.547	0.014	3.700	0.008	57.307	0.005	17.056	0.002
1399151_at	AI029110	similar to hypothetical protein FLJ11526 (predicted)	RGD1309585_predicted	0.938	0.919	1.593	0.021	0.813	0.549	1.402	0.071
1373451_at	BG380780	similar to hypothetical protein FLJ11712	MGC94780	0.789	0.197	0.764	0.288	0.910	0.541	1.141	0.538
1380815_at	AW523684	similar to hypothetical protein FLJ11752	LOC304923	0.848	0.249	1.698	0.017	0.874	0.660	1.652	0.029
1382972_at	BE103344	similar to hypothetical protein FLJ12787	RGD1310992	1.307	0.185	2.872	0.005	1.518	0.135	1.915	0.019
1393320_at	BF396985	Similar to hypothetical protein FLJ12787	RGD1310992	1.215	0.378	2.072	0.006	1.131	0.869	2.000	0.000
1383849_at	AW143311	similar to hypothetical protein FLJ12994 (predicted)	RGD1308795_predicted	0.630	0.281	0.764	0.766	1.010	0.936	0.919	0.342
1382139_at	BE108950	similar to hypothetical protein FLJ12994 (predicted)	RGD1308795_predicted	0.962	0.825	0.692	0.028	0.862	0.096	0.757	0.022
1377683_at	AI407061	similar to hypothetical protein FLJ13045 (predicted)	RGD1307615_predicted	0.804	0.206	1.011	0.367	0.597	0.997	1.162	0.484
1380667_at	AW251634	similar to hypothetical protein FLJ13045 (predicted)	RGD1307615_predicted	1.073	0.250	0.932	0.768	0.683	0.728	0.988	0.954
1372618_at	AI407147	similar to hypothetical protein FLJ13045 (predicted)	RGD1307615_predicted	0.860	0.364	1.275	0.182	0.871	0.828	1.054	0.106
1385066_a_at	BM390527	Similar to hypothetical protein FLJ13089	RGD1305685	1.585	0.032	2.144	0.004	1.751	0.010	2.273	0.002

1395524_at	AW525958	Similar to hypothetical protein FLJ13089	RGD1305685	1.239	0.287	1.195	0.968	2.146	0.006	1.168	0.175
1384553_at	BE118056	similar to hypothetical protein FLJ13089	RGD1305685	1.246	0.395	2.301	0.000	1.771	0.004	2.225	0.013
1394566_at	AI549119	similar to hypothetical protein FLJ13188 (predicted)	RGD1305500_predicted	0.723	0.069	0.455	0.013	0.666	0.578	0.579	0.102
1377439_at	BF408617	similar to hypothetical protein FLJ13231 (predicted)	RGD1310081_predicted	4.627	0.000	1.024	0.832	20.467	0.000	3.357	0.000
1382062_at	AA943385	similar to hypothetical protein FLJ13273 (predicted)	RGD1311822_predicted	0.700	0.246	1.008	0.958	0.737	0.009	0.983	0.741
1373866_at	AI228596	similar to hypothetical protein FLJ13448	RGD1359509	0.662	0.014	0.821	0.349	0.721	0.024	0.925	0.282
1382530_at	AI044286	Similar to hypothetical protein FLJ13910 (predicted)	RGD1309766_predicted	1.224	0.779	0.639	0.082	1.041	0.291	0.626	0.117
1383258_at	BM383065	similar to hypothetical protein FLJ14146	RGD1310587	0.703	0.338	0.667	0.428	0.963	0.395	1.187	0.526
1384956_at	AI556490	Similar to hypothetical protein FLJ14345 (predicted)	RGD1566248_predicted	1.125	0.716	1.223	0.868	1.489	0.980	1.589	0.086
1390031_at	BG378798	similar to hypothetical protein FLJ14466	RGD1311873	0.761	0.124	0.966	0.950	1.106	0.744	0.817	0.960
1392463_at	AI576058	similar to hypothetical protein FLJ14503 (predicted)	RGD1564852_predicted	1.001	0.542	0.613	0.010	1.317	0.093	0.933	0.322
1397373_at	AI575906	similar to hypothetical protein FLJ14503 (predicted)	RGD1564852_predicted	0.792	0.563	0.807	0.233	0.953	0.816	0.586	0.063
1374767_at	AI105450	similar to hypothetical protein FLJ14675	RGD1309592	0.684	0.011	0.468	0.048	0.531	0.027	0.678	0.092
1386425_at	H33472	Similar to hypothetical protein FLJ14675	RGD1309592	0.448	0.108	0.253	0.058	0.645	0.271	0.363	0.032
1398020_at	BF393027	Similar to hypothetical protein FLJ14675	RGD1309592	0.618	0.243	0.090	0.014	0.363	0.058	0.094	0.019
1392051_at	BE106315	similar to hypothetical protein FLJ14681 (predicted)	RGD1307907_predicted	0.889	0.451	0.783	0.067	0.863	0.378	0.718	0.050
1373018_at	BM390695	similar to hypothetical protein FLJ14800 (predicted)	RGD1561500_predicted	0.917	0.085	1.052	0.405	1.134	0.357	1.000	0.974
1383118_at	BI288120	similar to hypothetical protein FLJ14803	RGD1309682	0.326	0.010	0.325	0.006	0.383	0.013	0.387	0.263
1374660_at	BM385193	similar to hypothetical protein FLJ20003 (predicted)	RGD1309025_predicted	1.163	0.430	0.849	0.984	1.322	0.085	1.181	0.049
1376898_at	AI172467	Similar to hypothetical protein FLJ20035 (predicted)	RGD1561680_predicted	1.047	0.643	0.950	0.776	0.860	0.365	0.749	0.607
1392680_at	AA900508	Similar to hypothetical protein FLJ20037 (predicted)	RGD1311381_predicted	0.302	0.038	0.276	0.017	0.330	0.084	0.299	0.007
1394940_at	BI294811	similar to hypothetical protein FLJ20037 (predicted)	RGD1311381_predicted	0.203	0.055	0.361	0.004	0.322	0.006	0.530	0.000
1394745_at	AA850950	Similar to hypothetical protein FLJ20037 (predicted)	RGD1311381_predicted	0.469	0.056	0.354	0.067	0.305	0.039	0.313	0.066
1394695_at	BE111700	Similar to hypothetical protein FLJ20037 (predicted)	RGD1311381_predicted	0.597	0.170	2.266	0.005	0.640	0.128	2.245	0.028
1383496_at	BM387466	similar to hypothetical protein FLJ20171 (predicted)	RGD1560481_predicted	1.216	0.102	2.611	0.001	1.503	0.006	2.530	0.000
1382596_a_at	AI230388	similar to hypothetical protein FLJ20254	RGD1311324	0.634	0.007	0.683	0.084	0.689	0.040	0.697	0.053
1394530_at	AW535733	Similar to hypothetical protein FLJ20259 (predicted)	RGD1311095_predicted	1.720	0.430	1.440	0.050	0.800	0.464	1.455	0.150
1374227_at	BM386851	similar to hypothetical protein FLJ20272 (predicted)	RGD1305264_predicted	0.997	0.816	1.279	0.155	0.999	0.709	1.025	0.714
1374719_at	BF285339	Similar to hypothetical protein FLJ20302; similar to CG31653-PA (predicted)	RGD1307264_predicted	1.248	0.686	1.791	0.015	0.691	0.283	1.361	0.132
1377745_at	BE349673	similar to hypothetical protein FLJ20331	LOC310946	0.502	0.026	1.362	0.075	0.672	0.284	1.131	0.117
1382321_at	AI071312	Similar to hypothetical protein FLJ20422 (predicted)	RGD1307703_predicted	0.409	0.005	0.519	0.104	0.600	0.050	0.708	0.051
1388564_at	BF283612	similar to hypothetical protein FLJ20436	RGD1303127	1.139	0.079	2.149	0.001	1.245	0.189	1.794	0.002
1381108_at	BF387399	similar to hypothetical protein FLJ20436	RGD1303127	0.996	0.974	1.325	0.613	1.001	0.994	1.105	0.997
1373492_at	AA964545	similar to hypothetical protein FLJ20487	RGD1309216	0.979	0.974	0.908	0.051	1.228	0.334	0.966	0.620
1388635_at	BE113372	similar to hypothetical protein FLJ20507 (predicted)	RGD1309744_predicted	0.835	0.630	0.746	0.013	0.932	0.353	0.704	0.013
1389317_at	BF417627	similar to hypothetical protein FLJ20507 (predicted)	RGD1309744_predicted	0.921	0.915	1.255	0.089	0.852	0.871	1.177	0.451
1384330_at	AI763467	similar to hypothetical protein FLJ20546	LOC303067	0.645	0.509	1.687	0.092	0.469	0.033	1.137	0.464
1391530_a_at	BI291880	similar to hypothetical protein FLJ20604 /// similar to hypothetical protein FLJ20604	RGD1311092 /// LOC498451	0.738	0.641	1.451	0.118	1.309	0.303	3.143	0.038
1373248_at	BI292079	Similar to hypothetical protein FLJ20674 (predicted)	RGD1565800_predicted	1.028	0.747	0.892	0.096	0.892	0.750	0.785	0.098
1392454_at	BI296999	similar to hypothetical protein FLJ20729 (predicted)	RGD1308723_predicted	2.121	0.219	2.161	0.012	2.697	0.006	2.474	0.002
1382253_at	BF419062	similar to hypothetical protein FLJ21103	RGD1307173	1.041	0.809	0.974	0.808	1.034	0.384	0.911	0.936
1382117_at	BF417345	similar to hypothetical protein FLJ21148 (predicted)	RGD1560538_predicted	0.411	0.013	2.307	0.006	0.196	0.049	2.658	0.001
1392109_at	BG671422	Similar to hypothetical protein FLJ21439 (predicted)	RGD1562529_predicted	0.613	0.010	0.921	0.259	0.528	0.103	0.979	0.969
1376695_at	BE108967	similar to hypothetical protein FLJ21816 (predicted)	RGD1304759_predicted	1.020	0.914	0.590	0.021	1.007	0.752	0.628	0.044
1380943_at	BI301460	similar to hypothetical protein FLJ21820	RGD1311648	0.904	0.508	0.697	0.013	1.281	0.266	0.921	0.606
1372670_at	BI281686	similar to hypothetical protein FLJ21827	RGD1307682	0.506	0.061	0.348	0.014	0.304	0.048	0.326	0.064
1395984_at	AI043648	similar to hypothetical protein FLJ21827	RGD1307682	1.038	0.978	0.450	0.026	1.000	0.828	0.454	0.027
1376281_at	BM389698	Similar to hypothetical protein FLJ22349	LOC500909	1.268	0.112	1.084	0.063	1.234	0.569	1.045	0.426
1393804_at	BF388537	similar to hypothetical protein FLJ22490 (predicted)	RGD1307055_predicted	0.906	0.511	0.857	0.310	0.780	0.289	0.861	0.449
1379343_at	BF404452	similar to hypothetical protein FLJ22555	MGC94335	1.175	0.567	1.029	0.826	1.161	0.118	1.020	0.713
1367510_at	BG381690	similar to hypothetical protein FLJ22625	RGD1304696	0.435	0.483	0.465	0.004	0.473	0.015	0.424	0.005
1394891_at	BF548290	Similar to hypothetical protein FLJ22965 (predicted)	RGD1564541_predicted	1.504	0.091	1.198	0.873	1.273	0.281	0.992	0.304
1380185_at	BI303290	Similar to hypothetical protein FLJ22965 (predicted)	RGD1564541_predicted	0.932	0.727	0.695	0.033	1.115	0.823	0.490	0.019
1377854_at	AI406343	similar to hypothetical protein FLJ23375 (predicted)	RGD1305647_predicted	0.918	0.588	2.536	0.000	0.709	0.006	2.248	0.013
1374042_at	BG378161	similar to hypothetical protein FLJ23451 (predicted)	RGD1310453_predicted	0.904	0.141	1.473	0.033	1.210	0.699	1.035	0.433
1372338_at	AI599079	similar to hypothetical protein FLJ25059 (predicted)	RGD1565697_predicted	0.610	0.130	0.594	0.045	0.657	0.010	0.724	0.127
1386795_at	BF291091	similar to hypothetical protein FLJ25530 (predicted)	RGD1305697_predicted	0.654	0.007	0.169	0.000	0.643	0.326	0.184	0.046
1382235_at	BF549700	similar to hypothetical protein FLJ30596 (predicted)	RGD1306809_predicted	0.813	0.365	1.998	0.092	1.442	0.012	2.348	0.041
1375460_at	BE113248	similar to hypothetical protein FLJ30656 (predicted)	RGD1309441_predicted	0.779	0.088	1.008	0.045	0.621	0.026	0.988	0.549
1389627_at	BF550270	similar to hypothetical protein FLJ31413	RGD1306209	0.911	0.865	0.874	0.239	0.729	0.159	0.631	0.007

1399087_at	AI179711	similar to hypothetical protein FLJ31528	RGD1307410	0.651	0.104	1.011	0.235	1.096	0.394	0.544	0.042
1381924_at	BF412180	similar to hypothetical protein FLJ31606 (predicted)	RGD1561507_predicted	1.444	0.167	1.020	0.891	1.020	0.918	1.029	0.868
1391929_at	AI231461	Similar to hypothetical protein FLJ31846 (predicted)	RGD1306118_predicted	1.449	0.566	0.777	0.950	0.735	0.627	1.319	0.100
1383951_at	BE108661	similar to hypothetical protein FLJ31951 (predicted)	RGD1309561_predicted	0.443	0.009	0.777	0.131	0.625	0.050	0.934	0.716
1377178_at	AA998606	similar to hypothetical protein FLJ32356 (predicted)	RGD1310656_predicted	1.098	0.590	0.936	0.783	1.001	0.984	0.938	0.654
1398618_s_at	AW435170	Similar to hypothetical protein FLJ32743 (predicted)	RGD1306734_predicted	1.062	0.781	1.061	0.285	1.200	0.160	1.128	0.245
1393818_s_at	BE102234	similar to hypothetical protein FLJ32796 (predicted)	RGD1311142_predicted	0.960	0.999	0.926	0.075	1.015	0.888	0.999	0.929
1379636_at	AW528443	similar to hypothetical protein FLJ32954	LOC313840	1.080	0.558	0.886	0.387	1.004	0.977	0.554	0.011
1376776_at	AW915484	similar to hypothetical protein FLJ33084	LOC500528	0.821	0.303	0.307	0.047	0.622	0.054	0.365	0.013
1374076_at	AI408984	similar to hypothetical protein FLJ34389 (predicted)	RGD1305243_predicted	3.029	0.048	0.872	0.652	1.820	0.031	1.190	1.000
1392389_at	BF389942	Similar to hypothetical protein FLJ34389 (predicted)	RGD1305243_predicted	0.970	0.801	1.175	0.980	0.939	0.589	1.068	0.331
1372909_at	BE112384	similar to hypothetical protein FLJ36090 (predicted)	RGD1565619_predicted	0.480	0.058	0.784	0.110	0.678	0.259	1.060	0.548
1382420_at	AI146080	Similar to hypothetical protein FLJ37440 (predicted)	RGD1310131_predicted	1.577	0.353	0.523	0.026	1.888	0.769	0.566	0.039
1389182_at	AI603132	similar to hypothetical protein FLJ37953 (predicted)	RGD1311269_predicted	0.905	0.362	1.612	0.099	1.241	0.179	1.371	0.498
1384149_at	H32531	similar to hypothetical protein FLJ38348 (predicted)	RGD1311424_predicted	1.405	0.025	1.613	0.022	1.014	0.887	0.987	0.098
1390124_at	AA801136	similar to hypothetical protein FLJ38426 (predicted)	RGD1564603_predicted	0.896	0.816	1.741	0.009	0.705	0.892	1.143	0.044
1371932_at	AI232287	similar to hypothetical protein FLJ38482	RGD1309341	1.480	0.275	1.956	0.018	1.656	0.079	1.963	0.006
1393074_at	BF406819	Similar to hypothetical protein FLJ38984 (predicted)	RGD1563072_predicted	0.883	0.258	1.379	0.090	1.002	0.993	1.216	0.095
1380314_at	BI290787	similar to hypothetical protein FLJ38984 (predicted)	RGD1563072_predicted	0.999	0.956	0.906	0.597	0.988	0.884	0.844	0.387
1396200_at	BF419037	similar to hypothetical protein FLJ40283 (predicted)	RGD1305898_predicted	0.685	0.131	1.112	0.113	0.751	0.147	0.929	0.087
1384008_at	AI555224	Similar to hypothetical protein FLJ40283 (predicted)	RGD1305898_predicted	1.288	0.164	1.100	0.829	1.409	0.017	0.903	0.432
1398647_at	BI288939	Similar to hypothetical protein FLJ40283 (predicted)	RGD1305898_predicted	1.152	0.239	1.130	0.198	1.378	0.032	1.080	0.178
1380419_at	BF287246	Similar to hypothetical protein FLJ90013 (predicted)	RGD1309656_predicted	0.990	0.994	0.857	0.867	0.719	0.036	0.657	0.498
1397806_at	BF406662	similar to hypothetical protein FLJ90652	LOC293494	0.880	0.793	1.296	0.093	0.917	0.789	0.999	0.999
1396796_at	BF392949	Similar to hypothetical protein FLJ90709	RGD1311881	1.444	0.857	0.853	0.582	1.187	0.136	0.660	0.854
1390514_at	BI295160	similar to hypothetical protein from BCRA2 region	MGC94223	1.573	0.006	1.992	0.001	1.409	0.002	1.782	0.008
1383179_at	BI291413	Similar to hypothetical protein HSPC129	RGD1309219	1.536	0.055	3.031	0.001	1.207	0.048	2.108	0.003
1375697_at	AI407016	similar to Hypothetical protein KIAA0152	RGD1307736	0.714	0.658	1.663	0.020	0.654	0.008	0.869	0.135
1379046_at	BI290140	similar to Hypothetical protein KIAA0152	RGD1307736	0.666	0.780	1.555	0.063	0.731	0.083	0.834	0.696
1380907_at	BE109785	Similar to Hypothetical protein KIAA0297/KIAA0329 (predicted)	RGD1307503_predicted	1.079	0.996	1.054	0.378	1.093	0.091	0.874	0.682
1383883_at	BG380058	Similar to Hypothetical protein KIAA0469 (predicted)	RGD1309644_predicted	0.995	0.989	0.949	0.390	1.019	0.182	0.957	0.292
1384153_at	BF415575	similar to Hypothetical protein KIAA0555 (predicted)	RGD1559742_predicted	1.334	0.373	1.263	0.741	1.208	0.287	1.612	0.217
1393089_at	BI295973	similar to Hypothetical protein KIAA0586 (predicted)	RGD1311562_predicted	0.836	0.451	1.001	0.828	1.008	0.686	0.972	0.883
1384886_at	AW523423	similar to hypothetical protein LOC168850 (predicted)	RGD1560157_predicted	1.066	0.530	0.825	0.048	0.943	0.353	0.927	0.472
1383624_at	BF420279	similar to hypothetical protein LOC284018 isoform b (predicted)	RGD1565033_predicted	0.654	0.040	0.505	0.032	0.376	0.023	0.500	0.140
1390226_at	AI408343	similar to hypothetical protein LOC340061 (predicted)	RGD1562552_predicted	3.047	0.012	5.430	0.001	3.553	0.009	3.264	0.002
1374211_at	BG380798	similar to Hypothetical protein LOC73072 (predicted)	RGD1566084_predicted	0.272	0.098	0.679	0.024	0.344	0.109	0.661	0.142
1382471_at	AI709698	similar to hypothetical protein MGC10993	RGD1310320	0.412	0.021	0.912	0.105	0.176	0.006	1.693	0.097
1372971_at	BI291301	similar to Hypothetical protein MGC11690	RGD1305178	0.685	0.152	1.362	0.274	0.587	0.001	0.918	0.557
1379977_at	AI176858	similar to hypothetical protein MGC13024	RGD1306538	0.418	0.032	0.562	0.073	0.535	0.070	0.449	0.010
1374258_at	BF394021	Similar to hypothetical protein MGC13138 (predicted)	RGD1306928_predicted	0.978	0.818	0.925	0.358	0.979	0.825	0.979	0.443
1388683_at	AI411174	similar to hypothetical protein MGC14151 (predicted)	RGD1559617_predicted	0.599	0.067	0.984	0.121	0.684	0.038	1.017	0.200
1395351_at	BF543381	Similar to hypothetical protein MGC14151 (predicted)	RGD1559617_predicted	0.699	0.110	0.442	0.047	0.541	0.053	0.373	0.109
1379323_at	BE109498	similar to hypothetical protein MGC14327 (predicted)	RGD1306304_predicted	0.208	0.045	0.427	0.016	0.205	0.011	0.442	0.121
1389124_at	AI009814	similar to hypothetical protein MGC15396 (predicted)	RGD1310602_predicted	0.873	0.528	0.412	0.004	0.663	0.243	0.532	0.017
1373806_at	AI044859	similar to hypothetical protein MGC15407	RGD1311732	0.438	0.068	0.288	0.000	0.421	0.002	0.286	0.001
1394424_at	AI547622	similar to hypothetical protein MGC15407	RGD1311732	0.539	0.334	0.216	0.003	0.423	0.075	0.286	0.007
1399102_at	BG377901	similar to hypothetical protein MGC15523	RGD1306356	0.328	0.063	0.457	0.004	0.378	0.024	0.462	0.002
1373853_at	AI705797	similar to hypothetical protein MGC15716	RGD1308123	0.622	0.108	0.338	0.000	0.410	0.025	0.406	0.022
1388789_at	AI410352	similar to hypothetical protein MGC17943 (predicted)	RGD1563325_predicted	0.584	0.596	0.797	0.022	0.739	0.346	0.650	0.031
1392942_at	BM383823	similar to hypothetical protein MGC17943 (predicted)	RGD1563325_predicted	1.223	0.926	0.450	0.307	0.697	0.097	0.437	0.311
1372866_at	BM386202	similar to hypothetical protein MGC18873	RGD1311914	0.730	0.142	2.890	0.000	0.919	0.195	1.874	0.000
1372496_at	BG371538	similar to hypothetical protein MGC19604 (predicted)	RGD1561264_predicted	0.551	0.665	3.260	0.001	0.682	0.086	1.852	0.003
1373730_at	BI282077	Similar to hypothetical protein MGC20460 (predicted)	RGD1310651_predicted	1.756	0.302	4.172	0.001	1.047	0.733	3.782	0.001
1377793_at	BF407551	similar to hypothetical protein MGC20460 (predicted)	RGD1310651_predicted	1.087	0.718	0.910	0.815	1.492	0.824	0.881	0.267
1383198_at	AI598511	similar to hypothetical protein MGC20460 (predicted)	RGD1310651_predicted	0.926	0.902	1.084	0.746	0.500	0.278	0.688	0.635
1374899_at	BM383043	similar to hypothetical protein MGC20579 (predicted)	RGD1566042_predicted	0.448	0.514	0.212	0.084	0.562	0.390	0.186	0.094
1374670_at	BM384543	similar to hypothetical protein MGC20700 (predicted)	RGD1307722_predicted	3.432	0.002	2.520	0.008	9.022	0.003	2.794	0.005
1372807_at	BF402462	similar to hypothetical protein MGC21688 (predicted)	RGD1310480_predicted	0.980	0.342	0.498	0.061	1.932	0.071	0.690	0.028
1372786_at	BF284299	similar to hypothetical protein MGC2494	RGD1306126	0.950	0.219	0.419	0.040	0.981	0.213	0.589	0.026
1390620_at	BI278605	similar to Hypothetical protein MGC25529 (predicted)	RGD1306746_predicted	0.759	0.094	0.705	0.042	0.720	0.130	1.191	0.544

1397255_at	AW533685	similar to hypothetical protein MGC2574	MGC94720	0.641	0.294	2.275	0.278	0.373	0.089	1.849	0.088
1378958_at	AA998314	similar to hypothetical protein MGC2574	MGC94720	0.680	0.352	1.557	0.023	0.508	0.021	1.848	0.001
1375551_at	BG379782	similar to hypothetical protein MGC2574	MGC94720	0.551	0.895	1.632	0.221	0.465	0.027	1.751	0.028
1389637_at	AI227731	Similar to hypothetical protein MGC26816 (predicted)	RGD1309338_predicted	0.863	0.410	1.022	0.761	0.869	0.460	0.986	0.924
1373135_at	AW531123	similar to hypothetical protein MGC2744	LOC619440	0.631	0.942	0.718	0.873	0.929	0.880	0.803	0.629
1382388_at	AW533941	Similar to hypothetical protein MGC27699 (predicted)	RGD1305013_predicted	0.972	0.847	0.690	0.015	1.001	0.990	0.728	0.008
1380872_at	BF396681	Similar to hypothetical protein MGC2817 (predicted)	RGD1562449_predicted	0.907	0.133	0.194	0.019	0.654	0.018	0.337	0.014
1371550_at	AW533431	Similar to Hypothetical protein MGC28888	LOC304361	1.693	0.021	1.314	0.182	2.317	0.005	1.505	0.599
1377159_at	BE120729	Similar to Hypothetical protein MGC28888	LOC304361	1.656	0.611	0.969	0.532	1.876	0.429	1.159	0.315
1372198_at	BG376471	similar to Hypothetical protein MGC28888	LOC304361	0.962	0.820	0.636	0.047	0.634	0.810	0.672	0.051
1372034_at	BF284106	Similar to hypothetical protein MGC29390 (predicted)	RGD1310490_predicted	23.406	0.000	11.803	0.002	52.253	0.001	26.183	0.003
1379613_at	BM390301	Similar to hypothetical protein MGC29390 (predicted)	RGD1310490_predicted	22.986	0.000	5.223	0.003	49.883	0.000	13.019	0.000
1390035_at	BI297073	similar to hypothetical protein MGC29875; novel putative protein similar to YIL091C yeast hypothetical 84 kD protein from SGA1-KTR7	LOC305076	0.982	0.735	0.980	0.929	0.914	0.012	1.044	0.577
1373209_at	AI599284	Similar to hypothetical protein MGC30618	RGD1305572	1.218	0.348	1.128	0.586	1.161	0.488	1.234	0.782
1372980_at	AA819250	similar to Hypothetical protein MGC30714 (predicted)	RGD1560915_predicted	0.594	0.011	0.539	0.010	0.472	0.005	0.604	0.126
1389559_at	AA892872	similar to Hypothetical protein MGC31278 (predicted)	RGD1564420_predicted	1.151	0.270	2.005	0.000	0.887	0.619	1.738	0.000
1390101_at	AI170609	similar to hypothetical protein MGC31967 (predicted)	RGD1560252_predicted	0.510	0.004	0.329	0.004	0.452	0.001	0.394	0.101
1379826_at	AA859429	similar to hypothetical protein MGC31967 (predicted)	RGD1560252_predicted	0.448	0.064	0.161	0.008	0.420	0.007	0.283	0.009
1376134_at	BI277596	similar to hypothetical protein MGC3207	RGD1307789	0.729	0.427	0.552	0.147	0.668	0.115	0.655	0.253
1392488_at	AI168950	Similar to hypothetical protein MGC32132 (predicted)	RGD1307915_predicted	0.904	0.653	1.016	0.841	1.338	0.254	1.015	0.774
1397251_at	BF389812	Similar to hypothetical protein MGC32132 (predicted)	RGD1307915_predicted	1.296	0.834	1.015	0.083	0.755	0.453	0.938	0.946
1378338_at	BE103735	similar to hypothetical protein MGC32132 (predicted)	RGD1307915_predicted	0.991	0.900	2.728	0.061	0.968	0.534	1.463	0.148
1374605_at	AA818020	similar to hypothetical protein MGC33214 (predicted)	RGD1309660_predicted	0.971	0.541	1.277	0.088	1.008	0.967	1.516	0.019
1375513_at	BG376846	Similar to hypothetical protein MGC33214 (predicted)	RGD1309660_predicted	0.919	0.782	1.045	0.347	0.976	0.925	1.351	0.353
1376904_at	AI716115	similar to hypothetical protein MGC33486 (predicted)	RGD1310680_predicted	19.250	0.011	2.353	0.025	14.190	0.005	5.376	0.004
1390801_at	AI412174	similar to hypothetical protein MGC34760	RGD1359349	1.487	0.057	0.919	0.780	2.474	0.018	1.328	0.254
1370901_at	AI407120	similar to hypothetical protein MGC36831 (predicted)	RGD1306215_predicted	0.490	0.051	1.098	0.475	0.373	0.002	0.744	0.182
1378606_at	AI010216	similar to hypothetical protein MGC37079 (predicted)	RGD1310484_predicted	0.874	0.170	0.618	0.002	0.824	0.043	0.642	0.007
1392993_at	BG665293	similar to hypothetical protein MGC37079 (predicted)	RGD1310484_predicted	1.186	0.213	0.741	0.006	1.092	0.405	0.669	0.001
1374249_at	AI168962	similar to Hypothetical protein MGC38513	RGD1304580	0.564	0.054	0.643	0.037	0.811	0.075	0.557	0.069
1373251_at	BI289957	similar to hypothetical protein MGC38837	LOC499671	0.595	0.038	0.745	0.230	0.696	0.166	0.826	0.787
1393352_at	BI293882	similar to hypothetical protein MGC38960 (predicted)	RGD1310552_predicted	0.641	0.015	0.619	0.012	0.573	0.045	0.548	0.010
1374574_at	AI547611	Similar to hypothetical protein MGC38960 (predicted)	RGD1310552_predicted	0.587	0.024	0.234	0.006	0.858	0.545	0.456	0.028
1398425_at	AI101458	similar to hypothetical protein MGC39325-like protein	MGC109194	0.456	0.548	0.826	0.127	0.750	0.067	0.805	0.206
1373574_at	BI285607	similar to hypothetical protein MGC40499 (predicted)	RGD1307636_predicted	1.075	0.968	0.760	0.037	1.147	0.904	0.331	0.092
1392014_at	BF416257	Similar to hypothetical protein MGC40841; similar to hypothetical protein MGC4707	RGD1309540	1.569	0.405	0.902	0.907	1.279	0.843	0.957	0.696
1382770_at	BG376622	similar to hypothetical protein MGC52110 (predicted)	RGD1565095_predicted	0.734	0.491	1.132	0.460	0.575	0.086	1.067	0.657
1393512_at	AA957880	Similar to hypothetical protein MGC5297	RGD1309729	2.046	0.077	1.280	0.034	1.020	0.897	1.237	0.236
1384011_a_at	BF287623	similar to hypothetical protein MGC5297	RGD1309729	1.151	0.712	0.982	0.918	2.169	0.012	1.299	0.568
1381057_at	AW526130	Similar to hypothetical protein MGC5391 (predicted)	RGD1561764_predicted	0.469	0.028	0.954	0.751	0.674	0.063	0.830	0.288
1389114_at	AW523874	similar to Hypothetical protein MGC59076	RGD1309144	0.997	0.988	0.575	0.012	0.999	0.416	0.726	0.064
1373299_at	BI295816	similar to hypothetical protein MGC6696	RGD1309471	1.484	0.168	1.903	0.016	1.634	0.000	2.148	0.010
1388499_at	AW531384	similar to hypothetical protein MGC7537	RGD1359380	0.748	0.104	1.034	0.692	0.903	0.552	0.971	0.732
1392538_at	BE110656	similar to Hypothetical protein MGC75937 (predicted)	RGD1562826_predicted	0.948	0.077	1.810	0.031	1.171	0.184	1.211	0.262
1373388_at	BI279290	Similar to Hypothetical protein MGC75937 (predicted)	RGD1562826_predicted	1.232	0.086	1.001	0.078	1.231	0.234	0.954	0.781
1378201_at	BF392915	Similar to Hypothetical protein MGC75937 (predicted)	RGD1562826_predicted	0.987	0.865	1.001	0.968	0.997	0.975	0.997	0.934
1390653_at	AI171174	similar to hypothetical protein MGC9907	RGD1307393	0.954	0.373	1.365	0.181	1.330	0.129	1.527	0.092
1376581_at	AW433895	similar to hypothetical protein MGC9912 (predicted)	RGD1309138_predicted	0.470	0.031	0.544	0.019	0.651	0.074	1.274	0.222
1372329_at	BM389011	similar to hypothetical protein PRO0971	RGD1311435	2.483	0.007	2.419	0.017	2.382	0.004	1.750	0.027
1382682_at	AI172217	Similar to hypothetical protein PRO0971	RGD1311435	2.429	0.090	1.779	0.125	3.959	0.099	1.356	0.092
1376209_at	BG669208	similar to hypothetical protein supported by AL449243 (predicted)	RGD1311310_predicted	0.884	0.628	1.125	0.921	0.731	0.077	1.094	0.521
1367523_at	AI409145	similar to hypothetical protein, 2-6 (predicted)	RGD1304906_predicted	0.883	0.575	2.268	0.023	0.443	0.015	1.968	0.000
1389343_at	H35203	similar to Hypothetical UPF0327 protein (predicted)	RGD1560187_predicted	0.667	0.504	1.017	0.259	0.747	0.073	0.966	1.000
1383579_at	BE109121	Similar to IKEN cDNA 6720480D16	LOC502282	1.154	0.244	0.828	0.595	1.005	0.977	1.060	0.402
1375285_at	AI407169	Similar to IL-17D (predicted)	RGD1563436_predicted	1.001	0.995	1.047	0.510	1.000	0.945	1.156	0.366
1371284_at	AJ391310	similar to immunoglobulin 4G6 heavy chain variable region (predicted)	RGD1564284_predicted	1.007	0.988	0.998	0.972	1.000	0.995	1.023	0.596
1393366_at	BF521857	Similar to Inner nuclear membrane protein Man1 (LEM domain containing protein 3) (predicted)	RGD1561001_predicted	0.783	0.103	0.549	0.074	0.721	0.127	0.651	0.264
1398599_at	BG664929	similar to integral membrane protein 1 (predicted)	RGD1565793_predicted	0.977	0.108	0.960	0.806	0.924	0.199	1.021	0.983
1377950_at	AA955213	similar to interferon-inducible GTPase	RGD1309362	63.412	0.001	29.135	0.009	235.043	0.001	142.184	0.006
1392637_at	AA923988	Similar to interferon-inducible GTPase	MGC108823	33.348	0.018	13.693	0.013	78.149	0.006	38.101	0.001

1373992_at	AI408440	similar to interferon-inducible GTPase /// similar to MGC108823 protein (predicted) /// similar to MGC108823 protein	MGC108823 /// RGD1559715_predicted /// LOC498872	140.487	0.000	144.379	0.000	482.198	0.000	370.848	0.001
1371582_at	BM389129	similar to interleukin enhancer binding factor 2	LOC310612	0.972	0.782	1.284	0.018	0.827	0.007	1.071	0.032
1382551_at	BF417645	similar to Intersectin 2 (SH3 domain-containing protein 1B) (SH3P18) (SH3P18-like WASP associated protein)	LOC313934	1.362	0.034	1.678	0.033	1.247	0.431	1.302	0.245
1377903_at	AI408914	Similar to Intersectin 2 (SH3 domain-containing protein 1B) (SH3P18) (SH3P18-like WASP associated protein)	LOC313934	0.842	0.097	0.642	0.049	0.692	0.091	0.919	0.447
1396256_at	AI045614	similar to Intersectin 2 (SH3 domain-containing protein 1B) (SH3P18) (SH3P18-like WASP associated protein)	LOC313934	1.144	0.458	1.009	0.427	0.665	0.277	0.759	0.317
1379459_at	BI301276	similar to intracellular membrane-associated calcium-independent phospholipase A2 gamma (predicted)	RGD1311444_predicted	1.121	0.344	0.563	0.835	1.000	0.996	0.512	0.140
1395725_at	BF557088	similar to intracellular membrane-associated calcium-independent phospholipase A2 gamma (predicted)	RGD1311444_predicted	0.975	0.447	0.964	0.075	1.091	0.908	0.889	0.020
1394234_x_at	AA848540	Similar to IQ motif and WD repeats 1 (predicted)	RGD1561961_predicted	0.490	0.016	0.450	0.023	0.641	0.167	0.411	0.036
1377807_a_at	BF389856	Similar to IQ motif and WD repeats 1 (predicted)	RGD1561961_predicted	0.688	0.046	0.652	0.189	0.621	0.319	0.474	0.093
1390852_x_at	BF389856	Similar to IQ motif and WD repeats 1 (predicted)	RGD1561961_predicted	0.613	0.061	0.481	0.123	0.682	0.228	0.358	0.079
1386473_at	AA848540	similar to IQ motif and WD repeats 1 (predicted)	RGD1561961_predicted	0.750	0.163	0.516	0.004	0.495	0.136	0.529	0.047
1377808_at	BF389856	Similar to IQ motif and WD repeats 1 (predicted)	RGD1561961_predicted	0.573	0.185	0.496	0.076	0.737	0.316	0.331	0.080
1395232_at	AI011035	similar to IQ motif and WD repeats 1 (predicted)	RGD1561961_predicted	0.760	0.283	0.336	0.077	0.852	0.601	0.309	0.070
1384402_a_at	H31119	similar to IQ motif and WD repeats 1 (predicted)	RGD1561961_predicted	0.711	0.514	0.245	0.099	1.079	0.770	0.167	0.035
1385546_at	AA998195	similar to IQ motif and WD repeats 1 (predicted)	RGD1561961_predicted	0.843	0.752	0.861	0.671	0.651	0.277	0.688	0.055
1383312_at	BF396751	Similar to JM11 protein (predicted)	RGD1561596_predicted	1.292	0.011	0.991	0.946	1.281	0.193	0.968	0.531
1382051_at	AA955489	similar to J-type co-chaperone HSC20 (predicted)	RGD1311005_predicted	0.993	0.500	1.005	0.743	0.923	0.235	1.158	0.186
1393199_at	AA955145	similar to Jumonji/ARID domain-containing protein 1C (SmcX protein) (predicted) /// similar to Jumonji/ARID domain-containing protein 1C (SmcX protein) (predicted)	RGD1560601_predicted /// RGD1566193_predicted	0.956	0.812	2.335	0.052	0.888	0.912	1.004	0.686
1377818_at	AW532426	Similar to junction-mediating and regulatory protein (predicted)	RGD1563506_predicted	1.484	0.311	1.319	0.424	1.563	0.141	1.340	0.174
1375887_at	BI282089	similar to kaiso protein (predicted)	RGD1566309_predicted	0.920	0.725	0.650	0.089	0.966	0.690	0.829	0.240
1373968_at	AI176016	Similar to KB07 protein (predicted)	RGD1561940_predicted	1.011	0.880	1.301	0.065	0.757	0.012	1.052	0.193
1384788_at	BF393298	similar to KCCR13L (predicted)	RGD1310193_predicted	0.494	0.013	0.786	0.045	0.480	0.005	0.695	0.082
1396556_at	BF413366	Similar to KCNMA1 protein	LOC498438	1.201	0.939	1.678	0.020	1.003	0.946	1.507	0.066
1376730_at	BE103377	Similar to kelch/ankyrin repeat containing cyclin A1 interacting protein isoform a (predicted)	RGD1561025_predicted	0.761	0.022	0.664	0.065	0.709	0.092	0.652	0.051
1392340_at	BF416150	similar to Kelch-like protein 3 (predicted)	RGD1565218_predicted	0.707	0.964	0.880	0.741	0.845	0.659	0.861	0.680
1399124_at	AI598517	similar to KIAA0090 protein (predicted)	RGD1310427_predicted	0.690	0.102	0.531	0.003	0.759	0.197	0.456	0.010
1382364_at	BI293914	similar to KIAA0090 protein (predicted)	RGD1310427_predicted	1.106	0.619	0.460	0.008	0.970	0.709	0.385	0.012
1389717_at	AI171467	similar to KIAA0157 gene product is novel. (predicted)	RGD1308918_predicted	0.673	0.559	0.772	0.166	0.934	0.457	0.870	0.729
1398607_at	AI717510	Similar to KIAA0240 (predicted)	RGD1305680_predicted	0.782	0.356	0.827	0.240	0.479	0.166	0.591	0.004
1394405_at	AI232356	Similar to KIAA0303 (predicted)	RGD1310139_predicted	2.515	0.005	1.508	0.028	1.788	0.017	1.253	0.065
1379114_at	BF412325	Similar to KIAA0303 (predicted)	RGD1310139_predicted	3.578	0.013	1.053	0.591	3.382	0.104	0.423	0.131
1384940_at	AI136655	similar to KIAA0335	RGD1305314	0.745	0.476	0.817	0.043	0.795	0.945	0.882	0.349
1373292_at	AI176553	similar to KIAA0339 protein	RGD1311624	0.996	0.852	1.221	0.089	0.869	0.239	1.132	0.184
1393683_at	BF415479	similar to KIAA0368 (predicted)	RGD1306148_predicted	1.425	0.001	1.121	0.635	1.569	0.003	0.999	0.997
1389277_at	BI285258	similar to KIAA0368 (predicted)	RGD1306148_predicted	1.038	0.266	1.578	0.084	1.419	0.598	1.243	0.088
1395875_at	BG379050	similar to KIAA0372 gene product (predicted)	RGD1306062_predicted	0.743	0.587	1.125	0.404	0.841	0.101	0.934	0.137
1390876_at	BM386308	similar to KIAA0377-like protein (predicted)	RGD1311552_predicted	1.713	0.036	1.702	0.430	1.232	0.410	1.304	0.326
1393065_at	BI276770	similar to KIAA0406-like protein (predicted)	RGD1562582_predicted	0.670	0.131	0.365	0.000	0.527	0.056	0.467	0.011
1384172_at	BF398262	Similar to KIAA0423 (predicted)	RGD1310474_predicted	0.974	0.643	0.870	0.377	1.235	0.080	1.163	0.078
1386217_at	AI639048	similar to KIAA0423 (predicted)	RGD1310474_predicted	1.043	0.715	1.000	0.997	1.039	0.423	0.972	0.724
1378831_at	BE108135	Similar to KIAA0456 protein (predicted)	RGD1566016_predicted	1.540	0.048	1.220	0.833	0.950	0.397	1.033	0.719
1381126_at	BE099652	similar to KIAA0456 protein (predicted)	RGD1566016_predicted	0.953	0.752	2.453	0.001	0.956	0.758	1.531	0.018
1398224_at	BF393183	Similar to KIAA0456 protein (predicted)	RGD1566016_predicted	0.999	0.976	1.007	0.296	1.498	0.051	1.009	0.980
1395958_at	BF396619	similar to KIAA0460 protein (predicted)	RGD1308268_predicted	0.810	0.600	1.105	0.291	0.546	0.013	1.124	0.785
1384384_at	BF543289	similar to KIAA0528 protein (predicted)	RGD1304592_predicted	0.771	0.067	1.415	0.096	0.734	0.301	1.617	0.113
1390338_at	BG373138	similar to KIAA0556 protein	LOC361646	0.976	0.929	1.154	0.214	1.018	0.642	1.258	0.046
1383933_at	AI136714	Similar to KIAA0564 protein (predicted)	RGD1308772_predicted	0.642	0.020	0.497	0.000	0.534	0.019	0.587	0.015
1380431_at	AA893000	similar to KIAA0564 protein (predicted)	RGD1308772_predicted	0.731	0.164	0.308	0.114	0.642	0.097	0.655	0.407
1393230_s_at	AI136714	Similar to KIAA0564 protein (predicted)	RGD1308772_predicted	0.804	0.251	0.710	0.071	0.699	0.087	0.754	0.100
1372395_at	AA850978	Similar to KIAA0597 protein (predicted)	RGD1565757_predicted	0.442	0.035	0.816	0.034	0.350	0.003	0.717	0.053
1381715_at	BE107590	Similar to KIAA0605 gene product (predicted)	RGD1305459_predicted	1.233	0.233	1.074	0.978	1.202	0.505	0.999	0.730
1398691_at	AI408578	Similar to KIAA0669 gene product	LOC499624	1.900	0.977	1.556	0.018	0.926	0.104	1.658	0.045
1373581_at	BG380767	Similar to KIAA0672 gene product	RGD1305664	1.779	0.135	1.704	0.027	2.466	0.077	2.364	0.001
1383677_at	AA925701	Similar to KIAA0794 protein (predicted)	RGD1306346_predicted	0.745	0.441	0.825	0.081	0.632	0.175	1.376	0.183
1384416_at	BE115686	Similar to KIAA0794 protein (predicted)	RGD1306346_predicted	1.263	0.944	0.897	0.862	1.103	0.640	1.042	0.757
1376104_at	BG381010	Similar to KIAA0802 protein (predicted)	RGD1308319_predicted	0.907	0.231	0.664	0.017	0.711	0.074	0.649	0.045
1389636_at	AI231088	similar to KIAA0833 protein	LOC362665	0.806	0.241	0.972	0.847	0.567	0.016	1.154	0.879
1379664_at	BF419602	similar to KIAA0853 protein (predicted)	RGD1307729_predicted	1.472	0.024	2.403	0.079	1.632	0.026	1.498	0.078

1382080_at	AW523680	similar to KIAA0853 protein (predicted)	RGD1563689_predicted	1.381	0.100	1.802	0.003	1.226	0.165	1.688	0.028
1395154_at	BI288548	similar to KIAA0853 protein (predicted)	RGD1307729_predicted	1.050	0.627	0.935	0.190	1.339	0.122	0.722	0.901
1379027_at	BM390702	similar to KIAA0869 protein (predicted)	RGD1308329_predicted	2.349	0.003	2.381	0.109	1.352	0.014	1.996	0.088
1378972_at	AI071547	Similar to KIAA0869 protein (predicted)	RGD1308329_predicted	0.997	0.985	1.822	0.043	0.978	0.765	1.237	0.092
1394439_at	AW523921	similar to KIAA0892 protein (predicted)	RGD1308759_predicted	1.767	0.248	0.867	0.578	0.973	0.989	0.936	0.928
1390315_a_at	AA875438	similar to KIAA0913 protein (predicted)	RGD1309414_predicted	1.724	0.081	0.928	0.290	1.115	0.575	0.972	0.444
1380979_a_at	AW523336	similar to KIAA0913 protein (predicted)	RGD1309414_predicted	1.359	0.573	1.139	0.053	1.087	0.559	1.003	0.939
1376414_x_at	BE109634	similar to KIAA0913 protein (predicted)	RGD1309414_predicted	1.045	0.752	1.093	0.400	1.003	0.963	1.305	0.002
1372629_at	BF285818	similar to KIAA0925 protein	LOC300768	0.727	0.376	0.693	0.050	0.729	0.084	0.618	0.030
1398022_at	BF404957	Similar to KIAA0953 protein (predicted)	RGD1310845_predicted	0.928	0.806	0.789	0.480	0.931	0.780	0.842	0.405
1376560_at	BM388282	Similar to KIAA0962 protein	LOC362652	0.925	0.254	0.277	0.011	1.093	0.867	0.849	0.375
1383299_at	BI291730	Similar to KIAA0965 protein (predicted)	RGD1564793_predicted	0.349	0.053	0.265	0.000	0.983	0.952	0.340	0.014
1373709_at	BI281706	similar to KIAA0974 protein	RGD1359592	0.549	0.211	0.502	0.007	0.740	0.018	0.592	0.099
1397289_at	AI228245	Similar to KIAA0974 protein	RGD1359592	0.748	0.669	1.450	0.327	0.717	0.289	1.013	0.687
1398951_at	BE109021	similar to KIAA1007 protein; adrenal gland protein AD-005	RGD1308009	1.174	0.066	0.981	0.333	1.117	0.059	1.209	0.039
1392727_at	AI235560	similar to KIAA1009 protein	RGD1307365	1.256	0.427	0.712	0.400	1.002	0.616	1.000	0.565
1390838_at	BE115823	similar to KIAA1034-like DNA binding protein (predicted)	RGD1562369_predicted	0.910	0.359	0.996	0.464	0.885	0.708	1.062	0.470
1375091_at	BE111801	similar to KIAA1052 protein (predicted)	RGD1561243_predicted	1.182	0.031	1.091	0.859	1.073	0.997	1.010	0.894
1392468_at	AW526683	similar to KIAA1078 protein (predicted)	RGD1310950_predicted	0.765	0.012	0.599	0.015	0.756	0.021	0.668	0.032
1395080_at	BF389061	Similar to KIAA1078 protein (predicted)	RGD1310950_predicted	0.785	0.127	1.087	0.710	1.499	0.670	1.564	0.068
1397201_at	BE107286	similar to KIAA1078 protein (predicted)	RGD1310950_predicted	0.912	0.201	0.947	0.679	0.909	0.210	1.000	0.995
1384039_at	BF558912	similar to KIAA1078 protein (predicted)	RGD1310950_predicted	0.747	0.696	0.569	0.030	0.809	0.886	0.602	0.062
1392738_at	AI602954	similar to KIAA1096 protein (predicted)	RGD1566064_predicted	0.859	0.124	2.194	0.057	1.368	0.834	1.461	0.323
1398633_at	AI136344	Similar to KIAA1096 protein (predicted)	RGD1566064_predicted	1.256	0.267	0.985	0.879	0.838	0.645	1.028	0.864
1399079_at	AI101659	similar to KIAA1096 protein (predicted)	RGD1307838_predicted	1.049	0.795	1.008	0.121	1.009	0.278	1.048	0.327
1378155_at	BI289641	similar to KIAA1096 protein (predicted)	RGD1566064_predicted	0.794	0.911	0.716	0.546	0.785	0.484	0.962	0.244
1374120_at	BI296223	similar to KIAA1126 protein (predicted)	RGD1309971_predicted	0.973	0.311	1.575	0.609	1.106	0.590	0.713	0.478
1382265_at	AI070061	similar to KIAA1128 protein (predicted)	RGD1304626_predicted	1.004	0.769	1.102	0.221	1.053	0.281	1.000	0.834
1373985_at	BI282311	Similar to KIAA1183 protein (predicted)	RGD1560435_predicted	0.219	0.061	0.086	0.000	0.174	0.056	0.135	0.027
1385491_at	BF403514	similar to KIAA1183 protein (predicted)	RGD1560435_predicted	0.479	0.098	0.223	0.002	0.357	0.135	0.168	0.009
1378978_a_at	AW520354	Similar to KIAA1205 protein (predicted)	RGD1309896_predicted	0.809	0.741	1.422	0.569	0.928	0.306	1.359	0.155
1378979_x_at	AW520354	Similar to KIAA1205 protein (predicted)	RGD1309896_predicted	0.967	0.856	0.787	0.376	0.762	0.834	1.066	0.259
1392593_a_at	AI555789	similar to KIAA1205 protein (predicted)	RGD1309896_predicted	1.193	0.931	0.910	0.475	1.093	0.737	1.219	0.258
1382297_x_at	AI555789	similar to KIAA1205 protein (predicted)	RGD1309896_predicted	0.877	0.978	1.042	0.307	1.112	0.744	1.075	0.566
1380182_at	BF291123	similar to KIAA1217 (predicted)	RGD1563437_predicted	0.768	0.004	0.300	0.004	0.943	0.161	0.477	0.027
1397152_at	BE108638	Similar to KIAA1217 (predicted)	RGD1563437_predicted	1.382	0.789	0.734	0.153	1.633	0.256	1.250	0.359
1383165_at	BM390462	similar to KIAA1324 protein (predicted)	RGD1310209_predicted	0.818	0.180	0.543	0.000	0.814	0.087	0.563	0.002
1394760_at	BF387238	similar to KIAA1409 protein (predicted)	RGD1311117_predicted	0.657	0.097	0.208	0.000	0.897	0.395	0.447	0.085
1382373_at	AA964332	Similar to KIAA1411 protein (predicted)	RGD1304927_predicted	0.759	0.018	0.601	0.103	0.551	0.025	0.918	0.341
1386154_at	AI639161	similar to KIAA1411 protein (predicted)	RGD1304927_predicted	0.730	0.140	0.884	0.015	0.442	0.002	0.931	0.296
1389769_at	BI285697	similar to KIAA1440 protein (predicted)	RGD1308908_predicted	0.647	0.494	1.398	0.141	0.862	0.633	1.088	0.606
1383803_at	BF283176	Similar to KIAA1546 protein (predicted)	RGD1311625_predicted	1.562	0.021	1.072	0.262	1.246	0.365	0.819	0.127
1376260_at	BI274279	similar to KIAA1627 protein (predicted)	RGD1304822_predicted	0.767	0.055	1.386	0.035	0.927	0.294	1.447	0.026
1380900_at	BE120504	Similar to KIAA1731 protein (predicted)	RGD1311723_predicted	0.638	0.027	0.429	0.006	0.464	0.170	0.510	0.042
1397811_at	AI137142	similar to KIAA1731 protein (predicted)	RGD1311723_predicted	0.991	0.415	0.861	0.449	0.914	0.882	0.762	0.020
1380286_x_at	BM386844	similar to KIAA1731 protein (predicted)	RGD1311723_predicted	0.965	0.920	1.271	0.029	1.021	0.984	1.199	0.059
1377245_a_at	AI146147	similar to KIAA1731 protein (predicted)	RGD1311723_predicted	0.972	0.931	1.600	0.015	0.960	0.942	1.304	0.016
1382875_at	BF386519	similar to KIAA1838 protein (predicted)	RGD1310304_predicted	0.702	0.037	1.405	0.034	0.854	0.016	1.138	0.463
1377648_at	BF414047	similar to KIAA1838 protein (predicted)	RGD1310304_predicted	0.740	0.130	0.383	0.009	0.633	0.062	0.394	0.007
1383431_at	BF404209	Similar to KIAA1841 protein (predicted)	RGD1305110_predicted	0.748	0.187	0.800	0.045	0.485	0.035	0.728	0.176
1393909_at	BF544438	similar to KIAA1841 protein (predicted)	RGD1305110_predicted	0.996	0.975	0.784	0.007	1.008	0.917	0.722	0.008
1391805_at	BE096676	Similar to KIAA1900 protein (predicted)	RGD1310364_predicted	1.854	0.012	1.027	0.127	1.908	0.006	1.433	0.141
1391767_at	AI548603	similar to KIAA1919 protein (predicted)	RGD1310495_predicted	1.001	0.258	0.999	0.209	1.002	0.803	1.003	0.890
1385660_at	AA924079	similar to KIAA2010 protein (predicted)	RGD1309059_predicted	1.199	0.287	1.343	0.054	1.406	0.114	1.102	0.380
1394555_at	AI501080	Similar to KIAA2010 protein (predicted)	RGD1309059_predicted	0.904	0.755	1.638	0.365	1.432	0.817	1.088	0.631
1384799_at	BF416137	similar to KIAA2022 protein (predicted)	RGD1561931_predicted	1.040	0.519	0.467	0.045	0.808	0.456	1.005	0.186
1390699_at	BF390453	similar to KIAA2026 protein	RGD1311595	1.186	0.518	1.030	0.801	1.132	0.158	1.363	0.096
1372811_at	BI289779	similar to kinectin (predicted)	RGD1563957_predicted	1.236	0.704	1.304	0.009	1.118	0.156	1.283	0.097
1376451_at	BG377849	similar to krev interaction trapped-1A	LOC362317	1.562	0.006	1.355	0.135	1.773	0.015	1.666	0.057
1396078_at	BF389439	similar to krev interaction trapped-1A	LOC362317	1.066	0.364	1.215	0.188	1.156	0.224	1.108	0.880
1382856_at	BI295313	similar to Ku70-binding protein 3	LOC299828	1.866	0.061	0.807	0.444	1.951	0.008	1.143	0.244

1398887_at	BE113217	similar to Late endosomal/lysosomal Mp1 interacting protein (p14) (predicted)	RGD1562501_predicted	0.692	0.447	0.715	0.062	0.693	0.433	0.900	0.475
1391044_s_at	BM390051	similar to Lck-interacting transmembrane adaptor protein LIME (predicted)	RGD1562795_predicted	0.323	0.111	0.811	0.082	1.252	0.961	0.537	0.038
1378810_at	BE114206	Similar to lemur tyrosine kinase 2	LOC304286	0.902	0.307	1.207	0.090	0.910	0.417	1.162	0.202
1374737_at	AW528218	similar to Lethal giant larvae homolog 2 (predicted)	RGD1560307_predicted	0.912	0.390	2.009	0.038	0.968	0.210	0.947	0.849
1372831_at	BE349838	Similar to leucine zipper, down-regulated in cancer 1; breast cancer, up-regulated 1 (predicted)	RGD1306472_predicted	0.269	0.000	0.287	0.041	0.473	0.004	0.625	0.035
1383342_at	BE098779	similar to Leucine-rich repeat-containing 14	MGC108882	0.747	0.333	0.688	0.033	0.732	0.328	0.882	0.677
1373168_at	BG380214	Similar to LEYDIG CELL TUMOR 10 KD PROTEIN	LOC288913	0.515	0.147	0.902	0.191	0.552	0.018	1.144	0.143
1398316_at	X62277	similar to LEYDIG CELL TUMOR 10 KD PROTEIN	LOC288913	0.856	0.399	1.250	0.233	0.702	0.017	1.760	0.111
1372769_at	AI105290	similar to ligatin	LOC498225	0.703	0.122	1.311	0.138	0.930	0.347	1.413	0.384
1398067_at	BF393939	Similar to LIM domain only 3 (predicted)	RGD1561357_predicted	1.391	0.350	1.265	0.050	1.042	0.908	1.125	0.121
1385765_at	BF406563	similar to lin-9 homolog (C. elegans)	LOC360888	1.193	0.078	0.769	0.009	1.027	0.234	0.817	0.134
1376682_at	AI709541	similar to lipin 3	LOC362261	1.053	0.756	1.173	0.149	1.099	0.984	1.073	0.063
1380839_at	BF401620	Similar to lipoma HMGIC fusion partner-like 3 (predicted)	RGD1559727_predicted	1.054	0.837	1.013	0.691	1.024	0.889	0.997	0.106
1374548_at	BE104797	Similar to Liver-expressed antimicrobial peptide 2 precursor (LEAP-2)	LOC497901	1.099	0.122	1.172	0.033	1.223	0.035	1.287	0.077
1372234_at	AA800950	similar to Lix1 homolog (mouse) like	LOC499677	1.364	0.333	1.413	0.021	1.657	0.065	1.534	0.021
1392070_at	AI112117	similar to Lix1 homolog (mouse) like	LOC499677	1.056	0.727	0.811	0.446	1.542	0.004	0.994	0.275
1382386_at	BI274268	similar to Lmbr1 protein (predicted)	RGD1563910_predicted	0.797	0.029	2.335	0.014	0.426	0.027	2.273	0.011
1376018_at	BF398513	similar to Lmnb2 protein (predicted)	RGD1563803_predicted	0.664	0.384	1.073	0.300	0.939	0.307	0.827	0.033
1394537_at	AI178429	similar to Lmo6 protein	LOC317380	1.034	0.562	1.037	0.885	1.036	0.189	0.998	0.651
1372478_at	AI137605	similar to LNV	LOC501065	0.998	0.506	0.761	0.012	1.254	0.846	0.597	0.012
1373782_a_at	AW253957	similar to LOC495800 protein	LOC499770	0.505	0.032	1.022	0.723	0.863	0.423	1.160	0.411
1373685_at	BI291430	similar to low density lipoprotein receptor-related protein binding protein (predicted)	RGD1565715_predicted	0.407	0.000	2.061	0.186	0.680	0.303	1.532	0.074
1384440_at	BM385619	Similar to LRRGT00021 (predicted)	RGD1562496_predicted	1.043	0.913	0.958	0.791	0.998	0.953	0.995	0.945
1373121_at	BE097240	similar to LRRGT00031	LOC499572	0.839	0.463	2.711	0.007	0.567	0.041	2.101	0.026
1384134_at	AI059390	Similar to LRRGT00057 (predicted)	RGD1563911_predicted	1.028	0.903	1.044	0.801	1.860	0.019	1.120	0.998
1396155_at	BF283527	similar to LRRGT00057 (predicted) /// similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH	RGD1564501_predicted /// LOC501761	1.109	0.775	1.006	0.115	0.844	0.968	0.944	0.315
1385461_at	AW529460	similar to LRRGT00108 /// similar to LRRG00135 (predicted)	LOC500675 /// RGD1562616_predicted	1.041	0.550	0.518	0.209	0.829	0.370	0.922	0.356
1393759_at	BM385963	similar to LRRGT00194 (predicted)	RGD1561564_predicted	1.018	0.241	0.652	0.061	0.791	0.612	0.755	0.020
1383906_at	BF416847	similar to lung inducible neuralized-related C3HC4 RING finger protein	LOC316326	178.200	0.000	117.719	0.003	255.497	0.000	99.708	0.001
1388347_at	AI233210	similar to lymphocyte antigen 6 complex, locus E	LOC362934	1.753	0.025	1.370	0.053	3.290	0.000	2.927	0.002
1393776_at	AA955277	Similar to lymphocyte antigen 6 complex, locus E	LOC362934	1.848	0.114	1.197	0.307	2.763	0.134	1.360	0.356
1373372_at	BM389227	similar to lymphocyte antigen 6 complex, locus E ligand	LOC501282	0.556	0.916	1.474	0.398	0.538	0.204	1.338	0.697
1377744_at	BF392982	Similar to macrophage actin-associated-tyrosine-phosphorylated protein (predicted)	RGD1563090_predicted	2.556	0.004	2.186	0.006	0.969	0.768	1.578	0.010
1378092_at	AI408718	similar to magnesium-dependent phosphatase-1 (predicted)	RGD1311147_predicted	0.712	0.252	0.922	0.710	0.533	0.082	1.299	0.168
1386266_at	AI227948	Similar to male sterility domain containing 1 (predicted)	RGD1565966_predicted	0.912	0.176	0.460	0.194	0.669	0.111	0.491	0.178
1382629_at	BM383809	similar to male sterility domain containing 2	LOC499247	2.422	0.069	2.793	0.003	1.713	0.023	2.435	0.070
1377307_at	BM385387	similar to mammary tumor receptor 2 isoform-like protein	LOC498968	0.987	0.460	0.991	0.571	1.279	0.350	1.009	0.835
1372029_at	BI281957	similar to mannose-6-phosphate receptor binding protein 1	LOC316130	1.002	0.973	2.173	0.011	1.002	0.803	1.449	0.024
1398924_at	AA849774	similar to mannosidase, beta A, lysosomal-like	MGC109145	0.982	0.536	1.789	0.503	1.156	0.551	1.905	0.057
1374550_at	BI277482	similar to map kinase interacting kinase	MGC112775	1.011	0.938	0.843	0.002	0.976	0.897	0.900	0.439
1370141_at	NM_021846	similar to MAP/microtubule affinity-regulating kinase 4 (MAP/microtubule affinity-regulating kinase like 1) (predicted)	RGD1561096_predicted	1.418	0.139	8.571	0.001	1.743	0.138	5.501	0.007
1372740_at	AA925557	similar to Map4k6-pending protein	LOC303259	0.924	0.303	1.718	0.005	1.260	0.061	1.528	0.038
1392133_at	AI502069	Similar to MAPK-interacting and spindle-stabilizing protein (predicted)	RGD1311455_predicted	3.091	0.014	4.256	0.003	3.308	0.004	1.946	0.781
1382565_at	BE108260	Similar to MAPK-interacting and spindle-stabilizing protein (predicted)	RGD1311455_predicted	2.217	0.021	4.200	0.040	1.700	0.124	1.866	0.064
1374112_at	BI296251	similar to MAPK-interacting and spindle-stabilizing protein (predicted)	RGD1565431_predicted	1.093	0.062	0.816	0.069	0.840	0.111	0.736	0.047
1381758_at	AI535566	similar to MDM2 Binding protein (predicted)	RGD1565672_predicted	1.237	0.673	0.739	0.104	0.960	0.788	1.181	0.245
1381353_at	AI179244	similar to melanoma antigen family A, 5	MGC114427	1.340	0.111	1.053	0.910	1.545	0.215	0.984	0.837
1395760_at	BF552848	Similar to membrane protein expressed in epithelial-like lung adenocarcinoma (predicted)	RGD1307493_predicted	0.811	0.465	0.901	0.897	1.066	0.783	0.912	0.223
1388578_at	BI288621	similar to membrane targeting translocation system protein like (2A562)	LOC289378	1.597	0.060	0.839	0.444	1.396	0.170	0.770	0.128
1395710_at	BI275003	similar to mesoderm induction early response 1 (MI-ER1) (predicted)	RGD1562337_predicted	1.060	0.554	1.005	0.857	1.053	0.136	1.096	0.273
1399077_at	AI411253	similar to Metaxin 1, isoform 2	LOC295241	0.530	0.031	1.024	0.030	0.609	0.046	1.219	0.118
1393094_at	AI385367	Similar to methyl-CpG binding protein MBD2	LOC498883	1.225	0.494	0.210	0.004	0.987	0.802	0.238	0.005
1381280_at	BF415212	Similar to methylenetetrahydrofolate dehydrogenase (NAD) (EC 1.5.1.15) / methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9) precursor - mouse (predicted)	RGD1310879_predicted	1.889	0.157	1.042	0.466	0.774	0.474	0.990	0.967
1372808_at	AW251324	similar to methylenetetrahydrofolate dehydrogenase (NAD) (EC 1.5.1.15)/methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9) precursor (predicted)	RGD1564040_predicted	1.045	0.809	1.410	0.024	0.855	0.511	1.359	0.173
1382903_at	BF420492	similar to mFLJ00191 protein	LOC310958	1.457	0.253	2.572	0.006	0.738	0.474	2.166	0.013
1372872_at	BI291271	Similar to mFLJ00191 protein	LOC310958	1.067	0.919	0.451	0.034	0.935	0.634	0.778	0.065

1377393_at	H31625	similar to MGC14161 protein (predicted)	RGD1561554_predicted	0.554	0.045	0.549	0.008	0.410	0.014	0.403	0.037
1375294_at	BF415950	Similar to MGC14161 protein (predicted)	RGD1561554_predicted	0.825	0.529	0.714	0.039	0.933	0.397	0.720	0.047
1396619_at	BF403306	Similar to MGC14161 protein (predicted)	RGD1561554_predicted	1.000	0.940	1.010	0.997	1.001	0.977	1.011	0.927
1381827_at	AW527316	similar to MGC4645 protein (predicted)	RGD1565864_predicted	1.275	0.255	1.395	0.072	1.430	0.050	1.008	0.054
1385128_at	BE108716	Similar to MGC68837 protein (predicted)	RGD1565710_predicted	2.320	0.045	1.044	0.879	2.493	0.116	1.953	0.046
1379577_at	AW527171	similar to MIC2L1 (predicted)	RGD1559441_predicted	1.004	0.993	0.942	0.049	1.120	0.583	1.213	0.148
1379153_at	BF387484	Similar to microfilament and actin filament cross-linker protein isoform a	LOC362587	0.668	0.118	0.661	0.291	0.683	0.235	0.656	0.007
1371940_at	AW920000	similar to microfilament and actin filament cross-linker protein isoform a	LOC362587	0.992	0.890	0.589	0.014	0.869	0.240	0.682	0.084
1373333_at	AI102732	similar to Microsomal signal peptidase 23 kDa subunit (SPase 22 kDa subunit) (SPC22/23)	MGC109340	0.826	0.532	0.512	0.016	0.526	0.180	0.395	0.010
1386090_at	BF289454	similar to minichromosome maintenance protein 8 isoform 1 (predicted)	RGD1560557_predicted	1.057	0.709	1.265	0.986	0.763	0.074	0.765	0.162
1379748_at	AA819629	Similar to minor histocompatibility antigen precursor	LOC310968	19.808	0.002	12.384	0.003	46.552	0.000	39.999	0.002
1373020_at	BG379323	similar to mitochondria-associated granulocyte macrophage CSF signaling molecule (predicted)	RGD1564452_predicted	0.698	0.085	1.492	0.046	0.680	0.070	1.355	0.000
1379632_at	AI502790	Similar to mitochondrial carrier family protein	RGD1308774	0.369	0.035	0.496	0.028	0.446	0.007	0.603	0.106
1380307_at	AI556551	Similar to mitochondrial carrier family protein	RGD1308774	1.359	0.477	0.885	0.463	1.156	0.859	1.038	0.672
1395621_at	H33102	similar to Mitochondrial carrier triple repeat 1 (predicted)	RGD1565119_predicted	0.845	0.802	1.179	0.240	0.879	0.673	0.675	0.010
1371649_at	BI289411	similar to mitochondrial ribosomal protein S24 (predicted)	RGD1564681_predicted	0.503	0.258	1.052	0.612	0.436	0.010	0.780	0.983
1397264_at	AA859819	Similar to mitochondrial tryptophanyl tRNA synthetase 2 (predicted)	RGD1565226_predicted	1.064	0.282	0.999	0.977	0.926	0.744	1.017	0.934
1372977_at	BI291366	similar to mitogen-activated protein kinase kinase kinase kinase 5 isoform 2 (predicted)	RGD1562028_predicted	1.001	0.976	1.289	0.986	0.906	0.533	1.106	0.346
1383558_at	BI290282	similar to MJ0495-like protein SelB (predicted)	RGD1560552_predicted	0.349	0.077	1.843	0.048	0.344	0.006	1.941	0.010
1372010_at	BF283797	similar to MK-5 type 2	MGC116327	0.897	0.771	1.687	0.024	0.645	0.005	1.260	0.099
1374799_at	AI407418	similar to mKIAA0159 protein (predicted)	RGD1562596_predicted	0.844	0.056	0.934	0.553	0.879	0.689	0.605	0.481
1395248_at	BF418342	similar to mKIAA0212 protein (predicted)	RGD1563633_predicted	1.335	0.475	1.517	0.110	1.166	0.070	1.198	0.421
1384186_at	AI556447	similar to mKIAA0212 protein (predicted)	RGD1563633_predicted	1.724	0.522	1.045	0.893	1.593	0.096	0.926	0.441
1383528_at	BI276223	similar to mKIAA0215 protein (predicted)	RGD1563945_predicted	0.709	0.058	1.125	0.575	0.532	0.074	1.143	0.192
1376013_at	BF282700	similar to mKIAA0227 protein (predicted)	RGD1565985_predicted	0.769	0.164	0.801	0.851	0.568	0.009	0.756	0.025
1392632_at	AI044816	similar to mKIAA0227 protein (predicted)	RGD1565985_predicted	1.003	0.995	0.885	0.473	1.005	0.964	0.766	0.664
1381958_at	BE107587	similar to mKIAA0259 protein (predicted)	RGD1562949_predicted	0.715	0.203	1.213	0.311	0.318	0.011	0.943	0.780
1379061_at	BI290700	similar to mKIAA0323 protein (predicted)	RGD1565688_predicted	1.000	0.991	2.436	0.068	1.001	0.661	1.153	0.641
1385004_at	BE107527	Similar to mKIAA0376 protein	RGD1309570	1.004	0.615	0.999	0.188	1.319	0.241	1.012	0.941
1377190_at	AI010237	Similar to mKIAA0386 protein	RGD1306939	1.512	0.250	1.157	0.827	1.393	0.260	1.005	0.384
1374766_at	BE103616	Similar to mKIAA0493 protein (predicted)	RGD1564703_predicted	0.440	0.000	0.443	0.000	0.566	0.002	0.431	0.004
1385408_at	BI288589	similar to mKIAA0518 protein (predicted)	RGD1561597_predicted	2.491	0.097	1.330	0.395	1.357	0.075	1.581	0.023
1371984_at	AI598442	Similar to mKIAA0613 protein (predicted)	RGD1564875_predicted	0.930	0.950	1.045	0.534	1.011	0.952	0.912	0.451
1389129_at	BF282876	similar to mKIAA0665 protein	RGD1308952	1.549	0.102	1.534	0.307	1.174	0.167	1.118	0.516
1390200_at	BM388794	similar to mKIAA0674 protein (predicted)	RGD1304816_predicted	1.231	0.348	1.296	0.231	1.421	0.091	1.143	0.479
1384616_at	AW523666	similar to mKIAA0674 protein (predicted)	RGD1304816_predicted	0.991	0.655	1.086	0.124	1.005	0.052	1.197	0.563
1389672_at	BI301467	similar to mKIAA0701 protein	LOC363009	0.816	0.046	0.545	0.018	0.830	0.532	0.631	0.208
1392559_at	BM383442	similar to mKIAA0701 protein	LOC363009	0.949	0.969	2.146	0.011	0.973	0.889	1.946	0.051
1384110_at	AI045668	similar to mKIAA0716 protein (predicted)	RGD1561724_predicted	2.479	0.003	0.500	0.040	3.508	0.001	0.896	0.701
1397226_at	AI100942	similar to mKIAA0716 protein (predicted)	RGD1561724_predicted	2.549	0.024	0.839	0.059	2.329	0.024	0.932	0.141
1376034_at	AW141824	similar to mKIAA0738 protein (predicted)	RGD1565474_predicted	0.741	0.136	0.407	0.007	0.620	0.483	0.715	0.032
1380309_at	BI273829	similar to mKIAA0804 protein (predicted)	RGD1309443_predicted	0.962	0.949	1.138	0.348	1.018	0.485	1.182	0.143
1374576_at	BF283857	similar to mKIAA0841 protein (predicted)	RGD1564266_predicted	1.005	0.887	1.389	0.055	0.946	0.556	1.041	0.995
1397368_at	BE120588	Similar to mKIAA0843 protein (predicted)	RGD1565118_predicted	0.680	0.497	1.224	0.544	0.633	0.286	1.021	0.596
1391528_at	AA858509	similar to mKIAA0863 protein (predicted)	RGD1308279_predicted	0.720	0.098	0.685	0.135	0.721	0.488	1.033	0.808
1382552_at	AW522677	similar to mKIAA0934 protein (predicted)	RGD1560155_predicted	1.038	0.470	2.062	0.007	0.580	0.026	1.725	0.003
1380969_at	BE106363	Similar to mKIAA0940 protein (predicted)	RGD1564670_predicted	1.423	0.637	0.998	0.804	0.894	0.473	0.733	0.141
1378147_at	BE109576	similar to mKIAA0978 protein (predicted)	RGD1561878_predicted	1.163	0.858	1.635	0.142	1.424	0.068	1.365	0.088
1398493_at	BG377873	Similar to mKIAA0981 protein	LOC316457	1.138	0.597	0.879	0.136	1.152	0.280	0.930	0.566
1379916_at	BE108030	Similar to mKIAA0998 protein (predicted)	RGD1563583_predicted	1.003	0.771	0.998	0.930	1.018	0.866	1.005	0.975
1373814_at	BI291270	similar to mKIAA1002 protein	RGD1310066	2.607	0.021	1.239	0.737	1.118	0.795	1.019	0.582
1382066_at	AI549105	similar to mKIAA1002 protein	RGD1310066	1.216	0.622	0.299	0.120	0.713	0.439	0.703	0.759
1381422_at	AA817889	Similar to mKIAA1002 protein	RGD1310066	1.393	0.999	0.703	0.468	1.141	0.084	0.822	0.996
1377653_at	BI293195	similar to mKIAA1011 protein	LOC366669	1.482	0.944	0.884	0.474	1.370	0.529	0.856	0.106
1374322_at	AA893980	similar to MKIAA1064 protein	LOC499087	0.895	0.182	0.311	0.006	1.362	0.299	0.466	0.032
1392148_at	BF391605	Similar to mKIAA1107 protein (predicted)	RGD1306921_predicted	0.181	0.008	0.613	0.019	0.445	0.073	0.516	0.044
1373179_at	BI300727	similar to mKIAA1107 protein (predicted)	RGD1306921_predicted	0.144	0.018	0.481	0.006	0.199	0.017	0.388	0.096
1397758_at	BI301535	Similar to mKIAA1208 protein (predicted)	RGD1564821_predicted	0.806	0.083	0.676	0.012	0.667	0.096	0.573	0.022
1382584_at	BE116720	similar to mKIAA1321 protein (predicted)	RGD1564405_predicted	1.424	0.156	1.275	0.280	1.434	0.350	1.448	0.171
1381586_at	BI296171	similar to mKIAA1386 protein	LOC368062	1.178	0.020	0.997	0.965	1.009	0.882	0.998	0.950
1377657_at	AW525218	Similar to mKIAA1417 protein (predicted)	RGD1565019_predicted	0.908	0.032	0.935	0.575	1.026	0.771	1.015	0.965

1374230_at	BI395805	Similar to mKIAA1429 protein (predicted)	RGD1559904_predicted	0.497	0.668	0.550	0.003	0.521	0.087	0.674	0.024
1391192_at	BF414558	Similar to mKIAA1429 protein (predicted)	RGD1559904_predicted	0.817	0.773	0.921	0.119	1.280	0.890	1.009	0.958
1392548_at	BF394282	similar to mKIAA1604 protein (predicted)	RGD1565385_predicted	1.384	0.994	1.361	0.051	0.657	0.077	0.984	0.159
1374725_at	AW252811	similar to mKIAA1631 protein	LOC310756	32.943	0.002	13.783	0.002	74.845	0.005	13.632	0.010
1381820_at	BI286742	Similar to mKIAA1631 protein	LOC310756	1.544	0.586	2.497	0.348	2.016	0.092	1.086	0.875
1392900_at	AW888327	Similar to mKIAA1631 protein	LOC310756	1.058	0.754	0.988	0.901	1.170	0.579	1.189	0.098
1379139_x_at	BF406217	Similar to mKIAA1737 protein (predicted)	RGD1309492_predicted	1.963	0.317	1.003	0.473	0.808	0.303	0.809	0.435
1374568_at	BF284775	Similar to mKIAA1737 protein (predicted)	RGD1309492_predicted	1.158	0.906	1.279	0.029	1.091	0.829	1.298	0.009
1386311_at	AI008479	Similar to mKIAA1737 protein (predicted)	RGD1309492_predicted	1.242	0.956	0.807	0.284	1.105	0.181	0.548	0.546
1378705_at	AW254450	similar to mKIAA1757 protein (predicted)	RGD1310433_predicted	1.690	0.015	1.044	0.828	1.320	0.091	0.960	0.577
1399070_at	AI180081	similar to mKIAA1757 protein (predicted)	RGD1310433_predicted	2.115	0.045	3.652	0.043	1.089	0.366	2.317	0.000
1391170_at	BE115521	similar to mKIAA1757 protein (predicted)	RGD1310433_predicted	1.257	0.087	1.595	0.052	1.438	0.477	1.175	0.386
1373330_at	AI406704	similar to mKIAA1783 protein (predicted)	RGD1560214_predicted	0.476	0.019	0.284	0.002	0.496	0.027	0.195	0.013
1372614_at	BF390044	similar to mKIAA1797 protein (predicted)	RGD1311849_predicted	0.603	0.629	1.157	0.979	0.503	0.052	0.907	0.315
1398115_at	BF393962	Similar to mKIAA1797 protein (predicted)	RGD1311849_predicted	1.371	0.701	0.839	0.137	0.891	0.936	1.005	0.790
1374364_at	BI277805	similar to mKIAA1931 protein (predicted)	RGD1562335_predicted	0.958	0.356	1.219	0.169	1.307	0.441	0.992	0.913
1380079_at	AW533923	similar to mKIAA2005 protein	LOC500015	5.842	0.001	1.530	0.183	34.077	0.001	9.980	0.018
1376920_at	BF408536	similar to mKIAA2005 protein (predicted) /// similar to mKIAA2005 protein (predicted) /// similar to mKIAA2005 protein	RGD1561472_predicted /// RGD1563965_predicted /// LOC500015	58.330	0.000	11.098	0.008	239.421	0.000	51.352	0.001
1390312_at	BG670441	similar to mKIAA2005 protein (predicted) /// similar to mKIAA2005 protein (predicted) /// similar to mKIAA2005 protein	RGD1561472_predicted /// RGD1563965_predicted /// LOC500015	7.621	0.044	1.343	0.001	51.275	0.001	14.989	0.007
1397528_at	BE112252	Similar to mKIAA3013 protein	LOC312030	0.887	0.035	1.032	0.873	0.839	0.054	0.946	0.930
1376049_at	AA925805	Similar to mKIAA3013 protein	LOC312030	0.504	0.086	0.612	0.199	0.574	0.057	1.005	0.960
1374154_at	AI411610	Similar to mKIAA3013 protein	LOC312030	1.430	0.101	2.892	0.001	1.028	0.900	2.498	0.002
1383043_at	AA955140	Similar to mKIAA3013 protein	LOC312030	1.372	0.200	1.398	0.108	0.957	0.864	1.085	0.979
1373303_at	BM383325	similar to mKIAA3013 protein	LOC312030	1.008	0.950	1.638	0.116	0.588	0.168	1.350	0.262
1373496_at	AI137294	similar to Mkrn1 protein	MGC94941	1.054	0.447	1.073	0.777	0.697	0.164	1.351	0.306
1376626_at	AI145815	similar to Mkrn1 protein	MGC94941	0.920	0.734	1.516	0.016	0.888	0.586	1.315	0.026
1372606_at	BM390528	Similar to MLTK-beta (predicted)	RGD1561394_predicted	1.130	0.901	2.446	0.032	1.888	0.025	5.793	0.006
1371998_at	AI176611	similar to Mob4B protein	MGC124888	1.187	0.037	1.591	0.031	1.127	0.166	1.371	0.016
1392961_at	AW534383	similar to Mob4B protein	MGC124888	1.687	0.473	1.427	0.158	2.333	0.704	1.277	0.465
1397372_at	BI289004	similar to Mob4B protein	MGC124888	1.055	0.531	0.857	0.992	1.410	0.099	0.780	0.273
1388820_at	BI286365	similar to modulator of estrogen induced transcription	RGD1307526	0.951	0.222	2.156	0.001	0.917	0.359	1.941	0.004
1390989_at	BG667374	similar to Mospd2 protein (predicted)	RGD1563952_predicted	0.662	0.844	0.775	0.002	0.864	0.454	0.759	0.141
1382743_at	AI578576	Similar to mouse LOC212632	LOC641315	2.296	0.034	2.609	0.044	1.134	0.628	1.435	0.072
1371720_at	AI599839	similar to Mrpl20 protein (predicted)	RGD1562345_predicted	0.389	0.274	0.275	0.018	0.376	0.042	0.553	0.344
1373705_at	AI235502	similar to Mrpl28 protein	LOC497876	0.520	0.004	0.624	0.063	0.527	0.002	0.776	0.149
1379831_at	AW252506	similar to multiple hat domains (predicted)	RGD1311017_predicted	0.880	0.742	1.046	0.889	0.721	0.057	0.727	0.294
1393595_at	BI289182	similar to multiple hat domains (predicted)	RGD1311017_predicted	0.865	0.765	0.944	0.437	0.942	0.998	0.942	0.160
1391786_at	BI297047	Similar to Murine homolog of human ftp-3	LOC308650	1.032	0.863	0.578	0.006	1.578	0.012	0.661	0.056
1373635_at	BF393090	similar to Myb protein P42POP (predicted)	RGD1565160_predicted	0.838	0.273	0.790	0.131	0.939	0.468	0.782	0.128
1371877_at	BM391502	similar to MYLE protein (Dexamethasone-induced protein) (predicted)	RGD1564938_predicted	0.557	0.003	0.943	0.558	0.724	0.205	0.689	0.945
1389165_at	AI178292	similar to myocardial ischemic preconditioning upregulated protein 2 (predicted)	RGD1565589_predicted	1.096	0.224	1.354	0.037	0.670	0.059	1.222	0.052
1394400_at	BF542890	Similar to myocardial ischemic preconditioning upregulated protein 2 (predicted)	RGD1565589_predicted	0.953	0.417	0.860	0.730	1.297	0.550	0.751	0.301
1392472_at	BI281877	similar to myocyte enhancer factor 2C	LOC309957	1.160	0.141	2.846	0.015	1.195	0.994	1.665	0.046
1371817_at	BI285489	similar to myo-inositol 1-phosphate synthase A1	LOC290651	0.585	0.018	1.467	0.014	0.768	0.173	1.013	0.933

1373177_x_at	AI409900	similar to Myosin IXb (Unconventional myosin-9b) /// hypothetical LOC287921 /// RGD1561528 (predicted) /// similar to spermatogenesis associated glutamate (E)-rich protein 4d /// similar to spermatogenesis associated glutamate (E)-rich protein 4d (predicted) /// similar to protein phosphatase 1 (predicted) /// hypothetical LOC363367 /// similar to spermatogenesis associated glutamate (E)-rich protein 4d /// hypothetical LOC363423 /// hypothetical gene supported by BC082068 /// hypothetical gene supported by BC082068 /// hypothetical gene supported by BC082068 /// hypothetical gene supported by BC082068 /// LOC501300 /// hypothetical gene supported by BC082068 /// similar to spermatogenesis associated glutamate (E)-rich protein 4d /// hypothetical gene supported by BC082068 /// similar to spermatogenesis associated glutamate (E)-rich protein 4d /// similar to spermatogenesis associated glutamate (E)-rich protein 4d /// hypothetical gene supported by BC082068 /// similar to spermatogenesis associated glutamate (E)-rich protein 4d /// hypothetical gene supported by BC082068 /// hypothetical gene supported by BC082068 /// similar to spermatogenesis ass	/// RGD1561528_predicted /// LOC301986 /// RGD1564288_predicted /// RGD1564721_predicted /// LOC363367 /// LOC363398 /// LOC363423 /// LOC501220 /// LOC501234 /// LOC501239 /// LOC501276 /// LOC501300 /// LOC501302 /// LOC501303 /// LOC501304 /// LOC501310 /// LOC501319 /// LOC501320 /// LOC501325 /// LOC501329 /// LOC501331 /// LOC501332 /// LOC501334 /// LOC501340 /// LOC501343 /// LOC501345 /// LOC501348 /// LOC501362 /// LOC501364 /// LOC501370 /// LOC501372 /// LOC501377 /// RGD1563206_predicted /// LOC501381 /// LOC501383 /// LOC501384 /// LOC501421 /// LOC501468 /// LOC501469 /// LOC501474 /// LOC501477 /// LOC501482 /// LOC501486	0.678	0.173	0.722	0.118	0.419	0.020	0.617	0.003
1376789_at	AI410679	Similar to Myosin light chain kinase 2, skeletal/cardiac muscle (MLCK2) (predicted)	RGD1305801_predicted	1.289	0.367	0.981	0.749	1.383	0.133	1.297	0.409
1390277_at	BF399451	Similar to Myosin VI (predicted)	RGD1560646_predicted	1.771	0.036	1.424	0.338	1.105	0.043	2.135	0.558
1376804_at	BM386777	similar to Myosin VI (predicted)	RGD1560646_predicted	0.506	0.171	1.356	0.017	0.622	0.082	1.207	0.032
1382895_at	AI044640	Similar to myosin XVIIIa	LOC360570	1.000	0.418	0.902	0.424	1.033	0.597	0.991	0.302
1371866_at	BM389317	similar to myosin XVIIIa	LOC360570	0.997	0.984	1.516	0.016	0.786	0.286	2.080	0.012
1371304_a_at	BI285502	similar to myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (predicted) /// myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (predicted)	RGD1559821_predicted /// Myl6_predicted	1.088	0.811	1.344	0.113	0.856	0.336	1.112	0.025
1398513_at	AI556479	Similar to Na+ dependent glucose transporter 1 (predicted)	RGD1559971_predicted	0.893	0.566	0.501	0.023	1.012	0.940	0.604	0.108
1372362_at	BE329241	similar to N-acetylgalactosamine kinase (GalNAc kinase) (Galactokinase 2)	LOC296117	0.619	0.663	1.674	0.011	0.706	0.207	1.475	0.005
1392444_at	AW531000	Similar to N-acetylglucosamine 6-O-sulfotransferase (predicted)	RGD1561144_predicted	0.739	0.049	0.072	0.001	1.266	0.312	0.107	0.033
1394264_at	BF558607	similar to N-acetylglucosamine 6-O-sulfotransferase (predicted)	RGD1561144_predicted	0.556	0.105	0.089	0.010	0.899	0.100	0.189	0.002
1373560_at	AI233172	similar to N-acetylglucosaminyltrasnferase IVb (predicted)	RGD1562836_predicted	1.790	0.052	2.851	0.002	1.208	0.179	1.950	0.029
1373575_at	BE111722	similar to NADH dehydrogenase (ubiquinone) Fe-S protein 2	LOC498279	0.991	0.622	0.995	0.927	0.997	0.625	0.991	0.993
1388403_at	AI172491	similar to NADP+-specific isocitrate dehydrogenase	LOC361596	0.448	0.121	1.523	0.020	0.255	0.007	1.471	0.015
1389746_at	BM386322	similar to Naglu (predicted)	RGD1564228_predicted	0.582	0.164	0.995	0.247	0.435	0.166	0.769	0.159
1385481_at	AW526551	similar to NCAG1 (predicted)	RGD1307724_predicted	0.340	0.008	0.510	0.014	0.371	0.003	0.370	0.026
1370903_a_at	AI146115	similar to Ndr3 protein	LOC296318	0.508	0.026	0.456	0.019	0.551	0.053	0.808	0.065
1392364_at	BE102708	Similar to nebulette non-muscle isoform (predicted)	RGD1559911_predicted	1.012	0.655	1.049	0.779	1.054	0.696	0.919	0.972
1381631_at	BF394093	Similar to nebulette non-muscle isoform (predicted)	RGD1559911_predicted	1.001	0.941	0.999	0.926	1.002	0.945	0.997	0.802
1391222_at	AA965076	similar to Nedd4 binding protein 1 (predicted)	RGD1305179_predicted	3.028	0.089	3.140	0.087	5.220	0.115	2.397	0.070
1390859_at	BI290968	similar to Nedd4 binding protein 1 (predicted)	RGD1305179_predicted	1.229	0.133	2.908	0.022	1.370	0.162	1.720	0.127
1380164_at	AI411787	Similar to Nedd4-binding brain specific protein BEAN (predicted)	RGD1562003_predicted	2.533	0.005	1.490	0.142	2.819	0.001	1.930	0.143
1385613_at	AI112079	Similar to nemo like kinase (predicted)	RGD1561602_predicted	0.654	0.248	1.008	0.967	0.657	0.807	0.968	0.891
1382365_at	AA997745	Similar to nemo like kinase (predicted)	RGD1561602_predicted	1.144	0.255	0.606	0.006	1.233	0.577	0.933	0.067
1378806_at	BF392451	Similar to nemo like kinase (predicted)	RGD1561602_predicted	1.225	0.372	0.615	0.078	1.238	0.090	0.459	0.020
1379218_at	BE101792	similar to nemo like kinase (predicted)	RGD1561602_predicted	1.005	0.914	0.653	0.004	1.174	0.980	0.925	0.045
1385266_at	BF404261	similar to nemo like kinase (predicted) /// similar to nemo like kinase /// similar to nemo like kinase (predicted)	RGD1561440_predicted /// LOC365949 /// RGD1561602_predicted	1.397	0.040	0.780	0.028	1.307	0.034	0.938	0.480

1379765_at	AI111738	similar to nemo like kinase (predicted) /// similar to nemo like kinase /// similar to nemo like kinase (predicted)	RGD1561440_predicted /// LOC365949 /// RGD1561602_predicted	1.168	0.409	0.916	0.179	1.056	0.288	0.755	0.219
1383146_at	BM388077	similar to neurobeachin (predicted)	RGD1562629_predicted	0.707	0.036	0.540	0.012	1.031	0.439	0.668	0.021
1380008_at	BI291914	similar to Neurofilament triplet H protein (200 kDa neurofilament protein) (Neurofilament heavy polypeptide) (NF-H) (predicted)	RGD1311283_predicted	1.088	0.212	1.864	0.003	1.217	0.145	1.367	0.028
1391028_at	AI511126	Similar to neuronal interacting factor X 1 (NIX1) (predicted)	RGD1565949_predicted	1.002	0.207	5.186	0.000	0.999	0.985	6.508	0.019
1394923_at	AW528728	similar to neuronal interacting factor X 1 (NIX1) (predicted)	RGD1565949_predicted	0.997	0.523	1.152	0.250	0.995	0.956	1.001	0.800
1383547_at	AI137593	similar to neuropathy target esterase homolog (predicted)	RGD1564611_predicted	0.961	0.877	0.998	0.105	0.990	0.962	1.004	0.995
1378359_at	AI072632	similar to NF-kappa-B-repressing factor (Transcription factor NRF) (predicted)	RGD1563950_predicted	0.621	0.010	0.658	0.207	0.497	0.015	0.901	0.456
1375630_at	AA859366	similar to NHP2-like protein 1 (High mobility group-like nuclear protein 2 homolog 1) ([U4/U6.U5] tri-snRNP 15.5 kDa protein) (OTK27)	MGC72932	0.432	0.257	1.522	0.035	0.387	0.068	1.107	0.402
1397412_at	BE107094	Similar to NICE-3	LOC361985	1.642	0.039	1.265	0.073	1.118	0.957	0.998	0.549
1388382_at	AI407017	similar to NICE-3	LOC361985	1.114	0.641	1.211	0.376	0.981	0.714	1.227	0.223
1392994_at	AW522671	similar to Nicotinamide riboside kinase 1	LOC499330	0.813	0.550	0.170	0.003	0.827	0.084	0.362	0.123
1381434_s_at	AW253721	similar to nidogen 2 (predicted)	RGD1566091_predicted	2.969	0.020	8.355	0.002	2.387	0.035	5.665	0.002
1373232_at	AI008975	similar to nidogen 2 (predicted) /// similar to nidogen 2 protein /// similar to nidogen 2 protein /// similar to nidogen 2 protein /// similar to nidogen 2 protein	RGD1566091_predicted /// LOC317070 /// LOC363405 /// LOC367653 /// LOC501271	1.949	0.388	2.444	0.008	1.424	0.254	2.193	0.015
1396219_at	BF542315	similar to nidogen 2 protein /// similar to Mic2l1 (predicted) /// similar to nidogen 2 protein (predicted) /// similar to nidogen 2 protein /// similar to nidogen 2 protein (predicted) /// similar to nidogen 2 (predicted) /// similar to nidogen 2 (predicted)	LOC302022 /// RGD1564559_predicted /// RGD1559500_predicted /// LOC367653 /// RGD1562856_predicted /// RGD1563545_predicted /// RGD1561103_predicted	1.263	0.660	1.332	0.744	1.470	0.099	1.609	0.771
1376175_at	BF283433	similar to NipSnap2 protein (Glioblastoma amplified sequence)	LOC498174	0.991	0.974	0.677	0.016	1.004	0.178	0.613	0.008
1373095_at	AI408081	similar to nitric oxide synthase (predicted)	RGD1560063_predicted	0.756	0.099	1.088	0.898	1.017	0.959	0.940	0.959
1391223_at	BF394238	Similar to nitric oxide synthase (predicted)	RGD1560063_predicted	1.347	0.469	0.621	0.116	0.810	0.115	0.603	0.125
1367467_at	BG380638	similar to nitrogen fixation cluster-like (predicted)	RGD1309562_predicted	0.604	0.355	0.774	0.149	0.597	0.010	0.888	0.076
1383339_at	BF567255	similar to NNX3 (predicted)	RGD1310358_predicted	1.305	0.306	0.860	0.823	1.256	0.667	0.918	0.492
1399157_at	AA849312	similar to NNX3 (predicted)	RGD1310358_predicted	1.133	0.556	0.956	0.656	0.902	0.875	1.110	0.376
1374962_at	BM385683	similar to NOGO-interacting mitochondrial protein (predicted)	RGD1563384_predicted	0.727	0.088	0.965	0.037	0.730	0.066	0.990	0.832
1390987_at	AI406858	Similar to novel protein (predicted)	RGD1565283_predicted	5.363	0.007	1.248	0.092	3.073	0.001	1.098	0.756
1373665_at	AI598689	similar to novel protein (predicted)	RGD1563106_predicted	0.444	0.017	1.157	0.180	0.616	0.043	1.099	0.655
1380564_at	AW522823	Similar to novel protein (predicted)	RGD1562276_predicted	1.327	0.045	0.739	0.299	0.994	0.773	0.965	0.723
1378468_at	BM390127	similar to novel protein (predicted)	RGD1564005_predicted	1.140	0.187	1.022	0.919	1.004	0.963	1.050	0.982
1378072_at	BE115405	similar to novel protein (predicted)	RGD1561464_predicted	2.542	0.370	0.657	0.321	1.224	0.602	1.123	0.795
1381955_at	AA957487	similar to novel protein (predicted)	RGD1561932_predicted	1.006	0.697	0.837	0.194	0.997	0.162	0.801	0.216
1393012_at	BI294441	similar to novel protein (predicted)	RGD1560636_predicted	1.447	0.867	0.528	0.077	1.669	0.279	0.568	0.135
1375526_at	AI171327	similar to novel protein of unknown function (DUF423) family member (predicted)	RGD1563438_predicted	0.674	0.454	1.911	0.068	0.893	0.040	1.288	0.252
1388906_at	BM389311	similar to novel protein similar to Tensin Tns (predicted)	RGD1564930_predicted	1.262	0.014	0.865	0.018	1.315	0.001	1.019	0.559
1372364_a_at	AA894101	similar to N-terminal asparagine amidohydrolase	RGD1305160	0.589	0.031	0.450	0.015	0.569	0.005	0.548	0.006
1383207_at	BE103628	Similar to N-terminal asparagine amidohydrolase	RGD1305160	0.830	0.548	1.228	0.013	0.694	0.016	1.080	0.123
1392655_at	AA997266	Similar to Nuclear autoantigen Sp-100 (Speckled 100 kDa) (Nuclear dot-associated Sp100 protein)	LOC363269	8.446	0.000	1.710	0.018	23.506	0.000	5.608	0.007
1385571_at	AA923865	Similar to Nuclear autoantigen Sp-100 (Speckled 100 kDa) (Nuclear dot-associated Sp100 protein)	LOC363269	5.702	0.011	1.956	0.021	8.238	0.003	1.695	0.021
1374792_at	BM389058	Similar to nucleolar protein 7, 27kDa (predicted)	RGD1565934_predicted	0.842	0.684	1.028	0.129	0.864	0.172	0.826	0.594
1374857_at	AI579023	similar to nucleolar protein family A, member 1	LOC499709	0.599	0.025	2.310	0.019	0.513	0.203	1.742	0.033
1394027_at	AI179798	Similar to Nucleoporin 62 (predicted)	RGD1564353_predicted	1.089	0.795	0.877	0.962	1.059	0.593	1.046	0.692
1390212_at	BI287987	similar to nucleoporin like 2 (predicted)	RGD1560934_predicted	1.044	0.981	1.188	0.208	1.045	0.991	1.285	0.036
1379529_at	BE121400	similar to Nucleosome binding protein 1	LOC501603	0.567	0.858	0.316	0.010	0.927	0.271	0.368	0.013
1391459_at	BI296636	similar to nudix (nucleoside diphosphate linked moiety X)-type motif 11 (predicted)	RGD1564763_predicted	0.413	0.001	0.560	0.029	0.391	0.001	0.770	0.168
1398326_at	BI282332	similar to Nur77 downstream protein 2	MGC105647	0.545	0.601	1.458	0.073	0.356	0.013	1.006	0.083
1374768_at	BI279857	similar to NYD-SP28 protein	LOC362994	0.997	0.992	0.842	0.182	0.997	0.993	0.847	0.190
1375056_at	AA943310	similar to OCIA domain containing 2 (predicted)	RGD1565826_predicted	0.839	0.804	0.343	0.000	0.685	0.574	0.423	0.032
1389390_at	AI599847	similar to ODAG protein	LOC500005	1.417	0.058	1.760	0.011	1.088	0.881	1.836	0.010
1372605_at	AA925258	similar to ODAG protein	LOC500005	0.789	0.694	0.561	0.020	0.685	0.385	0.556	0.025
1376693_at	AA998964	similar to OEF2 (predicted)	RGD1563091_predicted	148.179	0.002	48.442	0.006	285.273	0.002	110.052	0.002
1378043_at	AW532890	similar to OEF2 (predicted)	RGD1563091_predicted	16.690	0.009	5.784	0.069	35.566	0.001	14.235	0.011
1376964_at	BM384263	similar to Ofd1 protein (predicted)	RGD1562231_predicted	0.914	0.956	0.578	0.020	0.836	0.793	0.739	0.048

1389023_at	AI599504	Similar to Oligosaccharyl transferase 3 CG7748-PA	RGD1311563	0.588	0.245	0.530	0.001	0.656	0.023	0.572	0.002
1383631_at	BI296244	similar to Oligosaccharyl transferase 3 CG7748-PA	RGD1311563	0.466	0.298	0.961	0.304	0.566	0.103	0.763	0.086
1382057_at	AI058311	similar to oocyte-testis gene 1 (predicted)	RGD1564078_predicted	0.909	0.843	0.706	0.248	0.673	0.187	0.924	0.225
1385070_at	BE111420	Similar to Opa-interacting protein 5 (predicted)	RGD1564263_predicted	1.772	0.042	0.998	0.524	0.997	0.965	1.003	0.988
1388575_at	AA943740	Similar to Opa-interacting protein 5 (predicted)	RGD1564263_predicted	0.873	0.229	0.695	0.068	1.816	0.474	1.044	0.730
1373743_at	BI295567	similar to open reading frame 5	RGD1305062	0.979	0.178	0.862	0.762	1.295	0.065	0.996	0.386
1391147_at	BF404398	Similar to opioid growth factor receptor (predicted)	RGD1562096_predicted	1.273	0.122	1.001	0.750	1.130	0.586	0.775	0.050
1374264_at	BM384751	similar to ORC5-related protein	LOC362304	0.946	0.209	1.141	0.135	1.160	0.180	0.903	0.852
1398939_at	BF284885	similar to ORM1-like 3	LOC360618	0.712	0.374	1.205	0.134	0.844	0.057	1.043	0.828
1396763_at	BF412954	Similar to ortholog of human amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19)	LOC301455	0.772	0.767	0.810	0.074	3.504	0.175	1.039	0.116
1390793_at	BI295759	similar to osmosis responsive factor (predicted)	RGD1564042_predicted	0.932	0.930	0.638	0.358	0.554	0.324	0.967	0.458
1397904_at	BI292042	Similar to osteoclast inhibitory lectin (predicted)	RGD1563148_predicted	2.727	0.016	1.185	0.155	4.266	0.003	3.489	0.039
1397676_at	BF290784	Similar to osteoclast inhibitory lectin (predicted)	RGD1563148_predicted	2.837	0.019	1.974	0.003	5.531	0.000	2.855	0.001
1383862_at	BF404050	Similar to osteoclast inhibitory lectin (predicted)	RGD1563148_predicted	1.507	0.160	1.244	0.024	2.256	0.026	2.181	0.054
1384752_at	BF407755	similar to osteoclast inhibitory lectin (predicted)	RGD1563033_predicted	1.165	0.957	1.186	0.420	1.149	0.477	0.970	0.747
1398581_at	AA956307	similar to osteopetrosis associated transmembrane protein 1	LOC365611	0.707	0.131	0.408	0.000	0.555	0.009	0.379	0.018
1395454_at	AW920180	similar to osteopetrosis associated transmembrane protein 1	LOC499474	0.916	0.665	1.260	0.033	1.043	0.358	1.317	0.027
1389144_at	AA818759	similar to OTTHUMP00000018508 (predicted)	RGD1560745_predicted	1.194	0.792	1.693	0.184	1.165	1.000	1.550	0.074
1384428_at	AI043872	similar to OTTHUMP00000040081 (predicted)	RGD1566403_predicted	0.946	0.436	1.281	0.277	0.679	0.336	1.248	0.128
1397780_at	BE096283	similar to OTTHUMP00000040479 (predicted)	RGD1564192_predicted	1.089	0.138	0.965	0.817	1.759	0.067	0.968	0.673
1373898_at	BM387873	similar to OTTHUMP00000042400	LOC360760	1.412	0.041	0.937	0.072	1.385	0.050	0.991	0.835
1384254_at	AI717553	similar to OTU domain containing 1 (predicted)	RGD1563344_predicted	5.435	0.000	4.414	0.000	4.964	0.004	3.758	0.000
1389614_at	AI172472	similar to ovary-specific MOB-like protein (predicted)	RGD1562983_predicted	0.997	0.862	1.122	0.216	0.724	0.134	0.881	0.526
1388646_at	BM391469	similar to p150 target of rapamycin (TOR)-scaffold protein containing WD-repeats (predicted)	RGD1311784_predicted	0.603	0.206	0.368	0.006	0.536	0.003	0.354	0.012
1382275_at	AI236989	similar to PAK/PLC-interacting protein 1	MGC125015	0.886	0.645	1.909	0.000	1.068	0.995	1.198	0.122
1389918_at	BM391364	similar to palladin	LOC290704	4.315	0.013	3.869	0.002	1.726	0.131	3.057	0.047
1384253_at	AW251334	similar to palladin; CGI-151 protein	LOC364558	0.696	0.020	0.276	0.004	0.888	0.535	0.641	0.204
1383324_at	AI703599	Similar to PALS2-alpha splice variant (predicted)	RGD1562141_predicted	1.422	0.006	3.731	0.000	1.276	0.102	2.171	0.008
1398627_at	AA819889	Similar to PALS2-alpha splice variant (predicted)	RGD1562141_predicted	1.483	0.200	0.626	0.102	0.836	0.226	0.762	0.108
1397419_at	AI101314	Similar to PALS2-alpha splice variant (predicted)	RGD1562141_predicted	1.272	0.256	1.663	0.052	0.957	0.788	1.665	0.026
1391825_at	BE120422	Similar to part of a novel protein (predicted)	RGD1562324_predicted	0.409	0.013	1.041	0.572	0.335	0.011	0.863	0.370
1390366_at	BI291884	similar to PC-LKC gene product (predicted)	RGD1560576_predicted	0.857	0.759	0.511	0.346	0.671	0.109	0.841	0.710
1392556_at	BF410961	similar to PDZ domain actin binding protein Shroom	RGD1310470	1.319	0.065	1.143	0.322	1.411	0.339	1.136	0.309
1388664_at	BI282719	similar to PDZ-domain protein scribble (predicted)	RGD1565055_predicted	1.004	0.696	1.272	0.430	1.078	0.864	0.929	0.613
1399081_at	AI712911	similar to pellino protein (predicted)	RGD1564594_predicted	2.209	0.032	1.003	0.720	3.057	0.018	1.002	0.404
1396292_at	BG379069	Similar to peptide N-glycanase	LOC361014	0.440	0.005	0.880	0.310	0.700	0.013	0.831	0.303
1384205_at	BM385969	similar to peptide N-glycanase	LOC361014	0.732	0.173	0.957	0.427	0.781	0.165	1.019	0.800
1398480_at	AW531492	similar to Peroxidasin CG12002-PA (predicted)	RGD1308720_predicted	0.997	0.991	0.992	0.994	0.999	0.997	0.996	0.986
1390531_at	BE098021	Similar to Peroxisomal proliferator-activated receptor A interacting complex 285 kDa protein (PPAR-alpha interacting complex protein 285) (predicted)	RGD1306056_predicted	7.195	0.001	1.755	0.052	13.438	0.003	4.269	0.004
1376595_at	BF282695	similar to peroxisome biogenesis factor 1 (predicted)	RGD1559939_predicted	0.838	0.100	0.282	0.001	1.093	0.405	0.519	0.051
1385561_at	BF561031	similar to peroxisome biogenesis factor 1 (predicted)	RGD1559939_predicted	1.014	0.997	0.600	0.118	1.012	0.999	0.599	0.121
1390506_at	BF396678	similar to peroxisome proliferator-activated receptor binding protein (predicted)	RGD1559552_predicted	1.175	0.166	1.289	0.080	1.534	0.142	1.782	0.095
1384962_at	BI295735	similar to peroxisome proliferator-activated receptor binding protein (predicted)	RGD1559552_predicted	1.114	0.984	3.612	0.100	1.112	0.970	1.047	0.919
1379520_at	BE103550	Similar to PEST-containing nuclear protein	LOC288165	3.447	0.027	0.858	0.497	2.238	0.049	0.635	0.116
1389040_at	AI170825	similar to PEST-containing nuclear protein	LOC288165	0.766	0.517	0.603	0.007	1.003	0.590	0.695	0.012
1391426_a_at	AI578071	similar to PEST-containing nuclear protein	LOC288165	1.094	0.546	1.178	0.359	1.089	0.918	1.310	0.101
1384518_at	BE107536	similar to PHD finger protein 14 isoform 1 (predicted)	RGD1563764_predicted	0.500	0.297	0.727	0.180	0.442	0.157	0.708	0.113
1393458_s_at	BE107536	similar to PHD finger protein 14 isoform 1 (predicted)	RGD1563764_predicted	0.846	0.753	0.787	0.031	0.689	0.280	0.716	0.020
1376043_at	BI292073	similar to PHD zinc finger containing protein JUNE1	MGC94192	1.327	0.118	2.893	0.006	0.940	0.173	2.274	0.107
1377674_at	AI408930	Similar to PHF21A protein (predicted)	RGD1560612_predicted	1.451	0.039	0.681	0.004	1.743	0.036	0.966	0.735
1374078_at	BI295133	similar to PHF21A protein (predicted)	RGD1560612_predicted	1.042	0.795	1.398	0.337	1.503	0.781	1.535	0.025
1371863_at	BM387059	similar to phosphatidylglycerophosphate synthase (predicted)	RGD1305052_predicted	3.422	0.008	5.272	0.001	2.846	0.001	2.595	0.002
1398557_at	BF389362	Similar to phosphoseryl-tRNA kinase (predicted)	RGD1564300_predicted	1.213	0.029	1.498	0.033	0.835	0.463	1.933	0.027
1373731_at	AI409901	similar to phosphoseryl-tRNA kinase (predicted)	RGD1564300_predicted	0.677	0.271	1.848	0.012	0.542	0.229	1.520	0.044
1390779_at	AA818912	Similar to phosphoseryl-tRNA kinase (predicted)	RGD1564300_predicted	0.831	0.510	0.881	0.274	1.056	0.924	0.916	0.274
1392038_at	BF387389	similar to PI-3-kinase-related kinase SMG-1 isoform 2 (predicted)	RGD1563508_predicted	2.173	0.014	5.263	0.003	1.979	0.079	2.679	0.001
1397709_at	BG672259	similar to PI-3-kinase-related kinase SMG-1 isoform 2 (predicted)	RGD1563508_predicted	1.302	0.014	1.109	0.109	1.585	0.051	1.042	0.986
1372830_at	BM384116	similar to PI-3-kinase-related kinase SMG-1 isoform 2 (predicted)	RGD1563508_predicted	1.357	0.198	1.289	0.004	1.361	0.118	1.375	0.006
1374111_at	BI301101	similar to pinin	LOC368070	1.311	0.017	1.135	0.153	2.422	0.003	1.414	0.026

1380001_at	AW526140	similar to pinin	LOC368070	1.648	0.040	1.096	0.972	3.007	0.014	1.407	0.667
1396463_at	BE127046	similar to pinin	LOC368070	1.080	0.279	1.132	0.368	1.851	0.098	0.963	0.778
1383336_at	BF549763	similar to pinin	LOC368070	1.128	0.847	1.165	0.495	2.385	0.006	1.383	0.054
1376762_at	BE112933	Similar to Pleckstrin homology domain-containing protein family A member 1 (Tandem PH domain containing protein-1) (predicted)	RGD1564153_predicted	1.524	0.075	2.268	0.025	0.989	0.815	2.823	0.034
1392230_at	BI287470	Similar to Pleckstrin homology domain-containing protein family A member 1 (Tandem PH domain containing protein-1) (predicted)	RGD1564153_predicted	1.362	0.739	1.105	0.972	2.315	0.184	1.649	0.257
1378094_at	BM389654	Similar to pleckstrin homology-like domain, family B, member 2	LOC360713	0.395	0.004	0.243	0.000	0.472	0.003	0.308	0.012
1377022_at	BF395328	similar to pleckstrin homology-like domain, family B, member 2	LOC360713	0.532	0.054	1.762	0.191	0.802	0.376	1.965	0.014
1381796_at	AI454286	Similar to PLU1 (predicted)	RGD1565602_predicted	0.884	0.586	1.072	0.957	0.991	0.479	1.514	0.147
1383082_at	BF522592	similar to PLU1 (predicted)	RGD1565602_predicted	1.008	0.614	1.044	0.675	0.995	0.985	1.001	0.991
1376347_at	BM383996	similar to PLU1 (predicted)	RGD1565602_predicted	0.988	0.685	1.231	0.124	0.998	0.933	0.969	0.307
1382152_at	AI234336	similar to PLU1 (predicted)	RGD1565602_predicted	0.913	0.848	0.966	0.828	0.994	0.787	1.009	0.948
1377863_at	BI303977	similar to PLU1 (predicted)	RGD1565602_predicted	0.978	0.947	0.585	0.025	0.704	0.159	0.833	0.060
1388852_at	AI406307	similar to pM5 protein; DNA segment, Chr 7, ERATO Doi 156, expressed (predicted)	RGD1305240_predicted	0.516	0.045	0.576	0.008	0.618	0.009	0.636	0.090
1374385_at	AI009789	similar to Pol(yrC)-binding protein 1 (Alpha-CP1) (hnRNP-E1) (predicted)	RGD1561319_predicted	0.968	0.957	2.192	0.001	1.026	0.810	1.758	0.000
1376056_at	BF291214	similar to poly (ADP-ribose) polymerase family, member 10 (predicted)	RGD1563511_predicted	3.548	0.075	1.364	0.707	2.794	0.007	1.503	0.047
1377970_at	BE105494	similar to poly (ADP-ribose) polymerase family, member 8	LOC294762	6.906	0.000	3.377	0.000	6.385	0.001	3.319	0.002
1373013_at	AI009693	similar to polyadenylate-binding protein-interacting protein 2	LOC361309	1.034	0.201	1.249	0.063	1.097	0.373	1.182	0.057
1399026_at	AI178191	similar to polyadenylate-binding protein-interacting protein 2	LOC361309	0.757	0.959	0.889	0.544	0.918	0.236	0.731	0.099
1392054_at	AW532414	similar to polybromo-1 (predicted)	RGD1565549_predicted	1.319	0.132	0.958	0.530	1.211	0.318	0.939	0.413
1395100_at	BI286690	similar to polybromo-1 (predicted)	RGD1565549_predicted	1.961	0.158	1.017	0.910	1.779	0.036	0.997	0.991
1379645_at	BE113614	similar to polybromo-1 (predicted)	RGD1565549_predicted	1.018	0.629	0.589	0.057	1.261	0.622	0.568	0.007
1382021_at	AA850650	Similar to polycystic kidney disease 2 (predicted)	RGD1559992_predicted	0.704	0.411	0.443	0.000	0.673	0.322	0.470	0.010
1378522_at	BG373062	Similar to polycystic kidney disease 2 (predicted)	RGD1559992_predicted	0.820	0.533	1.040	0.298	0.889	0.517	0.839	0.197
1376374_at	AI406775	Similar to polycystic kidney disease 2 (predicted)	RGD1559992_predicted	0.955	0.883	0.678	0.008	0.786	0.477	0.663	0.007
1398508_at	BF546374	similar to polyglutamine-containing protein	RGD1310994	1.011	0.798	0.742	0.125	0.947	0.742	0.819	0.366
1393205_at	AA997182	Similar to polymerase (RNA) II (DNA directed) polypeptide H (predicted)	RGD1561203_predicted	1.529	0.597	1.363	0.021	0.657	0.154	1.089	0.950
1372363_at	BF404414	similar to polymerase (RNA) II (DNA directed) polypeptide H (predicted) /// similar to polymerase (RNA) II (DNA directed) polypeptide H (predicted)	RGD1565904_predicted /// RGD1561203_predicted	1.092	0.553	1.115	0.277	0.760	0.238	0.973	0.355
1389247_at	BI274108	similar to polymerase (RNA) III (DNA directed) (155kD)	RGD1305574	0.726	0.304	1.255	0.727	0.943	0.457	0.880	0.789
1375896_at	BM392055	similar to polyploidy associated protein kinase PAPK-A (predicted)	RGD1559449_predicted	0.795	0.745	0.547	0.029	1.608	0.109	0.606	0.009
1384523_at	BF400964	similar to postmeiotic segregation increased 1	MGC72584	1.091	0.731	1.357	0.050	0.981	0.879	1.299	0.041
1399134_at	AW144008	similar to POT1-like telomere end-binding protein	LOC500054	0.656	0.062	0.711	0.006	0.562	0.234	0.504	0.003
1389988_at	BI301226	similar to Potassium channel tetramerisation domain containing protein 2 (predicted)	RGD1566063_predicted	0.577	0.077	1.000	0.995	0.635	0.192	1.003	0.918
1384002_at	BG663077	similar to Potential phospholipid-transporting ATPase IF (ATPase class I type 11B) (ATPase IR)	LOC361929	0.658	0.231	0.343	0.003	0.823	0.457	0.558	0.005
1370925_at	BG380816	similar to Potential phospholipid-transporting ATPase IIB	LOC291411	0.580	0.311	0.470	0.002	0.473	0.002	0.446	0.020
1399000_at	AI233289	Similar to Potential phospholipid-transporting ATPase IIB	LOC291411	0.791	0.943	1.231	0.636	1.092	0.690	1.001	0.997
1393502_at	AI071962	similar to predicted CDS, putative protein of bilaterial origin (4J193)	RGD1306153	0.816	0.110	1.401	0.006	0.853	0.910	1.108	0.033
1367495_at	AI412457	similar to prefoldin 4 (predicted)	RGD1560211_predicted	0.725	0.097	1.580	0.042	0.580	0.006	1.656	0.224
1388475_at	AA899150	Similar to prion protein interacting protein 1	LOC313535	0.848	0.088	0.847	0.070	0.896	0.409	0.849	0.052
1374082_at	BI275982	similar to PRO1853 homolog	RGD1311578	0.857	0.382	1.251	0.194	0.556	0.017	1.311	0.021
1395318_at	BF397354	similar to Probable chromodomain-helicase-DNA-binding protein KIAA1416	LOC307727	1.009	0.935	0.959	0.833	0.993	0.949	0.961	0.538
1374129_at	AI104518	similar to product is unknown~seizure-related gene (predicted)	RGD1562933_predicted	0.936	0.260	0.942	0.079	1.059	0.638	0.757	0.051
1397320_at	BI293372	Similar to Progesterone-induced blocking factor 1 (predicted)	RGD1305077_predicted	0.660	0.239	2.742	0.005	0.992	0.747	1.709	0.127
1389325_at	AA848545	similar to programmed cell death 10	MGC72992	1.744	0.107	1.948	0.019	1.855	0.057	2.033	0.002
1389852_at	AI598316	similar to proliferation associated nuclear element 1 isoform 1 (predicted)	RGD1307309_predicted	0.783	0.979	1.099	0.212	1.030	0.896	1.101	0.755
1389447_at	AA955470	similar to prolyl-4-hydroxylase-alpha NE2 CG9720-PA (predicted)	RGD1311848_predicted	0.521	0.514	0.953	0.922	0.612	0.175	0.864	0.329
1372643_at	BE110569	similar to protein 4.1G (predicted)	RGD1563977_predicted	0.431	0.023	0.512	0.052	0.452	0.015	0.410	0.011
1390957_at	AI112360	Similar to Protein C14orf101 homolog (predicted)	RGD1562018_predicted	0.820	0.426	0.625	0.015	0.610	0.195	0.842	0.141
1382855_at	BI295963	similar to Protein C20orf158 (predicted)	RGD1305899_predicted	1.019	0.392	0.876	0.079	0.859	0.304	0.706	0.054
1375667_at	AW434286	Similar to Protein C20orf177 (predicted)	RGD1311952_predicted	0.478	0.099	0.128	0.014	0.244	0.056	0.087	0.003
1393046_at	AI709474	similar to Protein C20orf20	RGD1308612	0.901	0.521	1.525	0.013	0.940	0.697	1.107	0.073
1389594_at	BI284608	similar to Protein C20orf22 homolog	LOC499913	0.451	0.440	0.712	0.188	0.435	0.067	0.463	0.099
1392576_at	AI175445	similar to protein C33A12.3	RGD1359508	0.558	0.883	0.878	0.354	0.997	0.987	0.847	0.611
1380553_at	BM390497	similar to Protein C8orf1 (hT41) (predicted)	RGD1306323_predicted	1.779	0.207	1.602	0.067	1.758	0.302	1.026	0.464
1391881_at	AI716506	Similar to Protein C9orf10 (predicted)	RGD1306643_predicted	1.323	0.187	1.038	0.791	0.737	0.234	1.207	0.410
1371386_at	AI407975	similar to Protein C9orf10 (predicted)	RGD1306643_predicted	0.787	0.428	0.869	0.057	0.747	0.039	0.828	0.053
1372028_at	AA893215	similar to Protein CGI-117 (Protein HSPC111) (predicted)	RGD1305727_predicted	0.723	0.338	1.547	0.015	1.007	0.523	1.596	0.022
1389980_at	AI412591	similar to Protein HSPC163 (predicted)	RGD1559740_predicted	1.715	0.044	2.725	0.001	1.466	0.101	2.241	0.002
1398458_at	BE104506	similar to protein kinase, lysine deficient 1; kinase deficient protein (predicted)	RGD1307284_predicted	0.399	0.067	0.403	0.003	0.342	0.022	0.456	0.003

1388949_at	BI297693	Similar to protein of unknown function (predicted)	RGD1566243_predicted	0.869	0.993	1.191	0.465	1.004	0.991	1.084	0.503
1377359_at	BM384440	similar to protein P3	LOC501665	0.247	0.105	0.513	0.178	0.368	0.075	0.649	0.285
1393890_at	BG670819	similar to protein phosphatase 1, regulatory (inhibitor) subunit 1C (predicted)	RGD1562095_predicted	0.770	0.746	0.965	0.375	1.315	0.229	0.743	0.319
1397786_at	BF391927	Similar to protein phosphatase 1, regulatory subunit 12C	LOC499076	1.722	0.230	0.828	0.639	2.859	0.059	1.236	0.699
1372625_at	AA851663	similar to protein phosphatase 1, regulatory subunit 12C	LOC499076	0.981	0.739	0.933	0.155	1.524	0.075	0.982	0.993
1393261_at	AI058850	Similar to protein phosphatase 2A B56 regulatory subunit gamma 3 isoform (predicted)	RGD1564600_predicted	0.550	0.175	0.309	0.002	0.643	0.262	0.306	0.003
1392498_at	BG670494	similar to protein phosphatase 2A B56 regulatory subunit gamma 3 isoform (predicted)	RGD1564600_predicted	0.437	0.470	0.612	0.188	0.368	0.034	0.673	0.010
1374812_at	AA818197	similar to protein Tyr phosphatase	LOC498331	1.020	0.860	0.972	0.909	1.307	0.433	0.995	0.986
1395437_at	BF287018	Similar to protein Tyr phosphatase	LOC498331	1.202	0.889	0.736	0.085	1.391	0.139	0.960	0.406
1371086_at	BE096879	similar to protein tyrosine phosphatase, receptor type, F (predicted)	RGD1564047_predicted	1.135	0.838	1.730	0.452	1.002	0.993	1.928	0.094
1382200_at	AW917547	similar to Prr6 protein (predicted)	RGD1565681_predicted	0.368	0.135	0.474	0.005	0.671	0.105	0.540	0.011
1395399_at	BM387829	similar to PS1D protein (predicted)	RGD1565267_predicted	0.659	0.981	0.956	0.965	0.948	0.567	0.825	0.496
1376315_at	BI282297	similar to putative alpha-mannosidase	RGD1303074	0.483	0.163	0.409	0.007	0.604	0.000	0.327	0.007
1389450_at	BF392737	similar to Putative methyltransferase HUSSY-03 (Williams-Beuren syndrome chromosome region 22 protein homolog) /// similar to Putative methyltransferase HUSSY-03 (Williams-Beuren syndrome chromosome region 22 protein homolog)	LOC360830 /// LOC368084	0.581	0.158	1.273	0.097	0.932	0.627	1.049	0.191
1373563_at	H35156	similar to putative nucleic acid binding protein RY-1; EST AI449063 (predicted)	RGD1310925_predicted	0.972	0.339	1.297	0.125	0.900	0.225	1.175	0.012
1377309_at	AA963085	Similar to putative pheromone receptor	LOC503293	1.116	0.924	1.100	0.143	1.292	0.275	1.242	0.596
1396892_at	AI548369	Similar to putative pheromone receptor (predicted)	RGD1563755_predicted	1.530	0.493	1.492	0.610	0.795	0.449	1.376	0.425
1378741_at	AA850260	similar to putative phosphatase subunit	RGD1309207	1.457	0.569	1.777	0.040	1.342	0.487	1.196	0.082
1373627_at	BI289104	Similar to putative phosphoinositide 5-phosphatase type II; C62	LOC287533	0.875	0.946	0.950	0.687	1.006	0.984	1.056	0.238
1376328_at	BI278776	similar to putative protein (5S487) (predicted)	RGD1310819_predicted	0.715	0.166	3.383	0.001	0.836	0.351	0.865	0.601
1379360_at	AI013789	similar to Putative protein 15E1.2 (predicted)	RGD1309698_predicted	0.703	0.325	1.003	0.668	0.720	0.332	0.867	0.155
1382866_at	BI285368	similar to Putative protein 15E1.2 (predicted)	RGD1309698_predicted	1.002	0.687	0.651	0.016	0.744	0.604	1.092	0.535
1393653_at	BM384831	similar to putative protein product of HMFN2073 (predicted)	RGD1560766_predicted	1.530	0.204	0.995	0.961	1.017	0.977	1.000	0.992
1376502_at	AW523504	similar to putative protein, with at least 9 transmembrane domains, of eukaryotic origin (43.9 kD) (2G415)	RGD1309228	1.176	0.053	1.094	0.206	1.025	0.246	1.153	0.853
1395537_at	BF523835	similar to putative protein, with at least 9 transmembrane domains, of eukaryotic origin (43.9 kD) (2G415)	RGD1309228	1.190	0.506	1.730	0.020	1.117	0.258	1.300	0.530
1378445_at	BM388759	similar to putative repair and recombination helicase RAD26L (predicted)	RGD1561537_predicted	0.708	0.112	0.844	0.298	0.807	0.584	0.926	0.229
1374170_at	AI172069	similar to putative TRAF and TNF receptor associated protein	LOC498749	0.822	0.307	1.159	0.203	1.499	0.303	1.116	0.408
1371620_at	BI279855	similar to px19-like protein	RGD1308082	0.703	0.207	1.310	0.006	0.611	0.038	1.211	0.117
1382028_at	BE115406	similar to PxF protein	LOC289233	1.000	0.915	0.686	0.009	1.055	0.124	0.734	0.002
1376710_at	BE113252	Similar to PYM protein	LOC503354	1.263	0.682	1.009	0.078	1.952	0.098	1.267	0.132
1369931_at	NM_053297	similar to pyruvate kinase (EC 2.7.1.40) isozyme M2 - rat (predicted)	RGD1561681_predicted	0.812	0.194	0.834	0.039	0.746	0.044	0.681	0.003
1398909_at	AA849634	similar to QIL1	LOC301124	0.710	0.634	0.578	0.045	0.568	0.031	0.561	0.058
1375378_at	BE108882	similar to QUAKING isoform 6	LOC499022	1.448	0.014	1.478	0.028	1.436	0.040	1.654	0.011
1384016_at	AI044937	similar to R31449_3 (predicted)	RGD1563634_predicted	1.005	0.976	1.337	0.057	0.804	0.991	1.939	0.005
1391955_at	BI291339	similar to RAB19, member RAS oncogene family	LOC500088	1.006	0.061	1.327	0.006	1.456	0.039	1.222	0.001
1383264_at	BI294715	Similar to RAB3 GTPase-activating protein (predicted)	RGD1306487_predicted	0.866	0.040	0.945	0.166	0.951	0.081	0.916	0.199
1391897_at	BG379295	similar to rab6 GTPase activating protein (GAP and centrosome-associated) (predicted)	RGD1304620_predicted	3.734	0.040	1.068	0.971	4.792	0.001	1.587	0.043
1396817_at	AI599545	Similar to RAD54B homolog isoform 1; RAD54, S. cerevisiae, homolog of, B (predicted)	RGD1306507_predicted	0.694	0.454	0.339	0.016	0.587	0.470	0.346	0.015
1385221_at	BE099682	Similar to RAD54B homolog isoform 1; RAD54, S. cerevisiae, homolog of, B (predicted)	RGD1306507_predicted	1.070	0.913	0.538	0.196	0.745	0.197	0.460	0.042
1396801_at	AI764598	Similar to Ran-binding protein 2 (predicted)	RGD1560047_predicted	1.890	0.114	0.839	0.274	1.246	0.296	1.346	0.458
1383172_at	BF543886	similar to Ran-binding protein 2 (predicted)	RGD1560047_predicted	0.865	0.420	0.746	0.320	1.099	0.059	0.905	0.868
1375371_at	BI296662	similar to Ran-binding protein 2 (predicted)	RGD1560047_predicted	1.039	0.892	1.374	0.110	0.944	0.807	1.123	0.804
1388477_at	AI598440	similar to RAN-binding protein 3 (RanBP3)	LOC501281	0.726	0.189	0.993	0.821	0.764	0.138	0.905	0.490
1371752_at	AI105088	similar to Ran-interacting protein MOG1 (predicted)	RGD1563195_predicted	0.845	0.510	1.163	0.293	1.247	0.306	1.070	0.102
1395264_at	BF545757	similar to Rap1-interacting factor 1 (predicted)	RGD1562474_predicted	0.610	0.038	0.912	0.405	0.719	0.062	0.944	0.223
1382384_at	BM383783	similar to Ras association (RalGDS/AF-6) domain family 6	MGC114410	0.696	0.033	1.252	0.157	0.426	0.005	0.972	0.563
1373036_at	BF283621	similar to Ras GTPase-activating-like protein IQGAP2 (predicted)	RGD1561455_predicted	0.842	0.643	1.011	0.969	0.863	0.708	1.010	0.973
1374165_at	AA818264	similar to Rasa4 protein (predicted)	RGD1565457_predicted	5.067	0.005	4.171	0.000	12.611	0.000	6.171	0.000
1398982_at	AI178239	similar to Ras-related protein Rab-1B	MGC105830	0.515	0.908	0.710	0.016	0.427	0.963	0.714	0.068
1384937_at	AI715121	Similar to RB-associated KRAB repressor (predicted)	RGD1562875_predicted	0.826	0.040	1.232	0.953	0.326	0.003	1.117	0.662
1377787_at	BF407266	similar to Rbm6 protein (predicted)	RGD1560367_predicted	1.223	0.186	1.113	0.141	1.013	0.941	1.127	0.137
1389868_at	AA850780	similar to RCK (predicted)	RGD1564560_predicted	0.661	0.162	0.835	0.228	0.727	0.126	0.737	0.005
1392854_at	BE116127	similar to RCK (predicted)	RGD1564560_predicted	0.622	0.625	0.492	0.164	0.457	0.104	0.500	0.197
1385168_at	BM387883	similar to receptor-interacting factor 1	RGD1306520	1.302	0.157	0.767	0.934	1.887	0.055	1.515	0.131
1396870_at	BF419761	Similar to regulator of G-protein signaling Z1	LOC362477	0.652	0.240	1.268	0.928	0.573	0.010	0.808	0.531
1396547_at	BI299163	Similar to regulator of G-protein signaling Z1	LOC362477	1.061	0.906	0.858	0.471	1.000	0.705	1.016	0.652
1382362_at	AA997890	Similar to regulator of sex-limitation candidate 16 (predicted)	RGD1566325_predicted	0.514	0.001	0.483	0.005	0.759	0.000	0.564	0.004
1393378_at	BM388654	Similar to regulator of sex-limitation candidate 16 (predicted)	RGD1566325_predicted	1.071	0.261	0.543	0.032	0.978	0.908	0.574	0.002
1381481_at	AI028912	Similar to regulator of sex-limitation candidate 16 (predicted)	RGD1566325_predicted	1.452	0.287	1.456	0.229	1.062	0.952	0.886	0.888

1393262_at	BG379771	Similar to regulatory factor X-associated protein	LOC499617	0.557	0.038	0.175	0.008	0.203	0.058	0.191	0.006
1395445_at	AI548975	similar to regulatory factor X-associated protein	LOC499617	1.484	0.302	1.267	0.193	0.874	0.616	0.664	0.533
1373382_at	AI408771	similar to RER1 homolog	RGD1306324	0.763	0.498	1.114	0.727	0.585	0.025	1.197	0.365
1381754_at	BE116951	similar to retinitis pigmentosa GTPase regulator-like protein (predicted)	RGD1563024_predicted	0.796	0.528	1.571	0.105	1.333	0.784	1.470	0.066
1392543_at	BI293462	similar to retinoblastoma binding protein 4 (predicted) /// retinoblastoma binding protein 4 (predicted)	RGD1563620_predicted /// Rbbp4_predicted	0.760	0.069	0.884	0.130	0.791	0.047	0.859	0.204
1376299_at	BI298889	similar to Retinoblastoma-binding protein 2 (RBBP-2)	LOC312678	0.662	0.321	1.234	0.469	0.663	0.003	0.997	0.296
1391689_at	BI282883	similar to Retinoblastoma-binding protein 2 (RBBP-2)	LOC312678	0.953	0.621	1.124	0.296	0.902	0.373	0.907	0.527
1379618_at	AI172526	Similar to Retinoblastoma-binding protein 8 (RBBP-8) (CtBP interacting protein) (CtIP) (Retinoblastoma-interacting protein and myosin-like) (RIM) (predicted)	RGD1308872_predicted	1.019	0.200	1.200	0.253	1.275	0.086	1.031	0.833
1391040_at	AA997052	similar to Retinoblastoma-binding protein 8 (RBBP-8) (CtBP interacting protein) (CtIP) (Retinoblastoma-interacting protein and myosin-like) (RIM) (predicted)	RGD1308872_predicted	1.151	0.309	1.009	0.874	1.427	0.038	1.142	0.062
1398995_at	BM389233	similar to retinoid x receptor interacting protein	RGD1307009	1.713	0.153	1.425	0.008	1.717	0.049	1.000	0.342
1379239_at	AI705987	Similar to retinoid x receptor interacting protein	RGD1307009	1.086	0.506	1.194	0.639	1.582	0.103	0.891	0.276
1391908_at	AW919097	Similar to retinoid x receptor interacting protein	RGD1307009	1.423	0.665	0.817	0.660	1.244	0.651	0.931	0.486
1382689_at	BI276519	similar to RGD1310870_predicted protein	LOC499242	0.546	0.116	1.309	0.456	0.563	0.004	1.074	0.141
1374708_at	BF408594	similar to Rho guanine nucleotide exchange factor (GEF) 10 (predicted)	RGD1565043_predicted	0.999	0.993	0.788	0.348	1.007	0.967	0.646	0.263
1398361_at	BI295127	similar to Rho-GTPase-activating protein PS-GAP-a (predicted)	RGD1562938_predicted	1.003	0.356	1.001	0.961	0.999	0.990	0.999	0.991
1395449_at	BG673211	Similar to ribosomal protein L24-like; 60S ribosomal protein L30 isolog; my024 protein; homolog of yeast ribosomal like protein 24	RGD1309784	0.959	0.584	1.099	0.735	0.953	0.497	1.112	0.139
1374957_at	AI408197	similar to ribosomal protein L27a (predicted)	RGD1560633_predicted	0.414	0.003	0.204	0.000	0.391	0.051	0.283	0.000
1393096_at	BF393086	similar to ribosomal protein L27a (predicted)	RGD1560633_predicted	0.672	0.008	0.586	0.000	0.520	0.002	0.600	0.008
1372043_at	BI282363	similar to ribosomal protein P0-like protein; 60S acidic ribosomal protein PO; ribosomal protein, large, P0-like (predicted)	RGD1311709_predicted	0.690	0.033	4.982	0.000	0.340	0.038	3.472	0.009
1398751_at	NM_031570	similar to ribosomal protein S7	LOC497813	0.873	0.784	1.030	0.661	0.764	0.025	1.038	0.356
1389202_at	AA944520	similar to Ribulose-5-phosphate-3-epimerase	MGC124653	1.504	0.038	1.500	0.038	1.840	0.023	1.586	0.002
1390093_at	BF404417	Similar to Ribulose-5-phosphate-3-epimerase	MGC124653	1.783	0.181	0.837	0.126	2.502	0.036	0.962	0.656
1371467_at	AA891221	similar to RIKEN cDNA 0610007P06	LOC293103	0.887	0.340	1.843	0.019	0.994	0.752	1.338	0.127
1373603_at	BG673166	similar to RIKEN cDNA 0610007P22 (predicted)	RGD1565744_predicted	0.694	0.079	2.709	0.020	0.652	0.010	1.747	0.000
1375297_at	AI168968	similar to RIKEN cDNA 0610008C08 (predicted)	RGD1565289_predicted	0.714	0.141	0.728	0.092	0.719	0.018	0.880	0.047
1371466_at	AI177397	similar to RIKEN cDNA 0610009B22	RGD1306925	0.490	0.099	0.249	0.000	0.606	0.010	0.325	0.011
1393492_at	BE107812	Similar to RIKEN cDNA 0610009F02 (predicted)	RGD1562328_predicted	1.058	0.241	0.911	0.276	1.692	0.042	1.209	0.113
1390421_at	AI232524	Similar to RIKEN cDNA 0610010D20 (predicted)	RGD1310475_predicted	1.046	0.788	0.466	0.522	1.025	0.696	0.865	0.890
1395383_at	BE116860	similar to RIKEN cDNA 0610011L14 gene	RGD1311066	0.864	0.251	0.758	0.042	0.770	0.064	0.910	0.283
1385496_at	AI043653	similar to RIKEN cDNA 0610011N22 gene	RGD735106	0.911	0.109	0.500	0.076	0.918	0.111	0.694	0.140
1385102_at	AI712625	similar to RIKEN cDNA 0610011N22 gene	RGD735106	1.273	0.328	0.965	0.105	1.234	0.225	0.645	0.046
1385101_a_at	AI712625	similar to RIKEN cDNA 0610011N22 gene	RGD735106	0.891	0.947	0.907	0.171	0.715	0.218	0.679	0.060
1398516_at	BF283013	similar to RIKEN cDNA 0610012C01 (predicted)	RGD1566310_predicted	0.823	0.153	0.981	0.905	0.596	0.030	0.926	0.177
1391679_at	AA944639	similar to RIKEN cDNA 0610012H03	LOC499850	1.152	0.267	1.249	0.705	1.011	0.495	1.239	0.693
1389312_at	AI104484	similar to RIKEN cDNA 0610016J10 gene	RGD1309929	0.573	0.024	0.588	0.008	0.564	0.001	0.718	0.009
1376083_at	BE112924	Similar to RIKEN cDNA 0610016J10 gene	RGD1309929	0.987	0.957	0.834	0.211	0.936	0.581	0.902	0.481
1393832_at	AI136337	similar to RIKEN cDNA 0610033I05	RGD1306676	11.880	0.000	4.786	0.003	19.993	0.000	8.437	0.006
1381601_at	BI293235	Similar to RIKEN cDNA 0610037L13	RGD1559786	0.899	0.185	0.984	0.655	0.948	0.850	0.967	0.800
1379288_at	BM389308	similar to RIKEN cDNA 0610037L13	RGD1559786	0.720	0.780	0.885	0.540	0.838	0.912	0.651	0.246
1373009_at	AI176734	similar to RIKEN cDNA 0610037L13	RGD1559786	0.945	0.926	1.120	0.112	0.884	0.221	1.435	0.012
1373454_at	AI230689	similar to RIKEN cDNA 0610037P05	RGD1305823	0.881	0.046	1.392	0.047	1.056	0.544	1.081	0.387
1388376_at	AI235498	similar to RIKEN cDNA 0610038D11 (predicted)	RGD1309710_predicted	1.039	0.856	1.746	0.035	0.914	0.074	1.627	0.025
1382331_at	AI180421	similar to RIKEN cDNA 0610038L10 gene (predicted) /// riboflavin kinase /// similar to riboflavin kinase (predicted)	RGD1560961_predicted /// Rfk /// RGD1563242_predicted	0.870	0.932	0.981	0.248	0.767	0.175	0.949	0.637
1373334_at	AI406609	Similar to RIKEN cDNA 0610039G24 gene (predicted)	RGD1310828_predicted	0.745	0.026	0.788	0.109	0.689	0.276	1.029	0.776
1391387_s_at	AI072956	Similar to RIKEN cDNA 0610039G24 gene (predicted)	RGD1310828_predicted	1.376	0.087	1.600	0.057	1.596	0.265	1.301	0.158
1395322_at	BE116752	Similar to RIKEN cDNA 0610039G24 gene (predicted)	RGD1310828_predicted	1.013	0.964	0.970	0.479	1.031	0.960	0.715	0.527
1389399_at	BG372451	similar to RIKEN cDNA 0610039J04	RGD1562218	0.677	0.072	0.733	0.837	0.746	0.354	0.985	0.737
1398372_at	BG380297	similar to RIKEN cDNA 0610039K22	MGC112682	0.682	0.204	0.872	0.119	0.906	0.992	0.922	0.076
1389054_at	BE113616	similar to RIKEN cDNA 0610040J01	LOC498368	0.621	0.675	0.725	0.226	0.349	0.014	0.847	0.347
1397717_at	BF285031	similar to RIKEN cDNA 0610042E07	RGD1309062	1.006	0.366	1.065	0.925	1.036	0.685	1.078	0.787
1372033_at	BM385414	similar to RIKEN cDNA 0610042E07	RGD1309062	1.145	0.748	1.528	0.730	1.631	0.123	1.596	0.214
1379759_at	BG377329	Similar to RIKEN cDNA 0710008K08 (predicted)	RGD1562691_predicted	0.988	0.921	1.220	0.013	0.994	0.960	1.193	0.022
1390844_at	AI230339	Similar to RIKEN cDNA 1110001A07 gene	RGD1307084	0.930	0.350	0.435	0.001	0.915	0.373	0.555	0.002
1382587_at	AA901257	Similar to RIKEN cDNA 1110001A07 gene	RGD1307084	0.733	0.478	0.779	0.162	1.052	0.145	0.900	0.502

1379261_at	BE111490	similar to RIKEN cDNA 1110001A07 gene	RGD1307084	1.203	0.529	0.724	0.021	0.951	0.660	0.603	0.020
1373371_a_at	AA892572	similar to RIKEN cDNA 1110001J03	MGC112899	0.358	0.301	0.955	0.644	0.393	0.099	0.783	0.669
1395898_at	BF396228	Similar to RIKEN cDNA 1110001M20 (predicted)	RGD1310313_predicted	0.924	0.054	1.290	0.142	0.982	0.881	0.964	0.809
1399012_at	BI285976	similar to RIKEN cDNA 1110001M20 (predicted)	RGD1310313_predicted	0.832	0.493	0.501	0.002	0.957	0.694	0.608	0.000
1375637_at	AI010441	similar to RIKEN cDNA 1110003E01	RGD1311122	0.716	0.092	0.782	0.022	0.681	0.247	0.643	0.030
1385110_at	AI029476	Similar to RIKEN cDNA 1110003E01	RGD1311122	0.776	0.998	1.515	0.019	0.886	0.902	1.344	0.016
1372675_at	BI291418	similar to RIKEN cDNA 1110004E09	RGD1306954	0.747	0.112	1.198	0.230	0.707	0.036	1.167	0.595
1383281_at	AA866227	similar to RIKEN cDNA 1110005A03	RGD1306284	0.785	0.182	0.706	0.001	1.272	0.768	0.791	0.009
1388344_at	BI283112	similar to RIKEN cDNA 1110005A23	RGD1305692	0.728	0.300	0.588	0.101	0.775	0.394	0.707	0.047
1374333_at	AI227700	similar to RIKEN cDNA 1110007C09 (predicted)	RGD1306058_predicted	0.457	0.141	0.493	0.041	0.285	0.025	0.423	0.018
1372596_at	BI284774	similar to RIKEN cDNA 1110007L15 (predicted)	RGD1311660_predicted	0.666	0.061	2.234	0.006	0.439	0.037	1.271	0.212
1376016_at	BF285425	similar to RIKEN cDNA 1110007L15 (predicted)	RGD1311660_predicted	0.534	0.091	0.741	0.006	0.583	0.004	0.627	0.000
1371478_at	AI409756	similar to RIKEN cDNA 1110008F13	RGD1307752	0.767	0.141	1.887	0.002	0.838	0.133	1.607	0.002
1386259_a_at	AI104152	similar to RIKEN cDNA 1110008J03 (predicted)	RGD1306772_predicted	1.416	0.675	0.642	0.433	0.701	0.086	0.974	0.754
1372946_at	AI411957	similar to RIKEN cDNA 1110012L19 (predicted)	RGD1562747_predicted	0.866	0.819	0.435	0.090	0.750	0.873	0.732	0.366
1388457_at	AI176633	similar to RIKEN cDNA 1110012M11	MGC72581	0.700	0.170	0.880	0.162	0.654	0.009	0.872	0.060
1389011_at	BG374333	similar to RIKEN cDNA 1110014D18	RGD1305156	1.282	0.086	1.213	0.148	1.233	0.394	1.033	0.850
1377692_at	BF558563	similar to RIKEN cDNA 1110018J12 (predicted)	RGD1565310_predicted	1.011	0.769	1.285	0.484	1.576	0.052	1.105	0.224
1377141_at	AI103397	Similar to RIKEN cDNA 1110018J18	LOC498685	0.363	0.020	0.220	0.000	0.293	0.010	0.223	0.003
1383443_at	AI146079	similar to RIKEN cDNA 1110018J18	LOC498685	1.007	0.871	0.962	0.975	1.264	0.219	1.083	0.731
1388665_at	BM390489	similar to RIKEN cDNA 1110020A23 (predicted)	RGD1308134_predicted	0.496	0.482	1.615	0.024	0.522	0.066	1.134	0.327
1388408_at	AA800199	similar to RIKEN cDNA 1110020C13	RGD1307129	1.162	0.189	1.167	0.036	1.101	0.079	1.205	0.105
1367529_at	BE113989	similar to RIKEN cDNA 1110021N07 /// similar to Der1-like domain family, member 1	RGD1311835 /// LOC500872	0.806	0.133	1.519	0.006	0.777	0.234	1.436	0.025
1374581_at	BM384392	similar to RIKEN cDNA 1110021N07 /// similar to Der1-like domain family, member 1	RGD1311835 /// LOC500872	0.908	0.215	1.734	0.001	0.799	0.323	1.431	0.004
1389615_at	BI284801	similar to RIKEN cDNA 1110021N07 /// similar to Der1-like domain family, member 1	RGD1311835 /// LOC500872	0.576	0.428	2.337	0.006	0.545	0.006	2.070	0.006
1384407_at	AI602856	similar to RIKEN cDNA 1110025F24 (predicted)	RGD1311451_predicted	0.801	0.440	0.382	0.051	0.814	0.199	0.557	0.057
1373822_at	BI275708	similar to RIKEN cDNA 1110025L05 (predicted)	RGD1565363_predicted	1.080	0.299	1.787	0.006	1.018	0.752	1.322	0.017
1388621_at	BG378803	similar to RIKEN cDNA 1110030J09 (predicted)	RGD1563202_predicted	0.593	0.649	0.896	0.159	0.567	0.139	0.663	0.101
1374292_at	BF414124	similar to RIKEN cDNA 1110031I02	RGD1305007	0.762	0.986	1.060	0.731	0.944	0.377	1.161	0.771
1372677_at	BM392053	similar to RIKEN cDNA 1110033C18	RGD1304783	0.986	0.347	1.852	0.000	0.798	0.068	1.307	0.070
1372644_at	BI282137	similar to RIKEN cDNA 1110038F14 (predicted)	RGD1304721_predicted	0.811	0.734	2.430	0.052	1.194	0.701	1.157	0.524
1373562_at	BF416880	similar to RIKEN cDNA 1110055N21 (predicted)	RGD1309370_predicted	0.806	0.035	1.004	0.374	0.840	0.185	0.997	0.983
1371623_at	AI411896	similar to RIKEN cDNA 1110058L19 (predicted)	RGD1309248_predicted	0.658	0.701	1.116	0.750	0.592	0.539	1.245	0.046
1372667_at	AI170752	similar to RIKEN cDNA 1110059E24	RGD1359158	1.101	0.105	1.889	0.122	0.733	0.442	1.404	0.067
1399117_at	BF546356	similar to RIKEN cDNA 1110059G10	RGD1311745	0.937	0.875	0.601	0.209	0.812	0.377	1.055	0.412
1371860_at	AA944016	similar to RIKEN cDNA 1110059P08	RGD1305031	1.041	0.452	1.263	0.261	0.803	0.815	1.373	0.151
1374145_at	BF414252	similar to RIKEN cDNA 1110061L23	RGD1309809	0.572	0.080	0.623	0.027	0.626	0.116	0.776	0.136
1383077_at	BI287209	similar to RIKEN cDNA 1110063F24 (predicted)	RGD1311622_predicted	0.866	0.153	1.049	0.397	0.954	0.254	0.973	0.647
1374560_at	AI137296	similar to RIKEN cDNA 1190002C06	MGC124825	1.422	0.099	3.688	0.023	1.200	0.119	2.124	0.641
1389629_at	AA819400	similar to RIKEN cDNA 1190003A07 (predicted)	RGD1307103_predicted	1.153	0.296	1.493	0.020	0.991	0.669	1.215	0.102
1373875_at	BG381541	similar to RIKEN cDNA 1190005P17 (predicted)	RGD1308261_predicted	0.923	0.186	2.269	0.001	0.714	0.058	2.022	0.015
1372918_at	BM385785	similar to RIKEN cDNA 1190017O12 (predicted)	RGD1566291_predicted	0.763	0.445	1.281	0.154	0.693	0.113	1.123	0.089
1399049_at	AI230073	similar to RIKEN cDNA 1200003C05 (predicted)	RGD1308917_predicted	0.529	0.097	0.851	0.175	0.524	0.052	0.846	0.113
1373588_at	H33457	similar to RIKEN cDNA 1200004M23	RGD1310323	2.888	0.011	3.285	0.000	3.572	0.010	3.597	0.001
1383471_at	BI286125	similar to RIKEN cDNA 1200006F02	RGD1307594	0.996	0.827	0.782	0.171	0.996	0.990	0.899	0.164
1382150_at	BG377042	similar to RIKEN cDNA 1200007B05 gene	RGD1305072	0.704	0.057	0.370	0.000	0.602	0.017	0.481	0.008
1386088_at	AW141957	similar to RIKEN cDNA 1200007B05 gene	RGD1305072	0.502	0.074	0.469	0.001	0.537	0.151	0.461	0.013
1389970_at	BG378319	similar to RIKEN cDNA 1200009B18; EST AA408438	RGD1310606	0.823	0.008	0.532	0.000	0.939	0.478	0.640	0.005
1375819_at	BI299678	similar to RIKEN cDNA 1200011I18	RGD1307254	0.635	0.064	0.796	0.016	0.621	0.034	0.796	0.124
1377252_at	BF411321	similar to RIKEN cDNA 1200011M11 (predicted)	RGD1306862_predicted	0.999	0.995	0.699	0.157	0.966	0.975	0.945	0.163
1388406_at	AI412090	similar to RIKEN cDNA 1200013P24	RGD1308915	0.313	0.048	0.649	0.301	0.323	0.000	0.840	0.041
1390264_at	BF413854	similar to RIKEN cDNA 1200014J11 (predicted)	RGD1308139_predicted	1.452	0.169	2.154	0.001	1.218	0.285	1.314	0.004
1394213_at	AI030380	similar to RIKEN cDNA 1200014J11 (predicted)	RGD1308139_predicted	1.482	0.514	1.729	0.064	0.884	0.182	1.000	0.989
1377268_at	BM390418	similar to RIKEN cDNA 1200014M14	RGD1310597	0.636	0.016	1.035	0.374	0.579	0.025	1.001	0.990
1390868_at	BF403073	similar to RIKEN cDNA 1200016B10 (predicted)	RGD1308695_predicted	0.811	0.139	3.101	0.066	1.156	0.712	2.116	0.163
1388907_at	BF400873	similar to RIKEN cDNA 1200016B17	RGD1306053	0.463	0.384	0.600	0.021	0.532	0.008	0.472	0.008
1371730_at	BF418786	similar to RIKEN cDNA 1300002A08	RGD1305466	0.797	0.016	0.879	0.222	0.687	0.096	0.856	0.027
1379254_at	AA945882	similar to RIKEN cDNA 1300007B12; clone MNCb-2755	RGD1309892	0.959	0.860	1.094	0.338	0.896	0.590	1.128	0.158

1374414_at	AI412962	similar to RIKEN cDNA 1300010M03	RGD1306844	0.783	0.343	1.052	0.696	0.540	0.019	0.801	0.021
1376087_at	BM386653	similar to RIKEN cDNA 1300010M03 (predicted)	RGD1561189_predicted	0.739	0.612	0.867	0.570	1.041	0.839	1.159	0.270
1381187_at	BE102551	Similar to RIKEN cDNA 1300017J02	RGD1310507	1.012	0.992	1.013	0.949	1.020	0.638	0.996	0.958
1398925_at	BI274664	similar to RIKEN cDNA 1300018I05	RGD1307801	1.288	0.176	0.638	0.037	1.596	0.002	0.824	0.011
1373655_at	BG371863	similar to RIKEN cDNA 1500002O20	RGD1309888	0.796	0.125	1.231	0.014	0.931	0.744	1.113	0.561
1376681_at	AI177038	similar to RIKEN cDNA 1500003O22	RGD1308302	0.685	0.187	1.091	0.518	0.919	0.442	1.284	0.088
1375712_at	AI600090	Similar to RIKEN cDNA 1500006O09 (predicted)	RGD1305475_predicted	0.789	0.521	1.001	0.868	0.712	0.003	1.291	0.156
1398385_at	AI169641	similar to RIKEN cDNA 1500006O09 (predicted)	RGD1305475_predicted	0.548	0.610	0.813	0.232	0.633	0.076	1.116	0.807
1377133_at	BE100973	Similar to RIKEN cDNA 1500009M05 (predicted)	RGD1566242_predicted	2.448	0.030	1.097	0.801	1.510	0.011	1.180	0.997
1392662_at	AI229905	similar to RIKEN cDNA 1500009M05 (predicted)	RGD1566242_predicted	0.748	0.755	2.746	0.011	0.554	0.225	2.367	0.007
1371828_at	BM386571	similar to RIKEN cDNA 1500011H22	RGD1310861	0.463	0.132	0.630	0.001	0.690	0.039	0.661	0.055
1372391_at	AI598937	similar to RIKEN cDNA 1500016H10 (predicted)	RGD1308469_predicted	0.914	0.938	1.306	0.012	0.820	0.094	1.629	0.016
1389013_at	BF420644	similar to RIKEN cDNA 1500016H10 (predicted)	RGD1308469_predicted	1.059	0.980	1.413	0.178	0.635	0.256	1.322	0.243
1373042_at	AW434104	similar to RIKEN cDNA 1500016L11 (predicted)	RGD1305050_predicted	1.001	0.998	1.162	0.176	1.040	0.178	1.006	0.990
1370360_at	AF146738	similar to RIKEN cDNA 1500031L02	RGD621352	0.378	0.197	0.285	0.001	0.308	0.007	0.440	0.002
1385711_at	AW507178	similar to RIKEN cDNA 1500031M22 (predicted)	RGD1311752_predicted	0.780	0.032	1.554	0.024	0.337	0.002	0.699	0.087
1391427_at	AW254563	Similar to RIKEN cDNA 1500031M22 (predicted)	RGD1311752_predicted	0.874	0.189	1.217	0.767	0.396	0.052	1.173	0.163
1389459_at	BE116947	Similar to RIKEN cDNA 1600012F09 (predicted)	RGD1306613_predicted	1.903	0.225	1.425	0.048	1.847	0.077	1.951	0.003
1392504_at	BI297184	similar to RIKEN cDNA 1600012F09 (predicted)	RGD1306613_predicted	0.623	0.248	2.425	0.017	0.293	0.028	1.239	0.337
1395696_at	BF560674	similar to RIKEN cDNA 1600012F09 (predicted) /// hypothetical protein LOC500028	RGD1306613_predicted /// LOC500028	0.998	0.857	1.024	0.830	1.005	0.993	0.995	0.983
1395887_at	BF283642	similar to RIKEN cDNA 1600029D21	LOC363060	1.119	0.047	1.030	0.635	1.007	0.892	0.996	0.843
1384696_at	BE113106	similar to RIKEN cDNA 1700001E04	MGC116197	0.993	0.819	1.008	0.855	1.003	0.952	0.998	0.495
1397537_at	BG665530	similar to RIKEN cDNA 1700001E04 /// similar to cDNA sequence AY358078 /// similar to RIKEN cDNA 4930555G01 /// similar to RIKEN cDNA 4930555G01 /// similar to RIKEN cDNA 1700001E04 /// similar to RIKEN cDNA 4930555G01 /// similar to cDNA sequence AY358078 /// similar to RIKEN cDNA 4930555G01 /// similar to RIKEN cDNA 1700001E04	LOC363433 /// LOC363434 /// LOC367381 /// LOC500070 /// LOC501091 /// LOC501092 /// LOC501221 /// LOC501222 /// LOC501399	1.016	0.978	1.006	0.045	1.267	0.374	0.984	0.050
1389600_at	AW524433	similar to RIKEN cDNA 1700001E04 /// similar to RIKEN cDNA 1700001E04 /// similar to RIKEN cDNA 1700001E04 /// hypothetical protein LOC363306 /// similar to RIKEN cDNA 1700001E04 /// similar to RIKEN cDNA 1700001E04 /// similar to RIKEN cDNA 1700001E04 /// similar to RIKEN cDNA 1700001E04 /// similar to RIKEN cDNA 4930555G01 /// similar to RIKEN cDNA 2610042L04 /// similar to cDNA sequence AY358078 /// similar to cDNA sequence AY358078 /// similar to RIKEN cDNA 1700001E04 /// similar to cDNA sequence AY358078 /// similar to Reticulocalbin 1 precursor /// similar to RIKEN cDNA 4930555G01 /// similar to cDNA sequence AY358078 /// hypothetical protein LOC501396 /// similar to RIKEN cDNA 1700001E04	LOC301748 /// LOC316186 /// LOC360998 /// LOC363306 /// LOC363320 /// LOC363433 /// LOC498374 /// LOC501091 /// LOC501092 /// LOC501093 /// LOC501221 /// LOC501225 /// LOC501226 /// LOC501245 /// LOC501250 /// LOC501253 /// LOC501393 /// LOC501396 /// LOC501399	1.128	0.761	1.667	0.229	1.625	0.084	1.839	0.041
1379347_at	BM389290	Similar to RIKEN cDNA 1700023M03	RGD1305457	0.383	0.003	0.824	0.008	0.562	0.006	0.568	0.036
1376689_at	BF282636	similar to RIKEN cDNA 1700023M03	RGD1305457	0.475	0.137	0.299	0.050	0.640	0.757	0.679	0.346
1390502_at	BF388757	similar to RIKEN cDNA 1700025G04 gene (predicted)	RGD1309104_predicted	0.997	0.979	1.195	0.170	1.083	0.731	1.083	0.982
1398371_at	AI409075	similar to RIKEN cDNA 1700034M03 gene	RGD1304751	1.710	0.005	1.984	0.026	1.428	0.031	2.464	0.007
1388563_at	AI169287	similar to RIKEN cDNA 1700034P14 (predicted)	RGD1305492_predicted	1.372	0.024	2.113	0.000	1.240	0.072	1.529	0.039
1396128_at	BG670404	similar to RIKEN cDNA 1700034P14 (predicted)	RGD1305492_predicted	1.003	0.735	1.774	0.124	0.633	0.159	1.193	0.473
1373436_at	AI171288	similar to RIKEN cDNA 1700040L02 (predicted)	RGD1306739_predicted	1.196	0.130	1.140	0.188	1.198	0.130	1.052	0.081
1386566_at	BF558962	Similar to RIKEN cDNA 1700047I17 (predicted)	RGD1562713_predicted	6.037	0.000	2.202	0.044	4.903	0.010	1.678	0.012
1382884_at	AI009813	Similar to RIKEN cDNA 1700047I17 (predicted)	RGD1562713_predicted	6.740	0.017	3.477	0.004	4.823	0.067	2.485	0.009
1376883_at	BI284887	similar to RIKEN cDNA 1700048E23	MGC93920	0.872	0.675	0.704	0.036	0.792	0.126	0.787	0.252
1393027_at	AI058848	similar to RIKEN cDNA 1700052N19	RGD1305235	1.291	0.545	1.173	0.111	0.993	0.796	1.696	0.017
1389187_at	BI286421	Similar to RIKEN cDNA 1700088E04	RGD1359634	1.519	0.783	1.449	0.702	0.968	0.305	1.278	0.557
1379044_at	AW534064	Similar to RIKEN cDNA 1700108L22	RGD1307509	0.828	0.477	0.737	0.071	0.972	0.135	0.424	0.030
1382219_at	AA945904	similar to RIKEN cDNA 1700108L22	RGD1307509	0.957	0.502	1.400	0.137	0.775	0.020	1.235	0.259
1379473_at	BI284815	similar to RIKEN cDNA 1700108L22	RGD1307509	0.929	0.792	0.986	0.932	0.974	0.240	0.500	0.121
1372090_at	AI231566	similar to RIKEN cDNA 1700108M19 (predicted)	RGD1560395_predicted	2.196	0.093	1.506	0.011	3.215	0.004	1.964	0.006
1377387_a_at	BF414330	similar to RIKEN cDNA 1810009K13 (predicted)	RGD1562184_predicted	1.001	0.076	1.041	0.855	2.898	0.053	1.218	0.268
1374183_at	AI705068	similar to RIKEN cDNA 1810011O16 (predicted)	RGD1309624_predicted	1.113	0.854	4.305	0.003	0.450	0.062	2.425	0.016
1377830_a_at	BF281728	similar to RIKEN cDNA 1810014F10 gene (predicted)	RGD1311186_predicted	0.326	0.018	0.566	0.241	0.307	0.027	0.752	0.372

1376861_at	AW525240	similar to RIKEN cDNA 1810018L05 /// similar to motile sperm domain containing 1	LOC317312 /// LOC501648	1.354	0.445	1.529	0.124	1.655	0.371	2.521	0.640
1383104_at	BI295116	similar to RIKEN cDNA 1810020D17 (predicted)	RGD1561459_predicted	0.942	0.775	0.574	0.072	0.841	0.612	0.929	0.087
1371634_at	BE107851	similar to RIKEN cDNA 1810020E01	RGD1305677	0.827	0.639	1.828	0.002	0.715	0.802	1.875	0.001
1373585_at	BE116774	similar to RIKEN cDNA 1810020G14 (predicted)	RGD1310781_predicted	0.476	0.224	0.463	0.004	0.409	0.254	0.536	0.009
1389561_at	BE110624	similar to RIKEN cDNA 1810021J13	RGD1311364	0.275	0.004	0.275	0.001	0.349	0.008	0.262	0.016
1388884_at	BM390774	similar to RIKEN cDNA 1810022C23	RGD1310224	0.774	0.427	0.505	0.014	1.073	0.681	0.776	0.423
1390579_at	BI294760	similar to RIKEN cDNA 1810029B16 (predicted)	RGD1305222_predicted	1.000	0.275	7.969	0.007	0.985	0.100	2.693	0.019
1394240_at	AI014154	Similar to RIKEN cDNA 1810030N24 (predicted)	RGD1305158_predicted	0.721	0.039	0.676	0.031	0.311	0.016	0.812	0.010
1399107_at	BE112193	similar to RIKEN cDNA 1810030N24 (predicted)	RGD1305158_predicted	0.534	0.041	0.472	0.068	0.264	0.044	0.685	0.236
1384550_at	AW917943	similar to RIKEN cDNA 1810030O07 (predicted)	RGD1565685_predicted	1.231	0.219	0.679	0.051	1.856	0.110	0.834	0.788
1383100_at	AI070897	similar to RIKEN cDNA 1810036I24 (predicted)	RGD1306343_predicted	0.647	0.097	0.916	0.532	0.777	0.091	1.056	0.487
1377654_at	BE328936	similar to RIKEN cDNA 1810037C20 (predicted)	RGD1562076_predicted	0.784	0.269	0.565	0.003	0.768	0.084	0.676	0.058
1388306_at	BM383758	similar to RIKEN cDNA 1810042K04 (predicted)	RGD1305593_predicted	0.656	0.427	1.045	0.770	0.599	0.035	1.021	0.881
1388770_at	BI275670	similar to RIKEN cDNA 1810045K17	RGD1304890	0.463	0.105	0.711	0.030	0.563	0.010	0.570	0.021
1372813_at	AA858862	similar to RIKEN cDNA 1810046J19 (predicted)	RGD1306682_predicted	0.622	0.626	1.253	0.435	0.709	0.295	1.141	0.851
1376086_at	AW528625	similar to RIKEN cDNA 1810047C23	RGD1311161	0.766	0.025	1.308	0.047	0.665	0.048	1.212	0.128
1373071_at	AI103101	similar to RIKEN cDNA 1810054G18 (predicted)	RGD1308901_predicted	0.953	0.777	2.367	0.003	0.597	0.395	1.829	0.007
1374233_at	BG372723	similar to RIKEN cDNA 1810055E12 (predicted)	RGD1308326_predicted	0.547	0.186	0.556	0.020	0.784	0.045	0.561	0.050
1375829_at	AW525101	similar to RIKEN cDNA 1810055E12 (predicted)	RGD1308326_predicted	0.989	0.611	1.760	0.052	0.996	0.975	0.940	0.239
1390232_at	BM388441	similar to RIKEN cDNA 1810055G02	RGD1311946	0.367	0.017	0.921	0.509	0.342	0.016	0.928	0.772
1389467_at	BM391248	similar to RIKEN cDNA 1810057C19	MGC108778	0.330	0.007	0.344	0.030	0.229	0.012	0.240	0.053
1383594_at	AW914775	similar to RIKEN cDNA 1810060J02	LOC312863	0.857	0.283	0.916	0.643	0.998	0.916	0.925	0.609
1386755_at	BF552559	similar to RIKEN cDNA 1810060J02	LOC312863	0.622	0.635	1.390	0.273	1.005	0.886	1.121	0.567
1374807_at	AI230067	similar to RIKEN cDNA 1810063B07 gene (predicted)	RGD1310877_predicted	0.878	0.521	0.671	0.007	1.169	0.237	0.584	0.087
1376896_at	AI227699	Similar to RIKEN cDNA 1810074P20 (predicted)	RGD1309308_predicted	0.637	0.305	0.762	0.094	0.817	0.106	0.724	0.094
1382526_at	BF281921	similar to RIKEN cDNA 1810074P20 (predicted)	RGD1309308_predicted	0.693	0.789	1.412	0.030	1.145	0.836	1.086	0.413
1372814_at	BF283084	similar to RIKEN cDNA 2010005O13	RGD1310623	1.118	0.708	0.766	0.068	1.124	0.743	0.813	0.108
1393005_at	AW916965	similar to RIKEN cDNA 2010005O13	RGD1310623	1.055	0.735	1.152	0.157	0.901	0.989	1.400	0.033
1381588_at	BG377308	similar to RIKEN cDNA 2010005O13	RGD1310623	0.968	0.948	1.025	0.893	0.967	0.944	1.043	0.913
1373244_at	AI412948	similar to RIKEN cDNA 2010008E23 gene	RGD1304758	1.184	0.172	1.241	0.000	1.396	0.087	1.228	0.001
1394807_at	AW522357	Similar to RIKEN cDNA 2010008E23 gene	RGD1304758	1.626	0.347	1.702	0.066	1.717	0.034	1.128	0.236
1389782_at	AI408993	similar to RIKEN cDNA 2010107G23 (predicted)	RGD1305587_predicted	0.547	0.050	0.554	0.003	0.554	0.062	0.772	0.027
1391776_at	BF403524	similar to RIKEN cDNA 2010110K16 (predicted)	RGD1305283_predicted	1.123	0.590	1.225	0.961	1.561	0.039	1.541	0.266
1377964_at	BM390539	similar to RIKEN cDNA 2010200O16 (predicted)	RGD1564454_predicted	0.879	0.490	4.142	0.004	0.639	0.418	2.736	0.013
1393186_at	BE117182	similar to RIKEN cDNA 2010200O16 (predicted)	RGD1564454_predicted	0.789	0.900	0.993	0.334	0.746	0.070	0.930	0.221
1389228_at	AI412292	Similar to RIKEN cDNA 2010309E21 (predicted)	RGD1304825_predicted	0.898	0.359	2.348	0.013	0.637	0.009	1.821	0.033
1371965_at	BF283269	similar to RIKEN cDNA 2010311D03	RGD1303272	0.648	0.296	0.519	0.004	0.506	0.059	0.673	0.003
1388542_at	BI283120	similar to RIKEN cDNA 2010315L10 (predicted) /// similar to 2010315L10Rik protein	RGD1306660_predicted /// LOC292282	0.962	0.355	0.824	0.165	0.940	0.300	0.836	0.051
1383774_at	BG376677	similar to RIKEN cDNA 2010316F05 (predicted)	RGD1308179_predicted	0.355	0.005	0.773	0.106	0.421	0.009	0.580	0.116
1379475_at	BF396403	similar to RIKEN cDNA 2210009G21 (predicted)	RGD1563120_predicted	0.626	0.393	0.273	0.009	0.565	0.085	0.458	0.148
1373112_at	BE110870	Similar to RIKEN cDNA 2210010N04 gene	RGD1306873	1.582	0.147	0.965	0.621	1.300	0.966	0.949	0.718
1375656_at	AI717725	similar to RIKEN cDNA 2210010N04 gene	RGD1306873	1.096	0.875	1.376	0.280	2.149	0.083	1.033	0.860
1372535_at	AI410203	similar to RIKEN cDNA 2210012G02	LOC366431	0.998	0.989	1.427	0.067	0.995	0.979	1.479	0.202
1372454_at	BG378568	similar to RIKEN cDNA 2210016L21 gene	RGD1311899	0.743	0.565	0.602	0.003	0.815	0.024	0.678	0.027
1389393_at	AI232269	similar to RIKEN cDNA 2210412D01	RGD1308210	1.645	0.068	1.604	0.048	1.547	0.135	1.198	0.274
1373315_at	AI176425	Similar to RIKEN cDNA 2210412D01	RGD1308210	0.681	0.107	0.872	0.904	0.468	0.002	0.833	0.512
1372604_at	BI289459	similar to RIKEN cDNA 2210421G13 (predicted)	RGD1565597_predicted	34.242	0.000	34.714	0.000	47.175	0.001	94.349	0.001
1397167_at	AW534046	Similar to RIKEN cDNA 2210421G13 (predicted)	RGD1565356_predicted	0.701	0.359	1.224	0.332	0.823	0.033	1.006	0.466
1374420_at	BE117936	similar to RIKEN cDNA 2310001A20	RGD1308874	0.761	0.866	0.837	0.065	0.776	0.857	0.820	0.193
1390382_at	BF414043	similar to RIKEN cDNA 2310003F16 (predicted)	RGD1311457_predicted	0.886	0.827	1.540	0.012	0.621	0.024	1.001	0.058
1392960_at	AI713860	similar to RIKEN cDNA 2310004I24 gene	RGD1309906	0.769	0.758	1.362	0.021	0.999	0.997	1.076	0.599
1376379_a_at	AW252141	similar to RIKEN cDNA 2310004I24 gene	RGD1309906	0.625	0.875	1.006	0.893	1.045	0.458	0.909	0.563
1373857_at	BM387116	Similar to RIKEN cDNA 2310005N03 gene	RGD1309105_predicted	0.304	0.094	0.363	0.005	0.345	0.024	0.487	0.088
1380821_a_at	AI072678	Similar to RIKEN cDNA 2310005N03 gene	RGD1309105_predicted	0.834	0.429	0.665	0.037	1.207	0.921	0.722	0.293
1372823_at	BE117126	Similar to RIKEN cDNA 2310005N03 gene	RGD1309105_predicted	1.104	0.760	1.657	0.007	1.021	0.405	1.346	0.004
1388570_at	AI232494	similar to RIKEN cDNA 2310005O14	LOC498909	0.552	0.012	0.820	0.539	0.476	0.030	0.902	0.415
1390491_at	BM390772	similar to RIKEN cDNA 2310005O14	LOC498909	0.547	0.339	1.098	0.587	1.750	0.344	1.200	0.552
1393537_at	AI060026	Similar to RIKEN cDNA 2310005P05	RGD1307401	1.513	0.883	0.973	0.769	0.733	0.387	0.800	0.058
1376985_at	AA866482	similar to RIKEN cDNA 2310007F12 (predicted)	RGD1562416_predicted	0.829	0.447	1.765	0.001	0.613	0.004	1.487	0.005
1372704_at	BE098941	similar to RIKEN cDNA 2310008M10 (predicted)	RGD1560708_predicted	0.708	0.238	0.836	0.014	0.618	0.071	0.774	0.043

1373791_at	BI289399	similar to RIKEN cDNA 2310011J03	RGD1359127	0.824	0.822	0.919	0.456	0.578	0.067	1.438	0.026
1377194_a_at	BE107471	similar to RIKEN cDNA 2310015N07	RGD1308637	1.205	0.118	1.539	0.018	1.180	0.135	1.523	0.004
1382590_at	BI277914	Similar to RIKEN cDNA 2310015N21 (predicted)	RGD1563347_predicted	1.141	0.169	0.997	0.973	0.709	0.962	0.989	0.988
1393165_at	BG377684	similar to RIKEN cDNA 2310028N02	RGD1359339	0.359	0.021	0.585	0.015	0.318	0.003	0.488	0.010
1397714_at	BF565706	similar to RIKEN cDNA 2310035C23 (predicted)	RGD1307235_predicted	1.905	0.010	0.991	0.810	1.549	0.054	1.118	0.634
1374253_at	BI291355	similar to RIKEN cDNA 2310035C23 (predicted)	RGD1307235_predicted	0.712	0.197	0.551	0.007	1.490	0.926	0.897	0.055
1394925_at	AI578037	similar to RIKEN cDNA 2310035C23 (predicted)	RGD1307235_predicted	1.222	0.282	1.242	0.941	1.941	0.021	0.993	0.781
1398952_at	AI233222	similar to RIKEN cDNA 2310036O22 (predicted) /// similar to RIKEN cDNA 2310036O22 (predicted)	RGD1564093_predicted /// RGD1563295_predicted	1.112	0.062	1.199	0.031	1.062	0.371	1.247	0.023
1388616_at	AI233746	similar to RIKEN cDNA 2310042G06	MGC72955	0.548	0.148	0.692	0.004	0.492	0.007	0.694	0.042
1399135_at	BI290646	similar to RIKEN cDNA 2310042P20	MGC94954	0.676	0.291	0.902	0.088	1.002	0.350	0.977	0.985
1382100_at	AA997169	similar to RIKEN cDNA 2310047O13 (predicted)	RGD1309605_predicted	0.576	0.007	0.947	0.279	0.655	0.007	0.865	0.681
1372488_at	BM386249	similar to RIKEN cDNA 2310057D15	RGD1309016	0.930	0.995	2.535	0.040	0.831	0.992	1.366	0.179
1385208_at	BF391430	similar to RIKEN cDNA 2310057M21	RGD1305014	1.168	0.550	0.837	0.808	1.015	0.707	1.205	0.896
1391634_at	BF552826	similar to RIKEN cDNA 2310057N15 (predicted)	RGD1562078_predicted	1.146	0.447	0.923	0.714	1.002	0.090	0.928	0.787
1372952_at	BI291286	similar to RIKEN cDNA 2310061F22	LOC292069	0.849	0.445	1.448	0.058	1.049	0.517	0.955	0.753
1372913_at	AA849734	similar to RIKEN cDNA 2310065K24	RGD1307433	1.493	0.014	1.347	0.011	3.001	0.006	1.440	0.220
1382490_at	BF284288	Similar to RIKEN cDNA 2310067G05	LOC301113	0.817	0.067	0.597	0.016	1.501	0.734	0.829	0.018
1379273_at	BE109836	similar to RIKEN cDNA 2310075A12	LOC300472	0.475	0.099	0.934	0.236	0.280	0.000	0.769	0.014
1395289_at	H33428	similar to RIKEN cDNA 2310075A12	LOC300472	0.479	0.139	0.788	0.853	0.525	0.036	0.475	0.116
1388412_at	BI284376	similar to RIKEN cDNA 2400003C14	RGD1307799	1.360	0.015	1.411	0.025	1.162	0.016	1.184	0.020
1374047_at	BM390427	similar to RIKEN cDNA 2400010D15	RGD1311805	0.694	0.210	0.663	0.022	0.968	0.173	1.026	0.462
1393009_at	AI535126	similar to RIKEN cDNA 2410002F23	RGD1309326	0.610	0.071	1.357	0.074	0.451	0.026	1.460	0.128
1385648_at	AA956840	Similar to RIKEN cDNA 2410002O22 gene	RGD1306583	1.917	0.013	1.555	0.026	0.562	0.114	0.646	0.042
1372547_at	AI175034	similar to RIKEN cDNA 2410002O22 gene	RGD1306583	0.634	0.100	0.953	0.639	0.608	0.012	0.919	0.379
1379795_at	AA819224	similar to RIKEN cDNA 2410002O22 gene	RGD1306583	0.439	0.170	0.649	0.139	0.864	0.879	0.606	0.286
1375918_at	AW917662	similar to RIKEN cDNA 2410003C20	LOC497967	0.636	0.275	0.851	0.574	0.397	0.073	0.906	0.852
1384105_at	BE109571	Similar to RIKEN cDNA 2410003C20	LOC497967	0.827	0.668	1.083	0.636	0.929	0.775	1.632	0.090
1374841_at	AI237644	similar to RIKEN cDNA 2410004B18 (predicted)	RGD1560065_predicted	1.164	0.389	0.558	0.057	0.687	0.148	0.571	0.166
1384710_at	BF403316	similar to RIKEN cDNA 2410004F06 (predicted)	RGD1562792_predicted	0.998	0.977	1.000	0.185	1.021	0.824	0.997	0.162
1374661_at	AW524523	similar to RIKEN cDNA 2410004H02	LOC361571	0.865	0.062	1.942	0.000	0.697	0.280	1.812	0.005
1389786_at	AA946272	Similar to RIKEN cDNA 2410005O16	LOC500419	1.222	0.598	0.801	0.424	1.797	0.051	0.999	0.479
1390967_a_at	AW919980	similar to RIKEN cDNA 2410006F12	RGD1306841	0.690	0.997	2.533	0.011	0.936	0.124	1.569	0.065
1374848_at	AI599867	Similar to RIKEN cDNA 2410016F19 (predicted)	RGD1307434_predicted	0.524	0.002	1.170	0.411	0.939	0.221	1.037	0.848
1384185_at	BI289594	similar to RIKEN cDNA 2410016O06 (predicted)	RGD1307704_predicted	0.690	0.348	1.127	0.318	0.586	0.007	1.004	0.511
1373639_at	BE115570	similar to RIKEN cDNA 2410022L05 (predicted)	RGD1565675_predicted	1.128	0.663	1.405	0.094	1.397	0.114	1.917	0.023
1379816_at	AI502578	Similar to RIKEN cDNA 2410025L10 (predicted)	RGD1563342_predicted	1.082	0.468	0.622	0.007	3.234	0.034	0.825	0.276
1392491_at	AI072533	Similar to RIKEN cDNA 2410127L17	RGD1311863	0.843	0.040	0.786	0.512	0.933	0.623	1.155	0.542
1371461_at	BF414239	similar to RIKEN cDNA 2410166I05	RGD1305453	0.719	0.447	0.941	0.701	0.616	0.021	0.998	0.877
1390392_at	BI301527	similar to RIKEN cDNA 2500001K11 (predicted)	RGD1309602_predicted	0.578	0.003	1.045	0.920	0.758	0.206	1.213	0.333
1398359_at	AI008549	similar to RIKEN cDNA 2500002L14; EST C77350	MGC94464	0.645	0.581	1.194	0.601	0.758	0.385	1.027	0.854
1371373_at	AI010460	similar to RIKEN cDNA 2500002L14; EST C77350	MGC94464	0.881	0.721	0.948	0.146	0.990	0.811	0.963	0.250
1384925_at	AI045021	Similar to RIKEN cDNA 2510005D08 (predicted)	RGD1306762_predicted	0.718	0.020	0.704	0.180	0.496	0.040	0.653	0.360
1390098_at	AA955687	similar to RIKEN cDNA 2510005D08 (predicted)	RGD1306762_predicted	0.728	0.724	0.840	0.402	0.808	0.027	0.656	0.769
1389682_at	BF284967	similar to RIKEN cDNA 2510006C20	RGD1309120	0.774	0.123	0.585	0.000	0.724	0.298	0.765	0.063
1374210_at	BM383870	similar to RIKEN cDNA 2510027N19	RGD1307760	1.672	0.213	1.939	0.060	1.753	0.014	1.892	0.051
1371654_at	BF417252	similar to RIKEN cDNA 2510039O18 (predicted)	RGD1305350_predicted	0.658	0.051	0.975	0.883	0.512	0.032	1.110	0.052
1388508_at	BM384233	similar to RIKEN cDNA 2510049I19 (predicted)	RGD1561287_predicted	0.595	0.193	1.376	0.174	0.761	0.015	1.274	0.834
1383779_at	BF566806	similar to RIKEN cDNA 2600005C20 (predicted)	RGD1305633_predicted	1.164	0.985	0.895	0.481	0.805	0.226	1.003	0.947
1372549_at	AI409460	similar to RIKEN cDNA 2600017H02 (predicted)	RGD1561781_predicted	0.881	0.053	0.997	0.844	0.775	0.008	1.000	0.990
1392923_at	H34314	Similar to RIKEN cDNA 2610001E06 (predicted)	RGD1308126_predicted	1.415	0.021	0.749	0.001	0.736	0.215	0.544	0.035
1392562_at	BM391400	similar to RIKEN cDNA 2610001E06 (predicted)	RGD1308126_predicted	1.179	0.127	1.731	0.014	0.995	0.856	0.888	0.322
1382436_at	BM386497	similar to RIKEN cDNA 2610002M06 (predicted)	RGD1566265_predicted	1.396	0.138	2.925	0.006	1.821	0.100	3.364	0.004
1374124_at	AA851397	similar to RIKEN cDNA 2610003J06	RGD1307381	0.589	0.319	0.743	0.050	0.811	0.239	0.589	0.016
1379318_at	BI296812	Similar to RIKEN cDNA 2610019F03	LOC498662	0.912	0.514	1.004	0.988	0.873	0.357	1.000	0.987
1399130_at	AW918690	similar to RIKEN cDNA 2610022G08	LOC502782	0.276	0.025	0.421	0.104	0.351	0.007	0.236	0.053
1372543_at	BI282107	similar to RIKEN cDNA 2610029G23 (predicted)	RGD1562502_predicted	1.177	0.919	1.547	0.021	0.879	0.150	1.636	0.002
1382186_a_at	AI136314	similar to RIKEN cDNA 2610029K21	RGD1311086	0.214	0.010	5.225	0.005	0.202	0.001	5.488	0.006
1393128_at	BI288424	similar to RIKEN cDNA 2610029K21	RGD1311086	0.525	0.139	1.526	0.935	0.467	0.097	1.534	0.936
1382188_at	BF397703	similar to RIKEN cDNA 2610029K21	RGD1311086	0.813	0.645	1.382	0.454	0.821	0.253	1.235	0.196
1382187_at	AI136314	similar to RIKEN cDNA 2610029K21	RGD1311086	0.991	0.997	1.007	0.985	0.992	0.987	1.354	0.046

1399009_at	BE329028	similar to RIKEN cDNA 2610034N24 (predicted)	RGD1305036_predicted	0.704	0.076	0.806	0.093	0.638	0.161	0.899	0.962
1381139_at	BM387383	Similar to RIKEN cDNA 2610039E05 (predicted)	RGD1560840_predicted	0.929	0.999	0.883	0.960	1.121	0.548	0.754	0.242
1378875_a_at	AW522817	similar to RIKEN cDNA 2610110G12	RGD1303066	0.611	0.385	0.373	0.001	0.971	0.927	0.515	0.107
1391554_at	BE113319	Similar to RIKEN cDNA 2610110G12	RGD1303066	0.968	0.522	0.737	0.052	1.122	0.631	0.895	0.047
1396713_at	BE121434	Similar to RIKEN cDNA 2610110G12	RGD1303066	0.995	0.990	0.749	0.606	1.006	0.979	0.999	0.995
1372066_at	AI170703	similar to RIKEN cDNA 2610204K14	RGD1310022	0.874	0.208	1.250	0.361	0.543	0.272	1.243	0.088
1372185_at	BF557934	similar to RIKEN cDNA 2610205E22	RGD1306582	0.842	0.573	3.493	0.019	0.785	0.184	2.222	0.026
1397468_at	BI288527	similar to RIKEN cDNA 2610207I16	RGD1305387	0.831	0.147	0.938	0.754	1.506	0.097	0.782	0.867
1384244_at	AA964752	similar to RIKEN cDNA 2610207I16	RGD1305387	0.787	0.207	1.508	0.001	1.602	0.015	2.069	0.009
1372553_at	AI233205	similar to RIKEN cDNA 2610301B20; EST AI428449	MGC94199	0.764	0.012	0.641	0.028	0.735	0.304	0.763	0.025
1390146_at	BF414998	similar to RIKEN cDNA 2610318G18 (predicted)	RGD1306105_predicted	0.479	0.007	0.595	0.005	0.687	0.028	0.792	0.049
1399013_at	AI412609	similar to RIKEN cDNA 2610318K02 (predicted)	RGD1310905_predicted	0.833	0.466	1.231	0.147	0.771	0.007	1.149	0.102
1393451_at	BI295149	similar to RIKEN cDNA 2610510J17	RGD1310953	1.757	0.769	0.993	0.049	1.001	0.992	0.998	0.992
1383560_at	BI303213	Similar to RIKEN cDNA 2610528A15	RGD1305984	0.407	0.074	1.058	0.976	0.462	0.089	0.708	0.594
1389810_at	BI275054	similar to RIKEN cDNA 2610528A15	RGD1305984	0.466	0.107	1.101	0.486	0.945	0.790	1.367	0.060
1374478_at	AA819329	similar to RIKEN cDNA 2610528J11 (predicted)	RGD1305347_predicted	0.435	0.027	0.515	0.024	0.283	0.013	0.375	0.014
1373074_at	AI171367	similar to RIKEN cDNA 2700002I20	RGD1307279	0.495	0.836	0.954	0.780	0.949	0.845	1.169	0.095
1381118_at	AW526652	similar to RIKEN cDNA 2700007P21	RGD1311463	0.350	0.002	0.485	0.067	0.408	0.013	0.407	0.064
1392967_at	BF550692	similar to RIKEN cDNA 2700062C07	MGC116121	0.702	0.013	0.525	0.006	0.863	0.985	0.653	0.016
1376638_at	BI288798	similar to RIKEN cDNA 2700067D09	RGD1305833	0.914	0.422	0.738	0.021	1.007	0.581	0.910	0.012
1374321_at	AI227598	Similar to RIKEN cDNA 2700081O15 (predicted)	RGD1560108_predicted	1.033	0.205	0.554	0.025	1.674	0.114	0.880	0.449
1374430_at	BI274617	similar to RIKEN cDNA 2700085E05	RGD1307010	0.665	0.322	0.954	0.366	0.754	0.045	0.939	0.164
1390284_at	BM383683	Similar to RIKEN cDNA 2700091N06 (predicted)	RGD1310710_predicted	0.887	0.467	1.063	0.851	0.833	0.176	0.981	0.876
1398374_at	BE101274	similar to RIKEN cDNA 2810002D13 gene	RGD1307128	0.994	0.935	0.729	0.136	0.745	0.074	0.695	0.191
1372265_at	AI172218	similar to RIKEN cDNA 2810002N01	RGD1304719	0.631	0.187	0.815	0.114	0.456	0.026	0.902	0.495
1375701_at	BF400575	similar to RIKEN cDNA 2810013M15	LOC360568	1.895	0.058	1.201	0.246	1.547	0.020	0.709	0.051
1376201_at	AI070397	similar to RIKEN cDNA 2810013M15	LOC360568	1.125	0.992	0.776	0.323	1.001	0.988	0.997	0.214
1373413_at	AW531093	similar to RIKEN cDNA 2810021O14 (predicted)	RGD1310481_predicted	0.870	0.872	0.778	0.080	0.991	0.681	0.846	0.294
1395336_at	BE098691	similar to RIKEN cDNA 2810022L02	LOC501207	1.018	0.700	1.003	0.935	1.016	0.946	0.999	0.989
1373946_at	AI409943	similar to RIKEN cDNA 2810037C14	RGD1305915	0.957	0.938	1.233	0.441	0.838	0.510	1.062	0.217
1392928_at	AA891693	similar to RIKEN cDNA 2810055F11 (predicted)	RGD1305721_predicted	0.829	0.883	1.107	0.046	1.144	0.065	1.504	0.067
1373474_at	BE115948	similar to RIKEN cDNA 2810403A07	RGD1565775	0.928	0.066	0.964	0.946	1.140	0.797	1.061	0.336
1395535_at	BF548555	similar to RIKEN cDNA 2810405J04	RGD1305486	1.078	0.266	1.002	0.946	1.328	0.049	1.000	0.997
1373870_at	BE110630	similar to RIKEN cDNA 2810405J04	RGD1305486	0.757	0.356	0.793	0.082	0.742	0.026	0.870	0.356
1397077_at	BF410515	Similar to RIKEN cDNA 2810409H07	RGD1307982	0.990	0.670	1.110	0.959	0.998	0.877	1.093	0.965
1388645_at	AI175494	similar to RIKEN cDNA 2810409H07	RGD1307982	0.969	0.861	1.558	0.001	1.219	0.064	2.103	0.000
1383891_a_at	AA997097	similar to RIKEN cDNA 2810417J12 gene (predicted)	RGD1311166_predicted	1.179	0.541	1.394	0.098	1.003	0.298	1.466	0.093
1379337_at	BI284334	similar to RIKEN cDNA 2810421I24	RGD1307883	1.065	0.562	2.441	0.053	0.731	0.054	2.715	0.097
1372108_at	BE098359	similar to RIKEN cDNA 2810422B04	LOC500199	0.418	0.042	0.751	0.587	0.840	0.035	0.710	0.463
1393834_at	BF402667	Similar to RIKEN cDNA 2810426N06 (predicted)	RGD1562094_predicted	1.356	0.079	0.951	0.568	2.932	0.016	1.370	0.529
1392956_at	BG373315	Similar to RIKEN cDNA 2810443J12 (predicted)	RGD1304868_predicted	0.961	0.798	0.711	0.813	0.759	0.325	1.457	0.069
1373198_at	BF283018	similar to RIKEN cDNA 2810451A06	RGD1311098	0.482	0.347	1.022	0.874	0.350	0.024	0.723	0.733
1373688_at	AA849532	similar to RIKEN cDNA 2810453I06	LOC498145	0.663	0.003	1.304	0.445	0.845	0.291	1.005	0.358
1378399_at	BE111635	similar to RIKEN cDNA 2810453I06	LOC498145	0.706	0.181	1.350	0.214	0.758	0.099	1.156	0.558
1379284_at	AI411760	similar to RIKEN cDNA 2810457I06 (predicted)	RGD1310357_predicted	0.995	0.696	1.334	0.062	0.999	0.984	1.064	0.016
1377703_at	AA819694	similar to RIKEN cDNA 2900009I07	RGD1310316	0.769	0.854	0.903	0.591	0.526	0.059	0.916	0.343
1373100_at	BI288811	similar to RIKEN cDNA 2900010J23	LOC499779	0.802	0.217	0.706	0.058	0.701	0.193	0.652	0.103
1380750_at	BF398240	Similar to RIKEN cDNA 2900010J23	LOC499779	0.646	0.951	0.727	0.060	0.840	0.828	0.649	0.020
1397901_at	BI298378	Similar to RIKEN cDNA 2900010J23 (predicted)	RGD1561465_predicted	1.064	0.317	0.858	0.124	0.616	0.109	0.723	0.198
1389033_at	AW918775	similar to RIKEN cDNA 2900010M23 (predicted)	RGD1306917_predicted	1.011	0.948	1.264	0.877	0.756	0.091	1.211	0.839
1392294_at	BE119402	Similar to RIKEN cDNA 2900016D05	LOC501285	1.188	0.883	1.077	0.718	1.113	0.077	1.048	0.802
1383128_at	AW921382	similar to RIKEN cDNA 2900024C23 (predicted)	RGD1308581_predicted	1.133	0.987	0.705	0.249	0.940	0.629	1.344	0.813
1397628_at	BM390965	similar to RIKEN cDNA 2900092E17	RGD1305592	1.734	0.176	1.775	0.137	1.289	0.479	2.167	0.076
1381765_at	AI137388	Similar to RIKEN cDNA 3010027G13	RGD1306193	0.779	0.086	1.081	0.480	0.625	0.014	1.006	0.920
1375146_at	BI282168	similar to RIKEN cDNA 3010027G13	RGD1306193	0.764	0.165	1.101	0.151	0.668	0.009	1.051	0.180
1371502_at	AI103666	similar to RIKEN cDNA 3100004P22	RGD1306184	0.730	0.368	0.890	0.365	0.822	0.204	0.832	0.443
1367483_at	AI170657	similar to RIKEN cDNA 3110001D03 (predicted)	RGD1309148_predicted	0.944	0.328	1.138	0.269	1.157	0.061	1.156	0.177
1380619_at	AI177390	similar to RIKEN cDNA 3110001I22 (predicted) /// similar to RIKEN cDNA 3110001I22 (predicted)	RGD1561986_predicted /// RGD1565661_predicted	1.194	0.093	1.404	0.004	1.433	0.002	2.245	0.011
1371424_at	BG378621	similar to RIKEN cDNA 3110005O21	RGD1304823	1.281	0.518	1.021	0.475	0.968	0.763	1.021	0.368
1396891_at	AW533248	Similar to RIKEN cDNA 3110007P09 (predicted)	RGD1564957_predicted	0.686	0.430	1.526	0.205	0.630	0.419	1.238	0.397

1389231_at	BI296728	similar to RIKEN cDNA 3110007P09 (predicted)	RGD1564957_predicted	1.010	0.852	0.998	0.124	1.013	0.994	1.147	0.680
1397708_at	BI289555	similar to RIKEN cDNA 3110009E18	LOC288978	0.507	0.037	0.696	0.035	0.601	0.042	0.550	0.020
1375816_at	BI296706	Similar to RIKEN cDNA 3110009E18	LOC288978	1.540	0.518	1.333	0.615	1.479	0.786	0.880	0.442
1379793_at	AW535749	similar to RIKEN cDNA 3110031B13	RGD1305356	0.963	0.084	0.956	0.789	0.958	0.627	0.843	0.053
1388775_at	AI176439	similar to RIKEN cDNA 3110031B13	RGD1305356	1.012	0.414	0.470	0.000	0.582	0.408	0.600	0.001
1379425_at	AI549208	similar to RIKEN cDNA 3110037I16 (predicted)	RGD1309802_predicted	1.710	0.669	0.968	0.780	0.998	0.303	0.959	0.308
1373833_at	BI288945	similar to RIKEN cDNA 3110040N11	RGD1305713	1.131	0.274	0.671	0.055	0.998	0.961	0.472	0.057
1390144_at	BF411622	similar to RIKEN cDNA 3110043O21	RGD1359108	0.518	0.269	1.373	0.036	0.608	0.407	0.963	0.768
1388996_at	AI406527	similar to RIKEN cDNA 3110052N05	RGD1308579	0.513	0.122	0.311	0.003	0.668	0.068	0.339	0.010
1372072_at	BI282268	similar to RIKEN cDNA 3110052N05	RGD1308579	0.931	0.340	0.707	0.153	0.755	0.181	0.772	0.573
1395503_at	BF564382	similar to RIKEN cDNA 3230401I01 (predicted)	RGD1307904_predicted	1.171	0.901	1.064	0.514	0.998	0.986	1.048	0.443
1377848_at	AW535219	similar to RIKEN cDNA 3830405G04	RGD1305287	0.353	0.007	0.271	0.008	0.517	0.047	0.381	0.007
1398968_at	AI168979	Similar to RIKEN cDNA 3930401K13	RGD1309459	0.722	0.949	0.666	0.002	0.910	0.111	0.614	0.083
1376028_at	BI285463	similar to RIKEN cDNA 4121402D02 (predicted)	RGD1564778_predicted	0.952	0.315	0.912	0.230	1.066	0.656	0.841	0.287
1389917_at	BF284375	Similar to RIKEN cDNA 4121402D02 (predicted)	RGD1564778_predicted	1.003	0.711	0.999	0.979	1.000	0.114	1.000	0.984
1372169_at	BE108809	similar to RIKEN cDNA 4121402D02 (predicted)	RGD1564778_predicted	1.055	0.810	0.866	0.027	0.939	0.023	0.781	0.066
1373390_at	AI178783	similar to RIKEN cDNA 4121402D02 (predicted)	RGD1564778_predicted	0.967	0.810	0.875	0.851	1.075	0.781	0.801	0.337
1399118_at	AI168933	similar to RIKEN cDNA 4121402D02 (predicted)	RGD1564778_predicted	1.363	0.865	2.083	0.009	1.397	0.879	1.345	0.066
1383307_at	AI717533	similar to RIKEN cDNA 4432406C05	MGC114379	0.650	0.261	0.576	0.004	0.496	0.037	0.653	0.019
1397410_at	BI301687	Similar to RIKEN cDNA 4631427C17 (predicted)	RGD1564895_predicted	1.070	0.763	0.475	0.002	0.831	0.825	0.484	0.019
1388637_at	AI579376	similar to RIKEN cDNA 4632411B12	RGD1309220	0.921	0.798	1.515	0.068	0.933	0.102	1.095	0.060
1374441_at	AI180035	similar to RIKEN cDNA 4633402N23 gene	RGD1306649	0.574	0.234	0.869	0.460	0.297	0.003	1.143	0.556
1375548_at	BI296537	similar to RIKEN cDNA 4732418C07 (predicted)	RGD1310351_predicted	0.640	0.329	0.576	0.009	0.898	0.455	0.596	0.003
1378962_at	BM385701	similar to RIKEN cDNA 4732496G21 gene	RGD1309655	1.362	0.194	1.112	0.049	1.619	0.339	0.960	0.312
1385204_at	AI639503	similar to RIKEN cDNA 4833418A01 (predicted)	RGD1565551_predicted	1.002	0.994	0.804	0.806	0.999	0.969	1.148	0.271
1379422_at	AI145871	similar to RIKEN cDNA 4833435D08 /// similar to glycosyltransferase 28 domain containing 1	LOC300284 /// LOC367759	0.869	0.175	0.467	0.015	0.893	0.599	0.480	0.031
1393369_at	BI300502	Similar to RIKEN cDNA 4921511I16	RGD1305302	1.860	0.015	0.854	0.010	1.321	0.101	0.870	0.252
1383617_at	BF401603	similar to RIKEN cDNA 4921511I16	RGD1305302	1.097	0.055	1.079	0.288	1.219	0.049	1.391	0.191
1388625_at	BM390149	similar to RIKEN cDNA 4921521J11 (predicted)	RGD1304711_predicted	0.750	0.012	0.858	0.089	1.177	0.329	1.016	0.144
1377644_at	BF284809	similar to RIKEN cDNA 4921524J17 (predicted)	RGD1308706_predicted	1.609	0.218	2.325	0.007	1.340	0.058	2.725	0.003
1389296_at	AI104356	similar to RIKEN cDNA 4921531G14 (predicted)	RGD1310430_predicted	0.620	0.036	1.172	0.314	0.530	0.071	0.966	0.697
1390875_a_at	BF290046	similar to RIKEN cDNA 4921537D05	RGD1359593	1.637	0.011	2.035	0.044	3.316	0.012	1.929	0.012
1377855_at	BE111774	similar to RIKEN cDNA 4921537D05	RGD1359593	1.479	0.121	0.988	0.603	2.252	0.056	1.229	0.350
1376668_at	BM388328	similar to RIKEN cDNA 4922503N01 (predicted)	RGD1311126_predicted	0.973	0.937	0.755	0.083	0.669	0.912	0.831	0.365
1389300_at	AI410415	similar to RIKEN cDNA 4930404J24 (predicted)	RGD1563498_predicted	0.979	0.899	1.475	0.057	0.621	0.112	1.464	0.067
1372378_at	BE111729	similar to RIKEN cDNA 4930429A22 (predicted)	RGD1560168_predicted	0.771	0.148	1.038	0.647	0.838	0.034	1.056	0.708
1394095_at	AA850714	similar to RIKEN cDNA 4930429M06Rik	RGD1307449	1.060	0.759	1.969	0.147	0.556	0.268	0.981	0.999
1391115_at	BM390642	similar to RIKEN cDNA 4930429O20	LOC498229	0.997	0.980	1.021	0.924	1.006	0.955	0.995	0.979
1384431_at	AI070150	Similar to RIKEN cDNA 4930431B11 gene	RGD1308555	2.446	0.038	4.261	0.004	1.639	0.026	5.491	0.009
1377053_at	BE117757	similar to RIKEN cDNA 4930444A02	RGD1310810	0.346	0.001	0.376	0.008	0.412	0.000	0.567	0.004
1382813_at	BG377386	similar to RIKEN cDNA 4930444A02	RGD1310810	0.445	0.028	0.374	0.003	0.560	0.031	0.438	0.022
1390913_at	AW435463	similar to RIKEN cDNA 4930506L13 (predicted)	RGD1308890_predicted	0.666	0.118	0.802	0.155	0.489	0.119	1.044	0.236
1378220_at	AI111983	similar to RIKEN cDNA 4930517K11	LOC497860	1.290	0.640	1.258	0.279	1.551	0.352	1.232	0.071
1382115_at	BE099174	similar to RIKEN cDNA 4930521E07 (predicted)	RGD1305166_predicted	0.520	0.039	0.448	0.009	0.516	0.261	0.396	0.101
1374980_at	BI282049	similar to RIKEN cDNA 4930527D15	RGD1307598	0.851	0.180	1.384	0.044	1.206	0.592	1.154	0.593
1388633_at	BM388921	similar to RIKEN cDNA 4930538D17	RGD1309313	0.607	0.090	0.638	0.016	0.814	0.074	0.701	0.027
1393464_at	BM383378	similar to RIKEN cDNA 4930550C14	RGD1311251	0.667	0.588	0.502	0.038	1.007	0.884	0.443	0.866
1374856_at	BF396478	similar to RIKEN cDNA 4930556P03 (predicted)	RGD1306433_predicted	1.078	0.856	1.215	0.090	1.056	0.810	1.354	0.067
1373613_at	AI408827	similar to RIKEN cDNA 4930570C03	LOC300191	0.968	0.417	0.998	0.983	0.968	0.669	1.025	0.075
1396737_at	BF403249	similar to RIKEN cDNA 4931400A14 (predicted)	RGD1307234_predicted	1.007	0.857	1.536	0.044	0.992	0.249	0.996	0.802
1371763_at	BI274533	similar to RIKEN cDNA 4931406C07	RGD1309534	0.270	0.027	0.218	0.001	0.175	0.004	0.267	0.011
1381305_at	BM383011	similar to RIKEN cDNA 4931406P16 (predicted)	RGD1308428_predicted	1.051	0.511	0.570	0.030	1.223	0.172	1.113	0.536
1392586_at	AI704512	similar to RIKEN cDNA 4932432K03	RGD1308087	0.878	0.392	0.816	0.287	1.134	0.094	0.921	0.896
1373123_at	BG372671	similar to RIKEN cDNA 4932432N11 gene (predicted)	RGD1310671_predicted	0.711	0.214	0.763	0.071	0.820	0.332	0.857	0.065
1372063_at	BG377807	Similar to RIKEN cDNA 4933402P03	LOC497938	0.736	0.456	0.513	0.010	1.163	0.963	0.575	0.065
1380261_at	BE328914	Similar to RIKEN cDNA 4933404M02	LOC499806	1.062	0.401	0.999	0.993	1.340	0.017	0.983	0.955
1393919_at	AW535116	similar to RIKEN cDNA 4933405A16	RGD1305778	2.612	0.078	5.531	0.024	3.667	0.009	3.969	0.003
1381888_x_at	AA848451	Similar to RIKEN cDNA 4933428G09 (predicted)	RGD1311045_predicted	1.028	0.772	1.304	0.076	1.375	0.441	1.082	0.605
1389269_at	BI285251	similar to RIKEN cDNA 4933433P14 gene	RGD1308470	0.942	0.543	1.090	0.663	1.031	0.042	1.316	0.149
1377613_at	BF403784	similar to RIKEN cDNA 5031400M07	RGD1307343	0.847	0.290	1.074	0.114	0.810	0.376	1.022	0.172
1386287_at	AI407974	similar to RIKEN cDNA 5033405K12 (predicted)	RGD1311593_predicted	2.468	0.034	6.674	0.003	1.832	0.033	6.194	0.004

1380032_at	BF407634	similar to RIKEN cDNA 5033405K12 (predicted)	RGD1311593_predicted	1.113	0.241	3.085	0.052	1.109	0.354	3.245	0.423
1373186_at	AI176617	similar to RIKEN cDNA 5033405K12 (predicted)	RGD1311593_predicted	0.946	0.443	0.901	0.060	1.037	0.334	0.991	0.263
1389444_at	AI179665	Similar to RIKEN cDNA 5033406L14	RGD1305755	1.330	0.115	0.687	0.073	1.255	0.695	0.687	0.070
1390802_at	AI170769	similar to RIKEN cDNA 5033414D02 (predicted)	RGD1306839_predicted	0.447	0.524	1.204	0.329	0.507	0.141	1.078	0.147
1395440_at	AW915843	similar to RIKEN cDNA 5133401N09	MGC125086	1.005	0.981	1.004	0.966	0.998	0.974	1.001	0.996
1371941_at	AI411390	similar to RIKEN cDNA 5230400G24	RGD1310230	0.778	0.223	0.791	0.021	0.739	0.011	0.732	0.052
1375024_at	AI410336	similar to RIKEN cDNA 5230400J09 (predicted)	RGD1559623_predicted	1.007	0.265	0.933	0.499	0.925	0.387	1.634	0.021
1382987_at	AA874945	Similar to RIKEN cDNA 5330414D10 (predicted)	RGD1307986_predicted	3.857	0.492	1.083	0.735	2.381	0.193	0.910	0.229
1384970_at	BM389861	similar to RIKEN cDNA 5330437I02 gene (predicted)	RGD1565246_predicted	0.999	0.773	0.997	0.986	1.004	0.962	1.000	0.994
1367542_at	AI411793	similar to RIKEN cDNA 5330440M15 /// similar to hypothetical protein SP192 (predicted) /// similar to 5330440M15Rik protein /// similar to 5330440M15Rik protein (predicted) /// similar to 5330440M15Rik protein /// similar to 5330440M15Rik protein (predicted)	LOC313519 /// RGD1564280_predicted /// LOC498424 /// RGD1563081_predicted /// LOC499711 /// RGD1563632_predicted	1.294	0.050	1.289	0.098	1.097	0.221	1.395	0.045
1372152_at	BI275874	similar to RIKEN cDNA 5430428G01 /// similar to RIKEN cDNA 5430428G01	RGD1312003 /// LOC499699	0.783	0.547	0.738	0.076	0.762	0.283	1.258	0.212
1371992_at	BG378110	similar to RIKEN cDNA 5430437P03	MGC94542	0.948	0.172	1.380	0.021	1.573	0.205	1.417	0.012
1385681_at	BG668520	similar to RIKEN cDNA 5430437P03	MGC94542	1.061	0.886	1.034	0.041	1.000	0.954	1.004	0.983
1389472_at	AI169015	Similar to RIKEN cDNA 5630401D24 (predicted)	RGD1311526_predicted	0.824	0.338	1.495	0.003	0.592	0.019	1.508	0.002
1393510_at	AW524463	similar to RIKEN cDNA 5730410E15 gene (predicted)	RGD1564335_predicted	1.203	0.314	3.747	0.054	1.571	0.026	2.996	0.092
1376793_at	BF397794	similar to RIKEN cDNA 5730414C17 (predicted)	RGD1308377_predicted	0.877	0.929	0.687	0.004	0.873	0.593	0.986	0.068
1389708_at	AW142960	similar to RIKEN cDNA 5730421E18	RGD1310006	0.554	0.060	0.901	0.822	0.626	0.148	1.226	0.363
1373846_at	BF408064	similar to RIKEN cDNA 5730434I03 gene (predicted)	RGD1311774_predicted	0.777	0.127	0.789	0.020	0.659	0.000	0.763	0.005
1373848_at	BM388575	similar to RIKEN cDNA 5730449L18 (predicted)	RGD1308584_predicted	0.828	0.483	1.237	0.677	0.618	0.076	1.297	0.565
1383141_a_at	AI236700	similar to RIKEN cDNA 5730453I16	RGD1305441	1.234	0.000	1.116	0.680	1.309	0.034	1.127	0.819
1390729_x_at	BM391768	similar to RIKEN cDNA 5730453I16	RGD1305441	0.924	0.515	1.442	0.001	1.310	0.193	1.097	0.418
1377496_at	BM391768	similar to RIKEN cDNA 5730453I16	RGD1305441	1.102	0.697	2.185	0.009	1.081	0.407	1.609	0.219
1375590_at	AA894335	similar to RIKEN cDNA 5730454B08 (predicted)	RGD1308290_predicted	1.004	0.964	1.335	0.004	1.066	0.257	1.001	0.994
1393583_at	BE119096	similar to RIKEN cDNA 5730466H23 (predicted)	RGD1560957_predicted	1.569	0.138	1.946	0.153	1.498	0.285	2.107	0.016
1393086_at	AI060055	similar to RIKEN cDNA 5730469D23 (predicted)	RGD1308324_predicted	1.090	0.759	0.997	0.134	1.124	0.910	0.810	0.034
1391236_at	BG380318	similar to RIKEN cDNA 5730469D23 (predicted)	RGD1308324_predicted	0.893	0.955	1.609	0.084	0.581	0.103	1.695	0.045
1372895_at	AI169367	similar to RIKEN cDNA 5730469M10	RGD1309676	4.050	0.022	10.944	0.001	15.114	0.008	13.719	0.000
1392116_at	BE102137	similar to RIKEN cDNA 5730470L24	RGD1311316	1.109	0.306	0.826	0.048	0.897	0.084	0.871	0.086
1371740_at	AI178732	similar to RIKEN cDNA 5730470L24	RGD1311316	0.837	0.809	0.419	0.016	0.842	0.411	0.405	0.023
1388693_at	BF418174	similar to RIKEN cDNA 5730502D15 gene (predicted)	RGD1310875_predicted	0.750	0.920	1.449	0.019	0.734	0.770	1.209	0.164
1395883_at	BF550469	Similar to RIKEN cDNA 5730509K17 gene (predicted)	RGD1561042_predicted	2.094	0.410	0.945	0.863	1.203	0.187	0.935	0.799
1374874_at	AI410818	similar to RIKEN cDNA 5730509K17 gene (predicted)	RGD1561042_predicted	0.982	0.877	0.313	0.002	0.992	0.934	0.312	0.006
1374487_at	AI169579	similar to RIKEN cDNA 5730536A07	RGD1307481	0.877	0.537	0.955	0.702	0.778	0.027	0.868	0.410
1378433_at	BI296242	similar to RIKEN cDNA 5730557B15 (predicted)	RGD1564227_predicted	4.032	0.008	1.667	0.175	2.374	0.108	2.222	0.161
1376177_at	AI179609	similar to RIKEN cDNA 5730593F17 (predicted)	RGD1561062_predicted	0.437	0.053	0.665	0.094	0.474	0.001	0.696	0.000
1383360_at	AI145787	similar to RIKEN cDNA 5830404H04	RGD735112	1.116	0.990	1.001	0.617	1.006	0.944	0.944	0.423
1395620_at	AI710510	similar to RIKEN cDNA 5830415L20	RGD1306302	1.006	0.230	1.274	0.084	1.673	0.721	1.518	0.082
1374009_at	BI282615	similar to RIKEN cDNA 5830415L20	RGD1306302	1.046	0.740	0.818	0.156	1.214	0.218	0.874	0.290
1383652_at	BF409138	similar to RIKEN cDNA 5830427H10	LOC502872	0.622	0.202	0.935	0.029	1.033	0.492	0.980	0.782
1392591_at	AI170983	Similar to RIKEN cDNA 5830433M19	MGC125002	0.589	0.071	0.586	0.004	0.786	0.300	0.684	0.006
1380035_at	BF523119	similar to RIKEN cDNA 5830433M19	MGC125002	0.716	0.100	0.833	0.027	0.553	0.029	0.976	0.681
1377218_at	BF414000	Similar to RIKEN cDNA 5830434P21	LOC296637	1.239	0.175	1.018	0.375	1.021	0.784	1.046	0.175
1393346_at	BI279863	similar to RIKEN cDNA 5830436D01 (predicted)	RGD1561673_predicted	0.924	0.759	0.514	0.001	0.663	0.066	0.698	0.083
1377756_at	AI232228	similar to RIKEN cDNA 5830446M03	RGD1307688	1.390	0.182	1.928	0.000	1.371	0.338	1.746	0.000
1391933_at	BF392746	Similar to RIKEN cDNA 5830457O10 (predicted)	RGD1306894_predicted	1.002	0.496	0.758	0.139	0.999	0.532	0.998	0.336
1374516_at	AI008492	similar to RIKEN cDNA 5830457O10 (predicted)	RGD1306894_predicted	0.736	0.974	0.497	0.001	0.600	0.327	0.730	0.099
1377067_at	AI137309	similar to RIKEN cDNA 6030443O07 (predicted)	RGD1305918_predicted	1.001	0.991	0.495	0.014	0.991	0.052	0.579	0.009
1376645_at	AW916327	Similar to RIKEN cDNA 6330406I15 (predicted)	RGD1307396_predicted	0.243	0.066	0.406	0.097	0.178	0.007	0.426	0.076
1374929_at	AI010233	similar to RIKEN cDNA 6330407D12 (predicted)	RGD1561171_predicted	0.399	0.066	0.748	0.102	0.324	0.008	0.495	0.003
1374515_at	AA848948	similar to RIKEN cDNA 6330409N04	RGD1306437	0.859	0.984	1.657	0.046	0.698	0.461	1.431	0.025
1393370_at	BG380685	similar to RIKEN cDNA 6330415M09 (predicted)	RGD1308384_predicted	2.021	0.216	0.994	0.961	2.332	0.025	1.614	0.538
1379987_at	BE100570	similar to RIKEN cDNA 6330416G13 gene (predicted)	RGD1304595_predicted	1.062	0.680	1.899	0.048	1.162	0.056	1.280	0.207
1383806_at	BF556825	similar to RIKEN cDNA 6330509G02	RGD1304726	2.060	0.097	0.726	0.560	1.113	0.790	0.759	0.059
1372938_at	AI575671	similar to RIKEN cDNA 6330509G02	RGD1304726	0.920	0.509	0.777	0.184	0.989	0.395	0.695	0.022
1382737_at	AI059118	similar to RIKEN cDNA 6430548M08 (predicted)	RGD1304884_predicted	1.010	0.497	1.101	0.401	1.005	0.466	1.014	0.844

1376583_at	BE095847	similar to RIKEN cDNA 6430548M08 (predicted)	RGD1304884_predicted	0.917	0.691	1.156	0.525	0.735	0.052	0.886	0.161
1384923_at	AI137998	Similar to RIKEN cDNA 6430571L13 gene; similar to g20 protein (predicted)	RGD1307461_predicted	1.027	0.374	1.004	0.119	1.234	0.009	0.996	0.980
1394419_at	BE109109	similar to RIKEN cDNA 6530401L14 gene	RGD1309107	1.226	0.057	1.015	0.678	1.057	0.823	0.871	0.446
1382466_at	BF407231	similar to RIKEN cDNA 6530403A03	RGD1309020	1.353	0.015	1.995	0.004	1.077	0.716	1.651	0.013
1377907_at	BF287924	similar to RIKEN cDNA 6530403A03	RGD1309020	1.371	0.823	0.683	0.046	0.956	0.826	0.708	0.041
1377616_at	BE114214	similar to RIKEN cDNA 6720467C03 (predicted)	RGD1310681_predicted	0.336	0.060	0.365	0.003	0.254	0.000	0.522	0.028
1378104_at	AI105459	similar to RIKEN cDNA 8430406I07	RGD1307465	0.899	0.693	0.878	0.078	0.934	0.691	0.748	0.018
1397238_at	AW524239	Similar to RIKEN cDNA 8430426H19 (predicted)	RGD1559768_predicted	0.913	0.064	0.286	0.001	0.958	0.505	0.366	0.012
1395323_x_at	BF398458	Similar to RIKEN cDNA 8430426H19 (predicted)	RGD1559768_predicted	1.469	0.447	0.814	0.101	1.166	0.240	0.724	0.239
1391410_at	BM392039	Similar to RIKEN cDNA 8430426H19 (predicted)	RGD1559768_predicted	0.691	0.481	0.418	0.012	0.574	0.076	0.512	0.031
1372714_at	BG668449	similar to RIKEN cDNA 8430437G11	RGD1307778	1.083	0.813	0.908	0.068	1.060	0.946	1.176	0.018
1388801_at	AA945103	Similar to RIKEN cDNA 9030221M09 gene (predicted)	RGD1305469_predicted	1.698	0.107	0.710	0.091	1.374	0.157	1.080	0.386
1389036_at	BM385629	similar to RIKEN cDNA 9030221M09 gene (predicted)	RGD1305469_predicted	1.449	0.154	1.892	0.026	1.736	0.067	1.664	0.247
1367514_at	AI235508	similar to RIKEN cDNA 9030624J02	LOC361635	1.044	0.866	1.045	0.330	1.004	0.833	0.969	0.340
1389435_at	BE329046	Similar to RIKEN cDNA 9130005N14 (predicted)	RGD1560201_predicted	0.686	0.974	0.576	0.001	0.551	0.029	0.426	0.004
1395226_at	BI274777	similar to RIKEN cDNA 9130023F12 gene (predicted)	RGD1311920_predicted	1.135	0.083	2.192	0.000	0.960	0.516	1.419	0.009
1390500_at	BG375508	similar to RIKEN cDNA 9130023F12 gene (predicted)	RGD1311920_predicted	0.965	0.921	0.560	0.019	0.637	0.038	0.714	0.005
1388482_at	BM384306	similar to RIKEN cDNA 9130404D14	RGD1307018	5.825	0.071	7.923	0.003	4.154	0.059	2.762	0.003
1390474_at	AA859508	similar to RIKEN cDNA 9330161F08 (predicted)	RGD1564315_predicted	0.656	0.386	0.762	0.021	0.688	0.205	0.670	0.100
1377701_at	AI012404	similar to RIKEN cDNA 9330177P20 (predicted)	RGD1561833_predicted	1.189	0.393	1.533	0.019	0.701	0.044	1.361	0.052
1372026_at	BI282651	similar to RIKEN cDNA 9430023L20	RGD1359310	1.069	0.284	2.877	0.020	1.004	0.973	2.909	0.048
1398337_at	AI169116	Similar to RIKEN cDNA 9430077D24 gene	LOC290341	0.846	0.883	0.845	0.015	1.001	0.989	0.903	0.199
1389148_at	AW254686	similar to RIKEN cDNA 9430083G14	RGD1549725	1.006	0.899	1.001	0.819	0.996	0.669	1.889	0.078
1399068_at	BM389499	similar to RIKEN cDNA 9430098E02 (predicted) /// similar to RIKEN cDNA 9430098E02 (predicted)	RGD1565407_predicted /// RGD1561454_predicted	0.544	0.032	0.739	0.263	0.571	0.231	0.657	0.141
1389197_at	BI290535	similar to RIKEN cDNA 9630046K23	RGD1306248	0.690	0.351	0.860	0.160	0.583	0.013	0.701	0.320
1398107_at	AI385379	similar to RIKEN cDNA A030007L17; EST AA673177 (predicted) /// similar to RIKEN cDNA A030007L17 (predicted)	RGD1304876_predicted /// RGD1560425_predicted	1.114	0.233	1.917	0.094	1.004	0.945	0.993	0.769
1392541_at	AW919608	similar to RIKEN cDNA A030007L17; EST AA673177 (predicted) /// similar to RIKEN cDNA A030007L17 (predicted)	RGD1304876_predicted /// RGD1560425_predicted	0.859	0.920	3.037	0.005	0.926	0.578	2.236	0.014
1376970_at	AW530127	Similar to RIKEN cDNA A130042E20; open reading frame 57 (predicted)	RGD1308722_predicted	1.000	0.969	0.857	0.101	1.001	0.972	0.826	0.116
1380904_at	BI300461	Similar to RIKEN cDNA A230102I05 (predicted)	RGD1311663_predicted	1.116	0.068	0.987	0.615	1.178	0.877	1.114	0.550
1380721_at	BE103115	Similar to RIKEN cDNA A230102I05 (predicted)	RGD1311663_predicted	1.861	0.324	0.848	0.217	1.847	0.166	1.013	0.619
1371443_at	AI409584	similar to RIKEN cDNA A430005L14	RGD1304567	0.328	0.006	1.022	0.400	0.314	0.004	0.886	0.488
1382424_at	AI071713	Similar to RIKEN cDNA A430005L14	RGD1304567	0.459	0.104	0.775	0.017	0.440	0.073	0.836	0.252
1392901_at	BM385213	Similar to RIKEN cDNA A430093J20 gene	LOC367113	2.586	0.003	1.140	0.594	1.955	0.015	1.002	0.237
1398411_at	BI278952	similar to RIKEN cDNA A430107P09 gene	LOC364357	0.760	0.543	0.619	0.062	1.140	0.437	0.701	0.050
1382181_at	AI555069	similar to RIKEN cDNA A530088I07 gene	LOC311984	4.749	0.012	2.245	0.042	13.768	0.000	2.144	0.159
1390289_at	BI283804	similar to RIKEN cDNA A530089I17 (predicted)	RGD1311375_predicted	0.389	0.026	0.291	0.002	0.465	0.018	0.312	0.032
1397305_at	BE110307	Similar to RIKEN cDNA A630054L15; hypothetical protein MGC38041 (predicted)	RGD1306064_predicted	0.677	0.134	0.861	0.518	0.924	0.613	0.872	0.484
1399150_at	AW144400	similar to RIKEN cDNA A630054L15; hypothetical protein MGC38041 (predicted)	RGD1306064_predicted	1.355	0.409	0.495	0.060	1.444	0.260	0.554	0.004
1383209_at	AW916721	similar to RIKEN cDNA A630054L15; hypothetical protein MGC38041 (predicted)	RGD1306064_predicted	1.018	0.433	0.807	0.347	1.108	0.247	0.940	0.167
1397350_at	BE096697	similar to RIKEN cDNA A730011L01 gene	LOC498029	1.854	0.299	0.945	0.671	10.529	0.006	1.017	0.467
1398219_at	BE109914	similar to RIKEN cDNA A930001M12 gene (predicted)	RGD1562567_predicted	0.441	0.013	0.141	0.001	0.334	0.048	0.151	0.012
1392015_at	BF392359	Similar to RIKEN cDNA A930008G19 (predicted)	RGD1310799_predicted	1.348	0.224	1.356	0.942	1.033	0.678	1.176	0.624
1396198_at	BF282909	Similar to RIKEN cDNA A930008G19 (predicted)	RGD1310799_predicted	0.835	0.589	0.908	0.524	1.043	0.736	1.110	0.618
1376654_at	AW521378	similar to RIKEN cDNA B130016O10 gene (predicted)	RGD1308448_predicted	0.717	0.208	0.615	0.012	0.748	0.049	0.948	0.067
1398426_at	AI409065	similar to RIKEN cDNA B130052G07 (predicted)	RGD1564105_predicted	0.740	0.973	0.940	0.738	0.740	0.974	0.635	0.644
1375006_at	BE121050	Similar to RIKEN cDNA B130055L09 (predicted)	RGD1309236_predicted	2.140	0.016	2.007	0.007	2.613	0.011	2.207	0.008
1390806_at	AW251111	similar to RIKEN cDNA B230118H07 (predicted)	RGD1309730_predicted	0.629	0.216	0.774	0.251	1.030	0.499	0.607	0.102
1371991_at	AA894318	Similar to RIKEN cDNA B230312A22	RGD1311249	1.003	0.389	0.652	0.102	1.052	0.723	0.564	0.063
1376863_at	BE109118	similar to RIKEN cDNA B230339M05 gene (predicted)	RGD1306861_predicted	0.736	0.033	1.116	0.263	0.456	0.017	1.099	0.280
1393505_x_at	AI045965	similar to RIKEN cDNA B230380D07 (predicted)	RGD1311456_predicted	0.822	0.324	1.125	0.391	0.718	0.092	0.953	0.666
1384609_a_at	AI045965	similar to RIKEN cDNA B230380D07 (predicted)	RGD1311456_predicted	0.707	0.332	0.784	0.981	0.256	0.043	1.045	0.618
1397774_at	BF290889	similar to RIKEN cDNA B230380D07 (predicted)	RGD1311456_predicted	1.021	0.609	0.904	0.232	0.948	0.718	0.727	0.016
1391169_at	BE120139	Similar to RIKEN cDNA B930062P21 gene (predicted)	RGD1562562_predicted	7.205	0.041	4.697	0.006	2.486	0.194	3.560	0.020
1381419_at	AI145119	Similar to Riken cDNA C230021P08 (predicted)	RGD1561571_predicted	0.903	0.774	0.903	0.651	1.385	0.068	1.320	0.284
1379356_at	AI574991	Similar to RIKEN cDNA C230093N12 (predicted)	RGD1310037_predicted	0.851	0.996	0.384	0.089	0.867	0.613	0.693	0.317
1372341_at	AI233213	Similar to RIKEN cDNA C330005L02	LOC501039	0.625	0.019	0.771	0.006	0.523	0.002	0.732	0.006
1380084_at	BF399367	Similar to RIKEN cDNA C330005L02	LOC501039	1.627	0.125	1.023	0.889	0.983	0.997	1.002	0.991
1392789_at	BI296353	Similar to RIKEN cDNA C330005L02	LOC501039	0.660	0.359	7.001	0.001	0.753	0.335	4.624	0.005

1390602_a_at	BG381320	similar to RIKEN cDNA C430004E15	LOC499749	1.010	0.955	1.686	0.029	0.526	0.016	0.942	0.543
1395624_at	BF546268	Similar to RIKEN cDNA C430008C19	RGD1307947	0.425	0.059	0.738	0.117	0.405	0.113	0.632	0.053
1389264_at	BI278594	similar to RIKEN cDNA C730048E16	RGD1309552	0.867	0.628	1.262	0.444	0.666	0.679	0.951	0.819
1395739_at	BG672302	similar to RIKEN cDNA C920006C10 (predicted)	RGD1305976_predicted	2.238	0.001	3.302	0.009	2.131	0.006	4.234	0.004
1389526_at	BG373853	similar to RIKEN cDNA C920006C10 (predicted)	RGD1305976_predicted	1.409	0.211	0.900	0.366	1.884	0.012	1.095	0.105
1390550_at	BF403636	similar to RIKEN cDNA C920006C10 (predicted)	RGD1305976_predicted	1.148	0.650	2.857	0.064	1.232	0.258	1.536	0.227
1374400_at	BI291528	similar to RIKEN cDNA C920006C10 (predicted)	RGD1305976_predicted	1.198	0.716	0.577	0.003	1.449	0.263	0.786	0.012
1374004_at	BM387902	similar to RIKEN cDNA D030028O16	RGD1310143	0.498	0.057	0.800	0.075	0.452	0.020	1.007	0.739
1381321_at	BE113257	Similar to RIKEN cDNA D030060M11	RGD1308076	1.403	0.406	1.262	0.265	1.172	0.681	1.066	0.539
1377480_at	BF387366	similar to RIKEN cDNA D030060M11	RGD1308076	1.104	0.431	1.280	0.038	1.478	0.764	1.373	0.010
1374479_at	BM390240	similar to RIKEN cDNA D030070L09	RGD1310199	1.295	0.248	0.913	0.589	1.406	0.662	1.016	0.970
1389302_at	BI289482	similar to RIKEN cDNA D030070L09	RGD1310199	1.449	0.452	0.920	0.277	0.965	0.773	1.006	0.964
1388425_at	BG671569	similar to RIKEN cDNA D130038B21	RGD1305890	3.503	0.077	3.776	0.041	3.306	0.053	4.400	0.026
1397959_at	AW534218	similar to RIKEN cDNA D130059P03 gene (predicted)	RGD1310722_predicted	1.905	0.047	1.305	0.068	1.407	0.091	1.195	0.892
1393091_at	H34096	similar to RIKEN cDNA D130064H19 (predicted)	RGD1311241_predicted	0.854	0.139	0.824	0.053	0.679	0.021	0.818	0.038
1375934_at	BE112948	similar to RIKEN cDNA D330045A20 (predicted)	RGD1566282_predicted	0.512	0.049	1.107	0.177	0.695	0.030	0.836	0.224
1383554_at	AW142796	similar to RIKEN cDNA D330045A20 (predicted)	RGD1566282_predicted	0.783	0.094	1.377	0.371	0.760	0.049	1.306	0.327
1384472_at	AA926022	similar to RIKEN cDNA D330050P16 gene	LOC362683	0.774	0.486	0.609	0.004	0.965	0.340	0.812	0.013
1383710_at	BE098872	similar to RIKEN cDNA D330050P16 gene /// similar to KIAA1414 protein	LOC362683 /// LOC362684	1.016	0.793	0.464	0.019	1.001	0.823	0.419	0.010
1376446_at	BE099060	similar to RIKEN cDNA D430028G21	MGC93707	1.004	0.758	0.958	0.841	1.032	0.367	0.933	0.600
1384858_a_at	AA964590	similar to RIKEN cDNA D530033C11 (predicted)	RGD1307179_predicted	0.980	0.896	1.627	0.024	0.955	0.725	1.448	0.034
1389476_at	AI010238	similar to RIKEN cDNA D630029K19	RGD1307100	1.421	0.001	0.660	0.005	1.452	0.057	0.690	0.011
1384483_at	BI274216	Similar to RIKEN cDNA E030034P13 (predicted)	RGD1309385_predicted	11.402	0.010	8.062	0.000	15.690	0.003	10.932	0.001
1372555_at	AI171778	similar to RIKEN cDNA E030034P13 (predicted)	RGD1309385_predicted	0.630	0.565	1.018	0.955	0.716	0.176	0.857	0.527
1374579_at	BF281860	Similar to RIKEN cDNA E230015L20 gene (predicted)	RGD1560873_predicted	1.473	0.939	0.559	0.015	1.267	0.648	0.607	0.070
1383095_at	BM387808	Similar to RIKEN cDNA E230015L20 gene (predicted)	RGD1560873_predicted	1.008	0.973	0.368	0.000	1.108	0.746	0.510	0.000
1391812_at	AI145876	Similar to RIKEN cDNA E330026B02 (predicted)	RGD1309172_predicted	0.392	0.006	0.059	0.002	0.571	0.035	0.122	0.023
1373086_at	AI102818	similar to RIKEN cDNA F730014I05 (predicted)	RGD1310800_predicted	0.680	0.171	1.259	0.877	0.897	0.546	1.118	0.595
1390278_at	BI279652	similar to RIKEN cDNA G430041M01 (predicted)	RGD1562563_predicted	1.252	0.061	1.261	0.198	1.572	0.008	1.260	0.195
1377762_at	BG381701	Similar to RIKEN cDNA G430041M01 (predicted)	RGD1562563_predicted	1.304	0.275	2.285	0.022	1.819	0.006	0.985	0.407
1394585_at	BE116089	Similar to RIKEN cDNA G430041M01 (predicted)	RGD1562563_predicted	1.075	0.534	1.687	0.154	1.874	0.104	0.938	0.532
1380489_at	BF389269	Similar to RIKEN cDNA G430041M01 (predicted)	RGD1562563_predicted	0.975	0.648	1.115	0.271	1.062	0.851	0.803	0.460
1392758_at	AA943056	similar to RIKEN cDNA G430041M01 (predicted)	RGD1562563_predicted	1.155	0.794	1.378	0.684	1.282	0.372	0.667	0.248
1378326_at	AW435059	similar to RIKEN cDNA G430055L02	LOC366012	1.306	0.072	1.081	0.026	1.048	0.250	1.173	0.430
1383260_at	BI289879	similar to RIKEN cDNA G630024C07 gene (predicted)	RGD1305903_predicted	0.891	0.990	0.823	0.352	0.961	0.303	0.928	0.349
1393018_at	AI071984	Similar to RING finger protein 33 (predicted)	RGD1565534_predicted	0.304	0.131	31.829	0.000	0.430	0.027	19.187	0.001
1373708_at	BG378168	similar to RNA binding motif protein 21	MGC125034	0.734	0.322	1.452	0.105	0.660	0.212	1.588	0.018
1392936_at	AW434972	similar to RNA binding motif protein 25 (predicted)	RGD1565486_predicted	1.173	0.071	0.857	0.242	0.953	0.676	0.820	0.011
1375898_at	AW252379	similar to RNA binding protein gene with multiple splicing (predicted)	RGD1561067_predicted	1.356	0.026	0.416	0.001	1.328	0.060	0.517	0.033
1372380_at	AI231308	similar to RNA binding protein gene with multiple splicing (predicted)	RGD1561067_predicted	0.976	0.728	2.710	0.002	0.910	0.255	2.370	0.012
1371351_at	AI233192	similar to RNA polymerase 1-3	MGC112727	0.964	0.740	1.892	0.000	0.905	0.480	1.183	0.266
1396410_at	BE116258	Similar to RNA-binding protein isoform G3BP-2a	RGD1309571	1.159	0.120	1.168	0.834	1.411	0.019	1.052	0.651
1375974_at	AI406315	Similar to RNA-binding protein isoform G3BP-2a	RGD1309571	1.489	0.140	1.094	0.388	1.491	0.109	1.053	0.298
1392572_at	BI282339	similar to RNA-binding protein Musashi2-S (predicted)	RGD1560397_predicted	1.186	0.004	1.665	0.055	1.417	0.002	1.825	0.011
1385427_at	BE118330	similar to RNA-binding protein Musashi2-S (predicted)	RGD1560397_predicted	1.519	0.012	1.209	0.199	1.468	0.031	1.462	0.280
1380541_at	AA957801	Similar to RNA-binding protein Musashi2-S (predicted)	RGD1560397_predicted	1.709	0.015	0.517	0.002	1.829	0.009	0.767	0.139
1388870_at	BF284305	Similar to RNA-binding protein Musashi2-S (predicted)	RGD1560397_predicted	1.243	0.162	0.361	0.008	1.659	0.103	0.622	0.079
1385809_at	AI070105	Similar to Rnf37-pending protein	RGD1305440	0.482	0.044	1.583	0.148	0.362	0.029	1.217	0.470
1389702_at	AI013041	similar to Rnf37-pending protein	RGD1305440	1.004	0.973	1.033	0.285	1.019	0.452	1.003	0.956
1383743_at	BI275464	similar to RP23-462P2.7 (predicted)	RGD1561607_predicted	1.669	0.009	0.901	0.028	1.586	0.009	1.373	0.091
1379055_x_at	BF410240	similar to Rpl17 protein (predicted) /// similar to Ac1147 (predicted) /// similar to Ac1147 /// similar to Ac1147 /// similar to Ac1147	RGD1565093_predicted /// RGD1561314_predicted /// LOC503301 /// LOC503405 /// LOC503410	1.300	0.866	1.253	0.170	1.447	0.195	1.249	0.220
1372554_at	AA943110	Similar to RW1 protein (predicted)	RGD1309266_predicted	0.791	0.719	0.566	0.009	0.694	0.079	0.800	0.010
1371350_at	AI412159	similar to S-adenosylmethionine synthetase gamma form (Methionine adenosyltransferase) (predicted)	RGD1560523_predicted	0.629	0.000	0.965	0.363	0.612	0.004	1.116	0.129
1390360_a_at	BI282944	similar to Safb2 protein	LOC301126	0.744	0.222	1.323	0.461	1.002	0.251	0.951	0.730
1374500_at	AI011571	similar to sarcoma antigen NY-SAR-27	LOC499691	0.757	0.030	0.971	0.263	1.216	0.615	0.803	0.916
1385455_at	BF397666	similar to sarcoma antigen NY-SAR-27	LOC499691	0.898	0.314	1.251	0.363	1.131	0.852	1.017	0.861
1379691_at	BM389372	similar to sarcoma antigen NY-SAR-27	LOC499691	0.768	0.352	0.709	0.196	0.744	0.539	0.543	0.027
1383371_at	AI712305	Similar to scavenger receptor cysteine rich domain containing, group B (4 domains) (predicted)	RGD1561163_predicted	0.509	0.084	0.556	0.020	0.829	0.229	0.990	0.476

1382601_at	AI237698	Similar to scavenger receptor type A SR-A (predicted)	RGD1564316_predicted	1.223	0.828	1.045	0.726	1.199	0.610	1.248	0.080
1378080_at	BI274498	similar to SCO cytochrome oxidase deficient homolog 1 (yeast) (predicted)	RGD1559538_predicted	0.972	0.993	1.321	0.073	0.963	0.957	0.929	0.548
1389024_at	BG380647	similar to Sec1 family domain containing protein 2 (Syntaxin binding protein 1-like 1) (Neuronal Sec1)	LOC498353	0.673	0.011	0.471	0.017	0.460	0.005	0.825	0.031
1388991_at	AA892491	similar to SEC14 and spectrin domains 1 (predicted)	RGD1562244_predicted	1.963	0.057	2.576	0.158	1.595	0.015	1.170	0.178
1388334_at	AI176849	similar to SEC14-like 1 (predicted)	RGD1563123_predicted	0.650	0.585	0.762	0.221	0.551	0.359	0.902	0.476
1398886_at	BI285703	similar to Selenoprotein H (predicted)	RGD1563348_predicted	0.898	0.884	2.087	0.006	0.590	0.016	2.254	0.002
1388705_at	BI282694	similar to selenoprotein SelM (predicted)	RGD1565037_predicted	0.653	0.643	1.010	0.359	0.493	0.108	0.740	0.854
1373508_at	AI180004	similar to Selenoprotein T precursor	LOC499625	0.571	0.278	0.773	0.029	0.696	0.098	0.717	0.031
1389354_at	BF285490	similar to semaF cytoplasmic domain associated protein 2	LOC365960	1.029	0.553	0.999	0.286	1.186	0.442	1.237	0.070
1381162_at	AI136863	Similar to septin 10 isoform 1	LOC309891	1.356	0.124	1.219	0.146	2.078	0.008	1.254	0.048
1372044_at	AI410321	similar to Ser/Thr-rich protein T10 in DGCR region (predicted)	RGD1310348_predicted	0.516	0.002	0.309	0.015	0.695	0.167	0.462	0.009
1389358_at	BF282740	Similar to serine/threonine kinase	LOC498312	1.312	0.215	0.797	0.033	0.726	0.698	0.673	0.024
1397880_at	BF389592	Similar to serine/threonine kinase	LOC498312	0.735	0.604	0.944	0.798	0.591	0.009	0.878	0.168
1389219_at	AI406322	Similar to serine/threonine kinase	LOC498312	0.987	0.774	0.906	0.050	0.617	0.269	0.975	0.102
1374584_at	BM388112	similar to Serine/threonine protein kinase 24 (predicted)	RGD1561742_predicted	0.953	0.360	1.073	0.063	0.739	0.011	0.944	0.646
1398089_at	BF401882	Similar to Serine/threonine protein kinase 24 (predicted)	RGD1561742_predicted	1.930	0.470	0.956	0.848	1.045	0.943	0.906	0.958
1375450_at	BF403864	similar to serologically defined colon cancer antigen 1 isoform a (predicted)	RGD1561973_predicted	1.193	0.216	0.601	0.535	0.966	0.349	0.601	0.571
1377212_at	BF416289	Similar to Serologically defined colon cancer antigen 13 (predicted)	RGD1564816_predicted	1.427	0.026	0.730	0.071	1.038	0.830	0.759	0.482
1384922_at	AW527642	Similar to SERTA domain containing 4 (predicted)	RGD1564561_predicted	0.255	0.004	0.055	0.001	0.256	0.000	0.211	0.006
1385073_at	AI145639	similar to SERTA domain containing 4 (predicted)	RGD1564561_predicted	0.359	0.041	0.189	0.051	0.229	0.012	0.183	0.087
1392711_at	AA996440	Similar to SERTA domain containing 4 (predicted)	RGD1564561_predicted	0.622	0.152	0.145	0.007	0.840	0.148	0.350	0.049
1388842_at	BG380385	similar to serum response factor (predicted)	RGD1559787_predicted	3.624	0.004	3.282	0.003	1.687	0.024	1.565	0.042
1374829_at	BF395579	similar to serum response factor (predicted)	RGD1559787_predicted	1.250	0.184	3.208	0.062	1.002	0.984	1.000	0.995
1391046_at	BM384217	similar to SET and MYND domain containing 3	LOC498295	0.981	0.318	1.460	0.037	0.976	0.221	1.237	0.012
1375171_at	BF396622	Similar to SET binding factor 2 (predicted)	RGD1559442_predicted	2.175	0.070	2.259	0.029	2.051	0.079	1.688	0.000
1372458_at	AI235220	similar to SET domain-containing protein	LOC498178	0.998	0.490	1.721	0.006	1.045	0.609	1.496	0.031
1372230_at	AI105430	similar to seven transmembrane domain protein	RGD1304706	0.462	0.193	1.022	0.880	0.709	0.032	1.119	0.593
1381623_at	BF391476	similar to Sfrs4 protein (predicted)	RGD1561347_predicted	1.225	0.354	2.076	0.005	1.591	0.332	1.886	0.001
1398084_at	BF419651	Similar to SH3 domain binding glutamic acid-rich protein like 2	LOC501026	2.256	0.064	2.040	0.445	1.605	0.133	1.389	0.420
1389639_at	BF283302	similar to Shb protein (predicted)	RGD1565350_predicted	3.283	0.008	2.949	0.008	2.726	0.018	1.696	0.026
1389575_at	BF284868	similar to sid2057p	RGD1311703	0.967	0.868	1.067	0.678	0.897	0.493	1.033	0.709
1393801_at	AI111841	similar to Sid3177p /// similar to Telomerase-binding protein p23 (Hsp90 co-chaperone) (Progesterone receptor complex p23) (Sid 3177)	LOC367808 /// LOC501566	0.794	0.083	1.705	0.062	0.685	0.025	1.191	0.338
1375552_at	BG372976	similar to signal recognition particle,72 kDa subunit	LOC498351	0.667	0.033	1.122	0.385	0.750	0.093	1.121	0.762
1399144_at	BG670238	Similar to signal recognition particle,72 kDa subunit	LOC498351	0.505	0.111	0.723	0.042	0.521	0.093	0.851	0.449
1367501_at	BM383845	Similar to signal recognition particle,72 kDa subunit	LOC498351	0.787	0.141	1.316	0.019	0.939	0.447	1.240	0.102
1392957_at	BF565151	similar to Single-stranded DNA-binding protein 2 (Sequence-specific single-stranded-DNA-binding protein 2) (predicted)	RGD1562968_predicted	0.660	0.013	0.664	0.062	0.462	0.083	0.820	0.141
1372491_at	AI229647	similar to Ski protein (predicted)	RGD1565591_predicted	1.417	0.462	1.119	0.154	0.650	0.150	0.661	0.759
1391633_at	BF390387	Similar to SLIT-ROBO Rho GTPase-activating protein 1 (predicted)	RGD1566260_predicted	1.515	0.528	1.650	0.038	0.509	0.404	0.991	0.966
1379542_at	BF522334	similar to Small nuclear ribonucleoprotein F (snRNP-F) (predicted) /// small nuclear ribonucleoprotein polypeptide F (predicted)	RGD1561993_predicted /// Snrpf_predicted	0.580	0.332	0.820	0.156	0.565	0.119	0.890	0.958
1377731_at	AI454091	similar to small unique nuclear receptor co-repressor (predicted)	RGD1560600_predicted	1.053	0.452	1.070	0.250	1.142	0.092	1.171	0.168
1372105_at	BF284932	similar to Smhs2 homolog (predicted)	RGD1309934_predicted	1.315	0.423	1.514	0.002	0.907	0.491	1.361	0.021
1371712_at	AI176503	similar to snRNP core protein SMX5d (predicted)	RGD1560193_predicted	0.516	0.773	2.221	0.010	0.544	0.028	1.857	0.021
1376936_at	BI296215	similar to sodium/calcium exchanger protein	LOC498185	1.623	0.171	1.146	0.265	0.948	0.646	1.014	0.762
1380105_at	C07059	similar to Solute carrier family 23, member 2 (Sodium-dependent vitamin C transporter 2) (predicted)	RGD1565367_predicted	0.983	0.390	0.205	0.000	0.888	0.747	0.279	0.005
1372289_at	AI170792	similar to solute carrier family 25 (mitochondrial carrier, Aralar), member 12 (predicted)	RGD1561141_predicted	0.555	0.131	0.934	0.567	0.553	0.992	0.779	0.485
1384413_at	AA900068	Similar to solute carrier family 35, member A5 (predicted)	RGD1564361_predicted	2.668	0.014	0.818	0.169	3.213	0.009	1.086	0.452
1389391_at	AI411981	Similar to Solute carrier family 35, member E3 (predicted)	RGD1564876_predicted	0.680	0.251	1.195	0.208	0.658	0.016	1.111	0.414
1378131_at	AI045015	Similar to solute carrier family 9 (sodium/hydrogen exchanger), isoform 9 (predicted)	RGD1560736_predicted	0.719	0.040	0.710	0.468	0.511	0.081	0.858	0.265
1394902_at	AA996417	Similar to sorting nexin 21 isoform a; sorting nexin L; sorting nexin 21 (predicted)	RGD1311169_predicted	1.473	0.590	1.362	0.077	1.212	0.097	1.139	0.326
1374745_at	BM391278	Similar to sorting nexin 21 isoform a; sorting nexin L; sorting nexin 21 (predicted)	RGD1311169_predicted	1.001	0.990	1.157	0.361	1.443	0.226	1.015	0.894
1384760_at	AI711126	similar to Sorting nexin 6 (TRAF4-associated factor 2) (predicted)	RGD1560591_predicted	1.001	0.973	0.623	0.002	1.003	0.773	0.623	0.002
1379942_at	AA858564	Similar to SOX2 protein (predicted)	RGD1565646_predicted	0.464	0.231	1.634	0.399	1.352	0.275	1.569	0.093
1379742_at	BI301216	similar to SP140 nuclear body protein isoform 1	LOC501175	1.198	0.770	1.108	0.113	4.158	0.005	2.414	0.042
1383103_at	BE110514	Similar to Sperm 1 POU-domain transcription factor (SPRM-1) (predicted)	RGD1305526_predicted	0.882	0.323	0.799	0.138	0.859	0.250	0.875	0.257
1389516_at	BI300082	Similar to Sperm 1 POU-domain transcription factor (SPRM-1) (predicted)	RGD1305526_predicted	1.347	0.448	1.043	0.809	1.319	0.932	0.934	0.519
1381393_at	BI301735	Similar to sperm antigen HCMOGT-1	RGD1309718	0.807	0.674	0.996	0.402	1.671	0.019	1.162	0.869
1397391_at	AI454739	Similar to spermatogenesis associated glutamate (E)-rich protein 4d	LOC296777	0.703	0.149	0.444	0.013	0.572	0.044	0.423	0.036
1395806_at	AI547628	similar to spermatogenesis associated glutamate (E)-rich protein 4d	LOC501290	1.772	0.399	0.820	0.152	1.134	0.634	0.648	0.201

1373592_at	AI407094	similar to SPI6	MGC94010	4.846	0.023	1.762	0.118	4.018	0.076	5.090	0.013
1384023_at	AI229556	similar to Spindlin-like (predicted)	RGD1560898_predicted	0.813	0.180	0.996	0.908	0.817	0.188	0.999	0.986
1379409_at	AW915474	similar to spinocerebellar ataxia 7 homolog (predicted)	RGD1562692_predicted	1.893	0.267	1.127	0.225	1.783	0.177	0.986	0.363
1388675_at	BE349771	similar to spinster-like protein	RGD1305613	0.817	0.861	1.998	0.009	0.772	0.884	2.077	0.058
1379221_at	AI716277	similar to SPla/RYanodine receptor SPRY (1J970) (predicted)	RGD1308847_predicted	1.071	0.505	1.198	0.766	1.220	0.086	1.003	0.906
1394441_at	AW528593	similar to SPla/RYanodine receptor SPRY (1J970) (predicted)	RGD1308847_predicted	1.058	0.752	0.791	0.021	1.260	0.158	0.867	0.269
1382056_at	AI145768	similar to splicing factor p54	LOC502603	0.988	0.086	1.163	0.474	0.723	0.427	0.914	0.637
1368212_at	NM_031021	similar to splicing factor p54	LOC502603	1.213	0.275	1.151	0.014	1.104	0.399	1.087	0.095
1371838_at	AI411155	similar to splicing factor, arginine/serine-rich 2	Sfrs2	1.106	0.264	1.428	0.001	1.133	0.300	1.326	0.003
1371839_at	AA819369	similar to splicing factor, arginine/serine-rich 2	Sfrs2	0.626	0.551	1.587	0.003	0.659	0.048	1.328	0.110
1373543_at	BI296461	Similar to Sprouty homolog 3 (Spry-3) (predicted)	RGD1564382_predicted	0.644	0.120	0.415	0.019	0.777	0.352	0.508	0.005
1385686_at	BI283251	similar to SPRR1b (predicted)	RGD1565265_predicted	0.639	0.174	0.992	0.947	0.676	0.204	0.999	0.964
1397635_at	BM390325	similar to squamous cell carcinoma antigen 2 (predicted)	RGD1562868_predicted	1.007	0.442	1.537	0.191	1.090	0.130	0.654	0.035
1373534_at	BE107209	similar to SR rich protein	RGD1307395	0.902	0.719	0.760	0.010	1.241	0.260	0.953	0.491
1373852_at	AA859922	similar to SRD5A2L	RGD1308828	1.398	0.082	1.220	0.182	0.834	0.637	0.617	0.063
1392813_at	AI548994	Similar to SRY sex determining region Y-box 9 protein (predicted)	RGD1563617_predicted	1.895	0.232	1.196	0.119	1.060	0.578	1.293	0.155
1382291_at	AI454332	Similar to SRY sex determining region Y-box 9 protein (predicted)	RGD1563617_predicted	1.888	0.477	2.188	0.421	1.446	0.909	1.607	0.439
1381935_at	BE115780	Similar to Sspn protein (predicted)	RGD1559723_predicted	1.002	0.317	0.867	0.207	0.858	0.104	0.999	0.986
1373871_at	AW435481	similar to STAGA complex 65 gamma subunit (predicted)	RGD1562206_predicted	0.637	0.247	0.517	0.001	0.569	0.265	0.774	0.039
1381461_at	AI058509	Similar to StAR-related protein 1-4E (predicted)	RGD1561783_predicted	1.385	0.015	0.414	0.002	1.274	0.006	0.526	0.015
1394275_at	BF559096	Similar to StAR-related protein 1-4E (predicted)	RGD1561783_predicted	1.616	0.052	0.285	0.000	0.629	0.128	0.397	0.000
1393183_at	H33503	similar to StAR-related protein 1-4E (predicted)	RGD1561783_predicted	0.800	0.397	0.298	0.000	1.028	0.806	0.403	0.009
1398588_at	BE098532	similar to step II splicing factor SLU7; DNA segment, Chr 11, ERATO Doi 730, expressed; DNA segment, Chr 3, Brigham & Womens Genetics 0878 expressed	LOC303057	0.906	0.788	1.313	0.125	0.908	0.530	0.963	0.543
1380226_at	BG376544	Similar to Sterile alpha motif domain containing 10 (predicted)	RGD1563203_predicted	0.707	0.172	0.730	0.099	0.842	0.040	1.019	0.854
1375073_at	BE107313	similar to sterile alpha motif domain containing 11 (predicted)	RGD1563779_predicted	0.807	0.275	1.189	0.045	1.015	0.058	1.225	0.018
1377918_at	AW526291	similar to Stomatin-like 1 (predicted)	RGD1559463_predicted	1.057	0.027	0.648	0.030	1.508	0.078	0.703	0.036
1373263_at	AW523737	similar to SUMO/sentrin specific protease 5 (predicted)	RGD1563140_predicted	0.506	0.305	2.942	0.001	0.713	0.962	2.738	0.004
1390555_at	AW530876	similar to Suppressor of cytokine signaling 5 (predicted)	RGD1564914_predicted	0.717	0.022	1.011	0.685	0.539	0.034	0.959	0.134
1379271_at	AA925076	similar to Suppressor of cytokine signaling 5 (predicted)	RGD1564914_predicted	0.774	0.475	1.163	0.223	0.717	0.264	1.009	0.829
1375068_at	AI410604	Similar to surfeit 5 isoform b (predicted)	RGD1564893_predicted	0.664	0.635	0.967	0.803	0.597	0.045	0.997	0.536
1376054_at	AI103054	similar to SWAP2	LOC499390	0.874	0.256	1.429	0.122	2.234	0.982	1.213	0.088
1371679_at	BE113393	similar to Synaptopodin-2 (Myopodin) (predicted)	RGD1564779_predicted	0.583	0.053	0.485	0.050	0.331	0.010	0.412	0.092
1384160_at	AI547837	similar to Synaptopodin-2 (Myopodin) (predicted)	RGD1564779_predicted	1.014	0.864	4.332	0.022	0.608	0.043	1.196	0.412
1388620_at	AA818192	similar to Tada3l protein	LOC362414	1.205	0.496	0.908	0.991	0.513	0.243	0.615	0.991
1380184_at	AW521222	Similar to TAFA5 (predicted)	RGD1562115_predicted	0.849	0.670	0.538	0.104	3.093	0.001	0.757	0.450
1380925_at	BF420093	Similar to talin 2 (predicted)	RGD1565416_predicted	1.812	0.011	0.998	0.875	2.082	0.029	0.942	0.661
1392944_at	AW251506	similar to talin 2 (predicted)	RGD1565416_predicted	1.061	0.838	1.049	0.171	1.632	0.838	0.965	0.824
1371381_at	AI007981	similar to TBC1 domain family member 4 (predicted)	RGD1561609_predicted	0.797	0.299	0.987	0.516	0.612	0.107	0.830	0.389
1378254_at	BM389480	similar to TBC1 domain family member 4 (predicted)	RGD1561609_predicted	1.013	0.919	0.841	0.472	0.712	0.147	0.638	0.194
1372129_at	BG378054	similar to TBC1 domain family, member 8; BUB2-like protein 1; vascular Rab-GAP/TBC-containing (predicted)	RGD1310147_predicted	1.072	0.538	0.954	0.286	1.020	0.538	0.919	0.231
1373467_at	BG374179	similar to TBP-associated factor 172 (TAF-172) (TAF(II)170) (predicted)	RGD1564130_predicted	1.613	0.108	1.775	0.097	2.049	0.034	2.590	0.005
1383429_at	BI289160	similar to T-Brain-1	LOC311078	0.666	0.448	1.285	0.002	0.725	0.112	1.211	0.012
1394082_at	BG662631	similar to T-Brain-1	LOC311078	0.564	0.747	1.165	0.380	0.399	0.555	1.060	0.668
1386073_at	AI043800	Similar to T-Brain-1	LOC311078	0.588	0.923	1.327	0.097	0.571	0.461	1.306	0.036
1379945_at	AI137329	similar to T-cell activation kelch repeat protein (predicted)	RGD1563166_predicted	1.239	0.904	0.355	0.002	0.599	0.901	0.505	0.030
1381570_at	BI293518	similar to T-cell activation NFKB-like protein (predicted)	RGD1308055_predicted	1.613	0.224	1.248	0.034	3.797	0.015	1.524	0.046
1397859_x_at	BI291927	Similar to T-cell receptor alpha chain (predicted)	RGD1565851_predicted	15.986	0.000	15.027	0.000	23.435	0.000	16.985	0.000
1377156_at	BI273936	Similar to TCF7L2 protein	LOC365486	12.088	0.001	1.035	0.913	14.076	0.008	2.796	0.053
1397210_at	BF396902	Similar to TCF7L2 protein	LOC365486	1.068	0.978	0.984	0.090	1.702	0.047	1.006	0.872
1395845_at	AW534087	Similar to TEL protein	LOC312777	1.725	0.057	1.070	0.669	2.014	0.199	1.000	0.999
1385294_at	BM387000	similar to TEL protein	LOC312777	1.754	0.181	4.807	0.010	1.063	0.840	1.905	0.087
1391444_at	BF285611	Similar to teratocyte-specific carboxylesterase (predicted)	RGD1564156_predicted	0.619	0.079	0.479	0.000	0.483	0.018	0.539	0.044
1397569_at	BF546710	Similar to teratocyte-specific carboxylesterase (predicted)	RGD1564156_predicted	0.816	0.290	0.436	0.020	0.416	0.074	0.311	0.000
1372237_at	BI298306	Similar to testes development-related NYD-SP22 isoform 1 (predicted)	RGD1561916_predicted	1.303	0.539	1.026	0.102	1.373	0.356	1.081	0.142
1389679_at	AI178923	Similar to testhymin (predicted)	RGD1563612_predicted	0.828	0.952	0.464	0.006	0.730	0.923	0.651	0.020
1389409_at	AI177869	similar to Testis derived transcript	LOC500040	0.637	0.938	2.419	0.008	0.477	0.821	2.019	0.059
1378941_at	AA957447	Similar to testis-specific chromodomain Y-like protein	LOC361237	1.317	0.237	1.706	0.004	1.291	0.325	1.730	0.021
1374494_at	AI137375	Similar to testis-specific chromodomain Y-like protein	LOC361237	0.840	0.988	2.097	0.116	0.783	0.317	2.905	0.014
1393496_at	BF566173	similar to testis-specific gene	LOC500799	1.141	0.322	1.028	0.869	1.003	0.868	0.993	0.969
1394949_at	BF399419	Similar to TGFB-induced factor 2 (predicted)	RGD1561562_predicted	1.001	0.626	0.653	0.299	1.586	0.429	0.565	0.067

1383428_at	AA923920	Similar to Thioredoxin domain containing protein 6 (Thioredoxin-like protein 2) (predicted)	RGD1564871_predicted	1.504	0.158	1.150	0.589	1.914	0.101	1.679	0.023
1382333_at	AI511250	Similar to THUMP domain containing 3 (predicted)	RGD1560852_predicted	0.610	0.036	0.891	0.124	0.596	0.034	0.787	0.068
1393317_at	BI303231	similar to THUMP domain containing 3 (predicted)	RGD1560852_predicted	0.902	0.239	1.983	0.018	0.854	0.572	1.743	0.026
1382049_at	AW530828	similar to thymus atrophy-related protein (predicted)	RGD1304607_predicted	0.529	0.093	0.334	0.045	0.470	0.087	0.464	0.047
1376119_at	BE100155	similar to thyroid adenoma associated (predicted)	RGD1560519_predicted	0.711	0.008	1.002	0.706	0.712	0.032	0.998	0.989
1397182_at	AI169397	similar to thyroid hormone receptor interactor 11	LOC314393	0.999	0.992	1.118	0.666	0.926	0.890	1.000	0.763
1372324_at	AW253391	similar to thyroid hormone receptor interactor 3	LOC497975	0.785	0.113	0.684	0.731	0.673	0.217	0.993	0.309
1384094_at	BF414316	Similar to timeless-interacting protein (predicted)	RGD1564084_predicted	1.373	0.211	1.772	0.562	0.587	0.275	0.891	0.388
1371546_at	BI284988	similar to TR4 orphan receptor associated protein TRA16	LOC361128	0.641	0.034	1.754	0.061	0.535	0.014	1.653	0.072
1380100_at	AW526268	similar to Traf2 and NCK interacting kinase, splice variant 4 (predicted)	RGD1561817_predicted	0.643	0.374	0.649	0.005	0.769	0.200	0.561	0.063
1396144_at	BF560978	similar to Traf2 and NCK interacting kinase, splice variant 4 (predicted)	RGD1561817_predicted	0.819	0.567	0.594	0.006	1.052	0.279	0.581	0.008
1383805_at	BG666454	similar to Traf2 and NCK interacting kinase, splice variant 4 (predicted)	RGD1561817_predicted	0.878	0.684	0.479	0.017	0.831	0.521	0.288	0.019
1373271_at	AI104034	similar to trafficking protein particle complex 5 (predicted)	RGD1563971_predicted	0.595	0.676	1.784	0.031	0.588	0.046	1.294	0.280
1377987_at	BI281852	similar to trafficking protein particle complex 5 (predicted)	RGD1563971_predicted	1.039	0.799	0.840	0.044	1.034	0.169	0.900	0.630
1384313_at	BF412520	similar to trafficking protein particle complex 5 (predicted)	RGD1563971_predicted	1.032	0.853	0.615	0.116	0.943	0.168	0.710	0.134
1382861_at	AA997486	similar to transcription elongation factor IIS - mouse	LOC498453	1.660	0.036	2.222	0.011	1.457	0.179	3.612	0.014
1392658_at	AI230409	Similar to transcription elongation factor IIS - mouse	LOC498453	1.718	0.120	2.428	0.003	1.978	0.158	3.054	0.000
1388867_at	AI227852	similar to transcription factor	MGC112830	0.720	0.076	0.613	0.021	0.679	0.042	0.447	0.020
1388964_at	AI232289	similar to transcription factor (p38 interacting protein)	RGD1307812	0.638	0.030	0.798	0.063	0.722	0.319	0.794	0.137
1394699_at	BG671896	Similar to transcription factor ONECUT2 (predicted)	RGD1564677_predicted	0.860	0.424	0.884	0.610	0.707	0.552	1.216	0.125
1379100_at	BF407311	similar to transcriptional regulating protein 132 (predicted)	RGD1306119_predicted	1.012	0.930	16.731	0.009	1.028	0.669	3.652	0.039
1389485_at	BE099784	similar to transformed mouse 3T3 cell double minute 1	LOC314859	0.686	0.212	1.112	0.523	0.563	0.119	0.808	0.368
1378675_at	BE119678	similar to transglutaminase E3 (predicted)	RGD1561831_predicted	1.058	0.338	0.447	0.082	1.019	0.994	0.402	0.000
1398973_at	BI296499	similar to transmembrane protein TM9SF3 (predicted)	RGD1564625_predicted	0.812	0.128	0.299	0.005	0.738	0.076	0.205	0.015
1395343_at	BF545305	similar to transmembrane protein TM9SF3 (predicted)	RGD1564625_predicted	0.385	0.129	1.249	0.812	0.881	0.827	1.062	0.695
1379627_at	AW534630	similar to transmembrane protein TM9SF3 (predicted)	RGD1564625_predicted	1.143	0.189	0.323	0.010	0.861	0.821	0.464	0.005
1371647_at	AA963367	similar to transmembrane protein TM9SF3 (predicted)	RGD1564625_predicted	0.878	0.755	0.816	0.061	0.971	0.883	0.875	0.324
1383721_at	AI556075	similar to transmembrane receptor	MGC112790	0.507	0.201	2.133	0.115	0.453	0.076	2.758	0.066
1388821_at	AI010430	similar to Tribbles homolog 2 (predicted)	RGD1564451_predicted	0.466	0.041	0.447	0.005	0.673	0.225	0.401	0.011
1390122_at	BI275740	Similar to triggering receptor expressed on myeloid cells-like 1 (predicted)	RGD1565175_predicted	2.150	0.010	1.465	0.016	2.272	0.003	1.493	0.041
1397183_at	BF404362	Similar to trinucleotide repeat containing 4 (predicted)	RGD1563168_predicted	1.079	0.832	0.573	0.045	1.036	0.852	0.475	0.196
1380769_at	BF394344	Similar to tripartite motif protein 24 (predicted)	RGD1562133_predicted	0.870	0.994	1.332	0.751	1.398	0.030	1.041	0.518
1373127_at	BM383645	Similar to Tripartite motif protein 44 (DIPB protein)	LOC502656	1.018	0.880	1.109	0.654	0.940	0.150	1.100	0.893
1374017_at	BI289517	Similar to tripartite motif protein 50 (predicted)	RGD1562778_predicted	3.057	0.006	0.343	0.028	4.558	0.005	0.274	0.028
1391027_at	AI236184	Similar to tripartite motif-containing 65 (predicted)	RGD1559497_predicted	1.165	0.527	1.008	0.729	0.972	0.916	0.948	0.754
1388951_at	BI294789	similar to Trithorax homolog 2 (Mixed lineage leukemia gene homolog 2 protein) (predicted)	RGD1308331_predicted	1.100	0.893	1.847	0.018	0.933	0.909	1.308	0.373
1376609_at	BG672064	similar to TRS85 homolog (predicted)	RGD1309102_predicted	1.072	0.531	1.119	0.444	1.118	0.623	1.058	0.437
1396115_at	BF566051	Similar to TRS85 homolog (predicted)	RGD1309102_predicted	0.840	0.971	0.820	0.024	1.195	0.895	0.998	0.990
1389139_at	BG665007	similar to Ttc15 protein (predicted)	RGD1566054_predicted	0.521	0.008	0.414	0.000	0.653	0.034	0.671	0.006
1382068_at	AA963991	similar to tubby super-family protein (predicted)	RGD1564487_predicted	1.100	0.298	1.293	0.142	1.183	0.187	1.071	0.517
1373718_at	BM384071	similar to tubulin, beta 2	LOC498736	3.379	0.008	2.320	0.021	2.101	0.198	2.002	0.002
1389108_at	AI710235	similar to tubulin-specific chaperone d	LOC363309	0.612	0.216	0.360	0.000	0.631	0.011	0.390	0.004
1372626_at	AI231999	Similar to tumor protein D53 (predicted)	RGD1564417_predicted	0.370	0.021	0.503	0.023	0.384	0.010	0.656	0.012
1393034_at	BI292899	similar to tyrosine kinase-associated leucine zipper protein LAZipII (predicted)	RGD1565584_predicted	1.108	0.232	1.201	0.104	1.624	0.182	1.247	0.058
1379723_at	BG673264	similar to tyrosine kinase-associated leucine zipper protein LAZipII (predicted)	RGD1565584_predicted	1.249	0.343	0.993	0.395	1.196	0.069	1.080	0.225
1376537_at	AW435010	Similar to Tyrosine-protein phosphatase, non-receptor type 3 (Protein-tyrosine phosphatase H1) (PTP-H1)	LOC500465	0.575	0.784	0.765	0.289	0.866	0.405	1.006	0.971
1394962_at	AI554981	Similar to U1 small nuclear ribonucleoprotein subunit, putative (predicted)	RGD1563251_predicted	0.994	0.560	1.022	0.846	1.001	0.798	0.948	0.833
1389874_at	BF404554	similar to U2 small nuclear ribonucleoprotein auxiliary factor 35 kDa subunit related-protein 1 (U2(RNU2) small nuclear RNA auxillary factor 1-like 1) (SP2)	LOC498425	0.809	0.457	1.104	0.660	1.017	0.665	1.090	0.883
1379590_at	AW527413	similar to U2 small nuclear ribonucleoprotein auxiliary factor 35 kDa subunit related-protein 1 (U2(RNU2) small nuclear RNA auxillary factor 1-like 1) (SP2)	LOC498425	1.020	0.819	1.296	0.525	0.721	0.065	0.929	0.519
1375058_at	BF396164	similar to U2af1-rs2 (predicted)	RGD1564881_predicted	0.472	0.009	0.738	0.011	0.413	0.021	0.877	0.013
1394672_at	BF414556	Similar to U5 snRNP-specific protein (Prp8-binding) (predicted)	RGD1309198_predicted	0.820	0.995	0.772	0.029	0.822	0.807	0.727	0.077
1383202_at	AA818406	similar to U6 snRNA-associated Sm-like protein LSm6 (Sm protein F) (predicted)	RGD1561937_predicted	1.002	0.272	0.931	0.698	1.074	0.799	1.349	0.001
1397874_at	AI548493	Similar to U7 snRNA-associated Sm-like protein Lsm11 (predicted)	RGD1565523_predicted	0.685	0.014	0.739	0.133	0.890	0.087	0.733	0.805
1375415_at	AI169233	similar to U7 snRNP-specific Sm-like protein LSM10	LOC366468	0.999	0.990	0.992	0.172	1.002	0.950	1.658	0.523
1371764_at	AI411771	similar to Ubc6p homolog	MGC94113	1.324	0.367	1.362	0.043	1.110	0.946	1.548	0.000
1389016_at	AI029306	similar to Ubiquitin carboxyl-terminal hydrolase 4 (Ubiquitin thiolesterase 4) (Ubiquitin-specific processing protease 4) (Deubiquitinating enzyme 4) (Ubiquitous nuclear protein)	LOC290864	1.025	0.882	1.719	0.047	0.956	0.832	1.129	0.360
1373409_at	BI294738	similar to ubiquitin protein ligase E3C (predicted)	RGD1559986_predicted	0.617	0.126	0.601	0.008	0.564	0.002	0.605	0.007
1380705_at	AW523627	Similar to ubiquitin protein ligase E3C (predicted)	RGD1559986_predicted	0.974	0.708	0.869	0.116	1.705	0.971	0.900	0.167

1390183_at	AI177708	similar to ubiquitin specific protease 34	LOC360990	1.362	0.019	1.074	0.110	1.174	0.054	1.165	0.059
1395426_at	AW142658	similar to ubiquitin-conjugating enzyme E2 variant 1 (predicted)	RGD1562209_predicted	1.619	0.327	1.071	0.770	1.812	0.647	0.881	0.476
1388640_at	BI279654	similar to Ubiquitin-like protein SMT3A precursor (Ubiquitin-related protein SUMO-2)	LOC499417	0.507	0.245	1.061	0.095	0.404	0.003	0.891	0.762
1367472_at	BG153295	similar to ubiquitin-protein ligase (EC 6.3.2.19) E1 - mouse	LOC314432	1.299	0.228	1.071	0.880	1.269	0.053	1.167	0.339
1383522_at	AI045086	similar to Ubiquitously transcribed tetratricopeptide repeat gene, X chromosome (predicted)	RGD1565134_predicted	1.240	0.454	0.997	0.562	0.953	0.874	1.286	0.373
1372115_at	AI408477	similar to Ubr2 protein (predicted)	RGD1561637_predicted	0.883	0.001	0.597	0.004	1.101	0.410	0.656	0.023
1391304_at	BM388658	similar to Ubr2 protein (predicted)	RGD1561637_predicted	1.837	0.127	1.024	0.779	1.125	0.735	1.010	0.715
1381349_a_at	AI231906	similar to Ubr2 protein (predicted)	RGD1561637_predicted	0.976	0.331	1.516	0.010	0.837	0.199	1.386	0.097
1389260_at	AI008393	similar to UBX domain-containing protein 1	LOC363332	1.134	0.753	1.407	0.349	1.146	0.983	2.180	0.018
1377572_at	AW434912	similar to UDP-glucose ceramide glucosyltransferase-like 2 (predicted)	RGD1563520_predicted	0.627	0.312	0.482	0.086	0.996	0.252	0.612	0.143
1379910_at	AI136097	similar to UDP-N-acteylglucosamine pyrophosphorylase 1 homolog (predicted)	RGD1561967_predicted	1.422	0.007	1.772	0.020	2.203	0.000	2.275	0.023
1378642_at	AI112858	similar to uncharacterized hypothalamus protein HT013 (predicted)	RGD1307071_predicted	0.777	0.586	2.010	0.019	1.471	0.207	2.017	0.015
1383643_at	BI282584	similar to UPF0197 protein C11orf10 homolog (predicted)	RGD1560328_predicted	0.794	0.071	1.030	0.761	0.472	0.046	1.002	0.301
1390110_at	BG372998	similar to Uridine-cytidine kinase 1-like 1 (predicted)	RGD1565465_predicted	0.721	0.158	1.069	0.432	0.819	0.121	1.067	0.747
1380038_at	BF393567	similar to vacuolar protein sorting 13C protein (predicted)	RGD1560364_predicted	1.050	0.973	0.986	0.985	1.001	0.996	0.997	0.967
1377145_at	BI296089	similar to very large G-protein coupled receptor 1 (predicted)	RGD1562101_predicted	1.133	0.048	0.993	0.846	0.996	0.997	1.061	0.994
1393304_at	BF386764	Similar to vesicle transport through interaction with t-SNAREs 1B homolog (predicted)	RGD1560475_predicted	0.975	0.785	1.462	0.011	1.006	0.984	1.179	0.247
1373145_at	BI281884	similar to Vps41 protein (predicted)	RGD1560511_predicted	0.775	0.280	0.618	0.006	0.884	0.249	0.767	0.023
1397512_at	BI281965	similar to Vps41 protein (predicted)	RGD1560511_predicted	0.979	0.779	0.768	0.679	1.018	0.567	0.847	0.313
1397824_at	BG665671	similar to WAC (predicted)	RGD1562407_predicted	2.210	0.066	1.500	0.626	3.096	0.047	1.062	0.807
1375644_at	AI170561	similar to WAC (predicted)	RGD1562093_predicted	1.800	0.181	2.208	0.005	1.753	0.258	1.612	0.005
1393686_at	AA818655	Similar to WAC (predicted)	RGD1562407_predicted	1.389	0.394	0.923	0.204	1.412	0.162	0.813	0.145
1391272_at	H33448	Similar to WAP four-disulfide core domain protein 8 precursor (Putative protease inhibitor WAP8)	LOC499942	2.798	0.525	0.955	0.994	1.229	0.847	1.011	0.996
1374669_at	AI600234	similar to WD repeat domain 11	LOC309016	0.756	0.342	0.622	0.200	0.689	0.233	0.553	0.075
1382489_at	BE116698	similar to WD repeat domain 11 protein (predicted)	RGD1564964_predicted	1.365	0.644	1.247	0.078	0.906	0.767	1.218	0.043
1391524_at	BE107185	similar to WD repeat domain 11 protein (predicted)	RGD1564964_predicted	0.983	0.705	1.100	0.545	1.037	0.900	1.163	0.928
1378318_at	BF420065	similar to WD repeat domain 53 (predicted)	RGD1559546_predicted	0.809	0.745	1.254	0.041	1.004	0.970	1.277	0.035
1386580_at	AW142797	similar to Wdr8 protein	LOC366515	0.639	0.636	1.188	0.101	0.970	0.605	0.899	0.669
1390811_at	BI290344	similar to Wdr8 protein	LOC366515	0.709	0.981	1.240	0.314	0.627	0.211	1.470	0.001
1388709_at	BF284695	similar to WD-repeat protein 43	LOC362703	0.505	0.288	1.064	0.721	0.729	0.150	1.149	0.090
1382679_at	BF396190	similar to WD-repeat protein 43	LOC362703	0.726	0.433	2.907	0.006	0.759	0.323	2.598	0.005
1383376_at	AI717529	similar to Williams-Beuren syndrome critical region protein 18	LOC368190	1.220	0.379	0.866	0.252	1.080	0.359	1.204	0.938
1380745_at	AA900859	Similar to Wilms tumor 1-associating protein (WT1-associated protein) homolog) (predicted)	RGD1563824_predicted	1.161	0.097	1.814	0.062	1.460	0.181	1.243	0.052
1382175_at	AW534129	Similar to Wilms tumor 1-associating protein (WT1-associated protein) homolog) (predicted)	RGD1563824_predicted	1.156	0.400	2.573	0.000	0.748	0.210	2.422	0.000
1391339_at	BI304052	Similar to Wilms tumor 1-associating protein (WT1-associated protein) homolog) (predicted)	RGD1563824_predicted	0.991	0.982	1.296	0.747	1.315	0.466	1.170	0.331
1390733_at	BI275867	Similar to WW domain-containing oxidoreductase isoform 2 (predicted)	RGD1565791_predicted	1.158	0.770	0.726	0.392	0.867	0.772	1.117	0.838
1377183_at	BE098555	Similar to WW-domain oxidoreductase (predicted)	RGD1564231_predicted	0.764	0.000	0.490	0.063	0.773	0.075	0.181	0.002
1388941_at	AI172403	similar to X83328 protein	RGD1304846	0.566	0.071	0.935	0.342	0.384	0.014	1.326	0.060
1376300_at	BI289802	similar to X83328 protein	RGD1304846	0.996	0.984	0.280	0.003	0.952	0.989	0.458	0.004
1380102_at	BM386836	similar to XAP-5 protein (predicted)	RGD1560964_predicted	0.484	0.015	0.829	0.285	0.342	0.003	0.860	0.051
1384354_at	BI288653	similar to X-linked lymphocyte regulated gene 4 (predicted)	RGD1565442_predicted	1.053	0.731	1.317	0.166	1.739	0.104	1.301	0.033
1373980_at	AW916138	similar to XPA binding protein 1 (predicted)	RGD1564506_predicted	0.894	0.129	1.684	0.005	0.726	0.044	1.537	0.018
1373941_at	BE103152	similar to YEATS domain containing 2 (predicted)	RGD1566176_predicted	1.103	0.498	1.070	0.115	1.093	0.799	1.033	0.687
1373149_at	BF285344	similar to yippee-like 3 (predicted)	RGD1564579_predicted	0.852	0.066	0.538	0.042	0.447	0.048	0.485	0.006
1372840_at	AI170289	Similar to Zbed4 protein (predicted)	RGD1560093_predicted	1.340	0.074	1.624	0.731	0.913	0.862	1.060	0.259
1379461_at	BE120147	similar to ZFP (predicted)	RGD1559144_predicted	1.354	0.047	0.838	0.089	1.563	0.018	0.766	0.238
1393105_at	BF288164	similar to zinc finger protein (predicted)	RGD1562173_predicted	0.425	0.064	1.002	0.454	0.395	0.064	0.909	0.204
1379104_at	BF400861	Similar to zinc finger protein 120 isoform 1 (predicted)	RGD1562845_predicted	1.089	0.018	1.442	0.073	1.305	0.372	2.017	0.000
1389709_at	AI146063	similar to Zinc finger protein 133	LOC499900	1.284	0.621	1.697	0.127	0.830	0.769	1.686	0.117
1396104_at	BF405150	Similar to Zinc finger protein 184 (predicted)	RGD1305084_predicted	1.022	0.970	0.878	0.840	1.475	0.003	0.959	0.867
1367547_at	BM388010	similar to zinc finger protein 198	LOC305913	1.220	0.092	1.153	0.189	1.380	0.127	1.094	0.318
1381733_at	BF404543	Similar to zinc finger protein 198	LOC305913	1.252	0.451	0.854	0.876	1.613	0.310	0.986	0.862
1393363_at	AI111670	similar to zinc finger protein 198	LOC305913	1.210	0.489	1.053	0.526	0.653	0.933	0.920	0.595
1380186_at	AI101272	Similar to Zinc finger protein 198 (Fused in myeloproliferative disorders protein) (Rearranged in atypical myeloproliferative disorder protein) (predicted)	RGD1306353_predicted	2.024	0.012	1.257	0.092	3.618	0.007	1.281	0.044
1382736_at	AI407047	Similar to Zinc finger protein 198 (Fused in myeloproliferative disorders protein) (Rearranged in atypical myeloproliferative disorder protein) (predicted)	RGD1306353_predicted	4.010	0.019	1.982	0.006	4.764	0.000	1.489	0.015
1390189_at	BF398121	similar to Zinc finger protein 277	LOC298977	1.247	0.445	1.643	0.067	1.278	0.393	2.032	0.011
1382228_at	BE095590	similar to Zinc finger protein 431 (predicted)	RGD1565971_predicted	0.777	0.064	0.616	0.009	0.902	0.533	0.582	0.006
1389657_at	AI175762	similar to zinc finger protein 524 (predicted)	RGD1565485_predicted	1.077	0.722	1.123	0.090	0.995	0.992	0.983	0.992
1389366_at	BI293689	similar to Zinc finger protein 553 (predicted)	RGD1561639_predicted	0.687	0.005	1.616	0.005	0.901	0.277	1.327	0.019

1397757_at	AW523345	Similar to zinc finger protein 560 (predicted)	RGD1565847_predicted	0.774	0.699	0.573	0.005	1.222	0.190	0.807	0.170
1393247_at	BI298190	Similar to zinc finger protein 560 (predicted)	RGD1565847_predicted	1.529	0.931	0.673	0.017	1.057	0.316	0.935	0.498
1375859_a_at	BM386823	Similar to zinc finger protein 565 (predicted)	RGD1560682_predicted	1.126	0.406	1.495	0.027	0.925	0.552	1.144	0.636
1389631_at	AA943109	Similar to zinc finger protein 609 (predicted)	RGD1561651_predicted	0.818	0.907	0.833	0.002	1.202	0.474	0.857	0.017
1390739_at	BE118828	similar to zinc finger protein 609 /// similar to zinc finger protein 609 (predicted)	LOC315766 /// RGD1561651_predicted	2.344	0.271	1.803	0.136	2.901	0.077	0.655	0.590
1398663_at	AI030120	similar to zinc finger protein 61	LOC499094	1.115	0.264	0.628	0.021	1.066	0.374	0.524	0.046
1386793_at	BF552772	similar to zinc finger protein 61	LOC499094	1.171	0.288	0.464	0.017	0.954	0.798	0.404	0.006
1380810_at	BE102637	Similar to zinc finger protein 610 (predicted)	RGD1560769_predicted	0.399	0.002	0.464	0.003	0.606	0.048	0.675	0.108
1392198_at	BF398283	Similar to zinc finger protein 610 (predicted)	RGD1560769_predicted	1.162	0.571	0.648	0.075	0.688	0.664	0.710	0.078
1379029_at	BI284478	Similar to Zinc finger protein 62 homolog (Zfp-62) (ZT3) (predicted)	RGD1560191_predicted	1.226	0.174	1.410	0.681	1.090	0.197	1.407	0.761
1396175_at	BG670617	similar to Zinc finger protein 62 homolog (Zfp-62) (ZT3) (predicted)	RGD1560191_predicted	1.497	0.724	1.023	0.426	1.192	0.791	1.242	0.218
1383538_at	BF545850	similar to zinc finger protein 650 (predicted)	RGD1565257_predicted	0.644	0.126	0.419	0.000	0.635	0.005	0.342	0.016
1382602_at	BE120211	similar to zinc finger protein 650 (predicted)	RGD1565257_predicted	0.800	0.129	0.388	0.001	0.828	0.069	0.383	0.009
1375059_at	AI178854	similar to zinc finger protein 652 (predicted)	RGD1566329_predicted	0.547	0.023	0.994	0.071	0.630	0.197	1.019	0.922
1393461_at	BM392157	Similar to zinc finger protein 75 (predicted)	RGD1565419_predicted	0.787	0.050	0.988	0.903	1.053	0.873	1.000	0.638
1377501_at	BM383704	similar to zinc finger protein 75 (predicted)	RGD1565419_predicted	1.966	0.103	1.012	0.648	1.346	0.676	0.647	0.684
1378973_at	BF396260	Similar to zinc finger protein Cezanne; cellular zinc finger anti-NF-kappaB Cezanne (predicted)	RGD1308111_predicted	2.651	0.041	3.053	0.027	1.476	0.179	2.283	0.049
1383311_at	AI716026	Similar to zinc finger protein Cezanne; cellular zinc finger anti-NF-kappaB Cezanne (predicted)	RGD1308111_predicted	2.481	0.068	1.601	0.081	2.374	0.084	1.321	0.274
1374348_at	BG373082	Similar to zinc finger protein Cezanne; cellular zinc finger anti-NF-kappaB Cezanne (predicted)	RGD1308111_predicted	1.172	0.083	1.005	0.785	1.087	0.548	1.080	0.253
1395651_at	AI511118	Similar to zinc finger protein Cezanne; cellular zinc finger anti-NF-kappaB Cezanne (predicted)	RGD1308111_predicted	1.019	0.163	0.497	0.024	1.251	0.281	0.501	0.022
1391507_at	BF417765	similar to zinc finger protein EZI	LOC500110	0.956	0.977	0.893	0.257	1.018	0.847	0.927	0.530
1391130_at	BI284481	similar to Zinc finger protein OZF (POZF-1)	RGD1308782	1.035	0.713	1.001	0.988	0.998	0.994	1.000	0.997
1385536_at	AI454433	Similar to zinc finger protein ZFP235 (predicted)	RGD1560762_predicted	2.025	0.075	1.183	0.421	0.641	0.172	3.193	0.154
1382453_at	BE118707	Similar to Zinc finger protein ZIC 3 (Zinc finger protein of the cerebellum 3) (predicted)	RGD1561261_predicted	1.121	0.732	1.567	0.273	1.235	0.696	1.658	0.365
1384769_a_at	AI136549	similar to Zinc finger X-linked protein ZXDB (predicted) /// similar to Zinc finger X-linked protein ZXDB (predicted)	RGD1563355_predicted /// RGD1563156_predicted	0.767	0.234	1.458	0.022	1.082	0.878	1.179	0.046
1372989_at	BI296586	similar to zinc finger, DHHC domain containing 14	LOC499014	1.141	0.054	1.746	0.005	1.009	0.072	2.053	0.003
1374949_at	BM385443	similar to Zinc finger, FYVE domain containing 19	LOC499871	1.009	0.928	1.988	0.004	1.409	0.415	1.760	0.020
1389509_at	BE097016	Sin3A associated protein 130 (predicted)	Sap130_predicted	0.616	0.063	0.871	0.113	0.431	0.050	0.903	0.163
1392465_at	AI228030	sin3-associated polypeptide, 18kDa	Sap18	0.667	0.271	1.303	0.024	0.548	0.051	1.093	0.072
1374904_at	AI175048	sine oculis homeobox homolog 1 (Drosophila)	Six1	1.647	0.466	1.501	0.689	1.256	0.038	0.882	0.668
1374080_at	AI407118	sine oculis-related homeobox 5 homolog (Drosophila) (predicted)	Six5_predicted	0.961	0.178	0.783	0.667	0.963	0.996	1.002	0.998
1378605_at	AA818702	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	Sigirr	0.591	0.386	0.646	0.372	0.647	0.215	1.030	0.900
1368517_at	NM_053358	single stranded DNA binding protein 3	Ssbp3	1.862	0.005	1.482	0.009	2.046	0.004	1.357	0.052
1372793_at	BE108903	single-stranded DNA binding protein 1	Ssbp1	0.470	0.011	0.587	0.004	0.570	0.062	0.817	0.069
1394884_s_at	AI171809	single-stranded DNA binding protein 1	Ssbp1	0.622	0.082	0.730	0.018	0.683	0.125	0.752	0.065
1375413_at	AA799614	sirtuin (silent mating type information regulation 2 homolog) 2 (S. cerevisiae)	Sirt2	0.850	0.897	1.614	0.115	1.178	0.296	1.924	0.000
1388925_at	AI171547	sirtuin 5 (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	Sirt5	0.887	0.840	1.621	0.025	0.783	0.361	1.174	0.068
1388638_at	AW525725	sirtuin 6 (silent mating type information regulation 2, homolog) 6 (S. cerevisiae)	Sirt6	0.937	0.883	1.073	0.631	0.782	0.297	1.070	0.931
1372933_at	AA892780	Sirtuin 7 (silent mating type information regulation 2, homolog) 7 (S. cerevisiae) (predicted)	Sirt7_predicted	0.936	0.909	1.442	0.050	0.701	0.056	1.101	0.318
1393706_at	BE109939	six transmembrane epithelial antigen of the prostate 1 (predicted)	Steap1_predicted	1.002	0.245	1.366	0.969	0.790	0.993	1.398	0.978
1387262_at	NM_031119	Sjogren syndrome antigen B	Ssb	1.001	0.115	0.959	0.184	1.068	0.399	0.956	0.366
1388655_at	AW252465	Sjogren's syndrome nuclear autoantigen 1 (predicted)	Ssna1_predicted	0.692	0.481	1.354	0.190	0.330	0.015	1.317	0.283
1383138_at	AI578268	slingshot homolog 3 (Drosophila)	Ssh3	0.867	0.553	0.879	0.391	1.398	0.836	0.905	0.141
1383231_at	AA955078	Smad nuclear interacting protein 1	Snip1	1.128	0.127	1.581	0.025	0.746	0.081	1.463	0.058
1398420_at	BF393807	SMAD specific E3 ubiquitin protein ligase 2 (predicted)	Smurf2_predicted	1.636	0.000	1.866	0.003	1.541	0.132	1.312	0.018
1372734_at	AI408095	small cell adhesion glycoprotein	Smagp	5.081	0.026	5.604	0.004	3.204	0.090	4.519	0.002
1388467_at	BG378576	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	Sgta	0.993	0.104	1.046	0.460	0.847	0.927	0.990	0.897
1377920_at	AI413026	Small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	Sgtb	1.525	0.009	2.630	0.007	1.524	0.029	1.030	0.954
1374279_at	BI288244	small inducible cytokine subfamily E, member 1	Scye1	0.858	0.819	1.942	0.004	0.670	0.052	1.679	0.003
1379810_at	AI454911	small inducible cytokine subfamily E, member 1	Scye1	0.952	0.975	2.060	0.003	0.966	0.969	2.086	0.006
1379320_at	AI102591	Small nuclear ribonucleoprotein D1 (predicted)	Snrpd1_predicted	0.674	0.016	1.408	0.068	0.668	0.094	1.460	0.001
1383107_at	BG670306	small nuclear ribonucleoprotein D1 (predicted)	Snrpd1_predicted	0.849	0.071	1.341	0.016	0.740	0.036	1.112	0.036
1371341_at	BG372885	small nuclear ribonucleoprotein D2 (predicted)	Snrpd2_predicted	0.802	0.573	1.617	0.091	0.566	0.022	1.354	0.173
1372333_at	BF555033	small nuclear ribonucleoprotein E (predicted) /// similar to small nuclear ribonucleoprotein E (predicted)	Snrpe_predicted /// RGD1565878_predicted	1.153	0.699	1.330	0.248	0.882	0.284	1.251	0.034
1388259_at	M29294	small nuclear ribonucleoprotein N	Snrpn	0.458	0.281	0.676	0.021	0.477	0.172	0.693	0.064
1368098_a_at	M29294	small nuclear ribonucleoprotein N	Snrpn	0.586	0.356	0.654	0.062	0.497	0.029	0.638	0.053
1369085_s_at	NM_130738	small nuclear ribonucleoprotein N /// SNRPN upstream reading frame	Snrpn /// Snurf	0.671	0.234	0.517	0.091	0.420	0.156	0.458	0.040
1389446_at	AI576586	small nuclear ribonucleoprotein polypeptide A' (predicted)	Snrpa1_predicted	1.116	0.434	3.092	0.006	1.163	0.452	2.492	0.008

1388117_at	AI411893	Small nuclear ribonucleoprotein polypeptides B and B1	Snrpb	1.002	0.577	1.037	0.781	1.049	0.770	1.089	0.137
1397294_at	AW529486	Small nuclear ribonucleoprotein polypeptides B and B1	Snrpb	0.968	0.865	0.804	0.235	0.882	0.245	1.003	0.993
1380265_at	BI294596	small nuclear RNA activating complex, polypeptide 1 (predicted)	Snapc1_predicted	0.792	0.795	0.870	0.243	0.654	0.096	1.051	0.730
1393161_at	AW916962	small nuclear RNA activating complex, polypeptide 3	Snapc3	1.134	0.605	1.548	0.002	1.191	0.464	1.850	0.005
1389641_at	BE349788	small nuclear RNA activating complex, polypeptide 4 (predicted)	Snapc4_predicted	0.830	0.697	1.457	0.005	0.882	0.410	0.983	0.868
1389792_at	BE329471	Small optic lobes homolog (Drosophila) (predicted)	Solh_predicted	0.747	0.366	1.390	0.130	0.945	0.290	1.350	0.130
1393041_at	AW535052	SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (predicted)	Smc2l1_predicted	0.767	0.333	1.271	0.210	0.772	0.040	1.104	0.576
1383008_at	AW535494	SMC4 structural maintenance of chromosomes 4-like 1 (yeast)	Smc4l1	0.922	0.522	1.473	0.433	0.600	0.151	0.681	0.018
1380257_at	BF419367	SMC5 structural maintenance of chromosomes 5-like 1 (yeast) (predicted)	Smc5l1_predicted	2.071	0.071	7.298	0.015	1.621	0.382	3.653	0.035
1390534_at	BG374727	SMC5 structural maintenance of chromosomes 5-like 1 (yeast) (predicted)	Smc5l1_predicted	1.109	0.091	0.976	0.651	1.098	0.709	1.364	0.479
1382790_at	AI639485	SMC5 structural maintenance of chromosomes 5-like 1 (yeast) (predicted)	Smc5l1_predicted	0.947	0.630	1.143	0.517	0.874	0.644	1.305	0.315
1378178_at	AA850777	SMC6 structural maintenance of chromosomes 6-like 1 (yeast) (predicted)	Smc6l1_predicted	1.554	0.096	1.230	0.041	1.507	0.106	0.924	0.063
1399095_at	AI407918	SMT3 suppressor of mif two 3 homolog 1 (yeast)	Sumo1	1.084	0.664	0.962	0.849	1.193	0.369	1.191	0.133
1367452_at	NM_133594	SMT3 suppressor of mif two 3 homolog 2 (yeast)	Sumo2	0.928	0.119	0.895	0.516	0.841	0.208	0.969	0.085
1367935_at	NM_057195	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	Smu1	0.750	0.139	0.977	0.628	0.712	0.001	0.991	0.911
1382006_at	AA996892	SNAP-associated protein	Snapap	0.755	0.017	0.710	0.028	0.799	0.062	0.799	0.351
1376366_at	BI278753	SNAP-associated protein	Snapap	0.999	0.472	0.702	0.000	0.914	0.996	0.877	0.241
1368596_at	NM_021693	SNF1-like kinase	Snf1lk	0.579	0.008	0.352	0.001	0.570	0.032	0.326	0.001
1391834_at	BM386419	Snf7 homologue associated with Alix 3	MGC108776	1.041	0.853	0.303	0.021	1.011	0.992	0.596	0.076
1372581_at	BF282487	SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae)	Snf8	0.660	0.059	0.830	0.064	0.772	0.012	0.723	0.096
1395406_at	BF552212	Sno, strawberry notch homolog 1 (Drosophila)	Sbno1	0.746	0.339	1.795	0.030	1.244	0.743	1.785	0.020
1389309_at	AW251323	sno, strawberry notch homolog 1 (Drosophila)	Sbno1	1.019	0.824	2.096	0.000	1.233	0.163	2.153	0.006
1379307_at	BF283256	sodium channel associated protein 1	Sap1	0.656	0.020	0.866	0.206	0.651	0.046	1.127	0.461
1373377_at	BG376162	sodium channel modifier 1 (predicted)	Scnm1_predicted	0.840	0.790	1.365	0.220	0.707	0.100	0.961	0.837
1369691_at	NM_013119	sodium channel, voltage-gated, type III, alpha polypeptide	Scn3a	1.225	0.648	0.503	0.046	1.067	0.747	0.541	0.006
1383435_at	BF542912	sodium channel, voltage-gated, type III, beta	Scn3b	1.751	0.146	0.418	0.019	1.950	0.533	0.441	0.079
1370850_at	AA685184	sodium channel, voltage-gated, type III, beta	Scn3b	0.979	0.832	0.359	0.000	1.276	0.114	0.537	0.016
1370973_at	BF285019	sodium channel, voltage-gated, type VII, alpha	Scn7a	1.113	0.826	0.259	0.042	1.588	0.403	0.291	0.039
1369693_a_at	NM_017215	solute carrier family 1 (glial high affinity glutamate transporter), member 2	Slc1a2	0.910	0.975	4.298	0.005	0.989	0.958	1.099	0.621
1368565_at	NM_019225	solute carrier family 1 (glial high affinity glutamate transporter), member 3	Slc1a3	0.733	0.110	0.661	0.091	2.169	0.116	1.057	0.400
1371130_at	X63744	solute carrier family 1 (glial high affinity glutamate transporter), member 3	Slc1a3	0.994	0.930	0.994	0.127	0.985	0.930	0.831	0.067
1370367_at	D63772	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	Slc1a1	7.193	0.008	1.240	0.145	7.776	0.014	0.962	0.374
1387932_at	U39555	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	Slc1a1	1.015	0.921	1.000	0.968	1.801	0.102	1.039	0.926
1368609_at	NM_017047	solute carrier family 10 (sodium/bile acid cotransporter family), member 1	Slc10a1	1.687	0.225	1.001	0.750	0.998	0.924	0.950	0.456
1367877_at	NM_013173	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	Slc11a2	9.325	0.000	17.194	0.002	2.864	0.024	3.877	0.021
1388059_a_at	AF029757	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	Slc11a2	2.139	0.213	1.588	0.037	1.458	0.347	1.085	0.433
1371525_at	BI277550	solute carrier family 12 (potassium/chloride transporters), member 7	Slc12a7	1.000	0.608	0.891	0.304	1.977	0.012	1.189	0.074
1393364_at	BM385460	solute carrier family 12 (potassium/chloride transporters), member 8	Slc12a8	0.571	0.032	0.798	0.196	0.525	0.033	0.647	0.008
1381253_at	BF398826	Solute carrier family 12, member 2	Slc12a2	1.613	0.532	1.325	0.130	0.923	0.419	1.057	0.772
1395748_at	AW528866	Solute carrier family 12, member 6	Slc12a6	1.111	0.993	0.638	0.123	1.340	0.077	0.758	0.057
1370440_at	AB000280	solute carrier family 15, member 4	Slc15a4	1.456	0.173	1.330	0.271	1.049	0.733	1.808	0.197
1370548_at	AB047324	solute carrier family 16 (monocarboxylic acid transporters), member 10	Slc16a10	0.219	0.079	0.108	0.000	0.369	0.003	0.250	0.025
1390036_at	BI289867	solute carrier family 16 (monocarboxylic acid transporters), member 6	Slc16a6	4.252	0.006	1.772	0.162	4.552	0.001	2.207	0.013
1394751_at	AI577528	Solute carrier family 16 (monocarboxylic acid transporters), member 6	Slc16a6	1.000	0.481	1.022	0.590	0.784	0.297	0.936	0.634
1392879_at	AA946069	Solute carrier family 16 (monocarboxylic acid transporters), member 6	Slc16a6	0.807	0.984	0.999	0.832	0.968	0.982	1.003	0.727
1376605_at	AA900983	solute carrier family 17 (anion/sugar transporter), member 5	Slc17a5	0.815	0.100	1.666	0.040	0.659	0.142	1.429	0.049
1387188_at	NM_133554	solute carrier family 17 (sodium phosphate), member 1	Slc17a1	1.001	0.996	0.997	0.928	1.283	0.402	1.054	0.750
1390591_at	AI169163	solute carrier family 17 (sodium phosphate), member 3	Slc17a3	2.051	0.002	7.003	0.005	1.161	0.497	7.051	0.006
1387999_at	M97380	solute carrier family 18 (vesicular monoamine), member 1	Slc18a1	1.247	0.510	1.004	0.980	1.268	0.374	0.995	0.975
1369131_at	NM_013031	solute carrier family 18 (vesicular monoamine), member 2	Slc18a2	0.679	0.068	0.749	0.118	0.522	0.073	0.523	0.005
1390863_at	BF283298	solute carrier family 19 (thiamine transporter), member 2	Slc19a2	1.112	0.601	3.217	0.000	0.908	0.583	2.478	0.006
1370848_at	BI284218	solute carrier family 2 (facilitated glucose transporter), member 1	Slc2a1	4.249	0.009	12.799	0.005	2.223	0.143	9.074	0.006
1380112_at	AW531114	Solute carrier family 2 (facilitated glucose transporter), member 1	Slc2a1	1.160	0.597	0.708	0.710	0.763	0.106	1.007	0.988
1387228_at	NM_012879	solute carrier family 2 (facilitated glucose transporter), member 2	Slc2a2	0.373	0.000	0.266	0.001	0.381	0.003	0.373	0.018
1368460_at	NM_031741	solute carrier family 2, member 5	Slc2a5	0.716	0.998	0.510	0.026	0.433	0.777	0.426	0.028
1370314_at	AB000489	solute carrier family 20 (phosphate transporter), member 1	Slc20a1	2.250	0.017	4.990	0.000	2.643	0.013	4.115	0.000
1372747_at	AI409899	solute carrier family 20, member 2	Slc20a2	0.790	0.795	1.275	0.059	0.748	0.572	1.571	0.115
1398435_at	BE112977	Solute carrier family 22 (organic cation transporter), member 15 (predicted)	Slc22a15_predicted	2.424	0.100	2.117	0.056	1.407	0.084	1.738	0.006
1371889_at	AW915448	solute carrier family 22 (organic cation transporter), member 17	Slc22a17	0.448	0.093	0.269	0.002	0.455	0.074	0.361	0.011
1367950_at	NM_019269	solute carrier family 22 (organic cation transporter), member 5	Slc22a5	1.564	0.072	1.535	0.047	1.078	0.754	0.733	0.139
1369169_at	NM_017315	solute carrier family 23 (nucleobase transporters), member 1	Slc23a1	0.856	0.664	1.084	0.946	0.800	0.579	1.001	0.641

1386454_at	AI639159	solute carrier family 23 (nucleobase transporters), member 3 (predicted)	Slc23a3_predicted	1.625	0.063	0.942	0.727	1.727	0.213	0.934	0.056
1398162_at	BF400617	Solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	Slc24a2	0.913	0.030	0.949	0.822	0.422	0.054	0.941	0.814
1388000_at	AF021923	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	Slc24a2	0.302	0.051	0.141	0.015	0.295	0.040	0.179	0.005
1392459_x_at	AI136271	Solute carrier family 24 (sodium/potassium/calcium exchanger), member 4 (predicted)	Slc24a4_predicted	1.887	0.424	0.986	0.324	1.358	0.418	1.872	0.082
1381965_at	AI136271	Solute carrier family 24 (sodium/potassium/calcium exchanger), member 4 (predicted)	Slc24a4_predicted	1.329	0.699	1.527	0.965	1.365	0.461	1.439	0.089
1398249_at	NM_053965	solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20	Slc25a20	0.763	0.466	1.273	0.033	0.780	0.143	0.899	0.268
1380111_at	AI578095	Solute carrier family 25 (mitochondrial carrier, Aralar), member 12 (predicted)	Slc25a12_predicted	1.043	0.359	0.961	0.986	0.998	0.454	1.119	0.829
1371534_at	AI407908	solute carrier family 25 (mitochondrial carrier, glutamate), member 22	Slc25a22	1.516	0.141	2.047	0.004	1.053	0.634	1.986	0.004
1390483_at	BF555120	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29	Slc25a29	1.000	0.545	1.000	0.976	1.176	0.329	1.002	0.992
1372538_at	BM389148	solute carrier family 25 (mitochondrial carrier, peroxisomal membrane protein), member 17 (predicted)	Slc25a17_predicted	0.483	0.042	0.783	0.126	0.369	0.007	0.636	0.011
1380909_at	BM385894	Solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 24 (predicted)	Slc25a24_predicted	2.091	0.000	1.303	0.005	1.968	0.000	1.277	0.048
1371754_at	AI177358	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	Slc25a25	0.579	0.133	0.569	0.011	0.540	0.007	0.625	0.005
1373283_at	BE113158	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 3	Slc25a3	0.487	0.082	2.119	0.016	0.210	0.003	1.407	0.034
1370277_at	M23984	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 3	Slc25a3	0.621	0.260	0.868	0.090	0.704	0.051	0.919	0.345
1396641_at	BF397278	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 3	Slc25a3	0.998	0.984	0.974	0.713	1.099	0.333	1.185	0.757
1388112_at	BG666999	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	Slc25a4	0.858	0.818	0.965	0.262	0.449	0.093	0.679	0.002
1388163_at	AI012445	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	Slc25a5	0.653	0.804	0.956	0.098	0.598	0.546	0.909	0.226
1370020_at	NM_133418	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10	Slc25a10	1.140	0.313	1.006	0.982	0.934	0.410	0.969	0.976
1393947_at	BG377383	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15	Slc25a15	0.998	0.181	0.504	0.007	1.107	0.155	0.509	0.007
1370060_at	NM_022398	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	Slc25a11	0.510	0.021	0.647	0.006	0.540	0.000	0.700	0.094
1380031_at	BE098261	Solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21	Slc25a21	0.624	0.149	1.474	0.069	1.559	0.007	0.935	0.780
1367773_at	NM_017307	solute carrier family 25, member 1	Slc25a1	1.227	0.996	0.573	0.016	0.906	0.638	0.681	0.008
1390416_at	H35736	Solute carrier family 25, member 30	Slc25a30	1.143	0.424	2.086	0.015	0.831	0.365	1.786	0.044
1381472_at	BE110276	Solute carrier family 25, member 32 (predicted)	Slc25a32_predicted	1.871	0.219	1.063	0.304	2.901	0.136	0.826	0.920
1393513_at	AI071445	Solute carrier family 26 (sulfate transporter), member 2	Slc26a2	1.510	0.498	0.950	0.571	1.491	0.350	1.173	0.155
1367789_at	NM_053580	solute carrier family 27 (fatty acid transporter), member 1	Slc27a1	0.423	0.013	0.439	0.071	0.912	0.196	0.608	0.024
1381028_at	BF417583	Solute carrier family 27 (fatty acid transporter), member 4	Slc27a4	1.096	0.226	1.867	0.009	0.671	0.191	1.107	0.520
1387585_at	NM_031738	solute carrier family 29 (nucleoside transporters), member 2	Slc29a2	1.002	0.881	1.003	0.878	1.000	0.430	1.001	0.952
1374200_at	BM392280	solute carrier family 29 (nucleoside transporters), member 3	Slc29a3	1.250	0.208	0.708	0.070	1.337	0.077	0.994	0.655
1398771_at	NM_019283	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	Slc3a2	0.989	0.897	2.168	0.002	0.671	0.418	1.765	0.030
1368440_at	NM_017216	solute carrier family 3, member 1	Slc3a1	0.238	0.022	0.109	0.006	0.460	0.046	0.168	0.009
1375182_at	BE109671	Solute carrier family 3, member 1	Slc3a1	0.335	0.034	0.129	0.000	0.368	0.006	0.236	0.013
1398264_at	NM_012890	solute carrier family 30 (zinc transporter), member 2	Slc30a2	0.997	0.680	0.996	0.978	1.002	0.988	0.904	0.104
1370357_at	Y16774	solute carrier family 30 (zinc transporter), member 4	Slc30a4	0.482	0.095	0.737	0.035	0.427	0.000	0.783	0.058
1373821_at	BF418332	solute carrier family 30 (zinc transporter), member 5 (predicted)	Slc30a5_predicted	0.497	0.384	0.935	0.207	0.452	0.052	0.769	0.033
1389133_at	AI104870	solute carrier family 30 (zinc transporter), member 6 (predicted)	Slc30a6_predicted	0.767	0.246	0.713	0.358	0.755	0.215	0.788	0.375
1374686_at	BF283406	solute carrier family 30 (zinc transporter), member 7	Slc30a7	0.887	0.603	1.188	0.874	1.295	0.076	1.005	0.952
1368045_at	NM_133600	solute carrier family 31 (copper transporters), member 1	Slc31a1	0.536	0.082	1.401	0.002	0.621	0.041	1.225	0.006
1373657_at	BF417391	solute carrier family 31, member 2	Slc31a2	1.092	0.738	0.314	0.004	1.258	0.233	0.392	0.005
1394954_at	BE101666	solute carrier family 31, member 2	Slc31a2	1.229	0.914	0.268	0.005	0.816	0.478	0.246	0.023
1393216_at	BI282044	solute carrier family 33 (acetyl-CoA transporter), member 1	Slc33a1	0.716	0.031	0.648	0.015	1.020	0.353	0.845	0.172
1370134_at	NM_022252	solute carrier family 33 (acetyl-CoA transporter), member 1	Slc33a1	0.569	0.305	0.885	0.509	0.769	0.197	1.037	0.516
1392317_at	BI288026	Solute carrier family 33 (acetyl-CoA transporter), member 1	Slc33a1	0.932	0.417	1.562	0.502	1.198	0.190	1.150	0.586
1370745_at	AB013454	solute carrier family 34 (sodium phosphate), member 1	Slc34a1	0.960	0.633	1.331	0.065	0.857	0.086	1.308	0.018
1386077_at	AA891822	Solute carrier family 35 (CMP-sialic acid transporter), member 1 (predicted)	Slc35a1_predicted	0.805	0.077	0.796	0.075	0.741	0.728	1.111	0.258
1386078_at	AI228537	solute carrier family 35 (CMP-sialic acid transporter), member 1 (predicted)	Slc35a1_predicted	1.110	0.300	0.750	0.162	0.810	0.347	0.712	0.109
1375254_at	BE103444	solute carrier family 35 (CMP-sialic acid transporter), member 1 (predicted)	Slc35a1_predicted	0.851	0.674	0.818	0.096	0.999	0.997	0.632	0.187
1376187_at	AI177887	Solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1 (predicted)	Slc35d1_predicted	0.970	0.280	0.926	0.268	0.800	0.160	0.900	0.323
1370303_at	AF406814	solute carrier family 35, member A4	Slc35a4	0.887	0.257	0.902	0.171	0.766	0.322	1.128	0.362
1375871_at	BM392047	solute carrier family 35, member B1	Slc35b1	0.934	0.457	1.370	0.092	1.021	0.157	1.012	0.416
1377143_at	BM388792	solute carrier family 35, member B1	Slc35b1	0.788	0.992	0.987	0.144	0.832	0.527	1.051	0.113
1376835_at	BI293600	Solute carrier family 35, member B2	Slc35b2	11.207	0.028	2.045	0.023	41.266	0.000	7.889	0.003
1390825_at	AI010067	solute carrier family 35, member B3 (predicted)	Slc35b3_predicted	1.243	0.015	1.111	0.237	1.613	0.296	1.227	0.009
1388760_at	BI296312	Solute carrier family 35, member B4 (predicted)	Slc35b4_predicted	0.450	0.028	0.749	0.124	0.957	0.649	0.874	0.108
1367499_at	BM390900	solute carrier family 35, member C1 (predicted)	Slc35c1_predicted	0.516	0.206	0.646	0.014	0.632	0.141	0.918	0.431
1383350_at	AA963524	Solute carrier family 35, member C2	Slc35c2	0.774	0.074	0.896	0.964	0.884	0.161	0.998	0.988
1383996_at	BI281608	Solute carrier family 35, member E1 (predicted)	Slc35e1_predicted	0.874	0.892	1.225	0.215	0.926	0.785	0.962	0.211
1387942_at	AF182714	solute carrier family 35, member E4	Slc35e4	0.999	0.989	1.424	0.063	0.997	0.968	1.122	0.252
1388732_at	AI009820	solute carrier family 35, member F5 (predicted)	Slc35f5_predicted	1.168	0.529	1.184	0.796	0.639	0.136	0.934	0.306
1398531_at	AI058947	Solute carrier family 36 (proton/amino acid symporter), member 4 (predicted)	Slc36a4_predicted	0.438	0.003	0.358	0.001	0.279	0.103	0.361	0.031

1382076_at	AA955403	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	Slc37a1	3.388	0.050	1.933	0.009	2.979	0.000	1.974	0.047
1386960_at	NM_031589	solute carrier family 37 (glycerol-6-phosphate transporter), member 4	Slc37a4	0.115	0.009	0.183	0.000	0.202	0.000	0.183	0.009
1370409_at	AF075704	solute carrier family 38, member 1	Slc38a1	0.831	0.897	4.248	0.016	0.887	0.896	3.495	0.001
1370286_at	AF249673	solute carrier family 38, member 2	Slc38a2	0.942	0.547	0.914	0.120	0.872	0.093	1.036	0.557
1369074_at	NM_130748	solute carrier family 38, member 4	Slc38a4	0.657	0.028	1.021	0.989	0.634	0.045	0.991	0.899
1387970_at	AF276870	solute carrier family 38, member 5	Slc38a5	0.453	0.069	0.114	0.000	0.496	0.027	0.134	0.003
1376972_at	AI407028	Solute carrier family 39 (iron-regulated transporter), member 1	Slc40a1	0.270	0.006	0.790	0.939	0.270	0.007	0.839	0.906
1390412_at	AI229664	Solute carrier family 39 (iron-regulated transporter), member 1	Slc40a1	0.143	0.027	1.456	0.435	0.352	0.068	1.912	0.117
1393162_at	AI502079	solute carrier family 39 (metal ion transporter), member 6	Slc39a6	1.396	0.202	1.684	0.003	1.482	0.880	1.272	0.312
1372482_at	AI600216	solute carrier family 39 (zinc transporter), member 13	Slc39a13	0.660	0.010	1.000	0.998	0.867	0.161	0.821	0.089
1373953_at	BI290779	solute carrier family 4 (anion exchanger), member 1, adaptor protein (predicted)	Slc4a1ap_predicted	0.660	0.683	0.940	0.470	1.069	0.903	1.173	0.158
1368082_at	NM_017048	solute carrier family 4, member 2	Slc4a2	0.938	0.801	0.889	0.739	0.627	0.014	0.885	0.028
1368772_at	NM_017049	solute carrier family 4, member 3	Slc4a3	0.924	0.208	1.033	0.394	0.717	0.342	0.787	0.005
1373326_at	AI716512	Solute carrier family 4, sodium bicarbonate transporter-like, member 10	Slc4a10	0.781	0.050	2.704	0.001	0.487	0.017	2.326	0.002
1383319_at	BI293444	solute carrier family 4, sodium bicarbonate transporter-like, member 11 (predicted)	Slc4a11_predicted	3.300	0.015	2.622	0.016	1.160	0.656	1.140	0.384
1379736_at	AI232440	Solute carrier family 43, member 2 (predicted)	Slc43a2_predicted	2.013	0.037	0.747	0.077	0.482	0.041	0.439	0.021
1384756_at	BF394311	Solute carrier family 43, member 2 (predicted)	Slc43a2_predicted	0.646	0.189	0.127	0.006	0.157	0.030	0.151	0.015
1376117_at	BI289103	solute carrier family 44, member 4	Slc44a4	2.459	0.130	2.604	0.018	4.514	0.004	3.226	0.007
1392349_at	BE116021	solute carrier family 5 (inositol transporters), member 3	Slc5a3	1.116	0.722	2.788	0.009	2.117	0.099	1.448	0.062
1383697_at	AW530905	Solute carrier family 5 (inositol transporters), member 3	Slc5a3	1.072	0.991	1.919	0.034	1.639	0.127	1.517	0.086
1377196_at	BI289660	Solute carrier family 5 (sodium/glucose cotransporter), member 10 (predicted)	Slc5a10_predicted	1.010	0.988	0.982	0.788	1.115	0.734	0.981	0.991
1368414_at	NM_022590	solute carrier family 5 (sodium/glucose cotransporter), member 2	Slc5a2	0.514	0.033	0.389	0.001	0.449	0.299	0.468	0.004
1367815_at	NM_130746	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	Slc5a6	0.573	0.171	1.486	0.142	0.631	0.365	1.543	0.043
1384303_s_at	AI712791	solute carrier family 6 (neurotransmitter transporter), member 17	Slc6a17	0.416	0.041	0.323	0.045	0.391	0.028	0.212	0.021
1384302_at	AI712791	solute carrier family 6 (neurotransmitter transporter), member 17	Slc6a17	0.298	0.094	0.400	0.005	0.188	0.021	0.264	0.022
1367810_at	AI412218	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	Slc6a8	2.192	0.051	23.339	0.001	0.461	0.196	14.009	0.000
1386934_at	NM_017348	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	Slc6a8	1.199	0.938	1.290	0.122	0.673	0.210	1.463	0.019
1373787_at	AA943735	Solute carrier family 6 (neurotransmitter transporter, glycine), member 9	Slc6a9	1.304	0.330	4.793	0.014	1.472	0.233	5.906	0.006
1378910_at	BG378480	Solute carrier family 6 (neurotransmitter transporter, taurine), member 6	Slc6a6	2.719	0.034	39.573	0.000	2.135	0.094	14.032	0.000
1368778_at	NM_017206	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	Slc6a6	1.683	0.117	1.300	0.413	1.101	0.621	0.701	0.013
1368391_at	NM_013111	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	Slc7a1	1.262	0.065	1.520	0.005	1.178	0.149	1.558	0.007
1368392_at	BF420160	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	Slc7a1	0.916	0.779	2.475	0.005	0.962	0.551	1.525	0.009
1369460_at	NM_022619	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	Slc7a2	1.112	0.375	2.915	0.014	0.594	0.447	1.425	0.135
1382145_at	AW531444	solute carrier family 7 (cationic amino acid transporter, y+ system), member 4 (predicted)	Slc7a4_predicted	0.467	0.056	0.229	0.004	0.367	0.012	0.361	0.040
1387280_a_at	NM_017353	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	Slc7a5	0.476	0.104	0.705	0.017	0.432	0.039	0.557	0.006
1373629_at	BE108272	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 (predicted)	Slc7a6_predicted	0.696	0.059	0.917	0.548	0.693	0.264	0.842	0.182
1387808_at	AF200684	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	Slc7a7	1.005	0.570	0.944	0.074	1.005	0.992	0.945	0.077
1387057_at	NM_053442	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 /// synaptic Ras GTPase activating protein 1 homolog (rat)	Slc7a8 /// Syngap1	0.706	0.087	0.279	0.001	0.429	0.017	0.257	0.006
1384831_at	AI233155	solute carrier family 7, (cationic amino acid transporter, y+ system) member 13	Slc7a13	0.592	0.482	1.207	0.628	1.253	0.606	0.651	0.324
1387793_at	NM_021594	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1	Slc9a3r1	0.849	0.582	0.636	0.048	0.936	0.580	0.992	0.138
1380531_at	AI102178	solute carrier family 9 (sodium/hydrogen exchanger), isoform 9 (predicted)	Slc9a9_predicted	0.426	0.037	1.040	0.151	0.651	0.077	0.995	0.841
1390440_at	BG380512	solute carrier family 9 (sodium/hydrogen exchanger), member 6 (predicted)	Slc9a6_predicted	0.713	0.288	0.385	0.000	0.674	0.012	0.477	0.004
1372899_at	AI104683	Solute carrier family 9 (sodium/hydrogen exchanger), member 8	Slc9a8	0.933	0.197	0.615	0.003	1.252	0.158	0.650	0.001
1367965_at	NM_012652	solute carrier family 9, member 1	Slc9a1	0.964	0.833	0.986	0.252	1.807	0.113	1.024	0.301
1370800_at	AF462063	Solute carrier family 9, member 1	Slc9a1	0.999	0.995	1.053	0.645	1.003	0.765	0.956	0.924
1368606_at	NM_030838	solute carrier organic anion transporter family, member 1a5	Slco1a5	1.217	0.642	1.150	0.575	2.471	0.237	1.991	0.002
1395039_at	BI289224	Solute carrier organic anion transporter family, member 3a1	Slco3a1	1.914	0.006	1.176	0.031	0.752	0.113	0.820	0.212
1373734_at	AI101171	Solute carrier organic anion transporter family, member 3a1	Slco3a1	0.506	0.141	0.380	0.003	0.801	0.088	0.306	0.015
1389067_at	AI180349	solute carrier organic anion transporter family, member 4a1	Slco4a1	2.124	0.024	1.663	0.112	1.410	0.074	0.966	0.871
1367762_at	NM_012659	somatostatin	Sst	0.476	0.005	0.083	0.005	0.478	0.019	0.077	0.048
1368598_at	NM_133522	somatostatin receptor 3 /// hypothetical gene supported by NM_133522	Sstr3 /// SSTR	2.172	0.043	1.987	0.039	0.722	0.929	1.103	0.845
1392523_at	AW144637	Son cell proliferation protein	Son	0.871	0.032	0.678	0.200	0.991	0.965	0.791	0.385
1391978_at	AW531885	Son cell proliferation protein	Son	1.284	0.187	0.563	0.032	1.167	0.534	0.833	0.589
1398989_at	BI275248	Son cell proliferation protein	Son	1.072	0.483	0.627	0.001	0.941	0.366	0.730	0.010
1369636_at	BI285149	sorbitol dehydrogenase	Sord	0.574	0.096	0.987	0.884	0.679	0.232	0.811	0.835
1372728_at	BE103745	Sortilin 1	Sort1	0.523	0.116	0.128	0.001	0.609	0.270	0.205	0.002
1391230_at	BF394904	Sortilin 1	Sort1	1.045	0.609	1.431	0.993	0.998	0.917	1.028	0.868
1390710_x_at	AA850618	sortilin-related receptor, L(DLR class) A repeats-containing (predicted)	Sorl1_predicted	0.615	0.007	0.244	0.000	0.643	0.011	0.419	0.000
1377457_a_at	AA850618	sortilin-related receptor, L(DLR class) A repeats-containing (predicted)	Sorl1_predicted	0.353	0.022	0.253	0.000	0.530	0.010	0.417	0.006
1377458_at	AA850618	sortilin-related receptor, L(DLR class) A repeats-containing (predicted)	Sorl1_predicted	0.798	0.064	0.287	0.001	0.773	0.120	0.346	0.000

1393933_at	AW144823	sortilin-related receptor, L(DLR class) A repeats-containing (predicted)	Sorl1_predicted	0.470	0.800	0.216	0.002	0.574	0.644	0.329	0.000
1388380_at	BI278122	sorting and assembly machinery component 50 homolog (S. cerevisiae)	Samm50	0.476	0.030	0.630	0.017	0.597	0.065	0.746	0.012
1368043_at	NM_053411	sorting nexin 1	Snx1	1.460	0.016	1.913	0.007	1.412	0.090	1.823	0.010
1383585_s_at	AI043753	Sorting nexin 10	Snx10	4.616	0.026	4.064	0.002	5.147	0.002	6.992	0.001
1383653_at	BG374126	sorting nexin 11	Snx11	2.449	0.067	1.397	0.994	3.578	0.003	1.156	0.986
1381699_at	BF389280	Sorting nexin 12 (predicted)	Snx12_predicted	2.021	0.150	0.808	0.333	1.578	0.739	0.680	0.146
1384410_at	AA964404	Sorting nexin 12 (predicted)	Snx12_predicted	1.286	0.415	0.527	0.039	0.935	0.263	0.651	0.486
1390280_at	BF396115	Sorting nexin 12 (predicted)	Snx12_predicted	0.994	0.966	0.954	0.123	1.002	0.607	0.929	0.197
1371555_at	AI599411	sorting nexin 12 (predicted) /// similar to Sorting nexin 12 (predicted)	Snx12_predicted /// RGD1559528_predicted	0.783	0.448	1.017	0.989	0.977	0.497	0.948	0.355
1389647_at	BM387990	Sorting nexin 13 (predicted)	Snx13_predicted	0.917	0.330	0.652	0.122	1.037	0.681	0.755	0.049
1379388_at	BI296311	sorting nexin 13 (predicted)	Snx13_predicted	1.281	0.555	1.940	0.003	1.318	0.276	2.224	0.001
1374692_at	BE107598	Sorting nexin 14 (predicted)	Snx14_predicted	0.701	0.055	0.607	0.027	0.604	0.098	0.724	0.103
1372656_at	BI282899	sorting nexin 15	Snx15	1.963	0.012	4.904	0.000	2.009	0.010	3.601	0.000
1387510_at	NM_022289	sorting nexin 16	Snx16	1.530	0.126	2.549	0.021	1.603	0.046	2.050	0.017
1382643_at	BE102993	sorting nexin 16	Snx16	1.502	0.159	1.775	0.034	1.499	0.090	1.370	0.038
1373061_at	BE329329	sorting nexin 17	Snx17	0.448	0.457	0.624	0.277	0.401	0.066	0.769	0.140
1373832_at	AI009949	Sorting nexin 19 (predicted)	Snx19_predicted	0.999	0.986	0.837	0.155	0.848	0.037	0.862	0.292
1374401_at	AI549249	sorting nexin 2 (predicted)	Snx2_predicted	0.672	0.416	1.517	0.008	0.793	0.490	1.458	0.003
1386247_at	AA859100	sorting nexin 25	Snx25	0.910	0.028	0.972	0.444	0.879	0.110	1.040	0.867
1395405_at	BE116248	Sorting nexin 26 (predicted)	Snx26_predicted	0.716	0.541	0.606	0.066	0.603	0.967	0.588	0.013
1392704_at	AI029221	Sorting nexin 4 (predicted)	Snx4_predicted	2.258	0.032	1.692	0.148	1.565	0.041	1.158	0.999
1373305_at	BI280349	sorting nexin 4 (predicted)	Snx4_predicted	2.143	0.088	1.151	0.106	2.122	0.005	1.242	0.029
1391055_at	AA866467	Sorting nexin 5 (predicted)	Snx5_predicted	0.965	0.744	0.763	0.018	0.978	0.796	0.870	0.040
1371779_at	AI408852	sorting nexin 6 (predicted)	Snx6_predicted	1.742	0.191	1.826	0.177	1.235	0.361	1.428	0.060
1383944_at	AI144970	Sorting nexin 6 (predicted)	Snx6_predicted	1.581	0.662	1.181	0.643	1.687	0.023	0.862	0.043
1383742_at	AA997003	sorting nexin 7	Snx7	0.998	0.994	12.558	0.005	1.658	0.080	14.921	0.002
1379804_at	AA900057	sorting nexin family member 27	Snx27	0.823	0.100	0.756	0.880	0.573	0.055	0.892	0.435
1372203_at	AI101286	sorting nexin family member 27	Snx27	0.788	0.118	0.796	0.091	1.054	0.926	0.705	0.085
1395216_at	AI176768	Sorting nexin family member 27	Snx27	0.636	0.590	1.000	0.039	0.849	0.699	1.329	0.090
1377603_at	BF284123	sorting nexing 24	Snx24	2.542	0.147	1.140	0.308	2.118	0.002	1.792	0.095
1381625_at	AI146135	Sorting nexing 24	Snx24	1.435	0.293	1.223	0.796	3.165	0.001	1.129	0.762
1382419_at	BI276776	SoxLZ/Sox6 leucine zipper binding protein in testis (predicted)	Solt_predicted	0.275	0.124	0.435	0.806	0.479	0.134	0.235	0.096
1392631_at	AA900254	Sp1 transcription factor	Sp1	1.674	0.145	2.712	0.126	0.945	0.964	2.049	0.179
1392180_at	AI705174	Sp1 transcription factor	Sp1	1.475	0.159	2.803	0.013	2.186	0.312	2.236	0.098
1371880_at	AI179662	Sp1 transcription factor	Sp1	1.631	0.279	2.609	0.006	1.327	0.193	2.087	0.007
1379384_at	BF288328	Sp1 transcription factor	Sp1	0.964	0.354	1.001	0.973	0.932	0.151	1.002	0.970
1372930_at	AI411381	SP110 nuclear body protein	Sp110	10.738	0.000	2.537	0.002	13.192	0.000	3.132	0.001
1394819_at	AI177957	SP110 nuclear body protein	Sp110	14.520	0.001	4.784	0.007	20.472	0.002	6.431	0.006
1396268_at	BF523991	SP110 nuclear body protein	Sp110	15.427	0.038	3.378	0.012	11.760	0.006	3.743	0.026
1374838_at	BI293504	SP140 nuclear body protein	Sp140	13.225	0.000	4.693	0.001	15.220	0.000	5.180	0.014
1382548_at	AI011760	Sp2 transcription factor (mapped)	Sp2_mapped	0.826	0.235	0.877	0.586	0.684	0.215	0.733	0.247
1393471_at	AI175908	Sp3 transcription factor	Sp3	1.113	0.494	3.119	0.046	1.168	0.257	1.159	0.648
1397734_at	AW524780	Sp3 transcription factor	Sp3	0.875	0.643	0.753	0.400	0.710	0.520	1.006	0.987
1373636_at	AI406342	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 1	Spock1	0.676	0.681	0.388	0.056	0.433	0.108	0.297	0.010
1383140_at	BG665046	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2 (predicted)	Spock2_predicted	1.003	0.510	0.735	0.048	0.985	0.959	0.452	0.005
1383839_at	AI576427	spastic paraplegia 20, spartin (Troyer syndrome) homolog (human)	Spg20	0.413	0.020	0.412	0.013	0.255	0.003	0.492	0.009
1388565_at	BI289536	spastic paraplegia 21 homolog (human)	Spg21	1.646	0.067	3.120	0.000	2.196	0.008	3.604	0.007
1374839_at	BE329255	spastic paraplegia 7 homolog (human)	Spg7	0.808	0.101	0.898	0.364	0.655	0.147	0.906	0.475
1395985_at	AI175636	spastic paraplegia 7 homolog (human)	Spg7	0.989	0.965	1.068	0.983	1.187	0.483	1.066	0.987
1383782_at	AI144975	spastin (predicted)	Spast_predicted	0.511	0.167	1.371	0.197	0.812	0.735	1.262	0.305
1378629_at	AI227638	special AT-rich sequence binding protein 1	Satb1	0.543	0.021	0.233	0.012	0.446	0.039	0.283	0.012
1379626_at	AA946353	Special AT-rich sequence binding protein 1	Satb1	0.851	0.056	0.232	0.001	0.965	0.414	0.364	0.003
1398367_at	BF283504	speckle-type POZ protein	Spop	1.826	0.011	1.248	0.002	1.578	0.033	1.253	0.055
1378604_at	BF396495	Speckle-type POZ protein	Spop	1.607	0.827	0.772	0.880	0.800	0.480	0.882	0.143
1390706_at	BF392456	spectrin beta 2	Spnb2	1.030	0.637	1.200	0.512	1.066	0.976	1.410	0.768
1371419_at	AW918614	spectrin beta 2	Spnb2	1.077	0.647	1.033	0.933	0.851	0.431	0.944	0.356
1395359_at	BF559566	Spectrin beta 2	Spnb2	1.021	0.805	1.796	0.007	0.923	0.366	1.856	0.029
1394926_at	AW527214	Spectrin beta 3	Spnb3	1.008	0.844	0.979	0.616	1.001	0.965	0.970	0.880
1386596_at	BF563673	Speedy homolog 1 (Drosophila)	Spdy1	1.193	0.137	2.347	0.182	1.466	0.162	2.033	0.021
1369469_s_at	NM_138855	speedy homolog 1 (Drosophila)	Spdy1	1.054	0.304	1.099	0.058	1.280	0.055	0.840	0.620

1386597_s_at	BF563673	speedy homolog 1 (Drosophila)	Spdy1	1.072	0.811	0.833	0.330	1.233	0.145	1.178	0.106
1389400_at	AW531716	SPEN homolog, transcriptional regulator (Drosophila) (predicted)	Spen_predicted	1.353	0.152	1.471	0.001	1.043	0.727	1.751	0.065
1387326_at	NM_053967	sperm adhesion molecule	Spam	1.045	0.158	1.139	0.993	1.044	0.812	1.136	0.993
1379028_at	BE118950	sperm associated antigen 7 (predicted)	Spag7_predicted	1.154	0.823	0.843	0.927	0.820	0.334	1.000	0.650
1394436_at	BF560163	sperm associated antigen 9 (predicted)	Spag9_predicted	0.895	0.064	0.721	0.102	1.415	0.404	0.784	0.370
1368903_at	NM_053416	spermatid perinuclear RNA binding protein	Strbp	0.731	0.322	1.474	0.007	0.845	0.035	1.298	0.007
1393724_at	BE113911	spermatogenesis associated 1	LOC362056	1.454	0.109	0.994	0.991	0.987	0.938	0.996	0.241
1375047_at	BI295760	spermatogenesis associated 5 (predicted)	Spata5_predicted	1.164	0.212	3.068	0.007	1.786	0.021	1.915	0.021
1377319_at	BF404163	Spermatogenesis associated 5 (predicted)	Spata5_predicted	1.010	0.952	1.427	0.216	1.407	0.449	1.029	0.897
1370398_at	AF094609	spermatogenesis associated 7	Spata7	0.513	0.147	1.060	0.786	0.589	0.128	1.148	0.938
1379018_at	BG375236	Spermatogenesis associated 7	Spata7	0.870	0.842	1.153	0.899	1.062	0.809	0.813	0.670
1391885_at	AA925352	Spermatogenesis associated 9 (predicted)	Spata9_predicted	0.450	0.043	0.154	0.009	0.624	0.128	0.357	0.015
1391839_at	AA891521	Spermatogenesis associated 9 (predicted)	Spata9_predicted	0.995	0.855	0.332	0.001	0.799	0.934	0.376	0.042
1390244_at	BF418231	spermatogenesis associated, serine-rich 2 (predicted)	Spats2_predicted	1.314	0.403	1.365	0.806	1.503	0.302	1.176	0.921
1369915_at	NM_139186	spermatogenesis-related protein (Srp)	Mki67ip	0.508	0.005	1.213	0.455	0.490	0.004	1.162	0.082
1395595_at	BG667615	Spermatogenesis-related protein (Srp)	Mki67ip	0.536	0.125	1.173	0.707	0.529	0.121	0.911	0.108
1388990_at	AA924622	Spermatogenesis-related protein (Srp)	Mki67ip	0.469	0.155	1.599	0.006	0.567	0.009	1.542	0.004
1367834_at	NM_053464	spermidine synthase	Srm	0.489	0.043	1.585	0.026	0.326	0.007	1.394	0.101
1371774_at	AA893220	spermidine/spermine N1-acetyl transferase (mapped)	Sat_mapped	2.230	0.006	11.183	0.000	1.571	0.130	8.696	0.000
1374892_at	AI410221	spermidine/spermine N1-acetyl transferase 2 (predicted)	Sat2_predicted	0.936	0.996	1.177	0.330	0.498	0.046	0.859	0.655
1374556_at	BI289700	spermine oxidase (predicted)	Smox_predicted	2.439	0.043	3.168	0.018	2.022	0.965	1.176	0.430
1394621_at	BI292153	spermine oxidase (predicted) /// similar to polyamine oxidase isoform 2 (predicted)	Smox_predicted /// RGD1564480_predicted	1.350	0.132	7.768	0.011	0.991	0.461	1.199	0.120
1375889_at	AI228536	spermine synthase	Sms	0.702	0.013	0.569	0.003	0.577	0.006	0.506	0.010
1394243_at	AI101062	spermine synthase	Sms	0.958	0.757	0.420	0.017	1.013	0.932	0.518	0.030
1371580_at	AI102725	SPFH domain family, member 1 (predicted)	Spfh1_predicted	0.848	0.691	2.019	0.001	0.667	0.001	1.863	0.008
1374209_at	AI010575	SPFH domain family, member 2 (predicted)	Spfh2_predicted	1.066	0.920	0.851	0.290	1.742	0.012	1.607	0.036
1372437_at	BM390921	S-phase kinase-associated protein 1A	Skp1a	0.614	0.408	0.515	0.009	0.665	0.096	0.522	0.003
1388552_at	BI283738	sphingomyelin phosphodiesterase 1, acid lysosomal	Smpd1	0.866	0.542	0.995	0.938	0.874	0.048	0.599	0.001
1368991_at	NM_053605	sphingomyelin phosphodiesterase 3, neutral	Smpd3	1.759	0.309	0.720	0.197	0.999	0.631	0.465	0.020
1388809_at	BM389498	sphingomyelin phosphodiesterase, acid-like 3A	Smpdl3a	1.091	0.493	1.136	0.410	0.427	0.017	1.385	0.196
1373542_at	BM386306	sphingosine kinase 2	Sphk2	1.634	0.599	1.363	0.979	1.003	0.905	1.055	0.770
1373874_at	AI169638	sphingosine-1-phosphate phosphatase 1	Sgpp1	0.356	0.305	0.650	0.004	0.755	0.068	0.734	0.072
1378047_at	AA901337	Spi-C transcription factor (Spi-1/PU.1 related) (predicted)	Spic_predicted	0.956	0.872	0.950	0.582	1.531	0.139	1.008	0.429
1376195_at	BI288682	spindlin	Spin	3.406	0.028	14.597	0.001	3.162	0.049	10.588	0.003
1399097_at	AI236783	Spindlin	Spin	1.894	0.036	1.635	0.000	1.737	0.024	1.486	0.049
1398601_at	AW143872	spire homolog 1 (Drosophila) (predicted)	Spire1_predicted	2.315	0.000	1.423	0.109	1.778	0.049	1.240	0.918
1380002_at	H31747	spire homolog 1 (Drosophila) (predicted)	Spire1_predicted	2.837	0.069	1.289	0.071	2.261	0.048	1.331	0.358
1396081_at	BM387505	spire homolog 1 (Drosophila) (predicted)	Spire1_predicted	1.412	0.072	1.312	0.178	1.269	0.404	0.998	0.981
1373742_at	AW526082	splA/ryanodine receptor domain and SOCS box containing 2	Spsb2	1.088	0.617	1.514	0.528	0.990	0.039	1.071	0.688
1377303_at	BG373000	SplA/ryanodine receptor domain and SOCS box containing 3 (predicted)	Spsb3_predicted	1.623	0.227	0.596	0.003	1.834	0.117	0.828	0.027
1372908_at	BM384449	splA/ryanodine receptor domain and SOCS box containing 3 (predicted)	Spsb3_predicted	0.591	0.476	1.078	0.737	0.738	0.202	1.090	0.280
1396863_at	AW535061	SplA/ryanodine receptor domain and SOCS box containing 4 (predicted)	Spsb4_predicted	0.962	0.903	1.599	0.559	1.223	0.143	0.997	0.570
1368186_a_at	U21683	spleen tyrosine kinase	Syk	1.000	0.852	1.000	0.997	0.999	0.850	0.999	0.993
1374668_at	AI230180	splicing factor 3a, subunit 1 (predicted)	Sf3a1_predicted	0.997	0.988	1.683	0.148	0.968	0.705	1.235	0.033
1383591_at	BM391839	splicing factor 3a, subunit 2, 66kDa	Sf3a2	1.491	0.437	0.978	0.789	1.518	0.317	1.057	0.866
1388669_at	BM391739	splicing factor 3a, subunit 3	Sf3a3	1.032	0.116	0.997	0.692	0.909	0.491	1.000	0.036
1373887_at	BF523561	splicing factor 3b, subunit 1	Sf3b1	1.218	0.070	0.717	0.024	1.740	0.030	0.719	0.004
1389840_at	BM384277	splicing factor 3b, subunit 1	Sf3b1	1.089	0.259	1.389	0.063	1.416	0.218	0.768	0.300
1390234_at	BE115465	splicing factor 3b, subunit 1	Sf3b1	1.066	0.419	1.408	0.035	1.250	0.203	1.639	0.108
1388614_at	BM386768	splicing factor 3b, subunit 2 (predicted)	Sf3b2_predicted	0.722	0.095	1.108	0.184	0.627	0.027	0.941	0.514
1377070_at	BE098910	splicing factor 3b, subunit 2 (predicted)	Sf3b2_predicted	0.672	0.691	1.508	0.063	0.800	0.216	1.088	0.093
1372501_at	BI285007	splicing factor 3b, subunit 3 (predicted)	Sf3b3_predicted	0.852	0.644	1.062	0.951	0.997	0.952	0.926	0.543
1374834_at	AA943520	splicing factor 3b, subunit 4	Sf3b4	0.992	0.967	1.975	0.003	0.953	0.708	1.254	0.022
1376164_at	BM383641	splicing factor 4	Sf4	0.689	0.024	1.033	0.613	0.699	0.115	0.955	0.885
1388132_at	BE107056	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	Sfpq	0.575	0.050	0.962	0.429	0.631	0.061	0.841	0.391
1383859_at	AA963376	Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	Sfpq	1.366	0.320	0.427	0.085	0.774	0.400	0.485	0.003
1368063_a_at	NM_133423	splicing factor YT521-B	Yt521	1.339	0.093	1.533	0.001	1.124	0.122	1.457	0.002
1374442_at	AI227831	splicing factor, arginine/serine rich 9	Sfrs9	0.660	0.005	1.181	0.555	0.612	0.011	0.974	0.875
1370189_at	BI290979	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	Sfrs10	0.994	0.891	0.892	0.071	1.033	0.798	0.969	0.338
1370188_at	AW252670	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	Sfrs10	1.020	0.952	2.182	0.006	1.044	0.693	1.409	0.087

1387824_at	NM_020092	splicing factor, arginine/serine-rich 12	Sfrs12	1.213	0.159	4.743	0.015	1.516	0.097	1.563	0.040
1377521_at	BF415552	Splicing factor, arginine/serine-rich 14 (predicted)	Sfrs14_predicted	0.857	0.270	0.726	0.518	0.699	0.471	0.712	0.600
1379685_at	AI502753	splicing factor, arginine/serine-rich 15	Sfrs15	1.123	0.431	1.335	0.189	1.523	0.274	0.952	0.716
1379010_at	AA956727	Splicing factor, arginine/serine-rich 3 (SRp20) (predicted)	Sfrs3_predicted	2.108	0.052	3.978	0.003	1.181	0.203	2.046	0.012
1374063_at	AI579288	splicing factor, arginine/serine-rich 3 (SRp20) (predicted)	Sfrs3_predicted	1.084	0.075	1.251	0.037	0.991	0.995	1.040	0.485
1376252_at	AI145784	splicing factor, arginine/serine-rich 3 (SRp20) (predicted)	Sfrs3_predicted	1.031	0.415	0.385	0.002	0.760	0.131	0.501	0.042
1368992_a_at	AI104005	splicing factor, arginine/serine-rich 5	Sfrs5	0.561	0.016	0.530	0.006	0.767	0.099	0.569	0.022
1380875_at	BE106717	Splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)	Sfrs8	0.763	0.033	1.014	0.603	0.614	0.237	1.012	0.884
1383676_at	AA996595	splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)	Sfrs8	1.020	0.498	1.084	0.058	1.000	0.247	1.130	0.156
1390919_at	AI230176	Splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)	Sfrs8	1.052	0.885	1.341	0.142	1.294	0.070	1.346	0.330
1391858_at	BM385930	splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)	Sfrs8	0.791	0.970	0.776	0.959	1.046	0.927	0.671	0.863
1370312_at	M88469	spondin 1	Spon1	1.376	0.177	0.993	0.975	1.311	0.072	1.014	0.946
1370847_at	AA801238	spondin 2, extracellular matrix protein	Spon2	1.209	0.204	1.106	0.505	1.805	0.079	0.904	0.495
1372954_at	BF404393	Sprague-Dawley UV73 mRNA, partial sequence	---	0.829	0.750	1.488	0.003	0.948	0.879	1.441	0.014
1374864_at	BM390457	sprouty homolog 2 (Drosophila)	Spry2	0.773	0.264	2.825	0.010	0.738	0.197	2.724	0.011
1392024_at	BF419641	Sprouty protein with EVH-1 domain 1, related sequence	Spred1	1.568	0.359	0.877	0.070	3.776	0.027	0.575	0.022
1392788_at	AA944323	Sprouty protein with EVH-1 domain 1, related sequence	Spred1	1.007	0.910	0.999	0.996	1.069	0.214	0.798	0.460
1377743_at	BI292687	Sprouty protein with EVH-1 domain 1, related sequence	Spred1	1.140	0.986	1.012	0.336	1.141	0.995	1.439	0.235
1389008_at	AI409218	Sprouty-related, EVH1 domain containing 2	Spred2	1.157	0.582	0.362	0.013	1.725	0.784	0.411	0.014
1387017_at	NM_017136	squalene epoxidase	Sqle	0.665	0.332	0.683	0.009	0.279	0.063	0.665	0.004
1384967_at	BM386930	Squamous cell carcinoma antigen recognized by T cells 2 (predicted)	Sart2_predicted	1.167	0.745	0.951	0.217	0.890	0.673	0.853	0.315
1387012_at	NM_031596	squamous cell carcinoma antigen recognized by T-cells 1	Sart1	1.029	0.776	2.234	0.004	1.174	0.812	1.767	0.001
1373003_at	BF414266	Squamous cell carcinoma antigen recognized by T-cells 3 (predicted)	Sart3_predicted	0.707	0.228	1.415	0.001	0.761	0.227	1.776	0.001
1376690_at	BI296277	SRB7 (suppressor of RNA polymerase B) homolog (S. cerevisiae) (predicted)	Surb7_predicted	0.912	0.821	0.942	0.098	1.005	0.980	1.114	0.315
1369979_at	NM_130413	src family associated phosphoprotein 2	Scap2	1.317	0.481	1.112	0.862	1.531	0.060	1.163	0.488
1396910_at	AW535180	Src homology 2 domain-containing transforming protein C1	Shc1	1.597	0.073	1.962	0.049	1.410	0.164	1.333	0.278
1377594_at	BF548525	Src homology 2 domain-containing transforming protein C1	Shc1	1.052	0.399	1.049	0.586	0.908	0.554	1.028	0.654
1389567_at	BE329208	SREBP cleavage activating protein (predicted)	Scap_predicted	0.872	0.028	1.454	0.015	0.772	0.055	1.330	0.007
1387275_at	NM_053349	SRY-box containing gene 11	Sox11	5.294	0.000	3.117	0.061	5.288	0.041	3.777	0.003
1383137_at	AA956294	SRY-box containing gene 4 (predicted)	Sox4_predicted	0.975	0.992	0.828	0.583	0.717	0.252	0.907	0.550
1373860_at	BI297183	SRY-box containing gene 4 (predicted)	Sox4_predicted	0.997	1.000	1.426	0.977	0.999	0.998	1.435	0.992
1392783_at	AI136436	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast)	Ssu72	0.635	0.044	0.567	0.023	0.879	0.241	0.688	0.051
1398517_at	BI295779	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast)	Ssu72	0.648	0.084	0.623	0.020	0.903	0.480	0.809	0.071
1371768_at	BM391850	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast)	Ssu72	1.287	0.470	1.143	0.634	1.610	0.133	1.095	0.990
1379078_at	BE105838	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	St3gal2	1.538	0.195	0.498	0.085	0.722	0.105	0.931	0.502
1373607_at	BF418530	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	St3gal3	0.814	0.303	0.672	0.033	1.024	0.742	0.650	0.012
1373224_at	BI295550	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	St3gal4	0.976	0.943	0.587	0.004	0.757	0.261	0.593	0.036
1368109_at	NM_031337	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	St3gal5	1.362	0.317	2.081	0.028	1.112	0.178	0.652	0.677
1383309_at	BF522030	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	St3gal6	2.053	0.221	1.249	0.256	2.159	0.142	0.777	0.458
1395389_at	BG663624	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	St3gal6	0.967	0.695	1.025	0.773	0.947	0.434	0.972	0.042
1387435_at	NM_013029	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	St8sia3	0.912	0.690	0.304	0.003	0.747	0.271	0.402	0.002
1370476_at	AY083159	Stam binding protein	Stambp	0.939	0.454	1.037	0.388	0.914	0.848	0.932	0.558
1370898_at	BF288101	stannin	Snn	1.002	0.985	1.024	0.840	1.002	0.988	1.001	0.878
1393559_at	AI235210	Stanniocalcin 1	Stc1	0.613	0.230	1.289	0.210	0.515	0.177	0.833	0.845
1377404_at	BM386683	stanniocalcin 1	Stc1	1.001	0.933	1.229	0.059	0.999	1.000	1.282	0.748
1367790_at	NM_022694	staphylococcal nuclease domain containing 1	Snd1	0.833	0.088	1.010	0.243	0.861	0.169	1.065	0.073
1374815_at	AA997695	STARD3 N-terminal like	Stard3nl	1.048	0.845	1.461	0.025	1.492	0.026	1.556	0.007
1392708_at	AI175745	STAR-related lipid transfer (START) domain containing protein 6	Stard6	0.689	0.414	0.922	0.514	0.706	0.415	0.646	0.766
1388948_at	AI104759	START domain containing 10	Stard10	0.733	0.415	0.877	0.513	0.582	0.031	0.728	0.759
1388562_at	BI282011	START domain containing 7 (predicted)	Stard7_predicted	0.834	0.073	0.759	0.010	0.932	0.958	0.773	0.025
1384665_at	BF549590	START domain containing 7 (predicted)	Stard7_predicted	0.922	0.773	0.867	0.554	1.218	0.193	0.872	0.608
1386857_at	NM_017166	stathmin 1	Stmn1	0.780	0.456	1.418	0.098	0.668	0.135	1.013	0.801
1370041_at	NM_053440	stathmin-like 2	Stmn2	1.793	0.022	0.774	0.008	1.151	0.490	0.738	0.017
1370042_at	BG668493	stathmin-like 2	Stmn2	1.525	0.276	0.758	0.142	1.319	0.110	1.147	0.739
1368157_at	NM_024346	stathmin-like 3	Stmn3	0.739	0.080	0.539	0.009	0.520	0.006	0.399	0.001
1387051_at	NM_053436	staufen RNA binding protein homolog 1 (Drosophila)	Stau1	0.875	0.286	1.046	0.566	0.597	0.003	0.920	0.151
1379754_at	AI070598	staufen, RNA binding protein, homolog 2 (Drosophila)	Stau2	7.721	0.002	2.374	0.003	8.366	0.005	2.804	0.015
1370680_at	AF483620	staufen, RNA binding protein, homolog 2 (Drosophila)	Stau2	6.281	0.008	2.189	0.027	6.102	0.006	2.581	0.017
1390558_at	AI502229	staufen, RNA binding protein, homolog 2 (Drosophila)	Stau2	1.157	0.717	0.921	0.291	0.950	0.787	0.649	0.055
1370355_at	J02585	stearoyl-Coenzyme A desaturase 1	Scd1	0.956	0.943	1.440	0.043	2.102	0.240	2.103	0.013
1388253_at	M15114	Stearoyl-Coenzyme A desaturase 2	Scd2	0.597	0.285	0.519	0.000	0.445	0.169	0.613	0.002

1367668_a_at	NM_031841	stearoyl-Coenzyme A desaturase 2	Scd2	0.755	0.340	0.769	0.035	0.690	0.054	0.799	0.148
1386889_at	BE107760	stearoyl-Coenzyme A desaturase 2	Scd2	0.830	0.969	0.374	0.027	0.823	0.108	0.293	0.020
1374007_at	AI178499	Step II splicing factor SLU7 (S. cerevisiae)	Slu7	0.528	0.018	1.052	0.224	0.566	0.105	0.974	0.766
1386856_a_at	AA859633	sterile alpha motif domain containing 4B	Samd4b	0.848	0.097	1.345	0.244	1.150	0.393	1.330	0.090
1393932_at	AI060175	sterile alpha motif domain containing 8	Samd8	0.919	0.690	4.268	0.005	1.155	0.382	3.500	0.004
1370420_at	J05035	steroid 5 alpha-reductase 1	Srd5a1	0.640	0.006	1.001	0.602	0.818	0.098	1.005	0.810
1371718_at	BI283124	steroid receptor RNA activator 1	Sra1	0.600	0.259	0.619	0.063	0.512	0.010	0.741	0.012
1368372_at	NM_012661	steroid sulfatase	Sts	0.805	0.701	1.184	0.142	1.083	0.921	1.237	0.723
1387896_at	M62763	sterol carrier protein 2	Scp2	0.817	0.551	0.545	0.003	1.575	0.566	0.671	0.096
1370296_at	M34728	sterol carrier protein 2	Scp2	0.752	0.569	0.426	0.006	0.764	0.236	0.498	0.017
1373869_at	AI012418	sterol O-acyltransferase 1	Soat1	0.251	0.044	0.278	0.000	0.204	0.000	0.250	0.001
1374976_a_at	AI548897	Sterol O-acyltransferase 1	Soat1	0.298	0.061	0.723	0.013	0.302	0.026	0.461	0.000
1388426_at	BF398848	sterol regulatory element binding factor 1	Srebf1	0.674	0.030	1.106	0.381	0.675	0.204	0.998	0.422
1383159_at	AW434445	Sterol regulatory element binding factor 1	Srebf1	0.989	0.534	1.125	0.046	0.934	0.769	1.265	0.199
1371979_at	AI170663	sterol regulatory element binding factor 2 (predicted)	Srebf2_predicted	0.869	0.469	0.448	0.009	0.870	0.900	0.431	0.009
1368275_at	NM_080886	sterol-C4-methyl oxidase-like	Sc4mol	0.864	0.763	1.349	0.033	0.685	0.785	1.099	0.573
1390777_at	AI710051	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae)	Sc5d	0.646	0.097	0.743	0.192	0.493	0.004	0.635	0.082
1387926_at	AB052846	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae)	Sc5d	0.512	0.557	0.525	0.007	0.236	0.003	0.471	0.002
1398910_at	BI280327	STIP1 homology and U-Box containing protein 1	Stub1	0.658	0.054	1.065	0.060	0.697	0.013	0.920	0.059
1398908_at	AA799462	stomatin (Epb7.2)-like 2	Stoml2	0.703	0.467	1.467	0.144	0.646	0.062	1.129	0.652
1383508_at	AW528853	stomatin (Epb7.2)-like 3 (predicted)	Stoml3_predicted	0.717	0.939	0.432	0.004	1.476	0.566	0.628	0.435
1380981_at	AW534519	Stonin 2 (predicted)	Ston2_predicted	2.061	0.314	1.620	0.082	0.878	0.783	1.072	0.090
1382210_at	BE117392	Strain Wistar Rap2a mRNA, 5' UTR	---	2.006	0.060	1.088	0.957	3.703	0.000	1.814	0.080
1375096_at	BF418337	stratifin (predicted)	Sfn_predicted	1.005	0.193	1.100	0.105	0.653	0.296	1.004	0.972
1392107_at	BI302669	strawberry notch homolog (Drosophila) (predicted)	Stno_predicted	2.283	0.026	1.178	0.071	1.477	0.111	1.053	0.813
1368844_at	NM_019271	stress 70 protein chaperone, microsome-associated, 60kD human homolog	Stch	0.731	0.659	0.951	0.613	0.856	0.539	1.001	0.616
1398877_at	BI283691	stress-induced phosphoprotein 1	Stip1	0.646	0.254	1.451	0.044	0.622	0.159	1.328	0.071
1392986_at	AI227920	striatin, calmodulin binding protein	Strn	0.824	0.717	1.415	0.119	0.973	0.944	1.163	0.498
1375537_at	BE107226	striatin, calmodulin binding protein 3	Strn3	1.448	0.370	1.165	0.473	1.457	0.203	1.205	0.134
1388835_at	AI575072	striatin, calmodulin binding protein 4 (predicted)	Strn4_predicted	0.865	0.394	0.593	0.029	0.708	0.189	0.707	0.006
1385241_at	AI071210	Stromal antigen 1 (predicted)	Stag1_predicted	1.186	0.918	1.061	0.296	1.137	0.516	1.056	0.355
1381259_at	BM391784	Stromal antigen 1 (predicted)	Stag1_predicted	0.725	0.988	0.905	0.906	1.320	0.329	0.770	0.343
1382332_at	AI549167	stromal antigen 2 (predicted)	Stag2_predicted	0.744	0.202	0.805	0.761	0.768	0.119	0.965	0.705
1371645_at	BI284339	stromal cell derived factor 2 (predicted)	Sdf2_predicted	0.663	0.815	0.900	0.162	0.873	0.256	0.894	0.244
1387778_at	NM_130412	stromal cell derived factor 4	Sdf4	0.812	0.626	0.698	0.004	0.826	0.007	0.642	0.001
1387016_a_at	NM_019380	stromal cell derived factor receptor 1	Sdfr1	1.084	0.013	0.864	0.031	1.251	0.008	1.072	0.351
1378160_at	AI179412	stromal cell derived factor receptor 2 (predicted)	Sdfr2_predicted	0.617	0.032	2.493	0.000	0.642	0.010	2.237	0.034
1376024_at	AW914992	stromal interaction molecule 1 (predicted)	Stim1_predicted	0.471	0.020	0.468	0.016	0.499	0.113	0.597	0.017
1382121_at	BI292282	stromal interaction molecule 1 (predicted)	Stim1_predicted	0.799	0.933	0.545	0.013	0.994	0.921	0.491	0.024
1379279_at	AI234719	stromal interaction molecule 2 (predicted)	Stim2_predicted	1.811	0.005	1.313	0.073	2.111	0.003	1.601	0.020
1398062_at	BF404303	stromal membrane-associated protein 1-like	Smap1l	1.442	0.065	1.879	0.029	1.248	0.057	1.432	0.269
1372561_at	AI234095	stromal membrane-associated protein 1-like	Smap1l	0.823	0.194	0.271	0.001	0.754	0.070	0.265	0.021
1390350_at	BE097445	stromal membrane-associated protein 1-like	Smap1l	1.018	0.739	0.291	0.015	0.844	0.107	0.279	0.000
1387026_at	NM_031683	structural maintenance of chromosomes 1 like 1 (S. cerevisiae)	Smc1l1	1.012	0.980	2.310	0.023	1.328	0.056	2.242	0.019
1388129_at	L08814	structure specific recognition protein 1	Ssrp1	0.838	0.337	1.906	0.018	0.766	0.075	1.957	0.031
1398880_at	BM388890	SUB1 homolog (S. cerevisiae)	Sub1	0.686	0.060	0.591	0.110	0.782	0.284	0.805	0.029
1367678_at	NM_130428	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	Sdha	0.657	0.192	1.212	0.265	0.722	0.080	1.248	0.402
1372123_at	AI172320	succinate dehydrogenase complex, subunit B, iron sulfur (Ip) (predicted)	Sdhb_predicted	0.840	0.730	1.429	0.007	0.587	0.044	1.318	0.011
1380813_at	AA891239	Succinate dehydrogenase complex, subunit B, iron sulfur (Ip) (predicted)	Sdhb_predicted	0.971	0.930	0.664	0.008	0.996	0.991	0.889	0.780
1371311_at	AI009817	succinate dehydrogenase complex, subunit C, integral membrane protein	Sdhc	0.828	0.370	0.854	0.089	0.911	0.544	0.897	0.080
1388294_at	AI176608	succinate dehydrogenase complex, subunit D, integral membrane protein	Sdhd	0.487	0.117	1.157	0.063	0.440	0.016	1.162	0.015
1371296_at	AI410703	succinate dehydrogenase complex, subunit D, integral membrane protein	Sdhd	0.494	0.251	0.991	0.969	0.443	0.029	1.144	0.245
1367642_at	NM_053752	succinate-CoA ligase, GDP-forming, alpha subunit	Suclg1	0.665	0.208	0.861	0.791	0.741	0.052	0.954	0.467
1388975_at	AA923982	succinate-Coenzyme A ligase, ADP-forming, beta subunit (predicted)	Sucla2_predicted	0.341	0.084	1.010	0.326	0.354	0.013	1.010	0.729
1373017_at	AI237518	succinate-Coenzyme A ligase, GDP-forming, beta subunit	Suclg2	0.837	0.829	0.647	0.001	0.843	0.189	0.889	0.056
1395293_at	BF388802	Sulfatase 2	Sulf2	1.001	0.440	0.811	0.357	1.285	0.363	0.913	0.666
1372422_at	AI175506	Sulfatase modifying factor 1 (predicted)	Sumf1_predicted	0.322	0.118	0.172	0.030	0.210	0.000	0.216	0.096
1389833_at	BF285924	Sulfatase modifying factor 1 (predicted)	Sumf1_predicted	0.517	0.208	0.211	0.008	0.513	0.209	0.212	0.001
1374588_at	BM389462	sulfatase modifying factor 1 (predicted)	Sumf1_predicted	0.871	0.728	1.336	0.006	0.840	0.221	1.185	0.174
1381979_at	AA964066	sulfatase modifying factor 2	Sumf2	0.701	0.138	0.999	0.681	0.436	0.109	0.908	0.699
1384331_at	H31896	Sulfiredoxin 1 homolog (S. cerevisiae)	Srxn1	0.370	0.018	4.564	0.023	0.364	0.007	4.396	0.001

1372510_at	AI172302	Sulfiredoxin 1 homolog (S. cerevisiae)	Srxn1	0.358	0.108	3.527	0.002	0.212	0.001	2.868	0.001
1370036_at	NM_031127	sulfite oxidase	Suox	0.279	0.112	0.082	0.002	0.319	0.007	0.125	0.014
1388526_at	AI169075	Sulfotransferase family, cytosolic, 2B, member 1 (predicted)	Sult2b1_predicted	0.275	0.006	0.191	0.000	0.392	0.006	0.192	0.036
1371650_at	BI275947	SUMO/sentrin specific peptidase 3	Senp3	0.890	0.036	0.778	0.022	0.811	0.033	0.869	0.054
1374580_at	AW535691	SUMO/sentrin specific peptidase 6 (predicted)	Senp6_predicted	0.948	0.362	1.145	0.049	0.836	0.034	1.145	0.019
1397812_at	H32530	SUMO/sentrin specific peptidase 6 (predicted)	Senp6_predicted	0.924	0.546	1.220	0.773	0.814	0.165	0.809	0.165
1372386_at	AW530777	SUMO/sentrin specific protease 2	Senp2	1.068	0.828	1.178	0.033	1.131	0.132	1.239	0.014
1391262_at	BE105606	SUMO/sentrin specific protease 5 (predicted) /// similar to SUMO/sentrin specific protease 5 (predicted)	Senp5_predicted /// RGD1564247_predicted	1.022	0.680	0.936	0.618	1.201	0.725	0.890	0.381
1394086_at	AI069981	SUMO1/sentrin specific protease 7 (predicted)	Senp7_predicted	1.737	0.013	0.979	0.556	3.111	0.010	0.882	0.596
1367641_at	NM_017050	superoxide dismutase 1	Sod1	0.771	0.374	0.781	0.032	0.763	0.021	0.834	0.134
1370173_at	BG671549	superoxide dismutase 2, mitochondrial	Sod2	6.741	0.000	7.513	0.002	7.021	0.000	5.526	0.000
1370172_at	AA892254	superoxide dismutase 2, mitochondrial	Sod2	8.687	0.001	13.068	0.000	9.232	0.001	9.183	0.000
1391004_at	AW535541	Supervillin (predicted)	Svil_predicted	2.581	0.024	0.691	0.057	1.057	0.076	0.628	0.138
1376572_a_at	AI045848	supervillin (predicted)	Svil_predicted	1.906	0.127	0.748	0.268	0.839	0.512	0.695	0.092
1398848_at	BG377057	suppression of tumorigenicity 13	St13	1.151	0.521	2.019	0.009	0.968	0.660	1.878	0.020
1387195_at	AB049189	suppression of tumorigenicity 14 (colon carcinoma)	St14	16.177	0.013	7.784	0.001	1.031	0.946	1.015	0.048
1370658_a_at	AF031942	suppression of tumorigenicity 18	St18	0.550	0.152	0.321	0.079	0.692	0.162	0.357	0.015
1373288_at	BG373023	suppression of tumorigenicity 5 (predicted)	St5_predicted	1.940	0.050	1.064	0.910	1.685	0.173	0.922	0.676
1392925_at	BI132374	suppression of tumorigenicity 7	ST7	0.932	0.900	1.247	0.290	1.164	0.422	1.441	0.006
1379842_at	H33639	suppression of tumorigenicity 7-like	St7l	0.745	0.332	0.979	0.847	0.634	0.190	0.997	0.957
1390977_at	AW527529	suppression of tumorigenicity 7-like	St7l	0.967	0.866	0.835	0.024	0.950	0.943	0.770	0.020
1375568_at	AI029171	Suppressor of cytokine signaling 1	Socs1	2.372	0.054	1.002	0.982	1.335	0.091	1.000	0.978
1376666_at	AI170864	suppressor of cytokine signaling 6 (predicted)	Socs6_predicted	0.903	0.516	1.510	0.007	1.282	0.665	1.369	0.040
1391484_at	BF284786	Suppressor of cytokine signaling 7 (predicted)	Socs7_predicted	1.322	0.034	1.246	0.005	1.530	0.024	1.409	0.028
1389060_at	BI297313	Suppressor of cytokine signaling 7 (predicted)	Socs7_predicted	1.439	0.367	1.274	0.125	1.694	0.051	1.777	0.566
1371378_at	BM389078	suppressor of initiator codon mutations, related sequence 1 (S. cerevisiae) (predicted)	Sui1-rs1_predicted	0.728	0.239	0.832	0.050	0.684	0.027	0.788	0.022
1388310_at	AI012372	suppressor of initiator codon mutations, related sequence 1 (S. cerevisiae) (predicted)	Sui1-rs1_predicted	0.976	0.991	1.495	0.001	0.750	0.099	1.372	0.001
1377281_at	BM388545	Suppressor of Ty 16 homolog (S. cerevisiae) (predicted)	Supt16h_predicted	0.596	0.041	0.841	0.059	0.583	0.057	0.967	0.400
1398980_at	AW253429	suppressor of Ty 16 homolog (S. cerevisiae) (predicted)	Supt16h_predicted	0.896	0.258	1.083	0.053	0.768	0.180	1.188	0.028
1398987_at	AW141261	suppressor of Ty 4 homolog 2 (S. cerevisiae) (predicted)	Supt4h2_predicted	1.027	0.941	0.977	0.186	0.876	0.011	1.052	0.074
1372094_at	BG380556	suppressor of Ty 5 homolog (S. cerevisiae)	Supt5h	0.885	0.295	1.263	0.605	0.844	0.275	1.208	0.272
1374398_at	AI178787	suppressor of Ty 6 homolog (S. cerevisiae)	Supt6h	0.764	0.008	1.015	0.980	0.715	0.011	0.982	0.826
1372350_at	BI297676	suppressor of var1, 3-like 1 (S. cerevisiae)	Supv3l1	0.997	0.976	1.102	0.970	1.000	0.968	1.019	0.626
1375981_a_at	AA997899	suppressor of variegation 3-9 homolog 1 (Drosophila) (predicted)	Suv39h1_predicted	1.950	0.001	6.036	0.002	2.761	0.001	4.466	0.014
1389620_at	AW525235	suppressor of variegation 4-20 homolog 2 (Drosophila) (predicted)	Suv420h2_predicted	0.856	0.228	1.961	0.100	1.160	0.256	1.277	0.199
1384664_at	AI233855	surfactant associated protein B	Sftpb	0.976	0.243	0.466	0.133	1.027	0.493	0.999	0.459
1398857_at	AF182952	surfeit 1	Surf1	0.604	0.082	0.917	0.245	0.659	0.014	1.143	0.576
1388658_at	AA942704	surfeit 2	Surf2	0.431	0.000	0.898	0.152	0.461	0.052	0.736	0.022
1389973_a_at	BE112262	surfeit 4	Surf4	0.657	0.017	1.174	0.059	0.722	0.069	0.977	0.654
1371791_at	AI227937	surfeit 4	Surf4	0.540	0.660	0.916	0.405	0.803	0.199	0.838	0.097
1390290_at	BF396659	surfeit gene 6 (predicted)	Surf6_predicted	1.466	0.130	1.936	0.022	1.226	0.025	1.634	0.016
1388979_at	BM390864	survival motor neuron domain containing 1	Smndc1	0.950	0.866	2.209	0.045	0.997	0.443	1.642	0.060
1382165_at	BI288396	survival motor neuron domain containing 1	Smndc1	0.887	0.881	1.495	0.586	1.265	0.182	1.794	0.183
1367883_at	NM_022509	survival of motor neuron 1, telomeric	Smn1	1.082	0.614	2.561	0.001	0.928	0.959	2.024	0.002
1368229_at	NM_053389	survival of motor neuron protein interacting protein 1	Sip1	0.407	0.069	0.599	0.130	0.387	0.059	0.715	0.149
1379960_at	AI406705	Sushi domain containing 3 (predicted)	Susd3_predicted	1.000	0.992	1.048	0.848	1.001	0.197	1.006	0.978
1373706_at	BI281981	Swi/SNF related matrix associated, actin dependent regulator of chromatin, subfamily a-like 1 (predicted)	Smarcal1_predicted	1.001	0.490	0.947	0.112	1.004	0.493	0.828	0.068
1384437_at	AI576309	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (predicted)	Smarca1_predicted	1.006	0.140	0.582	0.010	0.955	0.672	0.877	0.256
1394066_at	AA875609	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	Smarca2	0.426	0.039	0.428	0.035	1.120	0.776	0.716	0.157
1385074_at	BE102268	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	Smarca2	0.163	0.067	0.429	0.205	0.694	0.105	0.430	0.234
1376337_at	AI170385	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	Smarca2	0.734	0.103	0.510	0.000	1.108	0.296	0.800	0.046
1397165_at	BF547582	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	Smarca2	0.833	0.128	0.583	0.029	0.856	0.224	0.840	0.366
1373565_at	BE329013	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	Smarca4	0.786	0.385	0.864	0.183	0.676	0.098	0.799	0.069
1375469_at	BE111847	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	Smarca4	0.806	0.693	0.677	0.969	0.636	0.166	0.742	0.501
1384246_at	AA996404	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 (predicted)	Smarca5_predicted	0.751	0.011	0.570	0.001	0.816	0.002	0.704	0.009
1394093_at	BF557855	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 (predicted)	Smarca5_predicted	1.078	0.686	0.464	0.011	0.959	0.586	0.668	0.049
1379327_at	BI292524	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 (predicted)	Smarca5_predicted	0.856	0.909	1.596	0.004	0.904	0.557	1.163	0.075
1371914_at	AI406553	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	Smarcb1	0.978	0.749	1.250	0.114	0.837	0.196	1.227	0.083
1374182_at	AA965063	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1 (predicted)	Smarcc1_predicted	1.007	0.560	1.290	0.688	1.078	0.154	1.335	0.185
1370159_at	AB003505	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	Smarcd2	1.855	0.011	1.009	0.368	3.044	0.005	1.647	0.023

1377473_at	BE349749	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	Smarcd3	0.367	0.032	0.326	0.010	0.659	0.962	0.964	0.898
1398244_at	NM_133417	SYF2 homolog, RNA splicing factor (S. cerevisiae)	Syf2	1.467	0.164	1.841	0.033	0.878	0.619	1.683	0.041
1374733_at	BM387193	symplekin	Sympk	1.162	0.565	0.830	0.815	1.006	0.980	0.920	0.756
1379635_at	BF399325	synapse associated protein 1	Syap1	1.589	0.017	0.778	0.387	1.450	0.052	1.124	0.969
1392599_at	BE111132	synapse associated protein 1	Syap1	1.221	0.265	1.347	0.029	1.608	0.106	1.387	0.026
1390196_at	BG378858	Synapsin I	Syn1	2.724	0.129	1.184	0.502	3.559	0.000	1.609	0.099
1388811_at	BF401593	Synapsin II	Syn2	1.413	0.363	0.322	0.007	0.888	0.524	0.268	0.006
1383399_at	AI574728	synaptic vesicle glycoprotein 2a	Sv2a	0.563	0.122	0.540	0.016	0.306	0.013	0.755	0.178
1369628_at	BG672437	synaptic vesicle glycoprotein 2b	Sv2b	0.933	0.385	1.039	0.033	1.113	0.210	1.072	0.040
1370098_at	NM_053531	synaptobrevin-like 1	Sybl1	0.738	0.569	0.538	0.122	0.675	0.339	0.725	0.455
1369554_at	NM_053553	synaptogyrin 2	Syngr2	0.789	0.641	1.042	0.802	0.883	0.613	1.475	0.392
1388586_at	BG372397	synaptojanin 1	Synj1	1.606	0.030	1.240	0.005	1.341	0.153	1.060	0.170
1370070_at	NM_053476	synaptojanin 1	Synj1	1.249	0.155	0.912	0.556	1.252	0.072	0.880	0.094
1368038_at	AF260258	synaptojanin 2 binding protein	Synj2bp	0.630	0.091	0.383	0.013	0.782	0.438	0.598	0.069
1368040_at	BI285174	synaptojanin 2 binding protein	Synj2bp	0.393	0.516	0.663	0.162	0.543	0.132	0.584	0.033
1368041_at	BF284821	synaptojanin 2 binding protein	Synj2bp	1.162	0.634	1.124	0.574	0.474	0.251	0.901	0.354
1387553_at	NM_012810	synaptonemal complex protein 1	Sycp1	1.188	0.932	0.971	0.630	1.194	0.570	2.340	0.508
1368499_at	NM_130735	synaptonemal complex protein 2	Sycp2	0.658	0.082	0.819	0.128	1.174	0.852	0.600	0.059
1387614_at	NM_013041	synaptonemal complex protein 3	Sycp3	0.972	0.106	0.613	0.156	1.068	0.778	0.961	0.831
1368276_at	NM_012664	synaptophysin	Syp	0.805	0.493	0.492	0.039	0.497	0.052	0.469	0.060
1387073_at	NM_030991	synaptosomal-associated protein 25	Snap25	0.656	0.032	0.573	0.002	0.640	0.001	0.594	0.001
1373213_at	BI274180	synaptosomal-associated protein 29	Snap29	0.931	0.683	0.710	0.029	0.736	0.867	0.656	0.069
1398568_at	AW531009	Synaptosomal-associated protein, 91kDa homolog (mouse)	Snap91	1.134	0.050	1.080	0.168	1.908	0.022	1.103	0.395
1373865_at	BF281248	synaptosomal-associated protein, 91kDa homolog (mouse)	Snap91	1.520	0.092	0.745	0.066	2.493	0.001	1.097	0.125
1398741_at	BE096677	Synaptosomal-associated protein, 91kDa homolog (mouse)	Snap91	1.268	0.170	1.175	0.003	1.910	0.075	1.062	0.341
1394659_at	BF289445	Synaptotagmin binding, cytoplasmic RNA interacting protein	Syncrip	1.270	0.607	2.439	0.036	0.993	0.967	1.391	0.334
1382923_at	AI072424	synaptotagmin binding, cytoplasmic RNA interacting protein	Syncrip	0.517	0.691	6.247	0.020	0.509	0.108	3.357	0.002
1392071_at	BF392945	Synaptotagmin I	Syt1	1.068	0.487	0.995	0.883	2.035	0.170	1.001	0.993
1375877_at	AI454612	synaptotagmin IV	Syt4	0.614	0.039	0.948	0.658	0.632	0.000	0.875	0.240
1387662_at	L38247	synaptotagmin IV	Syt4	0.539	0.132	0.979	0.520	0.263	0.089	0.381	0.079
1368417_at	NM_019350	synaptotagmin V	Syt5	0.697	0.615	0.699	0.108	0.776	0.267	0.620	0.111
1374427_at	AI144986	Synaptotagmin XIII	Syt13	0.726	0.099	0.479	0.003	0.444	0.004	0.540	0.017
1387517_at	NM_030839	synaptotagmin XIII	Syt13	0.950	0.512	0.163	0.020	0.948	0.141	0.215	0.026
1369457_a_at	AF419342	synaptotagmin-like 4	Sytl4	0.776	0.460	0.113	0.006	0.778	0.450	0.097	0.001
1367849_at	NM_013026	syndecan 1	Sdc1	0.884	0.746	0.868	0.229	1.058	0.612	0.908	0.809
1370166_at	AI169682	syndecan 2	Sdc2	0.415	0.269	0.322	0.005	0.490	0.071	0.482	0.005
1370167_at	BG668421	syndecan 2	Sdc2	0.520	0.303	0.432	0.000	0.567	0.036	0.469	0.031
1367721_at	NM_012649	syndecan 4	Sdc4	8.336	0.003	2.754	0.006	10.825	0.002	2.453	0.005
1398762_at	NM_031986	syndecan binding protein	Sdcbp	1.442	0.001	2.297	0.002	1.234	0.052	1.575	0.011
1376973_at	BM386609	syndecan binding protein (syntenin) 2	Sdcbp2	2.604	0.078	1.051	0.550	1.344	0.062	1.080	0.274
1371827_at	AA946430	synovial apoptosis inhibitor 1, synoviolin	Syvn1	0.797	0.078	0.873	0.757	1.138	0.806	0.758	0.553
1397489_at	BE099670	Synovial sarcoma translocation, Chromosome 18	Ss18	1.667	0.348	1.397	0.674	1.005	0.204	0.944	0.700
1391628_at	BF418596	synovial sarcoma translocation, Chromosome 18	Ss18	1.517	0.466	1.546	0.017	1.578	0.004	2.036	0.026
1388431_at	AA851282	synovial sarcoma translocation, Chromosome 18	Ss18	0.966	0.545	0.592	0.012	1.101	0.156	0.690	0.029
1373146_at	AI716240	synovial sarcoma, X breakpoint 2 interacting protein	Ssx2ip	0.626	0.020	1.014	0.922	0.677	0.018	1.289	0.064
1384379_at	BG668700	Syntaxin 12	Stx12	0.861	0.612	0.891	0.468	0.985	0.892	0.893	0.150
1370192_at	BF283010	syntaxin 12	Stx12	0.689	0.959	1.013	0.973	0.580	0.491	0.899	0.279
1367530_at	AI412967	Syntaxin 16 (predicted)	Stx16_predicted	0.604	0.034	0.383	0.000	0.731	0.053	0.334	0.005
1370597_at	AF115435	syntaxin 17	Stx17	1.072	0.746	0.996	0.962	1.097	0.770	0.997	0.973
1372512_at	BE113340	syntaxin 18	Stx18	1.133	0.386	1.590	0.043	0.939	0.545	1.099	0.045
1370014_at	NM_031125	syntaxin 4A (placental)	Stx4a	1.196	0.644	1.282	0.224	1.564	0.027	1.875	0.010
1367878_at	NM_031704	syntaxin 5a	Stx5a	0.695	0.182	1.235	0.014	0.773	0.002	1.017	0.101
1380639_at	BI296446	syntaxin 5a	Stx5a	0.854	0.432	0.852	0.262	0.792	0.471	0.615	0.421
1386853_s_at	BI296446	syntaxin 5a	Stx5a	0.621	0.944	1.086	0.843	0.983	0.317	0.725	0.042
1388556_at	BG381589	syntaxin 6	Stx6	2.555	0.010	2.311	0.007	2.565	0.004	1.361	0.052
1387857_at	AI406531	syntaxin 7	Stx7	1.226	0.664	0.671	0.015	1.796	0.159	1.217	0.264
1397565_at	BI296579	Syntaxin 7	Stx7	1.014	0.826	1.011	0.971	1.616	0.076	1.001	0.996
1368070_at	NM_031656	syntaxin 8	Stx8	0.998	0.274	1.878	0.010	0.975	0.654	1.665	0.014
1398330_at	BM388715	syntaxin binding protein 1	Stxbp1	0.852	0.064	0.646	0.002	0.796	0.152	0.690	0.009
1370519_at	U06069	syntaxin binding protein 1	Stxbp1	0.733	0.977	0.481	0.027	0.658	0.351	0.544	0.003
1383871_at	BE120348	Syntaxin binding protein 2	Stxbp2	0.564	0.012	0.473	0.052	1.076	0.645	0.481	0.017

1369057_at	NM_031126	syntaxin binding protein 2	Stxbp2	0.879	0.402	0.819	0.281	0.724	0.362	0.801	0.284
1369414_at	NM_053637	syntaxin binding protein 3	Stxbp3	0.978	0.457	0.818	0.080	0.994	0.857	0.835	0.091
1387415_a_at	AF118889	syntaxin binding protein 5 (tomosyn)	Stxbp5	1.001	0.946	0.887	0.260	0.945	0.602	0.488	0.143
1367977_at	NM_019169	synuclein, alpha	Snca	1.004	0.754	1.381	0.879	0.663	0.225	0.577	0.135
1371568_at	AI145381	synuclein, beta	Sncb	0.285	0.001	0.537	0.109	0.204	0.003	0.389	0.064
1387474_at	J05097	tachykinin receptor 1	Tacr1	1.131	0.605	1.410	0.029	1.135	0.611	0.998	0.655
1368752_at	NM_017053	tachykinin receptor 3	Tacr3	0.883	0.701	0.813	0.751	0.687	0.254	0.872	0.402
1398963_at	BM392226	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor (predicted)	Taf10_predicted	0.444	0.281	0.919	0.506	0.379	0.003	0.741	0.000
1389025_at	BI278688	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf11	1.354	0.356	0.587	0.083	1.632	0.162	0.718	0.773
1374177_at	AI230912	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor (predicted)	Taf13_predicted	0.542	0.124	0.313	0.002	0.622	0.062	0.401	0.014
1383108_at	BE120513	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor (predicted)	Taf13_predicted	0.736	0.696	0.577	0.008	0.680	0.227	0.546	0.067
1393322_at	AI556910	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor (predicted)	Taf15_predicted	1.489	0.097	1.380	0.004	1.752	0.029	1.333	0.019
1392511_at	AA998513	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf2	0.748	0.878	0.474	0.001	0.957	0.863	0.695	0.035
1392561_at	BF396279	TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor (predicted)	Taf3_predicted	0.858	0.860	1.091	0.481	1.638	0.423	1.021	0.965
1376050_at	AI177663	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor (predicted)	Taf5_predicted	2.393	0.004	1.643	0.020	1.694	0.064	2.764	0.018
1373449_at	BG375861	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor	Taf5l	1.250	0.025	1.691	0.022	0.958	0.796	1.727	0.028
1384508_at	AI576469	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf6	1.376	0.052	1.149	0.438	3.509	0.091	1.241	0.012
1388058_at	D49446	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf6	1.128	0.180	1.385	0.186	1.706	0.101	1.550	0.003
1389174_s_at	AI234857	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf6	1.278	0.791	1.263	0.439	1.017	0.683	1.388	0.304
1375414_at	AA944572	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf9	0.618	0.423	1.250	0.369	0.486	0.039	1.013	0.909
1373632_at	AI172041	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf9	1.106	0.714	1.423	0.685	0.843	0.926	1.053	0.674
1368429_at	NM_133615	TAF9-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	Taf9l	0.918	0.896	0.249	0.004	0.936	0.319	0.385	0.034
1372008_at	BM385175	tafazzin (cardiomyopathy, dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndrome) (mapped)	Taz_mapped	0.414	0.010	0.543	0.007	0.503	0.040	0.591	0.011
1382036_at	AA900870	talin 1	Tln1	1.281	0.335	0.993	0.993	1.191	0.558	0.994	0.998
1389002_at	BI283756	talin 1	Tln1	0.999	0.781	1.078	0.744	1.155	0.851	0.998	0.461
1371610_at	AI411017	Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (predicted)	Tnks_predicted	0.835	0.073	0.765	0.036	0.835	0.200	0.993	0.404
1387140_at	NM_022702	TAO kinase 2	Taok2	0.647	0.974	0.724	0.104	0.943	0.679	0.973	0.597
1369726_at	NM_033098	TAP binding protein	Tapbp	5.627	0.039	8.768	0.001	4.270	0.001	14.864	0.003
1372962_at	AI599123	TAR (HIV) RNA binding protein 2	Tarbp2	0.789	0.649	1.387	0.268	0.623	0.902	1.263	0.434
1377608_a_at	BM392298	TAR DNA binding protein	Tardbp	0.871	0.142	0.795	0.021	0.953	0.639	0.883	0.162
1371367_at	BE107459	TAR DNA binding protein	Tardbp	0.926	0.412	0.397	0.003	0.831	0.031	0.507	0.004
1373927_at	BI283489	Target of myb1 homolog (chicken)	Tom1	1.201	0.028	1.255	0.186	1.204	0.047	1.255	0.712
1372020_at	BI285561	target of myb1 homolog (chicken)	Tom1	0.550	0.434	2.101	0.000	0.718	0.284	1.725	0.059
1382428_at	AA925658	taspase, threonine aspartase 1 (predicted)	Tasp1_predicted	0.961	0.160	1.524	0.186	1.271	0.534	0.983	0.933
1382035_at	AI535480	TATA box binding protein	Tbp	1.014	0.935	0.910	0.198	0.969	0.324	0.595	0.038
1373242_at	AW434020	TATA box binding protein-like 1 (predicted)	Tbpl1_predicted	1.198	0.335	1.292	0.336	1.095	0.394	1.399	0.673
1376554_at	BE121079	TatD DNase domain containing 1 (predicted)	Tatdn1_predicted	1.004	0.206	1.709	0.021	0.899	0.298	1.656	0.016
1398948_at	AI228250	Tax1 (human T-cell leukemia virus type I) binding protein 1	Tax1bp1	0.875	0.686	1.403	0.007	0.826	0.153	1.170	0.041
1388392_at	BI274159	Tax1 (human T-cell leukemia virus type I) binding protein 3	Tax1bp3	0.897	0.766	1.254	0.499	1.075	0.187	1.094	0.671
1391861_at	BI290684	taxilin beta (predicted)	Txlnb_predicted	1.065	0.900	1.561	0.372	1.030	0.862	1.194	0.511
1397115_at	BF409361	TBC1 domain family, member 1 (predicted)	Tbc1d1_predicted	1.938	0.374	0.811	0.527	4.222	0.040	0.606	0.377
1374101_at	BF282437	TBC1 domain family, member 10a	Tbc1d10a	0.806	0.091	2.066	0.006	0.954	0.860	1.684	0.074
1375226_at	BI287864	TBC1 domain family, member 10b (predicted)	Tbc1d10b_predicted	0.997	0.974	1.247	0.055	0.943	0.857	0.999	0.610
1388679_at	AI412244	TBC1 domain family, member 14	Tbc1d14	0.684	0.554	0.470	0.091	0.441	0.010	0.346	0.006
1388473_at	BF418041	TBC1 domain family, member 14	Tbc1d14	1.026	0.883	0.835	0.081	1.305	0.085	0.746	0.018
1382045_at	BI304056	TBC1 domain family, member 15	Tbc1d15	1.450	0.200	1.584	0.010	1.244	0.191	1.272	0.016
1385596_at	BF392191	TBC1 domain family, member 15	Tbc1d15	1.158	0.957	4.988	0.000	2.030	0.914	2.972	0.002
1379901_at	BG375857	TBC1 domain family, member 17 (predicted)	Tbc1d17_predicted	0.834	0.006	1.042	0.237	0.925	0.742	1.038	0.838
1396309_at	BI292839	TBC1 domain family, member 19 (predicted)	Tbc1d19_predicted	0.953	0.199	0.995	0.241	0.861	0.637	0.918	0.994
1383807_at	BG672767	TBC1 domain family, member 19 (predicted)	Tbc1d19_predicted	1.119	0.959	1.994	0.036	0.669	0.201	1.720	0.042
1395785_at	BE105453	TBC1 domain family, member 20	Tbc1d20	1.713	0.051	1.103	0.139	1.573	0.051	1.121	0.656
1372357_at	BI281833	TBC1 domain family, member 20	Tbc1d20	1.211	0.373	1.299	0.080	0.909	0.477	1.030	0.775
1373464_at	BF418962	TBC1 domain family, member 22a (predicted)	Tbc1d22a_predicted	2.285	0.155	1.411	0.218	0.913	0.638	1.072	0.605
1381109_at	BF412395	TBC1 domain family, member 22a (predicted)	Tbc1d22a_predicted	0.700	0.768	1.014	0.962	1.000	0.253	1.000	0.973
1383265_at	BF408403	TBC1 domain family, member 23 (predicted)	Tbc1d23_predicted	0.556	0.021	0.343	0.002	0.566	0.056	0.484	0.004
1385494_at	BM390350	TBC1 domain family, member 23 (predicted)	Tbc1d23_predicted	0.949	0.872	0.867	0.146	0.912	0.989	0.551	0.137
1372748_at	BE113335	TBC1 domain family, member 2B	Tbc1d2b	1.033	0.129	0.942	0.468	2.033	0.053	1.005	0.577
1391497_at	AA997515	TBC1D12: TBC1 domain family, member 12 (predicted)	Tbc1d12_predicted	5.647	0.000	2.972	0.051	3.307	0.052	3.249	0.064
1379232_at	AA955771	TBC1D12: TBC1 domain family, member 12 (predicted)	Tbc1d12_predicted	2.109	0.014	2.808	0.017	2.431	0.162	1.692	0.101
1375074_at	BE113756	TBK1 binding protein 1	Tbkbp1	2.610	0.020	2.330	0.000	1.580	0.006	1.230	0.024
1383916_at	AW533075	T-box 15 (predicted)	Tbx15_predicted	1.413	0.078	1.605	0.321	1.843	0.140	1.146	0.021

1374446_at	AI179464	TCDD-inducible poly(ADP-ribose) polymerase (predicted)	Tiparp_predicted	1.329	0.046	3.779	0.000	1.540	0.022	3.423	0.004
1385407_at	AI511405	TCDD-inducible poly(ADP-ribose) polymerase (predicted)	Tiparp_predicted	1.093	0.172	2.441	0.074	2.827	0.024	2.077	0.002
1367716_at	NM_133557	T-cell immunomodulatory protein	Cda08	0.535	0.476	0.427	0.000	0.868	0.087	0.492	0.005
1382448_at	AI071189	T-cell immunomodulatory protein	Cda08	0.776	0.581	1.047	0.416	1.018	0.313	0.926	0.737
1372507_at	AA901093	T-cell leukemia translocation altered gene	Tcta	0.406	0.307	0.461	0.008	0.418	0.002	0.455	0.002
1381167_at	BF390767	T-cell lymphoma invasion and metastasis 1	Tiam1	3.118	0.007	3.685	0.014	2.113	0.009	2.683	0.005
1374257_at	BM389265	T-cell lymphoma invasion and metastasis 1	Tiam1	2.823	0.012	1.989	0.139	4.010	0.018	1.560	0.066
1392980_at	AI716456	T-cell lymphoma invasion and metastasis 1	Tiam1	2.687	0.013	2.052	0.016	2.670	0.004	1.466	0.018
1371196_at	M23890	T-cell receptor beta-chain mRNA V-region (V-D-J-C), clone CRTB188	---	0.999	0.947	0.995	0.894	1.113	0.362	1.000	1.000
1380019_at	BM392376	T-cell, immune regulator 1	Tcirg1	1.403	0.367	1.177	0.941	2.219	0.153	1.003	0.967
1385224_at	AA819531	T-cell, immune regulator 1	Tcirg1	1.003	0.955	1.049	0.439	1.121	0.983	1.051	0.563
1388099_a_at	AB029495	TCF3 (E2A) fusion partner	Tfpt	1.010	0.956	1.847	0.016	0.929	0.891	1.838	0.057
1388471_at	AA800197	t-complex 11 (mouse) like 2	Tcp11l2	1.019	0.704	0.626	0.030	1.183	0.834	0.669	0.018
1388903_at	AI179335	T-complex associated-testis-expressed 1-like (Protein 91/23) /// similar to T-complex associated-testis-expressed 1-like (Protein 91/23) (predicted)	Tcte1l /// RGD1566162_predicted	0.964	0.951	0.411	0.002	0.784	0.173	0.567	0.002
1368049_at	NM_012670	t-complex protein 1	Tcp1	0.561	0.036	1.168	0.051	0.497	0.010	1.018	0.392
1386882_at	NM_031318	t-complex testis expressed 1	Tctex1	1.470	0.037	1.950	0.033	1.910	0.011	2.207	0.021
1370916_at	AI406496	tec protein tyrosine kinase	Tec	0.749	0.052	1.412	0.174	0.795	0.050	1.243	0.272
1368012_at	NM_022591	telomerase associated protein 1	Tep1	1.450	0.015	0.947	0.813	2.596	0.014	1.233	0.269
1394854_at	AA818755	telomeric repeat binding factor 1	Terf1	1.467	0.102	1.510	0.085	1.580	0.275	1.679	0.138
1388780_at	BF395792	telomeric repeat binding factor 2, interacting protein	Terf2ip	0.482	0.737	0.492	0.000	0.608	0.265	0.659	0.006
1371309_at	BI276999	testis enhanced gene transcript	Tegt	1.024	0.798	0.841	0.008	1.128	0.526	0.873	0.079
1369879_a_at	NM_019381	testis enhanced gene transcript	Tegt	1.019	0.911	1.792	0.038	0.880	0.415	1.640	0.048
1391440_at	AW521245	testis expressed gene 10 (predicted)	Tex10_predicted	1.278	0.147	3.638	0.023	1.149	0.429	3.229	0.011
1370453_at	AF347056	testis expressed gene 101	Tex101	0.984	0.862	0.995	0.953	0.998	0.612	0.996	0.923
1376038_at	AI411054	testis expressed gene 2	Tex2	0.420	0.149	0.518	0.004	0.427	0.023	0.611	0.006
1373539_at	BG380686	Testis expressed gene 261	Tex261	0.755	0.033	0.994	0.918	0.758	0.024	1.007	0.924
1389557_at	BM384037	testis expressed gene 261	Tex261	0.619	0.254	0.778	0.160	0.510	0.007	0.496	0.007
1388463_at	AW252660	testis expressed gene 264 homolog (mouse)	Tex264	1.260	0.376	4.045	0.001	0.705	0.181	2.379	0.003
1388209_at	AF092091	testis specific 10	Tsga10	0.245	0.056	0.040	0.000	0.239	0.057	0.041	0.000
1379708_at	BG381298	Testis specific 10	Tsga10	0.926	0.163	0.679	0.129	0.845	0.070	0.854	0.200
1395889_at	AA956651	Testis specific 10 interacting protein	Tsga10ip	0.781	0.087	0.760	0.390	1.003	0.083	0.996	0.987
1391228_at	BE106353	testis specific gene A2	Tsga2	1.088	0.844	0.973	0.073	1.124	0.951	0.788	0.064
1368687_at	NM_031578	testis specific protein kinase 1	Tesk1	1.020	0.969	1.535	0.024	0.668	0.038	1.090	0.041
1368736_at	NM_019203	testis specific X-linked gene	Tsx	1.483	0.255	0.731	0.023	3.548	0.057	1.173	0.214
1380091_at	BF287655	Testis-specific gene including a ubiquitin-likely domain	Anubl1	2.365	0.100	0.840	0.369	1.334	0.190	0.826	0.983
1394863_at	AI547767	Testis-specific kinase 2	Tesk2	1.305	0.394	0.591	0.212	0.776	0.941	0.549	0.968
1394772_at	AW521307	Testis-specific kinase 2	Tesk2	1.590	0.703	0.848	0.579	0.862	0.567	1.079	0.478
1374602_at	BF407207	testis-specific protein, Y-encoded-like	Tspyl	0.491	0.144	0.550	0.003	0.575	0.023	0.565	0.007
1372136_at	AA848776	tetraspanin 14 (predicted)	Tspan14_predicted	1.115	0.926	0.857	0.513	0.761	0.059	0.642	0.283
1398325_at	AI172464	tetraspanin 3	Tspan3	0.754	0.427	0.594	0.004	0.731	0.013	0.553	0.002
1372739_at	AA818865	tetraspanin 31	Tspan31	0.958	0.323	1.681	0.008	1.264	0.118	1.517	0.005
1381668_at	AW528482	Tetraspanin 5	Tspan5	0.771	0.127	1.414	0.431	0.885	0.310	1.211	0.921
1377089_a_at	BG381571	tetraspanin 5	Tspan5	0.919	0.589	0.741	0.298	0.622	0.021	0.733	0.118
1394316_a_at	AW920272	tetraspanin 5	Tspan5	0.866	0.708	0.733	0.275	0.501	0.038	0.780	0.571
1380725_at	AW251317	tetraspanin 5	Tspan5	0.886	0.791	5.917	0.004	0.266	0.002	3.755	0.002
1382146_at	BF412968	tetraspanin 6	Tspan6	0.502	0.319	0.290	0.004	0.627	0.111	0.314	0.050
1372286_at	BI295929	tetraspanin 6	Tspan6	0.774	0.728	0.436	0.025	0.725	0.204	0.506	0.004
1368052_at	NM_133526	tetraspanin 8	Tspan8	0.461	0.088	0.808	0.252	0.414	0.180	0.515	0.070
1381119_at	BM387763	tetratricopeptide repeat domain 1	Ttc1	0.925	0.234	1.118	0.129	0.951	0.359	1.001	0.983
1372712_at	BG380294	tetratricopeptide repeat domain 1	Ttc1	0.835	0.707	1.233	0.058	0.702	0.739	1.021	0.788
1389052_at	BI278584	tetratricopeptide repeat domain 13	Ttc13	0.467	0.036	0.484	0.002	1.033	0.839	0.574	0.027
1393758_at	AI535253	tetratricopeptide repeat domain 14 (predicted)	Ttc14_predicted	0.548	0.087	0.814	0.054	0.514	0.105	0.599	0.021
1372854_at	AI229046	tetratricopeptide repeat domain 17	Ttc17	0.706	0.042	0.819	0.406	0.860	0.526	0.715	0.953
1388806_at	AI176039	tetratricopeptide repeat domain 5	Ttc5	1.000	0.949	0.982	0.454	1.052	0.708	0.737	0.042
1393457_at	BI289669	Tetratricopeptide repeat domain 5	Ttc5	0.942	0.957	1.141	0.484	0.816	0.877	0.845	0.491
1376974_at	BG381669	tetratricopeptide repeat domain 7	Ttc7	2.565	0.028	2.894	0.004	2.674	0.018	1.666	0.028
1376035_at	BI274308	Tetratricopeptide repeat domain 7B (predicted)	Ttc7b_predicted	0.583	0.246	1.697	0.018	0.430	0.003	1.119	0.065
1376613_at	BI279201	tetratricopeptide repeat domain 9C	Ttc9c	1.466	0.009	1.165	0.144	2.040	0.001	1.403	0.007
1383730_at	BG668930	Tetratricopeptide repeat domain 9C	Ttc9c	1.364	0.018	0.814	0.062	1.434	0.089	0.857	0.323
1395375_at	BG672758	tetratricopeptide repeat domain 9C	Ttc9c	1.234	0.121	1.005	0.124	2.077	0.129	1.174	0.518

1378964_at	AI709953	Tetratricopeptide repeat domain 9C	Ttc9c	1.057	0.853	1.153	0.355	1.366	0.015	1.411	0.090
1373421_at	BM392224	TG interacting factor	Tgif	4.918	0.003	8.613	0.000	4.204	0.006	9.880	0.001
1383282_at	BF543075	THAP domain containing 11 (predicted)	Thap11_predicted	0.888	0.276	0.874	0.541	0.348	0.076	0.825	0.347
1371557_at	BI275281	THAP domain containing 4	Thap4	0.765	0.561	1.441	0.035	0.624	0.014	1.277	0.611
1390428_at	BF555924	THAP domain containing 6 (predicted)	Thap6_predicted	0.926	0.132	0.659	0.117	0.837	0.532	0.751	0.098
1374341_at	AI237866	THAP domain containing 7	Thap7	0.689	0.582	1.419	0.193	0.856	0.289	1.089	0.392
1372412_at	AA943723	THAP domain containing, apoptosis associated protein 3 (predicted)	Thap3_predicted	0.463	0.037	0.698	0.214	0.550	0.237	0.632	0.176
1388713_at	AW919094	thiamine triphosphatase	Thtpa	0.667	0.044	0.534	0.012	0.702	0.020	0.649	0.216
1388497_at	AI411426	thioesterase superfamily member 2 (predicted)	Them2_predicted	0.623	0.029	0.861	0.319	0.710	0.072	0.818	0.174
1374640_at	BE112158	thioesterase superfamily member 4	Them4	1.015	0.975	1.260	0.064	1.025	0.751	1.083	0.214
1370821_at	AF120100	Thiopurine methyltransferase	Tpmt	0.641	0.106	0.967	0.730	0.555	0.071	0.977	0.242
1378753_at	AI638971	thiopurine methyltransferase	Tpmt	0.707	0.111	1.063	0.489	0.675	0.775	1.175	0.028
1398839_at	NM_053800	thioredoxin 1	Txn1	1.320	0.150	1.537	0.004	1.391	0.018	1.733	0.000
1398844_at	AA800180	thioredoxin 2	Txn2	0.578	0.548	1.322	0.194	0.553	0.055	1.515	0.008
1390599_at	BE101766	Thioredoxin domain containing 1	Txndc1	0.556	0.047	0.418	0.037	0.731	0.152	0.414	0.009
1372067_at	AI179567	thioredoxin domain containing 1	Txndc1	0.680	0.208	0.851	0.061	0.691	0.025	0.954	0.477
1371565_at	BM390478	Thioredoxin domain containing 12 (endoplasmic reticulum)	Txndc12	0.598	0.099	1.006	0.612	0.483	0.005	0.961	0.441
1388523_at	BM392352	thioredoxin domain containing 12 (endoplasmic reticulum)	Txndc12	0.716	0.310	1.507	0.098	0.729	0.036	1.340	0.054
1379023_at	BF406975	Thioredoxin domain containing 12 (endoplasmic reticulum)	Txndc12	1.142	0.702	2.217	0.013	0.679	0.029	1.425	0.035
1375221_at	BE109676	thioredoxin domain containing 13	Txndc13	1.179	0.113	0.819	0.013	1.037	0.205	0.866	0.138
1372298_at	BE098766	thioredoxin domain containing 4 (endoplasmic reticulum)	Txndc4	0.865	0.197	1.003	0.943	0.855	0.032	0.857	0.045
1395693_at	BF553613	thioredoxin domain containing 4 (endoplasmic reticulum)	Txndc4	0.552	0.871	0.670	0.020	0.973	0.571	0.670	0.005
1371391_at	BM390196	thioredoxin domain containing 5 (predicted)	Txndc5_predicted	0.532	0.382	0.701	0.043	0.519	0.008	0.600	0.029
1391927_at	BE100100	Thioredoxin domain containing 5 (predicted)	Txndc5_predicted	0.807	0.609	0.798	0.314	1.066	0.796	0.979	0.678
1379245_at	BI283491	Thioredoxin domain containing 9	Txndc9	0.711	0.587	0.892	0.071	0.744	0.178	0.833	0.012
1386958_at	U63923	thioredoxin reductase 1	Txnrd1	1.345	0.125	3.241	0.003	0.925	0.408	2.259	0.003
1398791_at	NM_031614	thioredoxin reductase 1	Txnrd1	1.064	0.278	1.654	0.013	0.805	0.290	1.499	0.003
1380191_s_at	BF555110	thioredoxin-like 1	Txnl1	0.715	0.077	1.571	0.000	0.784	0.032	1.271	0.001
1391789_at	BF555110	thioredoxin-like 1	Txnl1	0.835	0.239	2.552	0.013	0.956	0.453	1.315	0.119
1368936_at	NM_080887	thioredoxin-like 1	Txnl1	0.588	0.757	1.211	0.064	0.474	0.092	1.185	0.249
1367870_at	NM_032614	thioredoxin-like 2	Txnl2	0.703	0.057	2.118	0.001	0.727	0.004	2.351	0.000
1372795_at	BF285089	thioredoxin-like 4B	Txnl4b	1.299	0.571	1.536	0.082	1.092	0.765	1.422	0.164
1388555_at	AI104292	thioredoxin-like 5 (predicted)	Txnl5_predicted	0.736	0.628	1.496	0.071	0.621	0.098	1.109	0.192
1396281_at	BI274269	Thioredoxin-like 6 (predicted)	Txnl6_predicted	1.244	0.508	1.317	0.985	1.030	0.992	0.999	0.998
1371796_at	AA799476	Thioredoxin-related transmembrane protein 2	Tmx2	0.545	0.031	0.934	0.676	0.634	0.028	0.852	0.304
1379981_at	AI170356	THO complex 1	Thoc1	0.878	0.406	0.311	0.011	1.001	0.993	0.276	0.022
1376641_at	BM384228	THO complex 1	Thoc1	1.170	0.596	1.583	0.018	0.806	0.970	1.589	0.028
1386525_at	AI556851	THO complex 2 (predicted)	Thoc2_predicted	0.909	0.672	1.478	0.031	0.881	0.224	1.493	0.470
1379849_at	BE098416	THO complex 3 (predicted)	Thoc3_predicted	0.838	0.533	1.539	0.111	0.603	0.016	1.167	0.228
1392671_at	AA999074	THO complex 3 (predicted)	Thoc3_predicted	0.603	0.553	1.725	0.030	0.524	0.138	1.139	0.279
1392508_at	BE119831	three prime histone mRNA exonuclease 1	Thex1	1.376	0.077	1.693	0.001	1.694	0.094	1.683	0.015
1392120_at	AW526194	Threonine synthase-like 1	Thnsl1	0.967	0.999	0.910	0.305	1.402	0.095	0.909	0.399
1372145_at	BI289683	threonyl-tRNA synthetase	Tars	1.265	0.164	1.746	0.003	1.289	0.009	1.722	0.007
1373760_at	BE349725	threonyl-tRNA synthetase-like 1	Tarsl1	1.423	0.072	1.068	0.679	1.405	0.925	0.972	0.698
1368901_at	BG666306	thrombomodulin	Thbd	0.181	0.011	0.471	0.033	0.214	0.012	0.477	0.027
1375951_at	AA818521	thrombomodulin	Thbd	0.220	0.088	0.950	0.867	0.224	0.092	0.948	0.876
1388567_at	BF282947	THUMP domain containing 1	Thumpd1	0.496	0.021	0.458	0.000	0.437	0.003	0.500	0.001
1376090_at	AW252828	THUMP domain containing 2	Thumpd2	0.730	0.077	0.735	0.123	0.730	0.078	0.738	0.115
1398448_at	BE108346	Thymic stromal cotransporter (predicted)	Tscot_predicted	0.538	0.032	0.646	0.017	0.492	0.018	0.595	0.003
1368179_at	NM_134465	thymic stromal-derived lymphopoietin, receptor	Tslpr	1.796	0.009	1.344	0.443	1.710	0.066	0.967	0.986
1393044_at	BF282370	thymidylate kinase family LPS-inducible member (predicted)	Tyki_predicted	110.965	0.000	26.603	0.004	276.242	0.001	52.564	0.001
1383424_at	BI276216	thymidylate kinase family LPS-inducible member (predicted)	Tyki_predicted	93.299	0.006	43.348	0.001	156.711	0.005	78.594	0.000
1369499_at	NM_019179	thymidylate synthase	Tyms	1.087	0.292	1.634	0.045	1.416	0.179	1.395	0.164
1368268_at	NM_053729	thymine-DNA glycosylase	Tdg	1.171	0.492	1.463	0.102	0.814	0.583	1.428	0.132
1392387_at	AI549050	Thymocyte nuclear protein 1	Thyn1	0.777	0.188	0.779	0.786	0.491	0.021	1.140	0.232
1383623_at	BM383909	thymocyte nuclear protein 1	Thyn1	0.712	0.410	1.333	0.636	0.526	0.025	1.390	0.092
1393083_at	AI102529	Thymocyte selection-associated HMG box gene (predicted)	Tox_predicted	1.077	0.474	0.899	0.182	1.391	0.045	0.720	0.083
1379824_at	AI101139	Thymocyte selection-associated HMG box gene (predicted)	Tox_predicted	1.540	0.504	1.559	0.972	1.162	0.440	0.909	0.908
1383126_at	AA998057	Thymoma viral proto-oncogene 1	Akt1	0.646	0.295	0.519	0.041	0.662	0.002	0.672	0.023
1375178_at	BE111601	Thymoma viral proto-oncogene 1	Akt1	1.000	0.975	0.763	0.006	1.008	0.999	0.537	0.010
1368832_at	NM_017093	thymoma viral proto-oncogene 2	Akt2	1.020	0.907	0.998	0.981	0.911	0.864	0.998	0.990

1388765_at	AA946508	Thymoma viral proto-oncogene 2	Akt2	1.009	0.908	1.328	0.213	1.309	0.672	0.998	0.976
1387592_at	NM_031575	thymoma viral proto-oncogene 3	Akt3	0.962	0.101	2.455	0.035	0.850	0.676	1.601	0.014
1368136_at	NM_012887	thymopoietin	Tmpo	1.346	0.687	1.173	0.427	0.742	0.033	0.936	0.053
1370442_at	U25684	thymosin beta-like protein 1	Tmsbl1	0.816	0.146	0.644	0.048	0.867	0.064	0.775	0.074
1367655_at	NM_021261	thymosin, beta 10	Tmsb10	1.923	0.012	2.210	0.016	1.830	0.010	1.789	0.010
1387883_a_at	BG668902	thymosin, beta 4	Tmsb4x	1.493	0.331	0.720	0.277	0.927	0.698	0.723	0.059
1369744_at	AF221622	thyroglobulin	Tg	1.501	0.183	0.716	0.076	2.376	0.037	0.641	0.038
1395928_at	BE102495	Thyroid hormone receptor alpha	Thra	0.872	0.968	1.590	0.004	1.000	0.999	0.997	0.975
1386156_at	AI639451	thyroid hormone receptor associated protein 1 (predicted)	Thrap1_predicted	2.107	0.003	1.420	0.010	1.619	0.033	1.749	0.025
1379567_at	AI105643	thyroid hormone receptor associated protein 1 (predicted)	Thrap1_predicted	2.055	0.083	2.127	0.003	1.487	0.245	1.587	0.110
1385091_at	AW530801	thyroid hormone receptor associated protein 1 (predicted)	Thrap1_predicted	1.019	0.864	1.343	0.390	0.970	0.266	1.279	0.055
1367525_at	AI179833	thyroid hormone receptor associated protein 3	Thrap3	0.716	0.003	0.650	0.019	0.854	0.022	0.783	0.063
1398967_at	AI410050	thyroid hormone receptor associated protein 4	Thrap4	0.901	0.047	1.045	0.048	1.128	0.174	0.995	0.972
1399078_at	BG380479	thyroid hormone receptor associated protein 5 (predicted)	Thrap5_predicted	1.003	0.545	1.535	0.093	1.173	0.908	1.164	0.196
1377596_a_at	AI008698	thyroid hormone receptor associated protein 6 (predicted)	Thrap6_predicted	0.881	0.151	0.949	0.676	1.005	0.469	0.947	0.456
1386963_at	NM_053920	thyroid hormone receptor interactor 10	Trip10	1.565	0.796	4.393	0.026	1.629	0.550	3.913	0.026
1374795_at	AA891859	Thyroid hormone receptor interactor 12	Trip12	0.937	0.495	0.336	0.007	0.895	0.396	0.395	0.012
1374490_at	AI177845	thyroid hormone receptor interactor 12	Trip12	0.992	0.598	0.470	0.002	1.059	0.445	0.568	0.035
1376984_at	AW915048	Thyroid hormone receptor interactor 12	Trip12	1.178	0.610	0.460	0.002	1.078	0.638	0.613	0.004
1388873_at	AA891883	thyroid hormone receptor interactor 12	Trip12	1.163	0.648	1.310	0.005	1.045	0.727	1.114	0.641
1382288_at	AI172553	thyroid hormone receptor interactor 4 (predicted)	Trip4_predicted	0.687	0.593	1.725	0.011	0.646	0.081	1.002	0.858
1371400_at	AI169092	thyroid hormone responsive protein	Thrsp	1.050	0.889	0.985	0.502	0.998	0.893	1.001	0.649
1370302_at	AF348365	thyroid hormone-response protein-1	AF348365	1.001	0.852	0.860	0.070	0.716	0.021	0.690	0.077
1368912_at	M12138	thyrotropin releasing hormone	Trh	0.496	0.138	0.293	0.353	0.512	0.073	0.077	0.041
1388476_at	AI101391	Tial1 cytotoxic granule-associated RNA binding protein-like 1 (mapped)	Tial1_mapped	1.146	0.486	1.387	0.001	1.028	0.501	1.317	0.005
1397797_at	BE103164	Tigger transposable element derived 3 (predicted)	Tigd3_predicted	1.051	0.763	0.961	0.818	5.729	0.098	0.999	0.884
1375865_at	BF408844	tight junction associated protein 1 (predicted)	Tjap1_predicted	1.654	0.035	1.517	0.128	1.965	0.034	1.831	0.006
1372473_at	AW434048	tight junction protein 1 (predicted)	Tjp1_predicted	2.417	0.005	1.633	0.004	2.584	0.000	2.185	0.012
1370940_at	BG378746	tight junction protein 2	Tjp2	3.919	0.018	2.947	0.013	2.037	0.052	2.462	0.026
1378567_at	BI295961	tight junction protein 3 (predicted)	Tjp3_predicted	1.149	0.560	2.678	0.082	1.025	0.489	1.334	0.137
1368522_at	NM_031340	timeless homolog (Drosophila)	Timeless	1.004	0.637	1.003	0.875	1.002	0.991	0.994	0.935
1368323_at	NM_017200	tissue factor pathway inhibitor	Tfpi	0.986	0.593	0.102	0.001	0.999	0.817	0.136	0.002
1377340_at	AI179507	tissue factor pathway inhibitor 2	Tfpi2	0.997	0.991	0.718	0.035	1.001	0.949	1.037	0.244
1367712_at	NM_053819	tissue inhibitor of metalloproteinase 1	Timp1	15.285	0.001	20.152	0.000	18.594	0.000	19.444	0.000
1398953_at	BM386183	tissue specific transplantation antigen P35B (predicted)	Tsta3_predicted	0.617	0.007	0.942	0.406	0.398	0.003	0.802	0.338
1391559_at	AW525904	TLC domain containing 1	Tlcd1	1.119	0.510	2.421	0.011	1.055	0.803	2.292	0.001
1385838_a_at	BF287928	TM2 domain containing 1 (predicted)	Tm2d1_predicted	0.682	0.365	0.463	0.011	0.796	0.502	0.660	0.014
1385839_x_at	BF287928	TM2 domain containing 1 (predicted)	Tm2d1_predicted	0.720	0.442	0.460	0.012	0.747	0.412	0.626	0.004
1367550_a_at	BI287742	TM2 domain containing 1 (predicted)	Tm2d1_predicted	0.722	0.526	0.475	0.011	0.766	0.436	0.633	0.006
1398984_at	AA818129	TM2 domain containing 2	Tm2d2	0.300	0.077	0.520	0.000	0.482	0.001	0.655	0.002
1373277_at	BG373457	TM2 domain containing 3 (predicted)	Tm2d3_predicted	0.532	0.292	1.253	0.209	0.704	0.440	1.155	0.660
1381524_at	BF397008	TM2 domain containing 3 (predicted)	Tm2d3_predicted	1.183	0.723	0.851	0.918	0.735	0.667	1.070	0.986
1374675_at	BG374992	TMEM9 domain family, member B (predicted)	Tmem9b_predicted	0.999	0.219	0.973	0.397	0.536	0.063	0.928	0.895
1374058_at	BM384945	TMEM9 domain family, member B (predicted)	Tmem9b_predicted	0.793	0.279	0.838	0.052	0.761	0.217	0.837	0.027
1371551_at	BM383323	Tnf receptor associated factor 4 (predicted)	Traf4_predicted	1.470	0.035	1.786	0.067	1.403	0.002	1.725	0.018
1388769_at	BI287266	Tnf receptor-associated factor 7 (predicted)	Traf7_predicted	1.012	0.823	1.143	0.284	1.160	0.161	1.156	0.167
1374467_at	BM389034	TNF receptor-associated protein 1	Trap1	0.291	0.014	0.497	0.175	0.347	0.003	0.685	0.521
1388492_at	AW919111	TNFAIP3 interacting protein 1 (predicted)	Tnip1_predicted	28.231	0.000	5.140	0.000	35.164	0.000	6.443	0.000
1383655_at	BF545192	TNFAIP3 interacting protein 2	Tnip2	3.215	0.017	14.278	0.002	1.952	0.051	10.646	0.002
1390434_at	BM386846	TNFRSF1A-associated via death domain	Tradd	0.887	0.487	2.030	0.073	1.096	0.272	1.907	0.049
1378572_at	BF408962	toll interacting protein (predicted)	Tollip_predicted	3.268	0.077	6.994	0.007	1.950	0.006	1.899	0.107
1399052_at	AA957069	Toll interacting protein (predicted)	Tollip_predicted	1.370	0.152	1.280	0.007	0.920	0.927	1.034	0.981
1380808_at	BE112982	Toll interacting protein (predicted)	Tollip_predicted	1.378	0.480	1.305	0.099	0.860	0.827	0.998	0.388
1389944_at	AI014155	Toll-like receptor adaptor molecule 2 (predicted)	Ticam2_predicted	0.605	0.148	1.254	0.269	1.047	0.942	0.713	0.328
1373862_at	AI009673	Toll-like receptor adaptor molecule 2 (predicted)	Ticam2_predicted	0.772	0.192	0.975	0.421	0.801	0.098	0.924	0.321
1386477_at	AI170046	Toll-like receptor adaptor molecule 2 (predicted)	Ticam2_predicted	0.642	0.813	1.028	0.950	0.697	0.339	0.938	0.743
1369990_at	NM_022183	topoisomerase (DNA) 2 alpha	Top2a	0.411	0.196	1.177	0.052	0.341	0.004	1.102	0.297
1388650_at	BM385445	topoisomerase (DNA) 2 alpha	Top2a	0.999	0.745	0.062	0.002	1.088	0.185	0.061	0.000
1399046_at	BE116507	topoisomerase (DNA) I	Top1	1.243	0.020	0.826	0.054	1.159	0.067	0.753	0.094
1369421_at	NM_022615	topoisomerase (DNA) I	Top1	0.967	0.858	0.977	0.832	0.980	0.404	0.956	0.996
1373553_at	AI233765	topoisomerase (DNA) III beta (predicted)	Top3b_predicted	0.764	0.531	1.231	0.263	1.019	0.198	0.920	0.527

1392610_at	AI176588	topoisomerase I binding, arginine/serine-rich (predicted)	Topors_predicted	1.083	0.236	1.126	0.630	1.007	0.904	1.008	0.949
1388024_s_at	U20286	torsin A interacting protein 1	Tor1aip1	2.702	0.027	1.320	0.299	2.991	0.001	1.672	0.306
1387917_at	U19614	torsin A interacting protein 1	Tor1aip1	2.164	0.045	1.630	0.027	2.534	0.000	1.269	0.034
1375969_at	BI296555	torsin A interacting protein 2	Tor1aip2	1.930	0.018	3.020	0.003	1.890	0.042	2.285	0.066
1381980_at	BI278862	Torsin A interacting protein 2	Tor1aip2	1.492	0.034	1.037	0.238	2.038	0.013	0.932	0.462
1374798_at	AA924151	Torsin A interacting protein 2	Tor1aip2	0.541	0.094	0.417	0.004	0.733	0.052	0.609	0.003
1392656_at	AI073268	Torsin A interacting protein 2	Tor1aip2	1.010	0.964	1.735	0.114	1.005	0.970	1.004	0.974
1373406_at	BM384991	torsin family 1, member B	Tor1b	0.580	0.044	0.492	0.001	1.276	0.062	0.764	0.016
1382984_at	AI073272	torsin family 1, member B	Tor1b	0.616	0.486	0.687	0.629	0.693	0.199	0.797	0.667
1373662_at	AI178830	torsin family 2, member A	Tor2a	0.692	0.160	1.212	0.414	0.828	0.552	1.058	0.458
1384318_at	BE100696	Torsin family 2, member A	Tor2a	1.266	0.818	0.281	0.006	1.842	0.340	0.451	0.098
1372868_at	BF284295	torsin family 3, member A	Tor3a	1.737	0.001	2.151	0.001	2.670	0.000	2.589	0.000
1382114_at	BG379991	tousled-like kinase 1 (predicted)	Tlk1_predicted	1.505	0.010	1.125	0.075	1.356	0.001	1.069	0.890
1383827_at	AI059119	tousled-like kinase 1 (predicted)	Tlk1_predicted	1.603	0.012	1.238	0.108	1.551	0.041	1.424	0.012
1399088_at	AA819648	tousled-like kinase 2 (Arabidopsis) (predicted)	Tlk2_predicted	2.047	0.101	1.536	0.058	1.694	0.044	1.644	0.009
1379488_at	BI274525	TP53 regulating kinase (predicted)	Trp53rk_predicted	0.509	0.110	1.274	0.251	0.515	0.105	1.004	0.949
1376007_at	AI411772	Tp53rk binding protein	Tprkb	0.726	0.180	0.356	0.033	0.633	0.377	0.773	0.055
1390972_at	BI281729	Tp53rk binding protein	Tprkb	0.671	0.230	0.992	0.162	0.642	0.212	0.833	0.086
1373392_at	AW523924	TPA regulated locus	Tparl	0.987	0.964	0.648	0.013	0.831	0.606	0.755	0.060
1371122_at	AW140505	TRAF family member-associated Nf-kappa B activator /// hypothetical gene supported by NM_145788	Tank /// LOC497768	1.125	0.135	1.744	0.990	0.997	0.991	1.005	0.976
1382311_at	BM384466	TRAF2 binding protein	LOC310877	39.747	0.003	7.045	0.001	78.651	0.001	15.497	0.002
1391787_at	AI059620	TRAF3 interacting protein 3	Traf3ip3	0.717	0.019	0.965	0.607	0.698	0.120	0.681	0.119
1372252_at	BE112892	trafficking protein particle complex 1	Trappc1	0.518	0.004	0.475	0.000	0.523	0.008	0.497	0.015
1372284_at	AI104319	trafficking protein particle complex 3	Trappc3	1.022	0.945	0.864	0.358	0.763	0.483	0.962	0.736
1373907_at	BI288890	trafficking protein particle complex 4	Trappc4	1.024	0.937	1.416	0.094	0.744	0.229	1.496	0.018
1372283_at	AA800622	trafficking protein particle complex 6B (predicted)	Trappc6b_predicted	1.103	0.697	1.303	0.185	0.969	0.842	1.234	0.008
1372092_at	BI278968	trafficking protein, kinesin binding 2	Trak2	0.443	0.080	0.225	0.000	0.366	0.001	0.336	0.000
1369940_at	NM_031811	transaldolase 1	Taldo1	0.819	0.113	2.126	0.001	0.680	0.025	1.374	0.028
1367765_at	NM_022534	transcobalamin 2	Tcn2	0.684	0.668	0.553	0.000	0.420	0.020	0.535	0.008
1393351_at	BE109501	Transcribed locus	---	10.542	0.000	2.572	0.003	9.782	0.000	1.852	0.225
1380129_at	AA818937	Transcribed locus	---	8.755	0.000	10.515	0.002	10.502	0.000	11.448	0.002
1393494_at	AA866419	Transcribed locus	---	10.652	0.000	2.217	0.004	9.999	0.000	1.801	0.051
1383757_at	AI044802	Transcribed locus	---	53.430	0.000	21.195	0.000	37.958	0.000	37.808	0.002
1382933_at	BE102157	Transcribed locus	---	10.837	0.000	4.571	0.001	1.655	0.513	1.397	0.081
1379647_at	BI295140	Transcribed locus	---	0.232	0.000	0.223	0.000	0.276	0.019	0.254	0.023
1379477_at	AI555261	Transcribed locus	---	4.212	0.000	1.738	0.029	3.304	0.000	2.775	0.045
1383939_at	BG378849	Transcribed locus	---	15.308	0.000	4.169	0.004	20.279	0.000	9.791	0.001
1371627_at	BI277433	Transcribed locus	---	0.352	0.000	0.210	0.002	0.337	0.001	0.119	0.013
1373488_at	BF289154	Transcribed locus	---	4.087	0.000	0.801	0.040	5.003	0.000	1.288	0.210
1377826_at	AI176721	Transcribed locus	---	17.836	0.000	3.325	0.003	18.228	0.000	5.169	0.011
1391125_at	AI639331	Transcribed locus	---	3.046	0.000	2.336	0.014	3.665	0.000	2.273	0.002
1374075_at	AI175533	Transcribed locus	---	0.600	0.000	0.430	0.000	0.818	0.103	0.612	0.010
1377442_at	BF409997	Transcribed locus	---	0.169	0.000	0.209	0.022	0.233	0.000	0.419	0.030
1385380_at	AI044983	Transcribed locus	---	126.467	0.000	29.024	0.000	292.902	0.000	41.156	0.000
1389774_at	AI008371	Transcribed locus	---	0.423	0.000	0.264	0.000	0.679	0.060	0.276	0.020
1377345_at	AI502211	Transcribed locus	---	1.839	0.000	1.116	0.025	2.096	0.000	1.233	0.003
1388701_at	AI555336	Transcribed locus	---	7.229	0.000	0.983	0.751	7.515	0.002	0.982	0.747
1374823_at	BI291651	Transcribed locus	---	0.531	0.000	0.391	0.001	0.785	0.193	0.463	0.068
1374685_at	BE117446	Transcribed locus	---	0.540	0.000	0.411	0.001	0.644	0.003	0.503	0.016
1388759_at	BM389875	Transcribed locus	---	3.833	0.000	2.517	0.000	5.374	0.002	3.243	0.000
1384470_at	BE114218	Transcribed locus	---	0.362	0.000	0.382	0.005	0.176	0.015	0.277	0.020
1394456_at	AW525722	Transcribed locus	---	0.515	0.000	0.869	0.022	0.524	0.011	0.996	0.085
1380712_at	AI406475	Transcribed locus	---	0.307	0.000	0.143	0.000	0.395	0.031	0.064	0.015
1382171_at	AI454310	Transcribed locus	---	1.356	0.000	2.524	0.025	0.872	0.313	2.429	0.024
1379431_at	AW918368	Transcribed locus	---	0.602	0.000	0.333	0.001	0.799	0.004	0.335	0.019
1385381_at	AA996491	Transcribed locus	---	0.222	0.000	0.443	0.009	0.321	0.010	0.369	0.124
1384019_a_at	BM383449	Transcribed locus	---	1.591	0.000	1.356	0.004	1.791	0.003	1.607	0.024
1385926_at	BF550565	Transcribed locus	---	14.358	0.000	4.903	0.003	14.889	0.001	6.938	0.001
1374622_at	BE107309	Transcribed locus	---	11.960	0.001	2.002	0.047	11.295	0.004	2.098	0.006
1389206_at	BE116867	Transcribed locus	---	0.368	0.001	0.332	0.000	0.304	0.011	0.516	0.023
1376673_at	BM391853	Transcribed locus	---	4.409	0.001	2.216	0.002	4.435	0.002	2.319	0.004

1379073_at	AA859663	Transcribed locus	---	0.346	0.001	0.345	0.015	0.729	0.187	0.584	0.151
1390659_at	BI302830	Transcribed locus	---	16.855	0.001	13.404	0.001	14.540	0.000	9.852	0.001
1371821_at	BM391330	Transcribed locus	---	2.217	0.001	1.578	0.048	2.078	0.015	1.414	0.036
1385925_at	AA963975	Transcribed locus	---	22.343	0.001	5.828	0.001	18.753	0.001	7.430	0.001
1383189_at	AA818143	Transcribed locus	---	13.898	0.001	1.893	0.158	34.959	0.001	8.590	0.003
1381145_at	BE112469	Transcribed locus	---	4.079	0.001	1.465	0.695	2.817	0.008	0.861	0.724
1395081_at	BI290843	Transcribed locus	---	2.687	0.001	0.447	0.051	3.255	0.006	0.848	0.531
1394786_at	AW526631	Transcribed locus	---	0.486	0.001	0.127	0.001	0.705	0.061	0.258	0.002
1376637_at	AI102401	Transcribed locus	---	0.363	0.001	0.222	0.000	0.299	0.001	0.228	0.038
1397558_at	AW527159	Transcribed locus	---	2.309	0.001	0.693	0.314	1.989	0.045	0.899	0.570
1388573_at	BF288140	Transcribed locus	---	1.791	0.001	0.685	0.233	1.090	0.159	1.002	0.994
1383348_at	BF545309	Transcribed locus	---	2.715	0.001	2.735	0.001	2.438	0.002	2.832	0.004
1373055_at	AI407547	Transcribed locus	---	0.321	0.001	1.363	0.909	0.344	0.001	1.004	0.211
1393134_at	BG375377	Transcribed locus	---	0.433	0.001	0.501	0.032	0.642	0.010	0.781	0.318
1395480_at	BI303370	Transcribed locus	---	1.474	0.001	0.459	0.295	1.806	0.020	0.872	0.281
1382931_at	AA924607	Transcribed locus	---	2.899	0.001	1.622	0.026	2.138	0.014	1.070	0.549
1390809_at	AI599392	Transcribed locus	---	3.286	0.001	1.745	0.047	2.763	0.011	2.168	0.160
1392969_at	BI282309	Transcribed locus	---	0.432	0.001	0.183	0.002	0.171	0.022	0.192	0.084
1374429_at	AI598401	Transcribed locus	---	7.484	0.001	3.765	0.011	8.377	0.003	3.736	0.015
1389213_at	AI408955	Transcribed locus	---	2.078	0.001	0.485	0.113	2.464	0.000	0.726	0.978
1381081_at	AW523873	Transcribed locus	---	2.332	0.001	1.016	0.834	2.461	0.007	1.207	0.007
1374531_at	AA926305	Transcribed locus	---	1.542	0.001	0.835	0.094	1.225	0.011	0.794	0.020
1398412_at	BF402250	Transcribed locus	---	0.126	0.001	0.447	0.010	0.139	0.003	0.385	0.001
1388465_at	AA891733	Transcribed locus	---	0.491	0.001	0.642	0.008	0.415	0.007	0.649	0.007
1393478_at	AI029492	Transcribed locus	---	0.475	0.001	0.312	0.000	0.457	0.010	0.464	0.010
1390207_at	BM390283	Transcribed locus	---	0.521	0.001	0.379	0.045	0.423	0.054	0.527	0.000
1385016_at	AI136882	Transcribed locus	---	0.203	0.001	0.090	0.001	0.222	0.001	0.216	0.023
1379113_at	BE119226	Transcribed locus	---	0.550	0.001	0.828	0.311	0.405	0.002	0.780	0.093
1386022_at	AW921706	Transcribed locus	---	0.664	0.001	0.555	0.066	0.606	0.050	0.633	0.051
1390804_at	AI176434	Transcribed locus	---	1.724	0.001	0.850	0.029	1.873	0.004	1.037	0.763
1378783_at	AI144739	Transcribed locus	---	11.302	0.001	3.398	0.213	7.604	0.006	1.554	0.583
1376319_at	BM390322	Transcribed locus	---	2.031	0.002	3.465	0.001	1.698	0.015	2.907	0.003
1373923_at	BF283756	Transcribed locus	---	10.555	0.002	1.619	0.017	11.952	0.002	0.932	0.829
1372381_at	BM383457	Transcribed locus	---	0.195	0.002	0.140	0.000	0.259	0.006	0.184	0.013
1398440_at	BI292166	Transcribed locus	---	0.382	0.002	0.236	0.003	1.014	0.275	0.487	0.012
1381043_at	AI639256	Transcribed locus	---	0.223	0.002	0.490	0.119	1.084	0.853	1.043	0.975
1383938_at	BI286738	Transcribed locus	---	2.811	0.002	0.843	0.124	5.257	0.000	1.137	0.237
1390461_at	AI071102	Transcribed locus	---	0.702	0.002	1.057	0.093	0.452	0.009	0.779	0.447
1392518_at	AI577870	Transcribed locus	---	1.876	0.002	1.818	0.013	3.355	0.000	1.513	0.127
1383503_at	AI102821	Transcribed locus	---	0.617	0.002	0.715	0.030	0.540	0.043	0.840	0.574
1391106_at	BM385061	Transcribed locus	---	57.037	0.002	28.311	0.000	87.755	0.001	86.156	0.002
1385138_at	BF401469	Transcribed locus	---	0.231	0.002	0.610	0.015	0.326	0.007	0.631	0.011
1377994_at	AI501237	Transcribed locus	---	6.140	0.002	3.568	0.019	6.436	0.002	1.969	0.093
1382289_at	BI291954	Transcribed locus	---	0.569	0.002	0.197	0.000	0.960	0.733	0.240	0.018
1367540_at	AI044872	Transcribed locus	---	5.408	0.002	3.064	0.000	6.238	0.004	2.563	0.007
1395557_at	BF565718	Transcribed locus	---	4.434	0.002	4.128	0.001	4.423	0.012	3.224	0.010
1393728_at	AA964541	Transcribed locus	---	71.436	0.002	27.395	0.008	33.004	0.001	24.395	0.006
1390142_at	BE111888	Transcribed locus	---	2.461	0.002	0.890	0.294	3.025	0.001	1.216	0.752
1396770_at	BE099410	Transcribed locus	---	3.428	0.002	1.428	0.347	1.878	0.017	0.681	0.816
1391463_at	AI575264	Transcribed locus	---	8.933	0.002	5.004	0.000	14.629	0.000	14.723	0.006
1376520_at	BE117616	Transcribed locus	---	1.519	0.002	0.249	0.004	1.765	0.021	0.478	0.042
1372633_at	AI178531	Transcribed locus	---	0.466	0.002	0.276	0.002	0.387	0.001	0.447	0.007
1392600_a_at	AI176989	Transcribed locus	---	13.173	0.002	3.194	0.002	6.648	0.015	2.356	0.009
1397748_at	AW521583	Transcribed locus	---	0.512	0.002	0.484	0.001	0.710	0.271	0.708	0.083
1380137_at	BF406176	Transcribed locus	---	0.512	0.002	0.179	0.015	0.324	0.039	0.380	0.033
1394184_at	AI177746	Transcribed locus	---	1.297	0.002	0.896	0.975	3.079	0.046	1.124	0.074
1371707_at	AI235431	Transcribed locus	---	0.735	0.002	0.758	0.099	0.898	0.836	0.968	0.304
1373137_at	BI284360	Transcribed locus	---	0.604	0.002	0.835	0.181	0.489	0.009	0.778	0.036
1380119_at	AA996432	Transcribed locus	---	5.332	0.002	2.967	0.018	12.371	0.000	4.569	0.006
1383383_at	BE115992	Transcribed locus	---	1.379	0.002	1.567	0.001	1.395	0.008	1.489	0.019
1374542_at	AI409904	Transcribed locus	---	0.314	0.002	1.978	0.818	0.356	0.003	1.770	0.990

1398561_at	BI302791	Transcribed locus	---	6.568	0.002	1.366	0.016	9.396	0.000	1.981	0.016
1394399_at	AW523958	Transcribed locus	---	3.120	0.002	1.791	0.025	1.934	0.009	1.049	0.901
1376672_at	AW533083	Transcribed locus	---	2.718	0.002	0.648	0.020	3.457	0.003	0.815	0.123
1388447_at	AA800701	Transcribed locus	---	0.334	0.002	0.357	0.009	0.250	0.004	0.377	0.001
1398620_at	BF397903	Transcribed locus	---	7.046	0.002	2.397	0.045	11.908	0.001	3.476	0.026
1383511_at	BF409024	Transcribed locus	---	0.361	0.002	0.720	0.004	0.464	0.077	0.956	0.861
1389319_at	AA800719	Transcribed locus	---	0.546	0.002	0.709	0.007	0.575	0.010	0.720	0.025
1383486_at	AA926109	Transcribed locus	---	2.972	0.003	1.128	0.633	2.891	0.016	1.384	0.075
1374463_at	AI172068	Transcribed locus	---	1.331	0.003	1.874	0.001	1.075	0.440	1.569	0.026
1374337_at	AI408954	Transcribed locus	---	43.544	0.003	22.632	0.000	114.111	0.001	49.242	0.000
1376869_at	BE108193	Transcribed locus	---	2.209	0.003	0.790	0.045	2.083	0.016	1.125	0.065
1373164_at	AI012590	Transcribed locus	---	3.011	0.003	2.361	0.044	1.180	0.957	2.026	0.055
1374627_at	BF283727	Transcribed locus	---	10.625	0.003	7.756	0.001	8.497	0.010	8.243	0.001
1374578_at	AI409501	Transcribed locus	---	3.033	0.003	1.511	0.042	2.267	0.033	1.495	0.011
1397247_at	BI276505	Transcribed locus	---	10.343	0.003	9.110	0.001	10.576	0.015	4.668	0.001
1377103_at	AW525765	Transcribed locus	---	0.579	0.003	0.962	0.362	0.520	0.022	1.002	0.979
1382438_at	BF393639	Transcribed locus	---	0.265	0.003	0.598	0.127	0.205	0.011	0.290	0.043
1374968_at	AI599930	Transcribed locus	---	0.565	0.003	0.627	0.033	0.541	0.081	0.548	0.016
1379373_at	AI556457	Transcribed locus	---	0.217	0.003	0.057	0.006	0.209	0.004	0.099	0.021
1379269_at	BM385296	Transcribed locus	---	1.951	0.003	0.623	0.018	3.975	0.001	1.085	0.455
1377825_at	AI411841	Transcribed locus	---	1.349	0.003	0.939	0.292	1.060	0.855	0.881	0.206
1389395_at	BI275654	Transcribed locus	---	0.442	0.003	0.338	0.024	0.442	0.007	0.744	0.189
1392982_at	AA818059	Transcribed locus	---	0.274	0.003	0.337	0.004	0.137	0.010	0.241	0.005
1378211_s_at	BE114473	Transcribed locus	---	3.193	0.003	0.719	0.008	3.764	0.006	0.883	0.068
1396328_at	BF390586	Transcribed locus	---	0.461	0.003	0.184	0.001	0.368	0.004	0.238	0.023
1393193_at	BF522381	Transcribed locus	---	0.386	0.003	0.673	0.134	0.363	0.031	0.667	0.159
1389589_at	BE105898	Transcribed locus	---	0.511	0.004	0.499	0.065	0.560	0.014	0.799	0.237
1384163_at	BE103875	Transcribed locus	---	1.921	0.004	2.851	0.002	1.850	0.005	3.071	0.001
1374709_at	AI406795	Transcribed locus	---	1.196	0.004	0.629	0.080	1.002	0.925	0.641	0.041
1396307_at	BF522907	Transcribed locus	---	2.250	0.004	1.769	0.081	1.290	0.194	1.203	0.064
1379283_at	BE117687	Transcribed locus	---	0.468	0.004	0.857	0.061	0.510	0.003	0.677	0.007
1379267_a_at	AA924312	Transcribed locus	---	0.505	0.004	0.486	0.011	0.744	0.100	0.616	0.116
1377424_at	AI712672	Transcribed locus	---	0.109	0.004	0.081	0.004	0.228	0.003	0.183	0.027
1375979_at	AA945734	Transcribed locus	---	14.516	0.004	4.092	0.004	4.182	0.021	2.404	0.005
1391411_at	AI179941	Transcribed locus	---	7.657	0.004	2.815	0.002	6.423	0.002	3.008	0.010
1392125_at	BF390331	Transcribed locus	---	0.241	0.004	0.645	0.432	0.339	0.004	0.554	0.011
1374803_at	BG374219	Transcribed locus	---	0.731	0.004	0.821	0.024	0.746	0.045	0.981	0.239
1377879_at	BE102375	Transcribed locus	---	2.344	0.004	0.938	0.969	1.299	0.406	0.625	0.204
1373678_at	BE098848	Transcribed locus	---	3.285	0.004	3.310	0.003	4.456	0.001	3.609	0.001
1392716_at	BF282115	Transcribed locus	---	0.367	0.004	0.482	0.009	0.479	0.003	0.568	0.037
1376398_at	BF417784	Transcribed locus	---	0.131	0.004	0.065	0.008	0.083	0.001	0.109	0.043
1382462_at	BF290937	Transcribed locus	---	0.348	0.004	0.761	0.061	0.345	0.003	0.566	0.053
1389586_at	BE107169	Transcribed locus	---	2.681	0.004	0.938	0.720	2.209	0.002	1.144	0.215
1378421_at	BG671734	Transcribed locus	---	2.650	0.004	0.747	0.146	2.324	0.003	0.874	0.338
1372778_at	AA799420	Transcribed locus	---	2.595	0.004	2.121	0.003	2.839	0.001	2.390	0.001
1393050_at	BG664069	Transcribed locus	---	2.905	0.004	2.253	0.017	2.526	0.017	2.852	0.006
1377996_at	BE103975	Transcribed locus	---	1.850	0.004	1.270	0.366	1.728	0.012	1.661	0.144
1378496_at	BM384963	Transcribed locus	---	0.121	0.005	1.538	0.277	0.164	0.001	1.713	0.207
1390543_at	BF396416	Transcribed locus	---	0.301	0.005	0.259	0.001	0.278	0.059	0.331	0.027
1380200_at	AI102906	Transcribed locus	---	4.966	0.005	2.295	0.001	5.354	0.001	2.326	0.001
1374079_at	AW915055	Transcribed locus	---	0.690	0.005	0.434	0.001	0.705	0.191	0.534	0.033
1378373_at	BF522207	Transcribed locus	---	1.786	0.005	0.497	0.099	0.894	0.509	0.514	0.002
1390393_at	BF388422	Transcribed locus	---	0.383	0.005	0.695	0.418	1.040	0.376	1.789	0.044
1398368_at	AI406502	Transcribed locus	---	0.551	0.005	0.184	0.000	0.649	0.146	0.286	0.012
1376916_at	AW529183	Transcribed locus	---	4.450	0.005	4.699	0.004	1.715	0.076	3.161	0.056
1389150_at	AW524559	Transcribed locus	---	3.264	0.005	2.204	0.000	2.366	0.012	2.007	0.002
1378133_at	AW532618	Transcribed locus	---	2.934	0.005	14.676	0.000	1.489	0.080	8.822	0.000
1376395_at	AI145359	Transcribed locus	---	0.369	0.005	0.132	0.005	0.200	0.026	0.158	0.015
1390443_at	BE105661	Transcribed locus	---	0.716	0.005	0.752	0.506	0.709	0.004	1.066	0.672
1383795_at	BF521753	Transcribed locus	---	0.748	0.005	0.694	0.005	0.749	0.025	0.685	0.022
1391958_at	BE119699	Transcribed locus	---	5.504	0.005	2.787	0.013	12.923	0.003	3.628	0.000

1392761_at	BM389886	Transcribed locus	---	1.683	0.005	0.866	0.020	1.549	0.008	0.911	0.244
1376930_at	BI294860	Transcribed locus	---	0.757	0.005	0.634	0.001	0.629	0.016	0.672	0.020
1389465_at	AI231286	Transcribed locus	---	2.360	0.005	1.476	0.071	2.570	0.001	1.784	0.011
1399121_at	BE111600	Transcribed locus	---	2.087	0.005	1.352	0.035	1.917	0.019	1.219	0.019
1390856_at	BF289100	Transcribed locus	---	1.959	0.005	0.620	0.008	1.029	0.726	0.798	0.029
1391251_at	BI290666	Transcribed locus	---	0.464	0.005	0.942	0.926	0.463	0.002	0.794	0.942
1374160_at	BE111296	Transcribed locus	---	0.128	0.005	0.220	0.003	0.240	0.023	0.187	0.041
1396621_at	BF408910	Transcribed locus	---	0.293	0.005	0.438	0.082	0.279	0.023	0.970	0.926
1393528_at	AI059227	Transcribed locus	---	0.111	0.006	0.057	0.008	0.091	0.003	0.101	0.041
1384184_at	BE117485	Transcribed locus	---	5.056	0.006	2.605	0.000	1.769	0.006	3.016	0.005
1384460_at	AI072669	Transcribed locus	---	0.141	0.006	0.131	0.001	0.113	0.000	0.140	0.021
1390203_at	AI411149	Transcribed locus	---	0.387	0.006	1.295	0.208	0.457	0.006	0.822	0.300
1384242_at	BI303239	Transcribed locus	---	4.780	0.006	1.117	0.600	2.623	0.002	1.085	0.326
1374060_at	AI411374	Transcribed locus	---	0.329	0.006	0.269	0.016	0.422	0.083	0.249	0.026
1379301_at	BM384812	Transcribed locus	---	0.803	0.006	0.892	0.149	0.824	0.008	1.089	0.899
1379089_at	BM382838	Transcribed locus	---	3.486	0.006	1.757	0.044	2.715	0.012	1.753	0.023
1393699_at	BF391905	Transcribed locus	---	0.523	0.006	0.394	0.000	0.414	0.009	0.346	0.010
1383967_at	BI275739	Transcribed locus	---	0.221	0.006	0.853	0.815	0.072	0.001	0.972	0.638
1383484_at	AW920193	Transcribed locus	---	1.502	0.006	1.097	0.607	1.211	0.146	1.093	0.037
1383770_at	BE117323	Transcribed locus	---	4.436	0.006	1.940	0.007	3.205	0.031	1.375	0.024
1377411_at	BF404135	Transcribed locus	---	2.326	0.006	1.274	0.595	3.102	0.005	1.185	0.382
1379607_at	AW527767	Transcribed locus	---	0.282	0.006	0.393	0.054	0.372	0.012	0.302	0.011
1390841_at	BI290420	Transcribed locus	---	2.379	0.006	0.457	0.023	2.670	0.008	0.538	0.013
1372466_at	AI408571	Transcribed locus	---	3.944	0.006	2.535	0.003	5.889	0.008	2.513	0.006
1373438_at	BE329352	Transcribed locus	---	0.632	0.006	1.484	0.014	0.548	0.010	1.355	0.007
1385169_at	AI230598	Transcribed locus	---	1.397	0.006	1.192	0.059	1.262	0.009	1.069	0.487
1396441_at	BE108895	Transcribed locus	---	0.523	0.006	1.943	0.102	0.507	0.002	1.378	0.295
1389687_at	BI273981	Transcribed locus	---	0.250	0.006	0.176	0.000	0.297	0.003	0.356	0.018
1377236_at	BF405622	Transcribed locus	---	1.675	0.006	1.177	0.074	1.258	0.281	1.164	0.046
1371575_at	BF281185	Transcribed locus	---	1.934	0.006	1.199	0.026	1.718	0.140	1.195	0.281
1386195_x_at	AI176775	Transcribed locus	---	1.983	0.006	0.764	0.024	1.254	0.032	0.722	0.045
1371995_at	AI599225	Transcribed locus	---	0.718	0.006	1.452	0.006	0.732	0.013	1.014	0.223
1389706_at	AI007639	Transcribed locus	---	0.201	0.007	0.169	0.006	0.196	0.031	0.130	0.006
1377704_at	BE117155	Transcribed locus	---	1.298	0.007	1.307	0.628	1.290	0.048	1.243	0.152
1372850_at	AA799464	Transcribed locus	---	1.806	0.007	1.366	0.023	3.137	0.005	1.920	0.006
1382604_at	BE117925	Transcribed locus	---	0.406	0.007	0.565	0.034	0.332	0.000	0.606	0.018
1389718_at	AA956417	Transcribed locus	---	4.918	0.007	2.310	0.123	2.165	0.009	0.862	0.496
1383458_at	BF403759	Transcribed locus	---	0.666	0.007	0.294	0.005	0.881	0.226	0.376	0.032
1390832_at	BI294696	Transcribed locus	---	7.908	0.007	3.664	0.000	6.970	0.017	3.825	0.001
1397617_at	BM382925	Transcribed locus	---	1.329	0.007	1.477	0.024	0.781	0.470	1.186	0.115
1389474_at	AA818380	Transcribed locus	---	0.594	0.007	1.032	0.560	0.610	0.009	0.964	0.969
1375866_at	BF396191	Transcribed locus	---	3.301	0.007	1.938	0.005	1.657	0.168	1.896	0.009
1386252_at	BE349825	Transcribed locus	---	2.643	0.007	3.928	0.032	3.195	0.025	3.248	0.038
1379371_at	BF284791	Transcribed locus	---	9.103	0.007	6.541	0.000	10.197	0.005	5.111	0.009
1388561_at	AI412886	Transcribed locus	---	0.428	0.007	0.268	0.010	0.662	0.110	0.199	0.028
1391550_at	BE108780	Transcribed locus	---	1.664	0.007	0.995	0.109	2.610	0.017	1.208	0.027
1374736_at	AI172004	Transcribed locus	---	2.305	0.007	2.360	0.002	2.415	0.003	2.096	0.000
1373993_at	AA799470	Transcribed locus	---	0.657	0.008	0.580	0.002	0.596	0.010	0.553	0.001
1390457_at	BM385762	Transcribed locus	---	0.409	0.008	0.294	0.001	0.287	0.028	0.736	0.066
1377925_at	BE105762	Transcribed locus	---	2.176	0.008	1.899	0.025	1.275	0.340	1.438	0.022
1373843_at	BE107419	Transcribed locus	---	14.548	0.008	3.128	0.017	46.872	0.008	15.516	0.002
1390708_at	AI012518	Transcribed locus	---	3.171	0.008	1.978	0.019	2.438	0.031	1.878	0.009
1378603_at	BM387125	Transcribed locus	---	0.353	0.008	0.225	0.020	0.360	0.010	0.239	0.055
1374694_at	BF284602	Transcribed locus	---	0.742	0.008	0.516	0.041	1.002	0.138	0.700	0.136
1380400_at	BF402498	Transcribed locus	---	2.203	0.008	0.977	0.818	1.281	0.532	1.756	0.051
1393273_at	AW533027	Transcribed locus	---	0.269	0.008	0.310	0.004	0.229	0.024	0.327	0.006
1374752_at	AI408734	Transcribed locus	---	3.206	0.008	1.437	0.054	1.950	0.040	1.273	0.320
1394797_at	BI276075	Transcribed locus	---	2.215	0.008	1.321	0.095	1.493	0.399	1.647	0.110
1391828_at	AI030836	Transcribed locus	---	1.893	0.008	1.793	0.000	2.270	0.023	1.916	0.016
1391808_at	AI535140	Transcribed locus	---	3.738	0.008	2.707	0.025	5.747	0.009	3.345	0.073
1372515_at	BI281177	Transcribed locus	---	0.408	0.008	0.562	0.001	0.398	0.001	0.361	0.000

1377456_at	BE116775	Transcribed locus	---	0.418	0.008	0.312	0.023	0.610	0.006	0.353	0.129
1383929_at	AI230265	Transcribed locus	---	0.533	0.008	0.469	0.001	0.992	0.408	0.725	0.291
1390709_at	AI102364	Transcribed locus	---	2.385	0.008	1.683	0.025	1.817	0.013	1.501	0.089
1383786_at	AW915417	Transcribed locus	---	3.152	0.008	4.005	0.004	1.712	0.086	1.329	0.612
1382330_at	BE116838	Transcribed locus	---	0.550	0.008	0.536	0.038	0.554	0.016	0.623	0.098
1382497_at	AA875457	Transcribed locus	---	0.559	0.008	0.456	0.038	0.834	0.065	0.629	0.062
1390339_at	BE099435	Transcribed locus	---	0.437	0.008	0.522	0.021	0.226	0.005	0.494	0.029
1377757_at	AA858978	Transcribed locus	---	0.716	0.009	0.513	0.054	0.709	0.022	0.521	0.002
1373656_at	AI713313	Transcribed locus	---	0.304	0.009	0.318	0.002	0.280	0.005	0.364	0.001
1377790_at	BE115859	Transcribed locus	---	1.457	0.009	1.733	0.027	1.408	0.013	1.868	0.005
1379487_at	BF287099	Transcribed locus	---	2.195	0.009	0.638	0.067	1.950	0.421	1.014	0.594
1384699_at	BM384930	Transcribed locus	---	0.405	0.009	0.867	0.423	0.425	0.005	0.913	0.918
1397928_at	BF389357	Transcribed locus	---	0.376	0.009	0.604	0.056	0.882	0.734	0.994	0.623
1376066_at	AI103572	Transcribed locus	---	6.489	0.009	2.110	0.007	4.662	0.008	2.976	0.005
1395233_at	BE107671	Transcribed locus	---	0.542	0.009	0.940	0.846	0.341	0.024	0.963	0.968
1375793_at	BI295700	Transcribed locus	---	3.871	0.009	0.793	0.141	3.071	0.008	0.804	0.340
1392592_at	AI137045	Transcribed locus	---	4.348	0.009	2.546	0.014	6.254	0.006	4.316	0.014
1378070_at	BE099891	Transcribed locus	---	0.408	0.009	0.252	0.008	0.395	0.016	0.393	0.021
1379085_at	BF396507	Transcribed locus	---	1.217	0.009	1.099	0.223	1.272	0.067	0.652	0.093
1379719_at	AI408386	Transcribed locus	---	0.451	0.009	0.668	0.015	0.351	0.165	0.798	0.047
1374809_at	BG672598	Transcribed locus	---	0.542	0.009	0.506	0.003	0.857	0.029	0.634	0.000
1390907_at	AI145039	Transcribed locus	---	0.668	0.009	0.562	0.009	0.589	0.198	0.498	0.019
1392995_at	BG669396	Transcribed locus	---	0.807	0.009	0.976	0.204	0.639	0.002	0.865	0.587
1390895_at	AA957047	Transcribed locus	---	3.273	0.009	1.883	0.057	4.109	0.006	2.580	0.026
1380858_at	BE120316	Transcribed locus	---	0.423	0.009	0.417	0.023	0.469	0.084	0.242	0.008
1397871_at	AI144643	Transcribed locus	---	0.421	0.009	0.642	0.003	0.572	0.245	0.595	0.004
1380229_at	AW530004	Transcribed locus	---	14.165	0.009	54.328	0.001	9.311	0.003	26.059	0.000
1372258_at	AI102935	Transcribed locus	---	0.638	0.010	0.382	0.000	0.761	0.011	0.429	0.001
1397765_at	BF406754	Transcribed locus	---	0.553	0.010	0.314	0.001	0.646	0.063	0.582	0.010
1385379_at	AA998187	Transcribed locus	---	2.214	0.010	0.301	0.059	1.487	0.038	0.586	0.583
1376966_at	BE108930	Transcribed locus	---	0.312	0.010	0.298	0.001	0.465	0.019	0.326	0.002
1398393_at	BF414412	Transcribed locus	---	4.589	0.010	2.182	0.034	14.960	0.007	3.569	0.019
1390324_at	BE101809	Transcribed locus	---	0.092	0.010	0.103	0.002	0.065	0.011	0.251	0.056
1373594_at	BE097279	Transcribed locus	---	0.689	0.010	0.527	0.039	0.542	0.067	0.658	0.052
1372582_at	AI407847	Transcribed locus	---	1.210	0.010	1.240	0.245	1.375	0.046	1.322	0.008
1376590_at	AA818732	Transcribed locus	---	0.524	0.010	0.209	0.028	0.597	0.069	0.291	0.092
1398615_at	BG379594	Transcribed locus	---	2.092	0.010	1.341	0.043	1.628	0.027	1.269	0.034
1383527_at	BF418522	Transcribed locus	---	2.157	0.010	0.766	0.446	0.671	0.476	1.000	0.350
1381084_at	AA964619	Transcribed locus	---	0.563	0.010	0.527	0.062	0.924	0.881	1.010	0.492
1390400_a_at	BM390922	Transcribed locus	---	2.172	0.010	0.744	0.158	1.413	0.089	0.641	0.001
1378346_at	AI385237	Transcribed locus	---	3.067	0.010	1.601	0.170	2.323	0.020	1.531	0.405
1374885_at	AI172278	Transcribed locus	---	0.296	0.010	0.187	0.000	0.471	0.005	0.202	0.001
1377651_at	AI577848	Transcribed locus	---	3.009	0.011	1.235	0.820	1.020	0.072	0.974	0.404
1381400_at	AI137973	Transcribed locus	---	0.517	0.011	1.077	0.554	0.355	0.003	0.997	0.947
1398969_at	BE104323	Transcribed locus	---	1.474	0.011	0.820	0.168	1.248	0.212	0.797	0.083
1382440_at	AI410813	Transcribed locus	---	0.453	0.011	0.301	0.000	0.310	0.004	0.340	0.047
1375051_at	BE104792	Transcribed locus	---	1.474	0.011	0.943	0.074	1.716	0.107	1.000	0.984
1376292_at	BM383423	Transcribed locus	---	6.332	0.011	6.194	0.002	3.632	0.025	2.998	0.013
1373351_at	BI286775	Transcribed locus	---	2.244	0.011	0.841	0.901	2.670	0.007	1.248	0.327
1373197_at	AI578263	Transcribed locus	---	4.028	0.011	1.399	0.055	25.420	0.001	3.381	0.021
1388986_at	AI598339	Transcribed locus	---	9.356	0.011	2.865	0.010	8.003	0.007	2.255	0.011
1376006_at	BG373799	Transcribed locus	---	4.939	0.011	5.059	0.002	4.796	0.011	3.243	0.001
1383499_at	BG371995	Transcribed locus	---	0.595	0.011	0.458	0.016	0.512	0.081	0.356	0.009
1392876_at	BG375098	Transcribed locus	---	2.936	0.011	7.562	0.006	3.118	0.022	5.913	0.001
1391979_at	AA851345	Transcribed locus	---	0.524	0.012	0.164	0.000	0.526	0.013	0.180	0.010
1393561_at	BF396511	Transcribed locus	---	1.772	0.012	0.625	0.004	2.209	0.001	0.898	0.069
1398578_at	AI102019	Transcribed locus	---	1.961	0.012	1.131	0.926	1.046	0.527	0.732	0.505
1378292_at	BE096367	Transcribed locus	---	1.979	0.012	0.775	0.052	1.996	0.013	1.641	0.117
1397572_at	BE109994	Transcribed locus	---	0.642	0.012	0.570	0.005	0.701	0.030	0.620	0.007
1388771_at	BG668182	Transcribed locus	---	1.570	0.012	1.171	0.154	1.534	0.013	1.135	0.046
1378210_at	BE114473	Transcribed locus	---	2.046	0.012	0.815	0.140	2.490	0.003	1.021	0.860

1378457_at	AI179450	Transcribed locus	---	0.353	0.012	0.874	0.557	0.562	0.054	0.894	0.351
1378672_at	BG381207	Transcribed locus	---	0.316	0.012	0.512	0.125	0.797	0.341	0.542	0.009
1398497_at	BF391243	Transcribed locus	---	0.166	0.012	0.424	0.024	0.314	0.008	0.665	0.112
1397888_at	BM389787	Transcribed locus	---	0.641	0.012	0.524	0.000	0.775	0.082	0.303	0.003
1391866_at	AI014116	Transcribed locus	---	1.420	0.012	2.531	0.085	0.888	0.745	1.275	0.271
1377221_at	AI411226	Transcribed locus	---	1.252	0.013	0.441	0.003	1.485	0.007	0.321	0.012
1390727_at	BF398618	Transcribed locus	---	1.305	0.013	0.625	0.038	1.290	0.291	0.833	0.072
1389584_at	AI101266	Transcribed locus	---	0.261	0.013	0.131	0.005	0.127	0.001	0.091	0.030
1384268_at	AW435305	Transcribed locus	---	0.080	0.013	0.134	0.000	0.212	0.022	0.153	0.002
1391672_at	BF399539	Transcribed locus	---	0.337	0.013	0.053	0.000	0.297	0.010	0.110	0.015
1392762_at	BF559727	Transcribed locus	---	0.640	0.013	0.618	0.086	0.518	0.002	0.814	0.245
1377045_at	BG372832	Transcribed locus	---	0.484	0.013	0.217	0.003	0.740	0.103	0.373	0.012
1378091_at	AW528824	Transcribed locus	---	0.681	0.013	0.281	0.054	0.631	0.021	0.339	0.051
1376205_at	BI286851	Transcribed locus	---	2.213	0.013	1.440	0.016	2.403	0.003	1.757	0.016
1395536_at	BG673248	Transcribed locus	---	0.449	0.014	0.139	0.021	0.538	0.010	0.178	0.026
1395705_at	BF412848	Transcribed locus	---	0.454	0.014	0.376	0.072	0.669	0.662	0.343	0.094
1376996_at	AI556018	Transcribed locus	---	1.702	0.014	1.431	0.090	1.746	0.013	1.324	0.071
1388915_at	BI295753	Transcribed locus	---	5.128	0.014	1.490	0.089	6.296	0.000	2.540	0.009
1382381_at	AA818480	Transcribed locus	---	1.808	0.014	1.612	0.016	2.127	0.015	1.888	0.008
1379873_at	BI276971	Transcribed locus	---	0.638	0.014	1.048	0.547	0.630	0.043	1.122	0.638
1379382_at	AI144865	Transcribed locus	---	2.023	0.014	1.431	0.220	1.345	0.045	1.482	0.176
1398707_at	BE108582	Transcribed locus	---	0.245	0.014	0.114	0.001	0.203	0.015	0.277	0.035
1389602_at	BF396759	Transcribed locus	---	0.597	0.014	0.512	0.005	0.640	0.001	0.658	0.004
1390364_at	AI044316	Transcribed locus	---	6.074	0.014	3.891	0.002	7.136	0.006	1.946	0.043
1391802_at	BE107950	Transcribed locus	---	0.513	0.014	0.636	0.153	0.338	0.008	0.581	0.190
1380831_at	AI237035	Transcribed locus	---	1.383	0.014	1.523	0.077	1.201	0.252	1.231	0.698
1391003_at	BE117528	Transcribed locus	---	1.403	0.014	1.158	0.469	1.424	0.009	0.982	0.725
1376065_at	AI058889	Transcribed locus	---	0.547	0.014	2.538	0.005	0.378	0.013	2.400	0.001
1377273_at	BF389637	Transcribed locus	---	0.338	0.014	0.307	0.012	0.541	0.026	0.354	0.020
1374243_at	AI102744	Transcribed locus	---	0.623	0.014	0.500	0.002	0.808	0.265	0.702	0.004
1393052_at	BM392406	Transcribed locus	---	1.822	0.014	3.125	0.000	0.980	0.359	2.263	0.002
1398978_at	AA850525	Transcribed locus	---	0.654	0.014	0.545	0.001	0.770	0.217	0.747	0.000
1392026_at	BF391823	Transcribed locus	---	0.410	0.014	0.797	0.120	0.828	0.044	0.578	0.014
1373515_at	BI275737	Transcribed locus	---	0.536	0.015	0.558	0.004	0.642	0.045	0.682	0.019
1373679_at	AA946467	Transcribed locus	---	2.481	0.015	8.726	0.000	1.191	0.297	10.298	0.002
1390444_at	AI044433	Transcribed locus	---	0.630	0.015	0.434	0.147	1.051	0.103	0.448	0.036
1372347_at	BI289462	Transcribed locus	---	1.846	0.015	2.111	0.002	2.083	0.192	1.735	0.002
1389246_at	BF282414	Transcribed locus	---	1.846	0.015	1.692	0.026	1.727	0.026	1.598	0.030
1384882_at	AI229056	Transcribed locus	---	3.184	0.015	6.414	0.000	1.539	0.084	3.893	0.000
1382705_at	BE116909	Transcribed locus	---	0.577	0.015	0.539	0.120	0.813	0.138	0.424	0.055
1382610_at	AA957105	Transcribed locus	---	2.232	0.015	1.178	0.927	3.864	0.005	1.920	0.030
1374896_at	AI101385	Transcribed locus	---	0.495	0.015	0.296	0.000	0.695	0.031	0.373	0.020
1384892_at	AI029798	Transcribed locus	---	2.179	0.015	1.117	0.288	2.111	0.048	1.671	0.009
1372390_at	AI710604	Transcribed locus	---	0.810	0.015	0.565	0.003	0.918	0.200	0.624	0.005
1373269_at	AI407751	Transcribed locus	---	0.400	0.015	0.709	0.044	0.438	0.186	0.649	0.088
1383894_at	BI289486	Transcribed locus	---	5.541	0.015	10.412	0.005	1.150	0.710	3.820	0.012
1389613_at	AI234712	Transcribed locus	---	3.299	0.016	0.464	0.013	3.211	0.011	0.513	0.015
1372937_at	AI012601	Transcribed locus	---	1.918	0.016	1.001	0.959	1.376	0.041	0.994	0.969
1389794_at	AI044984	Transcribed locus	---	0.531	0.016	0.304	0.007	0.626	0.052	0.463	0.032
1373736_at	AI178446	Transcribed locus	---	0.625	0.016	0.368	0.001	0.634	0.010	0.644	0.024
1383444_at	AA964069	Transcribed locus	---	0.387	0.016	0.279	0.000	0.508	0.027	0.359	0.025
1381275_at	AI179171	Transcribed locus	---	2.130	0.016	0.984	0.992	1.885	0.032	1.169	0.333
1377748_at	BF410460	Transcribed locus	---	0.676	0.016	0.970	0.379	0.804	0.019	1.109	0.028
1375523_at	BE108178	Transcribed locus	---	0.564	0.016	0.173	0.000	0.614	0.043	0.216	0.017
1382777_at	BE108796	Transcribed locus	---	4.486	0.016	1.468	0.292	3.401	0.091	1.778	0.133
1390134_at	AI411274	Transcribed locus	---	3.325	0.016	1.665	0.008	4.125	0.012	2.171	0.012
1379310_at	AI101880	Transcribed locus	---	2.899	0.016	2.235	0.002	2.193	0.057	1.641	0.011
1375575_at	BF403410	Transcribed locus	---	0.654	0.016	0.519	0.007	0.560	0.002	0.403	0.033
1383660_at	AI713166	Transcribed locus	---	0.658	0.016	0.712	0.144	0.719	0.014	0.592	0.011
1375962_at	BE102925	Transcribed locus	---	2.113	0.016	1.673	0.085	1.994	0.064	1.197	0.199
1374480_at	BE107255	Transcribed locus	---	1.931	0.016	0.992	0.901	2.494	0.001	1.300	0.067

1373310_at	BF396512	Transcribed locus	---	1.283	0.016	1.272	0.073	1.449	0.012	1.473	0.019
1391445_at	AI009603	Transcribed locus	---	0.588	0.016	1.273	0.563	1.139	0.764	1.376	0.058
1398622_at	AI703807	Transcribed locus	---	2.643	0.016	1.663	0.465	1.379	0.322	1.358	0.827
1375873_at	AI231506	Transcribed locus	---	2.032	0.016	1.675	0.017	2.029	0.068	1.355	0.072
1383999_at	AW527651	Transcribed locus	---	2.607	0.016	1.105	0.865	4.895	0.005	1.645	0.016
1378391_at	AI511069	Transcribed locus	---	0.477	0.016	0.438	0.039	0.619	0.111	0.611	0.025
1372642_at	BE113397	Transcribed locus	---	0.640	0.016	1.324	0.006	0.590	0.003	1.131	0.053
1372964_at	BI294751	Transcribed locus	---	3.344	0.017	0.838	0.523	1.889	0.069	0.702	0.070
1374750_at	AI172313	Transcribed locus	---	2.260	0.017	3.161	0.000	2.110	0.001	2.647	0.000
1389640_at	BM391811	Transcribed locus	---	1.639	0.017	1.745	0.018	1.289	0.145	1.237	0.080
1377322_at	BE117290	Transcribed locus	---	1.550	0.017	0.802	0.646	1.763	0.057	0.985	0.876
1384267_at	BF547003	Transcribed locus	---	1.455	0.017	1.519	0.213	0.762	0.227	1.921	0.080
1378861_at	BE105498	Transcribed locus	---	0.455	0.017	0.117	0.002	1.370	0.353	0.155	0.002
1375723_at	AI385171	Transcribed locus	---	0.652	0.017	0.534	0.042	0.648	0.023	0.547	0.039
1378166_at	BE096995	Transcribed locus	---	1.111	0.017	0.882	0.408	1.750	0.017	1.103	0.901
1396119_at	AW534209	Transcribed locus	---	0.422	0.017	0.203	0.000	1.044	0.251	0.455	0.068
1391670_at	BI295819	Transcribed locus	---	0.516	0.017	0.393	0.041	0.424	0.017	0.500	0.073
1389804_at	BF392605	Transcribed locus	---	4.663	0.017	1.454	0.198	7.958	0.009	1.546	0.153
1381579_at	BF386959	Transcribed locus	---	2.881	0.017	0.845	0.040	2.354	0.037	0.765	0.035
1394475_at	BE096857	Transcribed locus	---	0.332	0.017	0.241	0.003	0.141	0.018	0.072	0.018
1398424_at	AA799515	Transcribed locus	---	0.325	0.018	0.467	0.013	0.387	0.004	0.485	0.049
1391822_at	AW253356	Transcribed locus	---	0.659	0.018	0.556	0.022	0.743	0.271	0.717	0.295
1378668_at	BG672426	Transcribed locus	---	1.759	0.018	0.794	0.870	2.266	0.018	0.910	0.396
1381534_at	BI278449	Transcribed locus	---	2.918	0.018	4.246	0.000	3.409	0.022	6.286	0.005
1390391_at	BF283381	Transcribed locus	---	4.468	0.018	15.686	0.000	13.151	0.019	10.101	0.001
1373097_at	BF282125	Transcribed locus	---	0.663	0.018	1.081	0.358	0.810	0.922	0.700	0.337
1372848_at	BI296915	Transcribed locus	---	0.192	0.018	0.368	0.005	0.182	0.021	0.279	0.011
1379092_at	AI712997	Transcribed locus	---	2.336	0.019	1.677	0.031	1.751	0.029	1.310	0.131
1390145_at	AW524532	Transcribed locus	---	0.587	0.019	0.322	0.000	0.997	0.615	0.534	0.028
1380174_at	BE116115	Transcribed locus	---	1.092	0.019	0.453	0.000	1.219	0.326	0.594	0.000
1389365_at	AI228291	Transcribed locus	---	4.057	0.019	2.604	0.000	7.752	0.000	3.706	0.007
1392777_at	BF287676	Transcribed locus	---	14.628	0.020	6.337	0.002	12.097	0.015	6.652	0.002
1377451_at	AI599250	Transcribed locus	---	1.361	0.020	1.549	0.068	1.097	0.582	1.003	0.978
1378112_at	BI304019	Transcribed locus	---	1.732	0.020	1.138	0.254	1.472	0.064	1.052	0.109
1373082_at	AA893743	Transcribed locus	---	2.371	0.020	2.017	0.002	2.199	0.027	1.857	0.006
1376877_at	AA893164	Transcribed locus	---	9.519	0.020	3.108	0.016	12.874	0.035	1.668	0.091
1392869_at	AI111868	Transcribed locus	---	0.266	0.020	0.868	0.128	0.236	0.026	0.997	0.221
1389713_at	AI602851	Transcribed locus	---	1.478	0.020	0.767	0.007	1.394	0.052	0.832	0.195
1374466_at	AI715484	Transcribed locus	---	0.575	0.020	0.266	0.005	0.917	0.970	0.443	0.001
1372236_at	BI279079	Transcribed locus	---	2.053	0.020	0.668	0.009	3.297	0.000	0.557	0.033
1376593_at	BF283990	Transcribed locus	---	2.128	0.020	2.051	0.016	1.201	0.243	1.387	0.079
1377084_at	BE106598	Transcribed locus	---	0.655	0.020	0.933	0.116	0.514	0.031	0.865	0.486
1386621_at	AW142419	Transcribed locus	---	2.251	0.021	1.590	0.052	2.038	0.020	1.192	0.093
1375585_at	BE111820	Transcribed locus	---	2.521	0.021	1.723	0.074	5.143	0.016	1.889	0.006
1394097_at	AA849706	Transcribed locus	---	0.525	0.021	0.970	0.420	0.413	0.001	0.654	0.015
1373070_at	AI406379	Transcribed locus	---	1.268	0.021	0.658	0.008	1.162	0.037	0.689	0.020
1390024_at	AI237685	Transcribed locus	---	4.018	0.022	1.818	0.152	13.952	0.000	4.139	0.001
1374760_at	BG374448	Transcribed locus	---	4.083	0.022	2.577	0.014	3.681	0.117	2.621	0.003
1397417_at	BG671626	Transcribed locus	---	1.391	0.022	1.101	0.087	1.734	0.024	1.214	0.107
1374935_at	AI412099	Transcribed locus	---	2.030	0.022	1.036	0.751	1.376	0.369	0.892	0.382
1374064_at	BG376942	Transcribed locus	---	0.590	0.022	0.967	0.594	0.757	0.005	0.902	0.894
1378018_at	BE098045	Transcribed locus	---	0.402	0.022	0.402	0.001	0.280	0.000	0.375	0.019
1389159_at	BM385437	Transcribed locus	---	0.391	0.022	0.422	0.004	0.369	0.009	0.411	0.000
1382023_at	AI407113	Transcribed locus	---	0.618	0.022	0.875	0.394	0.298	0.025	0.682	0.320
1399064_at	AI009591	Transcribed locus	---	0.459	0.022	0.674	0.011	0.601	0.074	0.582	0.072
1372921_at	AI073219	Transcribed locus	---	0.409	0.023	1.164	0.729	0.286	0.003	1.002	0.991
1388662_at	BF392884	Transcribed locus	---	1.899	0.023	1.466	0.131	1.779	0.083	1.187	0.243
1377893_at	BM390475	Transcribed locus	---	1.981	0.023	0.313	0.014	4.180	0.000	0.758	0.108
1373761_at	AI176129	Transcribed locus	---	1.510	0.023	4.497	0.002	2.617	0.015	2.985	0.001
1384435_at	AA964258	Transcribed locus	---	0.586	0.023	0.844	0.619	0.593	0.214	0.792	0.351
1383645_at	BF411062	Transcribed locus	---	0.362	0.023	0.234	0.004	0.467	0.065	0.216	0.008

1377376_at	BF397554	Transcribed locus	---	1.145	0.023	1.059	0.561	1.580	0.121	1.361	0.374
1381981_at	BE101088	Transcribed locus	---	0.772	0.023	0.879	0.327	1.026	0.638	1.039	0.970
1372449_at	AW253616	Transcribed locus	---	0.610	0.023	0.193	0.000	0.738	0.097	0.330	0.000
1380193_at	BM387449	Transcribed locus	---	1.998	0.023	0.396	0.618	1.303	0.025	0.394	0.587
1390463_at	BG378294	Transcribed locus	---	0.506	0.023	0.440	0.004	0.511	0.001	0.596	0.006
1373225_at	AI102618	Transcribed locus	---	2.078	0.023	1.315	0.010	2.215	0.000	1.267	0.036
1395751_at	AI501450	Transcribed locus	---	1.598	0.024	1.110	0.001	0.895	0.996	1.813	0.087
1390669_at	AI639410	Transcribed locus	---	1.447	0.024	0.799	0.024	2.205	0.002	1.072	0.860
1388999_at	BF397907	Transcribed locus	---	1.217	0.024	1.393	0.028	1.071	0.468	1.606	0.043
1384678_at	BF559356	Transcribed locus	---	1.556	0.024	1.134	0.636	1.233	0.363	1.662	0.110
1385841_at	BM383983	Transcribed locus	---	0.195	0.024	0.192	0.007	0.460	0.032	0.466	0.020
1372884_at	BG381486	Transcribed locus	---	0.498	0.024	0.313	0.006	0.373	0.009	0.559	0.012
1373998_at	BM389853	Transcribed locus	---	5.861	0.024	1.300	0.313	6.770	0.024	1.672	0.051
1396850_at	AI501434	Transcribed locus	---	1.782	0.024	1.129	0.892	1.618	0.172	0.980	0.929
1375647_at	BG671943	Transcribed locus	---	1.488	0.024	1.248	0.220	1.413	0.005	1.230	0.656
1378134_at	BI291629	Transcribed locus	---	1.821	0.024	0.767	0.008	0.922	0.932	0.656	0.042
1393732_at	AI071024	Transcribed locus	---	1.197	0.024	1.003	0.670	1.288	0.007	1.194	0.958
1394467_at	AI511367	Transcribed locus	---	0.106	0.024	0.050	0.043	0.472	0.034	0.044	0.047
1373176_at	AA943208	Transcribed locus	---	3.171	0.024	1.523	0.027	3.714	0.032	1.531	0.264
1371601_at	BE107520	Transcribed locus	---	0.788	0.024	0.689	0.008	0.713	0.009	0.618	0.027
1374653_at	BF413204	Transcribed locus	---	0.545	0.024	0.891	0.913	0.798	0.048	0.917	0.851
1382304_at	AW528823	Transcribed locus	---	0.847	0.025	0.360	0.038	1.062	0.368	0.546	0.012
1392653_at	BE118116	Transcribed locus	---	7.540	0.025	2.353	0.017	3.994	0.033	2.363	0.047
1389698_at	AI010312	Transcribed locus	---	0.606	0.025	0.376	0.002	0.683	0.346	0.362	0.026
1393117_at	BI286900	Transcribed locus	---	0.692	0.025	0.652	0.008	0.545	0.075	0.643	0.146
1371529_at	BF289001	Transcribed locus	---	2.352	0.025	1.286	0.081	3.627	0.002	1.876	0.043
1390351_at	AI231225	Transcribed locus	---	1.712	0.025	0.652	0.017	1.629	0.053	0.784	0.068
1397679_at	BF550199	Transcribed locus	---	1.406	0.025	1.213	0.028	1.365	0.237	1.032	0.550
1371485_at	BI283695	Transcribed locus	---	1.664	0.025	1.376	0.361	0.701	0.657	1.035	0.063
1384671_at	AI059958	Transcribed locus	---	8.231	0.025	1.527	0.177	1.829	0.160	0.772	0.395
1373986_at	AI410107	Transcribed locus	---	2.154	0.025	2.994	0.001	0.971	0.818	2.381	0.002
1391702_at	BM389392	Transcribed locus	---	0.649	0.026	0.488	0.001	0.857	0.737	0.611	0.013
1390470_at	BE107044	Transcribed locus	---	1.728	0.026	0.535	0.004	1.214	0.194	0.708	0.368
1378590_at	AW527807	Transcribed locus	---	1.456	0.026	1.087	0.612	1.489	0.054	0.770	0.782
1371726_at	AW433870	Transcribed locus	---	1.404	0.026	1.002	0.087	0.982	0.489	1.213	0.248
1373545_at	AI406964	Transcribed locus	---	0.637	0.026	0.256	0.075	0.633	0.026	0.370	0.072
1397731_at	AA998060	Transcribed locus	---	1.948	0.026	1.602	0.099	2.394	0.026	1.840	0.076
1377884_at	BG671879	Transcribed locus	---	1.251	0.026	1.055	0.705	0.936	0.051	1.075	0.073
1396297_at	BG374359	Transcribed locus	---	4.006	0.026	1.211	0.063	5.120	0.007	1.687	0.125
1394290_at	BG669921	Transcribed locus	---	3.078	0.026	1.977	0.051	1.976	0.059	2.122	0.243
1372225_at	BE119802	Transcribed locus	---	1.706	0.026	1.255	0.041	4.066	0.003	1.397	0.015
1388743_at	BI297291	Transcribed locus	---	0.508	0.026	0.109	0.001	0.624	0.072	0.174	0.022
1394942_at	AI408528	Transcribed locus	---	1.089	0.027	1.022	0.882	1.002	0.749	0.979	0.846
1371616_at	AW524495	Transcribed locus	---	2.306	0.027	0.591	0.058	3.043	0.014	0.873	0.437
1376357_at	AA875143	Transcribed locus	---	1.340	0.027	0.696	0.011	1.487	0.092	0.851	0.007
1382313_at	AI511408	Transcribed locus	---	0.660	0.027	0.779	0.061	0.746	0.367	0.707	0.076
1393482_at	AI045330	Transcribed locus	---	0.099	0.027	0.032	0.000	0.092	0.002	0.076	0.012
1378222_at	BF389961	Transcribed locus	---	1.416	0.027	0.630	0.055	1.377	0.039	1.010	0.883
1373328_at	AI009678	Transcribed locus	---	0.728	0.027	0.693	0.081	0.504	0.003	0.984	0.145
1379379_at	BF392753	Transcribed locus	---	7.234	0.027	1.455	0.411	14.214	0.000	3.652	0.006
1383363_at	BF418817	Transcribed locus	---	0.369	0.027	2.435	0.025	0.414	0.017	3.392	0.334
1374350_at	BM382988	Transcribed locus	---	0.329	0.028	0.176	0.000	0.473	0.061	0.292	0.016
1381036_at	AW434394	Transcribed locus	---	2.118	0.028	1.540	0.031	0.993	0.226	1.214	0.376
1390885_at	AW535696	Transcribed locus	---	1.965	0.028	0.870	0.173	1.272	0.035	0.727	0.084
1380365_at	BF403932	Transcribed locus	---	0.600	0.028	0.673	0.042	0.701	0.072	0.739	0.004
1396813_at	AW528749	Transcribed locus	---	2.150	0.028	0.994	0.826	3.046	0.030	1.112	0.429
1390356_at	AW535401	Transcribed locus	---	1.528	0.028	1.063	0.128	1.723	0.005	1.383	0.008
1373311_at	BF405581	Transcribed locus	---	1.586	0.028	3.223	0.020	1.048	0.728	2.201	0.040
1376842_at	BF395964	Transcribed locus	---	3.740	0.028	2.471	0.007	3.077	0.048	2.457	0.010
1374435_at	AA996970	Transcribed locus	---	1.218	0.029	1.046	0.531	1.295	0.008	1.078	0.062
1391571_at	BG666079	Transcribed locus	---	0.671	0.029	0.886	0.143	0.663	0.019	0.948	0.791

1390962_at	BM385344	Transcribed locus	---	1.093	0.029	1.005	0.992	1.341	0.107	1.028	0.705
1384059_at	BE115159	Transcribed locus	---	0.517	0.029	0.289	0.015	0.492	0.032	0.460	0.020
1373497_at	BE109208	Transcribed locus	---	1.224	0.029	1.155	0.150	1.367	0.036	1.296	0.080
1389437_at	BF392952	Transcribed locus	---	0.525	0.029	0.297	0.001	0.393	0.151	0.392	0.001
1397300_at	BG371544	Transcribed locus	---	0.626	0.029	0.601	0.040	0.998	0.851	0.881	0.618
1397348_at	BE118444	Transcribed locus	---	2.975	0.029	0.979	0.087	3.817	0.028	1.532	0.210
1393265_at	BF546659	Transcribed locus	---	1.508	0.030	0.791	0.207	1.007	0.983	0.819	0.409
1371766_at	BE113242	Transcribed locus	---	0.893	0.030	0.859	0.078	1.285	0.126	0.828	0.171
1380660_at	BI295181	Transcribed locus	---	1.080	0.030	1.011	0.995	1.034	0.409	1.000	0.977
1379251_at	BF398485	Transcribed locus	---	1.178	0.030	1.122	0.061	1.340	0.059	1.230	0.000
1398447_at	AA801323	Transcribed locus	---	0.580	0.030	0.491	0.001	0.884	0.216	0.625	0.009
1393516_at	AA892335	Transcribed locus	---	0.381	0.030	0.229	0.011	0.460	0.011	0.405	0.079
1384839_at	AW522827	Transcribed locus	---	0.384	0.030	0.498	0.009	0.953	0.849	0.586	0.046
1382341_at	AI136740	Transcribed locus	---	1.250	0.030	0.890	0.175	1.365	0.061	0.648	0.177
1384032_at	AI058837	Transcribed locus	---	1.947	0.030	0.588	0.004	2.499	0.003	1.073	0.689
1395779_at	BF523321	Transcribed locus	---	1.505	0.030	0.512	0.004	1.868	0.001	0.645	0.024
1397924_at	AW523490	Transcribed locus	---	0.551	0.030	0.967	0.419	0.998	0.321	1.200	0.203
1394120_a_at	AI176775	Transcribed locus	---	2.070	0.030	0.585	0.035	1.281	0.257	0.837	0.042
1398613_at	AW532063	Transcribed locus	---	0.911	0.030	0.399	0.021	0.905	0.059	0.398	0.013
1376127_at	BE117201	Transcribed locus	---	0.801	0.031	0.804	0.002	0.671	0.015	0.830	0.018
1373207_at	AI235503	Transcribed locus	---	0.911	0.031	0.634	0.003	0.900	0.106	0.775	0.036
1381807_at	BM383408	Transcribed locus	---	0.231	0.031	0.806	0.518	0.652	0.074	1.000	0.627
1374483_at	BE098873	Transcribed locus	---	0.364	0.031	0.975	0.565	0.264	0.050	1.681	0.002
1392516_a_at	AI236580	Transcribed locus	---	0.611	0.031	0.437	0.021	0.686	0.059	0.405	0.040
1381008_at	BF390077	Transcribed locus	---	0.587	0.032	1.243	0.282	0.626	0.095	1.151	0.122
1374796_at	AI413058	Transcribed locus	---	0.386	0.032	0.164	0.000	0.418	0.001	0.248	0.005
1380033_at	AI408858	Transcribed locus	---	0.778	0.032	0.570	0.000	0.719	0.127	1.027	0.780
1378299_at	BF397445	Transcribed locus	---	1.734	0.032	0.947	0.339	1.881	0.023	0.986	0.977
1380152_at	BF407782	Transcribed locus	---	0.696	0.032	0.485	0.037	0.668	0.086	0.448	0.172
1380064_at	BE113961	Transcribed locus	---	1.763	0.032	0.657	0.000	1.479	0.037	0.846	0.064
1390731_at	BI288533	Transcribed locus	---	2.154	0.032	2.224	0.025	1.728	0.494	1.503	0.583
1374702_at	BI291393	Transcribed locus	---	0.622	0.032	0.506	0.003	0.530	0.011	0.553	0.036
1374410_at	BI278611	Transcribed locus	---	3.640	0.032	1.450	0.034	3.959	0.033	1.784	0.033
1374150_at	AA875425	Transcribed locus	---	1.236	0.032	1.650	0.013	1.333	0.073	1.829	0.006
1371552_at	BF400684	Transcribed locus	---	0.520	0.032	0.697	0.158	1.095	0.172	0.835	0.601
1396460_at	AW522969	Transcribed locus	---	0.501	0.033	0.308	0.000	0.771	0.026	0.269	0.000
1391683_at	BF563946	Transcribed locus	---	1.564	0.033	1.224	0.662	1.465	0.049	1.097	0.567
1392698_a_at	AA899844	Transcribed locus	---	0.586	0.033	0.792	0.038	0.756	0.047	0.841	0.041
1383210_at	BF554576	Transcribed locus	---	4.543	0.033	2.216	0.184	2.836	0.109	3.294	0.098
1393413_at	BI290400	Transcribed locus	---	3.106	0.033	3.103	0.007	2.242	0.011	1.678	0.038
1377712_at	AI556865	Transcribed locus	---	0.723	0.033	0.451	0.166	0.431	0.018	0.634	0.162
1391774_at	AW526131	Transcribed locus	---	0.339	0.033	0.326	0.009	1.459	0.238	0.412	0.027
1383237_at	BE098240	Transcribed locus	---	1.532	0.033	1.250	0.055	0.726	0.181	1.079	0.414
1378004_at	BF287788	Transcribed locus	---	0.478	0.033	0.405	0.025	0.601	0.045	0.641	0.080
1396037_at	BF544069	Transcribed locus	---	1.720	0.034	0.608	0.254	1.617	0.114	0.963	0.494
1382755_at	AI058343	Transcribed locus	---	1.621	0.034	2.305	0.013	1.694	0.008	2.394	0.029
1392575_at	BE108929	Transcribed locus	---	0.727	0.034	0.777	0.009	0.687	0.014	0.819	0.107
1384277_at	BM388018	Transcribed locus	---	1.642	0.034	1.165	0.138	1.834	0.026	1.137	0.086
1374281_at	BE109901	Transcribed locus	---	1.360	0.034	1.520	0.027	1.135	0.098	1.569	0.014
1375897_at	AI101372	Transcribed locus	---	0.938	0.034	1.433	0.054	0.615	0.211	0.996	0.990
1374780_at	AI232806	Transcribed locus	---	0.857	0.034	0.520	0.045	0.759	0.073	0.607	0.001
1389722_at	BF408457	Transcribed locus	---	5.386	0.034	0.568	0.044	8.004	0.005	0.640	0.944
1397199_at	BF408180	Transcribed locus	---	1.241	0.034	1.082	0.553	0.717	0.266	0.972	0.574
1385014_at	BG377996	Transcribed locus	---	0.351	0.034	0.456	0.003	0.413	0.075	0.644	0.039
1371798_at	AI013011	Transcribed locus	---	0.524	0.035	0.613	0.001	0.472	0.004	0.761	0.014
1380369_at	AI058315	Transcribed locus	---	1.196	0.035	0.841	0.966	1.352	0.400	0.705	0.021
1381885_at	BE102910	Transcribed locus	---	1.167	0.035	1.826	0.029	1.111	0.362	1.328	0.093
1376330_at	BF393046	Transcribed locus	---	0.303	0.035	0.321	0.006	0.278	0.022	0.348	0.004
1373023_at	BF555947	Transcribed locus	---	0.632	0.035	0.223	0.002	0.550	0.032	0.302	0.002
1374703_at	BI304209	Transcribed locus	---	0.638	0.035	0.556	0.003	0.546	0.023	0.682	0.005
1377880_at	AI170633	Transcribed locus	---	0.559	0.035	1.069	0.203	0.808	0.222	1.039	0.743

1378467_at	AA851361	Transcribed locus	---	1.914	0.035	0.942	0.216	2.641	0.005	1.252	0.652
1377155_at	BI294806	Transcribed locus	---	0.258	0.035	0.169	0.000	0.238	0.049	0.359	0.008
1379381_at	AI045321	Transcribed locus	---	3.199	0.036	1.001	0.553	4.312	0.001	0.916	0.665
1389075_at	AI600221	Transcribed locus	---	0.391	0.036	1.836	0.079	0.321	0.021	1.460	0.024
1384847_at	AA924641	Transcribed locus	---	2.547	0.036	1.230	0.529	2.584	0.104	0.618	0.075
1384238_at	BM385249	Transcribed locus	---	0.632	0.036	0.246	0.000	0.328	0.001	0.260	0.010
1395704_at	BF561525	Transcribed locus	---	2.148	0.036	0.766	0.126	1.292	0.028	0.559	0.010
1382227_at	AW533203	Transcribed locus	---	0.328	0.036	0.199	0.000	0.404	0.075	0.234	0.001
1379260_at	BE115626	Transcribed locus	---	3.375	0.036	1.139	0.447	3.749	0.042	1.699	0.370
1380917_at	BE109049	Transcribed locus	---	1.447	0.036	5.866	0.001	2.939	0.007	10.359	0.001
1386583_at	AA859497	Transcribed locus	---	0.530	0.036	0.860	0.010	0.513	0.016	0.916	0.789
1380345_at	AW529036	Transcribed locus	---	0.507	0.036	0.375	0.002	0.392	0.178	0.573	0.155
1372978_at	BI291218	Transcribed locus	---	0.496	0.036	0.761	0.381	0.456	0.019	0.699	0.355
1378965_at	AA818967	Transcribed locus	---	0.503	0.036	0.342	0.001	0.425	0.020	0.457	0.015
1391334_at	BE106273	Transcribed locus	---	0.353	0.037	0.312	0.135	0.344	0.040	0.793	0.135
1391582_at	AI180053	Transcribed locus	---	1.813	0.037	1.690	0.149	1.096	0.312	1.019	0.796
1392149_at	AA997766	Transcribed locus	---	0.686	0.037	1.096	0.992	0.728	0.210	0.523	0.093
1376463_at	AA955579	Transcribed locus	---	0.243	0.037	0.062	0.000	0.179	0.019	0.057	0.000
1389635_at	BE120878	Transcribed locus	---	0.849	0.037	0.724	0.004	0.743	0.040	0.811	0.253
1388881_at	BG380656	Transcribed locus	---	0.400	0.037	0.618	0.037	0.305	0.035	0.628	0.022
1382098_at	AI228756	Transcribed locus	---	0.446	0.037	0.040	0.000	0.521	0.009	0.152	0.010
1381386_at	AI407297	Transcribed locus	---	0.232	0.037	0.660	0.195	0.394	0.004	0.529	0.354
1396775_at	BF403583	Transcribed locus	---	1.674	0.037	0.847	0.796	1.509	0.052	0.563	0.198
1380741_at	BF412788	Transcribed locus	---	0.218	0.037	0.097	0.000	0.157	0.000	0.144	0.011
1374329_at	BI286364	Transcribed locus	---	0.578	0.038	0.475	0.007	0.425	0.010	0.369	0.025
1389301_at	AI176665	Transcribed locus	---	0.575	0.038	0.482	0.000	0.568	0.003	0.644	0.003
1391197_at	BF399523	Transcribed locus	---	2.226	0.038	1.209	0.444	1.466	0.360	1.158	0.993
1377909_at	BF401445	Transcribed locus	---	1.312	0.038	0.586	0.038	1.355	0.376	1.376	0.974
1392844_at	BE119432	Transcribed locus	---	1.507	0.038	2.651	0.007	1.882	0.214	1.907	0.030
1389388_at	BF291161	Transcribed locus	---	0.378	0.038	0.344	0.000	0.450	0.274	0.490	0.012
1373922_at	BG377024	Transcribed locus	---	2.221	0.038	2.006	0.000	1.338	0.394	1.603	0.127
1398464_at	AI575255	Transcribed locus	---	3.867	0.038	2.368	0.025	3.243	0.002	2.082	0.092
1386063_at	BF559746	Transcribed locus	---	2.492	0.038	1.552	0.135	1.864	0.070	1.002	0.227
1372197_at	BI299775	Transcribed locus	---	0.764	0.038	0.948	0.454	1.490	0.318	1.082	0.454
1382480_at	AI060139	Transcribed locus	---	0.705	0.038	1.012	0.365	0.702	0.026	0.948	0.156
1373050_at	AW917731	Transcribed locus	---	2.362	0.038	0.646	0.465	3.570	0.001	0.526	0.519
1381626_at	BE105470	Transcribed locus	---	0.508	0.039	1.033	0.936	0.521	0.032	0.990	0.961
1389789_at	AI059662	Transcribed locus	---	4.395	0.039	0.916	0.427	5.849	0.004	1.465	0.045
1374473_at	BI282910	Transcribed locus	---	1.497	0.039	1.191	0.001	1.045	0.558	1.220	0.002
1373217_at	AI010234	Transcribed locus	---	1.330	0.039	0.978	0.783	1.015	0.383	0.825	0.174
1372951_at	BI274172	Transcribed locus	---	1.891	0.039	2.487	0.005	1.959	0.009	2.462	0.001
1393822_at	AA925789	Transcribed locus	---	11.771	0.039	4.783	0.024	9.231	0.049	4.810	0.007
1388702_at	BI285078	Transcribed locus	---	0.589	0.039	0.591	0.082	0.715	0.424	0.648	0.006
1377019_at	BF410042	Transcribed locus	---	0.590	0.039	0.999	0.773	0.588	0.032	1.145	0.116
1372910_at	AI408770	Transcribed locus	---	1.388	0.039	1.149	0.051	2.311	0.006	1.469	0.026
1377413_at	BF548480	Transcribed locus	---	1.554	0.039	1.369	0.025	1.382	0.051	1.526	0.009
1390240_at	BM389611	Transcribed locus	---	13.310	0.040	5.801	0.027	11.773	0.016	3.957	0.145
1398619_at	BG671918	Transcribed locus	---	1.567	0.040	0.806	0.031	1.969	0.027	0.754	0.131
1377167_at	AA964494	Transcribed locus	---	1.147	0.040	0.713	0.076	1.487	0.048	1.033	0.196
1374158_at	BF398160	Transcribed locus	---	1.751	0.040	1.027	0.759	1.686	0.021	1.102	0.713
1382867_at	AA849390	Transcribed locus	---	2.437	0.041	0.593	0.158	1.648	0.035	0.786	0.145
1395110_at	BE110272	Transcribed locus	---	19.822	0.041	5.927	0.012	16.509	0.000	1.889	0.019
1384451_at	BE116574	Transcribed locus	---	2.007	0.041	0.995	0.683	2.426	0.045	1.036	0.803
1385355_at	BF391308	Transcribed locus	---	1.492	0.042	1.152	0.759	2.003	0.142	0.956	0.924
1381508_at	BE098143	Transcribed locus	---	0.805	0.042	2.182	0.067	0.801	0.038	1.134	0.317
1371818_at	AW251204	Transcribed locus	---	0.662	0.042	1.036	0.878	0.513	0.014	1.075	0.568
1384520_at	AW523106	Transcribed locus	---	0.754	0.042	0.619	0.057	0.586	0.014	0.743	0.120
1390303_at	BF390840	Transcribed locus	---	0.425	0.042	0.219	0.005	0.697	0.466	0.401	0.039
1372889_at	AI407489	Transcribed locus	---	2.165	0.042	0.329	0.049	1.044	0.659	0.329	0.049
1379997_at	BF398462	Transcribed locus	---	2.164	0.042	0.986	0.615	1.097	0.962	1.143	0.508
1390509_a_at	BI294860	Transcribed locus	---	0.666	0.042	0.604	0.003	0.562	0.037	0.652	0.001

1375363_at	BG374402	Transcribed locus	---	1.678	0.042	0.970	0.804	1.180	0.222	0.895	0.710
1393972_at	BE096871	Transcribed locus	---	2.403	0.042	0.905	0.273	1.662	0.464	1.416	0.120
1393730_at	BI277836	Transcribed locus	---	5.026	0.042	2.221	0.223	3.787	0.170	1.536	0.927
1389383_at	BI289855	Transcribed locus	---	1.843	0.042	0.619	0.001	3.237	0.014	0.755	0.047
1392493_at	AI501338	Transcribed locus	---	1.603	0.042	1.102	0.077	1.512	0.062	1.273	0.165
1377272_at	BE112934	Transcribed locus	---	0.513	0.042	1.195	0.139	0.389	0.037	0.942	0.306
1379535_at	AI073064	Transcribed locus	---	2.029	0.043	1.480	0.030	2.646	0.015	1.367	0.036
1396088_at	AW914780	Transcribed locus	---	2.910	0.043	1.924	0.053	2.386	0.073	1.030	0.072
1382334_at	AI170308	Transcribed locus	---	1.946	0.043	1.879	0.444	2.812	0.031	1.647	0.408
1382814_at	AW521702	Transcribed locus	---	0.949	0.043	0.238	0.001	0.959	0.261	0.255	0.005
1385929_at	AI171447	Transcribed locus	---	0.613	0.043	0.534	0.036	0.345	0.010	1.151	0.585
1385098_at	AW526343	Transcribed locus	---	0.640	0.043	0.099	0.002	0.529	0.078	0.117	0.002
1392924_at	BG371591	Transcribed locus	---	0.675	0.043	0.590	0.001	0.660	0.025	0.659	0.026
1395183_at	BM391096	Transcribed locus	---	2.008	0.043	39.509	0.003	0.550	0.530	30.352	0.001
1378367_at	BF389087	Transcribed locus	---	0.737	0.043	0.376	0.007	1.173	0.513	0.522	0.044
1392492_at	AA956982	Transcribed locus	---	1.698	0.043	1.118	0.694	1.554	0.077	0.952	0.817
1374485_at	AI137762	Transcribed locus	---	1.491	0.043	0.698	0.487	1.526	0.062	0.862	0.251
1374553_at	AW535229	Transcribed locus	---	0.693	0.043	0.893	0.216	0.786	0.002	0.764	0.017
1389230_at	AA818910	Transcribed locus	---	1.181	0.043	2.104	0.023	0.832	0.372	2.199	0.053
1383362_at	BI275850	Transcribed locus	---	3.174	0.043	1.364	0.291	3.751	0.045	1.592	0.008
1382854_at	AI232286	Transcribed locus	---	1.787	0.044	1.072	0.666	1.006	0.984	1.106	0.147
1384124_at	AW534915	Transcribed locus	---	0.548	0.044	0.916	0.035	0.415	0.020	0.518	0.011
1383907_at	BE117969	Transcribed locus	---	0.736	0.044	0.484	0.000	0.928	0.637	0.724	0.062
1374263_at	BF396108	Transcribed locus	---	2.160	0.044	1.077	0.227	4.703	0.021	1.798	1.000
1396405_at	BE097557	Transcribed locus	---	0.658	0.044	0.254	0.000	0.890	0.706	0.353	0.004
1390996_at	BE101679	Transcribed locus	---	1.539	0.044	1.018	0.942	0.980	0.764	1.154	0.105
1384948_at	AI113157	Transcribed locus	---	1.537	0.044	0.753	0.074	1.561	0.021	0.779	0.135
1376808_at	BG672572	Transcribed locus	---	0.644	0.044	0.204	0.001	0.534	0.079	0.321	0.018
1382506_at	AI044841	Transcribed locus	---	3.615	0.044	0.593	0.202	2.927	0.018	0.775	0.084
1374241_at	AI406271	Transcribed locus	---	0.408	0.044	0.286	0.003	0.265	0.000	0.289	0.005
1394169_at	AI639265	Transcribed locus	---	0.693	0.045	0.293	0.002	0.691	0.087	0.347	0.061
1391480_at	BI296013	Transcribed locus	---	0.668	0.045	0.601	0.140	0.672	0.043	0.598	0.139
1396967_at	BF406294	Transcribed locus	---	0.718	0.045	0.498	0.105	0.721	0.045	0.513	0.108
1376814_at	BE107949	Transcribed locus	---	0.363	0.045	0.318	0.004	0.575	0.036	0.526	0.036
1391241_at	BF394755	Transcribed locus	---	2.505	0.045	0.544	0.417	3.400	0.026	0.989	0.977
1398985_at	AI716480	Transcribed locus	---	3.421	0.045	0.952	0.139	4.062	0.012	1.574	0.034
1391610_at	AI555319	Transcribed locus	---	0.827	0.045	0.956	0.960	1.510	0.161	0.990	0.570
1391744_at	AI548028	Transcribed locus	---	0.308	0.045	0.319	0.073	0.459	0.090	0.165	0.043
1393765_at	AI043706	Transcribed locus	---	0.399	0.045	0.415	0.000	0.808	0.220	0.500	0.008
1379244_at	AW522926	Transcribed locus	---	2.815	0.045	1.273	0.120	2.426	0.078	1.001	0.995
1372875_at	AI408520	Transcribed locus	---	1.778	0.045	1.438	0.039	1.428	0.075	1.310	0.092
1394342_at	BF557463	Transcribed locus	---	2.215	0.046	1.001	0.721	0.623	0.886	0.751	0.045
1383378_at	BI298932	Transcribed locus	---	0.432	0.046	0.634	0.086	0.318	0.040	0.586	0.178
1373633_at	BF399791	Transcribed locus	---	2.043	0.046	2.055	0.166	1.286	0.311	1.143	0.683
1372564_at	AI411375	Transcribed locus	---	1.632	0.047	1.454	0.038	1.356	0.189	1.390	0.034
1374868_at	AW535434	Transcribed locus	---	1.461	0.047	1.187	0.100	1.550	0.035	0.891	0.929
1377688_at	AI136703	Transcribed locus	---	2.304	0.047	1.425	0.159	2.032	0.146	0.978	0.418
1390394_at	AW251900	Transcribed locus	---	1.443	0.047	1.451	0.004	1.796	0.000	1.535	0.057
1393021_at	BE113061	Transcribed locus	---	0.422	0.047	0.704	0.015	0.637	0.180	0.667	0.023
1372371_at	BI303031	Transcribed locus	---	2.125	0.047	1.031	0.966	2.344	0.032	1.409	0.218
1393928_at	AA899202	Transcribed locus	---	1.953	0.047	2.366	0.052	2.254	0.544	2.179	0.019
1398902_at	BF282978	Transcribed locus	---	0.689	0.047	1.607	0.012	0.477	0.007	1.333	0.119
1378937_at	BE349836	Transcribed locus	---	0.445	0.047	0.934	0.708	0.635	0.000	0.984	0.588
1377890_at	AI411360	Transcribed locus	---	0.619	0.047	0.333	0.009	0.590	0.046	0.329	0.003
1379358_at	BE108208	Transcribed locus	---	1.323	0.047	1.323	0.682	3.092	0.027	1.321	0.295
1392733_at	BM391545	Transcribed locus	---	2.209	0.047	3.164	0.011	1.792	0.019	5.558	0.009
1373516_at	BE099830	Transcribed locus	---	0.761	0.048	0.663	0.054	0.445	0.030	0.743	0.250
1372452_at	BG666882	Transcribed locus	---	0.657	0.048	0.712	0.047	0.393	0.006	0.580	0.056
1391292_at	AI556811	Transcribed locus	---	0.440	0.048	0.732	0.016	0.390	0.003	0.647	0.051
1377500_at	BE119198	Transcribed locus	---	1.629	0.048	1.836	0.083	1.118	0.218	1.568	0.015
1383417_at	BE119990	Transcribed locus	---	0.539	0.048	1.060	0.819	0.529	0.080	0.908	0.682

1372204_at	BM391843	Transcribed locus	---	1.748	0.048	1.492	0.042	2.129	0.018	1.865	0.004
1392692_at	BE107050	Transcribed locus	---	1.254	0.048	0.754	0.225	1.406	0.035	0.880	0.673
1393465_at	BE103258	Transcribed locus	---	0.697	0.048	0.972	0.763	0.554	0.013	0.661	0.038
1382071_at	BI302916	Transcribed locus	---	1.238	0.048	1.162	0.456	1.271	0.073	1.125	0.314
1379076_at	BE328961	Transcribed locus	---	0.606	0.048	0.233	0.000	0.664	0.515	0.376	0.054
1377202_at	AI172197	Transcribed locus	---	0.673	0.049	0.404	0.007	1.045	0.984	0.462	0.041
1379994_at	AI070694	Transcribed locus	---	1.539	0.049	0.852	0.502	1.340	0.022	1.036	0.754
1375272_at	BE113423	Transcribed locus	---	1.147	0.049	1.279	0.043	1.232	0.023	1.177	0.086
1372768_at	AW251331	Transcribed locus	---	0.762	0.049	0.689	0.014	0.729	0.106	0.699	0.003
1382300_at	BF284236	Transcribed locus	---	0.639	0.049	1.059	0.922	0.856	0.896	1.127	0.115
1393600_at	AA817969	Transcribed locus	---	0.692	0.049	0.411	0.020	0.689	0.045	0.761	0.072
1378316_at	AI145009	Transcribed locus	---	0.528	0.049	0.879	0.242	0.773	0.460	0.930	0.134
1372276_at	BG378613	Transcribed locus	---	0.461	0.050	0.390	0.020	0.478	0.076	0.412	0.064
1382183_at	AA849479	Transcribed locus	---	0.379	0.050	0.219	0.001	0.404	0.053	0.408	0.038
1383750_at	BF418523	Transcribed locus	---	0.425	0.050	0.108	0.000	0.684	0.000	0.217	0.025
1376691_at	AI103213	Transcribed locus	---	0.194	0.050	0.579	0.009	0.447	0.015	0.433	0.022
1389591_at	BM388471	Transcribed locus	---	1.639	0.050	1.730	0.068	1.134	0.910	1.213	0.989
1391860_at	AI599816	Transcribed locus	---	1.336	0.050	1.185	0.151	1.272	0.406	0.998	0.919
1382654_at	AA859319	Transcribed locus	---	0.664	0.050	0.418	0.006	0.512	0.033	0.427	0.020
1391817_at	AA901178	Transcribed locus	---	2.260	0.050	2.422	0.002	3.259	0.032	1.598	0.039
1393019_at	BG372243	Transcribed locus	---	0.746	0.050	0.589	0.007	0.897	0.463	0.758	0.002
1379302_at	AA848916	Transcribed locus	---	1.214	0.050	1.638	0.118	0.904	0.830	0.950	0.543
1379324_at	AW535283	Transcribed locus	---	0.568	0.051	0.666	0.045	0.378	0.000	0.658	0.012
1390410_at	AA963369	Transcribed locus	---	0.866	0.051	0.846	0.196	0.786	0.211	0.866	0.040
1374265_at	BF395101	Transcribed locus	---	1.969	0.051	1.744	0.024	2.822	0.062	1.504	0.046
1375635_at	AI406410	Transcribed locus	---	3.714	0.051	0.856	0.014	4.344	0.036	1.167	0.167
1375437_at	BI298111	Transcribed locus	---	0.777	0.051	0.924	0.039	0.776	0.064	0.610	0.008
1393937_at	AI577369	Transcribed locus	---	0.884	0.051	0.399	0.002	0.922	0.540	0.543	0.048
1373078_at	AI409271	Transcribed locus	---	0.661	0.051	0.463	0.004	0.611	0.032	0.485	0.004
1383102_at	BE111057	Transcribed locus	---	1.249	0.051	0.861	0.506	1.422	0.143	1.292	0.210
1373091_at	AI102576	Transcribed locus	---	1.464	0.051	0.689	0.420	1.742	0.186	1.022	0.214
1391220_at	BG381455	Transcribed locus	---	0.718	0.051	1.248	0.072	0.605	0.026	1.254	0.043
1377312_at	BF401679	Transcribed locus	---	0.655	0.051	0.769	0.052	0.708	0.589	0.769	0.048
1391863_at	BE106361	Transcribed locus	---	1.330	0.051	0.994	0.957	1.074	0.447	0.999	0.374
1393308_at	BE110640	Transcribed locus	---	0.601	0.051	0.779	0.236	0.715	0.838	0.837	0.093
1385350_at	BF398122	Transcribed locus	---	0.685	0.052	1.229	0.540	0.545	0.051	1.407	0.707
1392849_at	AI044509	Transcribed locus	---	1.087	0.052	1.035	0.581	1.548	0.123	0.999	0.895
1383022_at	BF390046	Transcribed locus	---	1.268	0.052	0.423	0.016	0.729	0.038	0.611	0.041
1371494_at	BE110614	Transcribed locus	---	0.365	0.052	0.133	0.001	0.565	0.039	0.201	0.029
1372027_at	AI009713	Transcribed locus	---	1.477	0.052	1.112	0.765	1.112	0.391	0.927	0.910
1377469_at	AI103161	Transcribed locus	---	0.375	0.052	0.207	0.003	0.335	0.032	0.465	0.016
1385717_at	AW524331	Transcribed locus	---	0.437	0.052	0.397	0.000	0.518	0.015	0.553	0.018
1398495_at	BE121436	Transcribed locus	---	0.747	0.052	0.461	0.086	0.476	0.016	0.322	0.071
1377154_at	BI295766	Transcribed locus	---	1.724	0.052	0.690	0.265	1.183	0.685	0.689	0.265
1373113_at	AI231778	Transcribed locus	---	1.506	0.053	1.722	0.000	1.224	0.296	1.574	0.010
1378396_at	AI007647	Transcribed locus	---	0.725	0.053	0.589	0.060	0.925	0.652	0.588	0.023
1398397_at	AI407483	Transcribed locus	---	1.799	0.053	1.521	0.807	4.682	0.001	1.810	0.990
1372838_at	AI227902	Transcribed locus	---	0.701	0.053	0.684	0.143	0.787	0.056	0.689	0.106
1375843_at	BM383777	Transcribed locus	---	0.765	0.053	0.636	0.001	0.919	0.291	0.685	0.021
1392531_at	AI178693	Transcribed locus	---	1.905	0.053	2.304	0.014	1.649	0.031	2.091	0.013
1392217_at	AI172126	Transcribed locus	---	0.280	0.053	0.268	0.000	0.354	0.034	0.208	0.008
1385253_at	AW529791	Transcribed locus	---	1.471	0.053	2.010	0.017	2.151	0.030	1.431	0.067
1393143_at	AI045866	Transcribed locus	---	1.449	0.054	0.712	0.016	1.917	0.071	1.053	0.649
1380298_at	AW435308	Transcribed locus	---	0.834	0.054	0.999	0.995	0.846	0.076	1.002	0.955
1393817_at	AI070991	Transcribed locus	---	1.328	0.054	0.915	0.263	1.566	0.101	1.206	0.124
1393777_at	AA998104	Transcribed locus	---	0.255	0.054	0.797	0.530	0.586	0.219	0.960	0.395
1393344_at	AW528051	Transcribed locus	---	0.676	0.054	0.335	0.017	0.780	0.230	0.225	0.034
1377040_a_at	AI172225	Transcribed locus	---	0.573	0.054	0.902	0.974	0.520	0.019	0.769	0.074
1376660_at	BG672127	Transcribed locus	---	0.689	0.054	2.635	0.003	0.998	0.993	1.988	0.004
1374035_at	BI296482	Transcribed locus	---	0.168	0.055	0.141	0.005	0.137	0.001	0.126	0.037
1379698_at	AI178631	Transcribed locus	---	0.444	0.055	0.260	0.001	0.314	0.033	0.381	0.047

1392500_at	AA957990	Transcribed locus	---	1.518	0.055	0.867	0.315	1.440	0.053	0.961	0.310
1398389_at	AI236136	Transcribed locus	---	0.719	0.055	0.441	0.001	0.717	0.003	0.517	0.011
1378998_at	AI071538	Transcribed locus	---	0.723	0.055	0.934	0.931	0.781	0.102	1.048	0.974
1391077_at	AA851257	Transcribed locus	---	0.253	0.055	0.696	0.126	0.252	0.049	0.538	0.005
1389205_at	AI012582	Transcribed locus	---	1.094	0.055	0.908	0.342	2.349	0.004	1.028	0.661
1376167_at	AA799347	Transcribed locus	---	0.609	0.055	0.648	0.127	0.642	0.224	0.782	0.228
1381795_at	AA963295	Transcribed locus	---	1.787	0.056	1.206	0.274	2.206	0.001	1.272	0.122
1399061_at	H35275	Transcribed locus	---	0.728	0.056	0.763	0.010	0.764	0.586	0.913	0.167
1388830_at	BM390687	Transcribed locus	---	1.873	0.056	1.236	0.039	1.885	0.006	1.439	0.008
1390530_at	AI169239	Transcribed locus	---	0.473	0.056	0.392	0.012	0.661	0.028	0.370	0.024
1393077_at	AA925179	Transcribed locus	---	0.839	0.056	0.703	0.011	0.665	0.017	0.713	0.005
1396236_at	AI145896	Transcribed locus	---	1.413	0.056	1.001	0.997	1.411	0.053	0.996	0.901
1379619_at	BE104952	Transcribed locus	---	1.512	0.057	1.385	0.090	1.201	0.246	0.902	0.628
1376232_at	AW521352	Transcribed locus	---	1.766	0.057	0.740	0.287	2.650	0.004	0.761	0.042
1372821_at	AI236621	Transcribed locus	---	0.268	0.057	0.613	0.376	0.495	0.033	0.812	0.421
1377076_at	AI716131	Transcribed locus	---	0.511	0.057	0.694	0.004	0.667	0.129	0.566	0.062
1380158_at	BF284973	Transcribed locus	---	1.682	0.057	1.144	0.335	1.589	0.020	1.792	0.012
1378357_at	AI556522	Transcribed locus	---	0.457	0.057	0.828	0.620	0.535	0.026	0.456	0.186
1384135_at	AI575629	Transcribed locus	---	1.533	0.058	0.735	0.486	1.976	0.723	0.698	0.316
1389293_at	BM390250	Transcribed locus	---	0.496	0.058	0.584	0.009	0.930	0.517	0.770	0.075
1380947_at	BE108752	Transcribed locus	---	0.764	0.058	0.670	0.009	0.440	0.001	0.259	0.043
1381551_at	BG378461	Transcribed locus	---	2.993	0.058	1.824	0.499	2.240	0.272	2.445	0.460
1377331_at	AW532469	Transcribed locus	---	0.656	0.058	0.623	0.006	0.695	0.048	0.768	0.008
1374270_at	AA964789	Transcribed locus	---	0.230	0.058	0.281	0.047	0.286	0.077	0.274	0.046
1388472_at	AI177860	Transcribed locus	---	1.363	0.058	0.933	0.365	1.603	0.113	0.998	0.792
1396483_at	AW434740	Transcribed locus	---	0.777	0.058	0.925	0.452	0.933	0.321	1.223	0.749
1376631_at	BF283675	Transcribed locus	---	1.255	0.059	1.060	0.231	0.985	0.900	1.007	0.960
1372736_at	BG374196	Transcribed locus	---	0.313	0.059	0.244	0.007	0.252	0.001	0.246	0.014
1389612_at	AI410941	Transcribed locus	---	0.786	0.059	0.298	0.012	0.804	0.150	0.402	0.004
1372277_at	BI274673	Transcribed locus	---	3.228	0.059	1.012	0.929	4.781	0.005	1.210	0.354
1390986_at	AW526072	Transcribed locus	---	0.486	0.059	0.213	0.000	0.367	0.044	0.233	0.000
1375050_at	BI294558	Transcribed locus	---	0.717	0.059	1.013	0.257	0.393	0.037	0.654	0.036
1373469_at	BF408841	Transcribed locus	---	0.354	0.059	0.536	0.007	0.283	0.010	0.603	0.006
1385533_at	BE106145	Transcribed locus	---	0.579	0.059	0.803	0.440	0.885	0.213	1.022	0.386
1373376_at	BI285979	Transcribed locus	---	0.570	0.059	0.714	0.021	0.751	0.083	0.719	0.001
1397584_at	BF289504	Transcribed locus	---	0.311	0.059	1.296	0.160	1.220	0.068	1.495	0.488
1394207_at	AI236188	Transcribed locus	---	0.439	0.059	0.121	0.001	0.746	0.435	0.187	0.033
1384833_at	AA801117	Transcribed locus	---	0.672	0.060	1.167	0.664	0.705	0.195	0.799	0.010
1383393_at	AA858485	Transcribed locus	---	1.237	0.060	0.871	0.273	1.448	0.051	0.916	0.401
1389318_at	BF282986	Transcribed locus	---	1.375	0.060	0.690	0.019	2.133	0.001	0.950	0.231
1380552_at	AI555855	Transcribed locus	---	7.872	0.060	1.877	0.130	8.124	0.060	6.903	0.013
1396076_at	AW914907	Transcribed locus	---	1.760	0.060	0.911	0.732	1.001	0.210	0.905	0.296
1398484_at	AI070306	Transcribed locus	---	0.776	0.060	0.285	0.001	0.669	0.057	0.315	0.001
1393177_at	AA924403	Transcribed locus	---	2.681	0.060	1.637	0.010	4.022	0.000	1.537	0.178
1372486_at	AI236691	Transcribed locus	---	0.676	0.060	0.532	0.000	0.602	0.028	0.614	0.001
1395625_at	BF415216	Transcribed locus	---	0.607	0.061	0.586	0.002	0.630	0.012	0.625	0.105
1380255_at	AI235931	Transcribed locus	---	0.504	0.061	0.390	0.002	0.730	0.054	0.697	0.006
1389458_at	AW435191	Transcribed locus	---	0.653	0.061	1.085	0.030	1.202	0.779	1.150	0.075
1376002_at	AI406363	Transcribed locus	---	2.069	0.061	1.018	0.393	3.862	0.008	1.838	0.330
1373223_at	AI101361	Transcribed locus	---	1.938	0.061	0.792	0.409	2.906	0.003	3.030	0.008
1373370_at	AI407467	Transcribed locus	---	1.570	0.061	0.795	0.380	2.447	0.004	0.987	0.587
1381077_at	AA996843	Transcribed locus	---	0.524	0.061	0.258	0.002	0.520	0.051	0.249	0.011
1378000_at	AA801075	Transcribed locus	---	0.460	0.061	0.297	0.000	0.290	0.026	0.356	0.002
1374019_at	BF284939	Transcribed locus	---	0.655	0.061	0.489	0.063	0.654	0.261	0.724	0.130
1391210_at	AI175259	Transcribed locus	---	0.471	0.061	0.484	0.060	0.516	0.967	0.410	0.049
1379510_at	BF546306	Transcribed locus	---	1.101	0.062	1.159	0.993	1.039	0.986	1.427	0.389
1393014_at	AA849210	Transcribed locus	---	1.401	0.062	1.162	0.359	1.370	0.612	0.711	0.314
1382368_at	AA943075	Transcribed locus	---	2.066	0.062	1.080	0.438	1.223	0.505	1.636	0.048
1373075_at	BM390707	Transcribed locus	---	1.087	0.062	1.529	0.004	1.307	0.001	1.453	0.033
1375687_at	BE097926	Transcribed locus	---	0.747	0.062	0.698	0.001	0.650	0.018	0.775	0.021
1373309_at	BI281129	Transcribed locus	---	2.044	0.062	1.368	0.115	4.596	0.001	2.014	0.003

1393687_at	BE113870	Transcribed locus	---	1.591	0.062	0.878	0.679	1.155	0.096	1.061	0.204
1385585_at	AI111674	Transcribed locus	---	1.886	0.062	2.345	0.016	1.085	0.651	1.824	0.177
1378765_at	BM384731	Transcribed locus	---	1.839	0.062	0.853	0.982	2.236	0.016	1.002	0.909
1375947_at	AI171856	Transcribed locus	---	0.710	0.063	0.637	0.043	0.720	0.045	0.860	0.317
1372836_at	AI170399	Transcribed locus	---	0.386	0.063	0.690	0.036	0.619	0.087	0.597	0.020
1383964_at	AI549551	Transcribed locus	---	0.704	0.063	0.284	0.006	0.859	0.331	0.360	0.009
1385874_at	AA956418	Transcribed locus	---	1.452	0.063	0.772	0.016	1.109	0.951	0.883	0.061
1376490_at	BG378933	Transcribed locus	---	1.310	0.063	2.045	0.176	0.998	0.513	0.835	0.263
1390213_at	BF388763	Transcribed locus	---	1.376	0.063	0.907	0.698	1.161	0.400	0.953	0.751
1389121_at	AA998771	Transcribed locus	---	0.613	0.063	0.460	0.025	0.790	0.063	0.527	0.234
1390206_at	AW434946	Transcribed locus	---	0.681	0.063	0.607	0.219	1.418	0.298	0.640	0.269
1394950_at	AI502833	Transcribed locus	---	3.456	0.064	4.311	0.005	2.338	0.091	1.131	0.683
1378016_at	BE104462	Transcribed locus	---	1.416	0.064	0.977	0.791	1.075	0.168	1.078	0.851
1380926_at	AA957632	Transcribed locus	---	1.422	0.064	2.031	0.055	1.039	0.197	1.515	0.014
1397112_at	BF415784	Transcribed locus	---	1.716	0.064	1.612	0.216	1.554	0.364	0.893	0.680
1395442_at	BF398196	Transcribed locus	---	1.665	0.064	1.069	0.446	1.166	0.034	0.824	0.319
1395832_at	AW529599	Transcribed locus	---	1.039	0.064	0.661	0.027	1.001	0.898	0.579	0.036
1398120_at	AW531770	Transcribed locus	---	0.525	0.064	1.239	0.152	0.363	0.050	1.145	0.820
1383565_at	BE120852	Transcribed locus	---	1.849	0.064	0.852	0.355	1.040	0.746	0.995	0.444
1393107_at	BI303078	Transcribed locus	---	1.064	0.064	0.625	0.007	1.057	0.816	0.742	0.112
1379908_at	BE104836	Transcribed locus	---	2.092	0.064	1.342	0.808	2.410	0.116	1.118	0.959
1382578_at	AI178173	Transcribed locus	---	0.640	0.064	1.185	0.282	0.665	0.068	1.249	0.988
1374339_at	BI303362	Transcribed locus	---	0.654	0.064	0.561	0.000	0.751	0.019	0.706	0.207
1392536_at	AI136839	Transcribed locus	---	1.135	0.065	1.890	0.001	0.664	0.015	1.905	0.033
1389109_at	AI407351	Transcribed locus	---	1.152	0.065	1.208	0.143	2.711	0.045	1.558	0.008
1374645_at	AW535233	Transcribed locus	---	1.330	0.065	0.948	0.673	0.992	0.862	0.978	0.893
1373729_at	BG376772	Transcribed locus	---	0.703	0.065	0.649	0.013	0.983	0.593	0.657	0.001
1374676_at	AA818911	Transcribed locus	---	1.899	0.065	0.502	0.046	3.401	0.001	0.754	0.112
1373415_at	AI407050	Transcribed locus	---	1.017	0.066	0.402	0.003	1.045	0.248	0.447	0.037
1379249_at	AA900400	Transcribed locus	---	1.498	0.066	1.507	0.004	1.291	0.135	1.288	0.099
1384584_at	AA892774	Transcribed locus	---	2.226	0.066	2.562	0.003	1.954	0.044	2.098	0.006
1380347_at	AI030806	Transcribed locus	---	0.936	0.066	0.263	0.000	0.966	0.537	0.286	0.076
1396399_at	AW530442	Transcribed locus	---	2.974	0.066	1.100	0.436	2.747	0.074	0.962	0.919
1383232_at	AI716944	Transcribed locus	---	0.782	0.066	0.772	0.005	0.775	0.020	0.805	0.005
1382270_at	BM384387	Transcribed locus	---	0.473	0.066	0.292	0.021	0.567	0.161	0.340	0.001
1397453_at	BM390792	Transcribed locus	---	1.591	0.066	0.770	0.349	2.414	0.001	1.589	0.073
1394527_at	AI501679	Transcribed locus	---	2.444	0.067	1.074	0.015	3.774	0.016	1.316	0.119
1374543_at	AA858791	Transcribed locus	---	2.415	0.067	1.865	0.001	2.447	0.041	2.246	0.008
1383504_at	AW530604	Transcribed locus	---	0.704	0.067	0.538	0.000	0.834	0.485	0.648	0.002
1395948_at	BF410644	Transcribed locus	---	0.450	0.067	0.413	0.064	0.088	0.025	0.670	0.061
1380349_at	BF395595	Transcribed locus	---	0.913	0.067	0.363	0.006	0.717	0.026	0.420	0.007
1379903_at	AI059853	Transcribed locus	---	0.427	0.067	0.714	0.024	0.285	0.005	0.751	0.025
1378162_at	AI045884	Transcribed locus	---	2.166	0.067	2.132	0.118	1.492	0.025	2.037	0.041
1378261_at	BE102806	Transcribed locus	---	5.705	0.068	32.402	0.013	1.346	0.447	4.127	0.014
1381915_at	AI111735	Transcribed locus	---	1.489	0.068	2.245	0.001	1.327	0.139	1.895	0.007
1392889_at	AI112294	Transcribed locus	---	1.615	0.068	0.632	0.035	1.347	0.039	0.772	0.077
1381507_at	BE097981	Transcribed locus	---	2.665	0.068	0.736	0.201	1.349	0.198	0.515	0.013
1397804_at	BF411294	Transcribed locus	---	1.098	0.068	1.102	0.491	1.450	0.001	1.065	0.090
1374422_at	BI395803	Transcribed locus	---	1.020	0.068	0.817	0.177	1.437	0.033	0.806	0.038
1375990_a_at	BF284519	Transcribed locus	---	2.173	0.069	0.938	0.439	1.465	0.831	1.219	0.874
1372560_at	AW522495	Transcribed locus	---	0.569	0.069	2.511	0.023	0.583	0.079	0.971	0.042
1390395_at	BF284768	Transcribed locus	---	0.854	0.069	0.772	0.082	0.970	0.726	1.297	0.014
1391217_at	BI289843	Transcribed locus	---	1.272	0.069	1.100	0.901	0.814	0.529	0.722	0.031
1377742_at	AI170706	Transcribed locus	---	0.824	0.069	1.074	0.372	0.960	0.584	0.959	0.214
1375497_at	BE107853	Transcribed locus	---	2.019	0.069	1.034	0.331	1.029	0.866	0.873	0.326
1384582_at	BE107130	Transcribed locus	---	1.239	0.070	0.987	0.067	1.712	0.013	1.155	0.272
1374664_at	AI235511	Transcribed locus	---	1.824	0.070	2.614	0.009	1.201	0.445	1.791	0.029
1391060_at	BG371670	Transcribed locus	---	1.521	0.070	0.845	0.313	1.717	0.067	1.206	0.874
1374636_at	BI298596	Transcribed locus	---	0.842	0.070	1.427	0.001	0.605	0.135	1.206	0.008
1391436_at	BF283714	Transcribed locus	---	0.379	0.070	0.205	0.000	0.713	0.368	0.404	0.006
1374307_at	AI236027	Transcribed locus	---	0.702	0.070	0.294	0.001	0.556	0.032	0.263	0.018

1377883_at	AI717530	Transcribed locus	---	0.551	0.070	0.162	0.005	1.069	0.429	0.661	0.019
1379695_at	AW915505	Transcribed locus	---	1.302	0.070	0.997	0.082	4.659	0.033	1.014	0.951
1378044_at	AA964294	Transcribed locus	---	2.182	0.071	1.009	0.945	1.028	0.927	1.007	0.905
1395726_at	AW143353	Transcribed locus	---	0.300	0.071	0.208	0.000	0.463	0.023	0.183	0.016
1372263_at	BF396485	Transcribed locus	---	1.397	0.071	3.624	0.023	0.971	0.473	1.857	0.007
1378370_at	BF401705	Transcribed locus	---	1.112	0.071	0.903	0.012	1.538	0.044	1.116	0.057
1386653_at	AW917558	Transcribed locus	---	0.387	0.071	0.305	0.011	0.522	0.030	0.301	0.024
1375963_at	BF281523	Transcribed locus	---	1.077	0.072	1.051	0.775	1.168	0.077	1.126	0.452
1379581_at	BI288586	Transcribed locus	---	2.118	0.072	1.433	0.284	1.386	0.300	0.982	0.870
1382352_at	AI030845	Transcribed locus	---	0.383	0.072	0.391	0.007	0.532	0.003	0.302	0.007
1389216_at	AW523499	Transcribed locus	---	1.322	0.072	1.840	0.017	1.327	0.174	2.023	0.005
1386064_at	AI501693	Transcribed locus	---	2.435	0.072	2.156	0.057	1.641	0.141	1.179	0.080
1377071_at	BG375652	Transcribed locus	---	1.278	0.072	0.296	0.005	1.454	0.411	0.322	0.004
1372495_at	BI274679	Transcribed locus	---	2.296	0.073	0.992	0.796	1.987	0.180	1.152	0.367
1390476_at	BE101472	Transcribed locus	---	1.379	0.073	1.159	0.090	0.923	0.651	1.000	0.136
1374610_at	AI599365	Transcribed locus	---	2.616	0.073	6.795	0.004	1.136	0.800	4.832	0.005
1386052_at	BF290410	Transcribed locus	---	2.573	0.073	0.977	0.879	1.791	0.112	0.961	0.869
1373854_at	AI175795	Transcribed locus	---	0.291	0.073	0.643	0.015	0.189	0.065	0.735	0.016
1386035_at	BG381661	Transcribed locus	---	0.758	0.073	1.074	0.613	1.555	0.226	1.117	0.198
1395393_at	BG671174	Transcribed locus	---	0.701	0.073	0.993	0.892	0.892	0.287	0.857	0.539
1379774_at	AI137801	Transcribed locus	---	1.559	0.073	1.056	0.221	1.805	0.001	1.165	0.019
1377005_at	BM390962	Transcribed locus	---	0.496	0.074	0.231	0.006	0.628	0.043	0.355	0.008
1372532_at	BI289477	Transcribed locus	---	0.676	0.074	2.213	0.002	0.798	0.059	2.038	0.009
1375612_at	AA965147	Transcribed locus	---	0.833	0.074	0.785	0.055	0.757	0.016	0.677	0.009
1383723_at	BF418837	Transcribed locus	---	1.753	0.074	2.025	0.015	1.017	0.111	2.081	0.041
1395991_at	BE107556	Transcribed locus	---	0.580	0.074	0.362	0.013	0.919	0.125	0.487	0.084
1397524_at	AA942689	Transcribed locus	---	1.139	0.074	1.194	0.382	1.009	0.991	0.988	0.039
1382240_at	AI029959	Transcribed locus	---	1.320	0.075	0.534	0.008	1.426	0.121	0.631	0.038
1398211_at	BF413560	Transcribed locus	---	1.009	0.075	0.954	0.921	1.000	0.994	1.122	0.450
1398644_at	AI535104	Transcribed locus	---	2.178	0.075	1.181	0.267	1.713	0.011	1.258	0.260
1391338_at	AI603449	Transcribed locus	---	0.557	0.075	0.532	0.000	1.048	0.217	0.518	0.000
1394135_at	AI639109	Transcribed locus	---	1.225	0.075	0.697	0.013	0.836	0.764	0.964	0.781
1395518_at	BF544403	Transcribed locus	---	0.876	0.076	3.098	0.000	0.418	0.005	2.687	0.015
1388758_at	AI009074	Transcribed locus	---	0.654	0.076	0.431	0.002	0.709	0.106	0.646	0.010
1384615_at	AI071319	Transcribed locus	---	0.883	0.076	0.519	0.003	0.592	0.084	0.402	0.004
1372529_at	BE116914	Transcribed locus	---	0.543	0.076	0.938	0.399	0.476	0.022	1.217	0.031
1373524_at	AA946482	Transcribed locus	---	0.531	0.076	0.324	0.010	0.757	0.446	0.596	0.021
1391990_at	BF405569	Transcribed locus	---	2.215	0.076	0.743	0.072	1.535	0.087	0.944	0.626
1382839_at	AI009109	Transcribed locus	---	0.996	0.077	0.272	0.055	0.999	0.970	0.564	0.129
1393824_at	BG377414	Transcribed locus	---	1.225	0.077	1.087	0.151	1.410	0.261	1.127	0.295
1375733_at	AW520755	Transcribed locus	---	0.261	0.077	0.388	0.004	0.635	0.152	0.373	0.055
1395368_at	BF408886	Transcribed locus	---	0.717	0.077	0.180	0.001	0.663	0.023	0.256	0.060
1381482_at	AI555166	Transcribed locus	---	2.478	0.077	0.525	0.664	0.939	0.105	0.772	0.352
1371773_at	AI179413	Transcribed locus	---	0.964	0.077	0.775	0.020	0.619	0.019	0.860	0.184
1379984_at	AI411147	Transcribed locus	---	0.865	0.077	1.222	0.199	0.867	0.112	1.475	0.049
1395373_at	BF561546	Transcribed locus	---	0.611	0.077	0.559	0.305	0.563	0.071	0.645	0.127
1397766_at	BI291982	Transcribed locus	---	2.236	0.077	0.757	0.062	2.628	0.044	1.065	0.751
1379296_at	AI137435	Transcribed locus	---	0.463	0.077	0.963	0.326	0.935	0.358	1.003	0.827
1382684_at	BI293639	Transcribed locus	---	0.786	0.077	1.316	0.292	1.318	0.088	1.087	0.689
1374773_at	BF398048	Transcribed locus	---	1.565	0.078	1.653	0.040	0.966	0.158	1.258	0.016
1378899_at	BE108523	Transcribed locus	---	0.546	0.078	0.624	0.003	0.526	0.006	0.631	0.041
1376237_at	AI145040	Transcribed locus	---	1.488	0.078	1.682	0.011	0.907	0.625	1.679	0.001
1399129_at	AA924317	Transcribed locus	---	0.768	0.078	0.692	0.030	0.777	0.087	0.780	0.797
1371775_at	AI172057	Transcribed locus	---	0.727	0.078	0.515	0.034	1.368	0.752	0.413	0.020
1394430_at	AI511275	Transcribed locus	---	0.624	0.078	0.414	0.021	0.500	0.049	0.580	0.033
1385826_at	AA860047	Transcribed locus	---	0.813	0.078	0.288	0.005	0.379	0.049	0.352	0.043
1378003_at	BM391860	Transcribed locus	---	2.382	0.079	1.766	0.030	1.942	0.046	1.447	0.518
1383819_at	BI292866	Transcribed locus	---	0.963	0.079	0.781	0.045	0.868	0.071	0.844	0.196
1398956_at	BE113384	Transcribed locus	---	0.804	0.079	0.650	0.009	0.694	0.144	0.670	0.164
1393135_at	BM390238	Transcribed locus	---	0.690	0.079	0.715	0.190	0.820	0.094	1.000	0.998
1376032_at	BF283840	Transcribed locus	---	1.064	0.079	1.160	0.309	1.691	0.056	1.004	0.545

1374598_at	AW914984	Transcribed locus	---	0.842	0.079	0.766	0.018	0.745	0.291	0.746	0.450
1388649_at	BI291470	Transcribed locus	---	0.903	0.079	0.735	0.280	0.814	0.071	0.737	0.067
1372126_at	BI288075	Transcribed locus	---	0.633	0.079	0.654	0.001	0.458	0.026	0.575	0.010
1374259_at	BG378156	Transcribed locus	---	1.792	0.080	0.408	0.006	1.441	0.110	0.588	0.003
1373423_at	AI170766	Transcribed locus	---	0.542	0.080	0.804	0.039	0.825	0.399	0.830	0.078
1384018_at	BG663446	Transcribed locus	---	1.010	0.080	0.949	0.683	0.934	0.168	0.999	0.833
1399109_at	BI281673	Transcribed locus	---	0.479	0.080	0.363	0.000	0.696	0.284	0.457	0.028
1390057_at	AA875554	Transcribed locus	---	0.521	0.080	0.358	0.020	0.322	0.233	0.314	0.089
1399060_at	BE113005	Transcribed locus	---	1.213	0.081	0.750	0.004	1.128	0.381	0.751	0.004
1397046_at	BE120364	Transcribed locus	---	0.707	0.081	0.668	0.177	1.090	0.751	0.707	0.131
1384562_at	AI071755	Transcribed locus	---	2.213	0.081	0.821	0.026	1.625	0.316	1.210	0.202
1380341_at	BE096469	Transcribed locus	---	0.885	0.081	1.084	0.484	0.889	0.071	1.000	0.999
1391342_at	AI058512	Transcribed locus	---	0.587	0.081	0.998	0.971	0.591	0.082	0.999	0.999
1383240_at	BE110753	Transcribed locus	---	1.560	0.082	0.833	0.598	0.815	0.206	1.007	0.797
1386257_at	AA858641	Transcribed locus	---	0.557	0.082	0.377	0.006	0.558	0.176	0.402	0.003
1388738_at	AI411227	Transcribed locus	---	0.272	0.082	0.209	0.002	0.882	0.880	0.184	0.030
1376386_at	BF393799	Transcribed locus	---	0.455	0.082	0.853	0.809	0.957	0.123	1.013	0.808
1382158_at	BF557889	Transcribed locus	---	1.478	0.082	1.486	0.213	2.855	0.017	2.025	0.080
1374312_at	BI297050	Transcribed locus	---	0.764	0.082	1.132	0.462	0.609	0.024	0.843	0.109
1379506_at	AA963909	Transcribed locus	---	1.926	0.083	1.480	0.022	1.001	0.851	1.436	0.117
1391711_at	BM386534	Transcribed locus	---	2.243	0.083	1.433	0.095	2.268	0.093	1.300	0.493
1376860_at	BE105713	Transcribed locus	---	1.389	0.083	0.748	0.014	0.993	0.055	0.897	0.019
1372696_at	AA893807	Transcribed locus	---	0.826	0.083	0.464	0.011	0.799	0.108	0.670	0.015
1395213_at	BI289885	Transcribed locus	---	1.310	0.083	0.867	0.080	1.030	0.978	0.860	0.085
1398992_at	AI410311	Transcribed locus	---	1.670	0.084	0.667	0.020	1.410	0.088	1.070	0.479
1374514_at	BG671893	Transcribed locus	---	1.469	0.084	0.975	0.443	1.753	0.041	0.973	0.462
1393154_at	BM384240	Transcribed locus	---	0.449	0.084	1.109	0.184	0.279	0.000	1.308	0.096
1373336_at	AI411074	Transcribed locus	---	0.785	0.085	0.372	0.000	0.726	0.020	0.384	0.025
1390743_at	BF405616	Transcribed locus	---	1.282	0.085	2.955	0.021	1.261	0.226	2.423	0.058
1377201_at	BE109156	Transcribed locus	---	0.698	0.085	0.267	0.004	0.206	0.037	0.210	0.003
1395483_at	BI296524	Transcribed locus	---	1.921	0.085	0.749	0.981	1.018	0.853	0.930	0.930
1393133_at	BG381252	Transcribed locus	---	0.739	0.086	0.870	0.248	1.041	0.485	1.218	0.990
1385883_at	AI144842	Transcribed locus	---	0.743	0.086	0.671	0.001	0.665	0.074	0.737	0.001
1385542_at	BF402259	Transcribed locus	---	1.614	0.086	1.260	0.079	1.136	0.716	1.191	0.253
1382107_at	AI176848	Transcribed locus	---	1.416	0.086	0.988	0.919	1.760	0.019	1.241	0.096
1384419_at	AA944588	Transcribed locus	---	1.667	0.086	1.354	0.494	2.230	0.052	0.823	0.106
1391329_at	BM387817	Transcribed locus	---	1.297	0.087	1.029	0.896	1.010	0.228	1.004	0.999
1391274_at	BI292056	Transcribed locus	---	1.119	0.087	0.783	0.967	0.822	0.264	0.995	0.971
1382346_at	BF281960	Transcribed locus	---	1.508	0.087	0.979	0.977	1.427	0.617	1.413	0.501
1372024_at	AI104846	Transcribed locus	---	1.106	0.087	2.241	0.003	1.097	0.754	1.719	0.011
1379364_at	BI273752	Transcribed locus	---	0.727	0.087	1.018	0.094	0.688	0.061	0.946	0.488
1378185_at	AW528873	Transcribed locus	---	1.604	0.088	1.493	0.072	1.363	0.077	3.041	0.002
1396378_at	BF412429	Transcribed locus	---	2.109	0.088	2.159	0.070	2.097	0.126	1.739	0.118
1381902_at	BE116321	Transcribed locus	---	1.447	0.088	2.369	0.000	1.190	0.021	1.910	0.001
1376531_at	BF416276	Transcribed locus	---	0.766	0.088	0.529	0.113	0.738	0.086	0.679	0.210
1383216_at	BM390667	Transcribed locus	---	1.769	0.088	2.677	0.000	0.912	0.417	1.997	0.013
1384119_at	AI072851	Transcribed locus	---	1.180	0.088	0.998	0.927	1.005	0.974	0.972	0.179
1377597_at	BI300688	Transcribed locus	---	0.746	0.088	0.389	0.001	1.145	0.224	0.617	0.015
1382754_at	H33080	Transcribed locus	---	0.591	0.088	0.997	0.973	0.788	0.462	0.996	0.972
1376235_at	BI289136	Transcribed locus	---	0.895	0.089	0.496	0.004	0.912	0.142	0.619	0.043
1381058_at	AI548492	Transcribed locus	---	2.339	0.089	0.437	0.012	1.475	0.018	0.618	0.043
1395468_at	BF409952	Transcribed locus	---	0.627	0.089	0.218	0.000	1.869	0.171	0.312	0.023
1390132_at	BF282059	Transcribed locus	---	1.112	0.089	1.377	0.874	1.218	0.203	1.120	0.229
1377082_at	BF567763	Transcribed locus	---	0.598	0.089	1.247	0.771	1.130	0.348	0.761	0.140
1376047_at	BI285321	Transcribed locus	---	0.511	0.090	0.309	0.002	0.646	0.022	0.459	0.009
1378350_at	AA859902	Transcribed locus	---	0.322	0.090	0.160	0.000	0.295	0.090	0.240	0.003
1373999_at	AI406350	Transcribed locus	---	0.647	0.090	0.882	0.265	0.425	0.001	0.708	0.012
1388918_at	BG378074	Transcribed locus	---	0.521	0.090	0.377	0.000	0.647	0.019	0.456	0.013
1392633_at	AI045724	Transcribed locus	---	1.436	0.091	3.173	0.003	1.002	0.820	1.492	0.260
1388607_at	AI177408	Transcribed locus	---	1.717	0.091	1.256	0.069	0.982	0.178	1.306	0.048
1374269_at	BF398756	Transcribed locus	---	0.768	0.091	0.615	0.174	0.627	0.094	0.652	0.204

1372890_at	BM389696	Transcribed locus	---	1.049	0.091	1.097	0.474	1.538	0.097	1.202	0.344
1378631_at	BM388084	Transcribed locus	---	0.895	0.091	0.985	0.622	0.912	0.214	0.950	0.030
1371559_at	AI103384	Transcribed locus	---	0.555	0.091	0.617	0.008	0.537	0.014	0.651	0.007
1382455_at	BG379564	Transcribed locus	---	1.224	0.091	0.734	0.238	2.165	0.055	1.389	0.302
1378237_at	BG376172	Transcribed locus	---	1.450	0.091	1.183	0.058	2.688	0.004	1.598	0.010
1392199_at	BF398981	Transcribed locus	---	0.610	0.091	0.196	0.008	0.348	0.006	0.266	0.013
1391264_at	AA875301	Transcribed locus	---	0.890	0.092	0.478	0.004	0.776	0.125	0.636	0.004
1395601_at	BI302615	Transcribed locus	---	0.864	0.092	0.167	0.004	0.498	0.080	0.344	0.010
1379835_at	BF558512	Transcribed locus	---	0.759	0.092	0.325	0.020	0.246	0.108	0.419	0.037
1377052_at	AW533469	Transcribed locus	---	2.208	0.092	2.481	0.010	5.021	0.006	4.087	0.015
1380155_at	AI137306	Transcribed locus	---	1.882	0.092	1.992	0.012	1.596	0.035	1.497	0.075
1380685_at	AI103408	Transcribed locus	---	1.312	0.092	0.477	0.072	1.004	0.478	0.405	0.056
1397652_at	BE108399	Transcribed locus	---	0.651	0.093	0.203	0.002	0.446	0.099	0.489	0.022
1377444_at	BE120680	Transcribed locus	---	1.293	0.093	0.954	0.754	1.152	0.323	1.022	0.886
1371472_at	BG380581	Transcribed locus	---	1.574	0.093	0.982	0.734	1.048	0.775	0.926	0.743
1393120_at	BG381381	Transcribed locus	---	0.593	0.093	0.967	0.329	0.455	0.005	0.809	0.014
1390466_at	AW531623	Transcribed locus	---	0.611	0.093	0.501	0.001	0.936	0.084	0.497	0.010
1386279_at	AI235655	Transcribed locus	---	0.474	0.093	0.475	0.003	0.489	0.112	0.383	0.027
1383978_at	BM384029	Transcribed locus	---	0.460	0.093	0.744	0.087	0.441	0.007	0.743	0.046
1378132_at	AI716098	Transcribed locus	---	2.341	0.093	2.571	0.031	2.435	0.003	2.618	0.046
1389974_at	BF555171	Transcribed locus	---	0.544	0.094	0.639	0.032	0.461	0.203	0.499	0.202
1396995_at	BG376821	Transcribed locus	---	2.365	0.094	1.227	0.571	2.188	0.048	0.691	0.354
1374066_at	BG376309	Transcribed locus	---	1.004	0.094	1.668	0.034	1.319	0.027	1.804	0.054
1373265_at	BM383832	Transcribed locus	---	1.299	0.094	1.109	0.214	1.498	0.076	0.912	0.556
1380003_at	BI281665	Transcribed locus	---	1.284	0.094	1.782	0.012	0.763	0.043	2.778	0.004
1389372_at	BF394221	Transcribed locus	---	1.450	0.094	0.709	0.016	1.947	0.023	0.917	0.699
1383934_at	BI299169	Transcribed locus	---	0.418	0.094	0.510	0.001	0.630	0.154	0.612	0.000
1393226_at	BI275559	Transcribed locus	---	2.001	0.094	0.912	0.240	1.616	0.102	1.249	0.017
1376820_at	AI045220	Transcribed locus	---	0.592	0.094	0.102	0.000	0.996	0.079	0.123	0.007
1379739_at	BF408431	Transcribed locus	---	0.753	0.094	0.838	0.006	0.991	0.370	0.913	0.378
1399156_at	AA900891	Transcribed locus	---	1.324	0.094	0.611	0.038	1.671	0.018	0.803	0.000
1393298_at	BF566249	Transcribed locus	---	0.993	0.094	1.453	0.012	1.406	0.014	1.395	0.176
1385822_at	AI030314	Transcribed locus	---	0.786	0.095	0.361	0.017	1.076	0.770	0.546	0.048
1383226_at	BI293943	Transcribed locus	---	1.684	0.096	0.532	0.014	1.055	0.442	0.581	0.003
1376698_at	BF418869	Transcribed locus	---	0.854	0.096	0.583	0.073	0.870	0.618	1.006	0.155
1398415_at	BG380708	Transcribed locus	---	0.422	0.096	0.271	0.013	1.155	0.055	0.306	0.027
1374688_at	AA945696	Transcribed locus	---	0.742	0.096	0.259	0.003	0.917	0.825	0.447	0.015
1393174_at	AI412813	Transcribed locus	---	1.576	0.097	1.065	0.553	2.085	0.067	1.136	0.287
1391090_at	BG380796	Transcribed locus	---	0.563	0.097	0.327	0.006	0.564	0.093	0.277	0.006
1384204_at	BG379466	Transcribed locus	---	0.884	0.098	0.400	0.015	0.914	0.879	0.711	0.075
1390792_a_at	AI406827	Transcribed locus	---	1.407	0.098	1.005	0.979	1.001	0.821	1.038	0.369
1380395_at	AI230394	Transcribed locus	---	0.900	0.099	1.768	0.001	0.611	0.036	1.743	0.008
1390545_at	AI178155	Transcribed locus	---	0.622	0.099	0.522	0.020	0.512	0.002	0.552	0.008
1393062_at	BI275419	Transcribed locus	---	0.504	0.099	0.549	0.044	0.371	0.009	0.873	0.216
1374644_at	BM386365	Transcribed locus	---	0.391	0.100	0.404	0.003	0.439	0.052	0.641	0.012
1385755_at	BF396388	Transcribed locus	---	2.153	0.100	1.256	0.098	3.131	0.028	1.939	0.009
1390456_at	AW524471	Transcribed locus	---	0.592	0.100	0.392	0.000	0.679	0.068	0.451	0.000
1386641_at	BF546770	Transcribed locus	---	2.047	0.100	1.441	0.002	1.463	0.009	1.767	0.002
1397214_at	BF288533	Transcribed locus	---	0.321	0.101	0.174	0.007	0.566	0.060	0.236	0.015
1380409_at	BF413455	Transcribed locus	---	0.526	0.101	0.595	0.224	0.762	0.294	1.318	0.251
1391694_at	AW521119	Transcribed locus	---	0.629	0.101	0.245	0.001	0.793	0.181	0.334	0.001
1395414_at	BI296064	Transcribed locus	---	0.348	0.101	0.133	0.009	0.999	0.087	0.425	0.074
1383766_at	BG663338	Transcribed locus	---	0.554	0.102	0.473	0.013	0.478	0.180	0.246	0.014
1374673_at	BI292547	Transcribed locus	---	1.462	0.102	1.226	0.140	1.379	0.319	0.946	0.456
1383540_at	BF551093	Transcribed locus	---	1.000	0.102	0.470	0.006	0.905	0.231	1.070	0.539
1392955_at	BF548909	Transcribed locus	---	0.754	0.102	0.887	0.314	1.055	0.290	0.987	0.892
1389402_at	AI178746	Transcribed locus	---	1.658	0.102	5.277	0.009	1.926	0.106	3.049	0.013
1397015_at	BF386238	Transcribed locus	---	0.597	0.103	0.775	0.191	0.665	0.211	0.753	0.384
1390376_at	BF406135	Transcribed locus	---	1.356	0.103	0.658	0.648	1.900	0.014	1.089	0.550
1391535_at	BF284610	Transcribed locus	---	0.573	0.103	0.205	0.002	0.387	0.011	0.337	0.015
1380023_at	AA997863	Transcribed locus	---	1.788	0.103	1.001	0.996	1.749	0.009	0.808	0.155

1376975_at	AA849719	Transcribed locus	---	1.188	0.104	0.775	0.843	1.056	0.427	0.941	0.831
1376827_at	BE111290	Transcribed locus	---	1.407	0.104	1.189	0.278	0.984	0.941	1.126	0.396
1385150_at	AI045507	Transcribed locus	---	3.133	0.104	1.376	0.087	6.487	0.024	1.042	0.108
1390515_at	AA998383	Transcribed locus	---	1.935	0.104	1.815	0.080	2.007	0.093	1.846	0.060
1393236_at	AI137233	Transcribed locus	---	1.303	0.105	2.782	0.001	1.358	0.143	3.011	0.004
1383593_at	BE113211	Transcribed locus	---	1.260	0.105	0.396	0.002	1.754	0.002	0.442	0.049
1376763_at	AW915423	Transcribed locus	---	1.988	0.105	0.803	0.061	2.117	0.164	0.928	0.848
1390136_at	BE109274	Transcribed locus	---	2.706	0.105	5.883	0.013	2.438	0.013	5.599	0.008
1377681_at	AA925313	Transcribed locus	---	0.755	0.105	0.537	0.040	0.958	0.985	0.689	0.011
1373580_at	BI289991	Transcribed locus	---	0.743	0.106	0.501	0.013	0.816	0.068	0.628	0.107
1388342_at	BI291344	Transcribed locus	---	1.363	0.106	0.836	0.164	1.147	0.634	0.959	0.197
1384214_a_at	AI045459	Transcribed locus	---	0.502	0.106	0.266	0.004	0.753	0.784	0.420	0.036
1373453_at	AA849756	Transcribed locus	---	1.886	0.106	1.369	0.918	0.999	0.993	0.999	0.793
1384462_at	AA819526	Transcribed locus	---	2.068	0.106	1.306	0.824	3.532	0.001	1.143	0.614
1373634_at	AI177753	Transcribed locus	---	0.789	0.107	0.569	0.000	0.809	0.185	0.611	0.007
1389477_at	BI278855	Transcribed locus	---	0.708	0.107	2.024	0.012	0.681	0.082	1.309	0.474
1373859_at	AA819884	Transcribed locus	---	0.641	0.108	0.277	0.000	0.901	0.039	0.357	0.007
1382572_at	AI577469	Transcribed locus	---	0.604	0.108	0.937	0.195	0.983	0.108	0.590	0.095
1396202_at	BF401339	Transcribed locus	---	1.003	0.108	0.889	0.267	1.168	0.399	1.097	0.200
1389522_at	BE109446	Transcribed locus	---	0.420	0.108	0.199	0.004	1.147	0.391	0.425	0.018
1394448_at	BG380768	Transcribed locus	---	0.850	0.108	0.874	0.900	0.568	0.049	1.005	0.695
1375880_at	AI170384	Transcribed locus	---	0.379	0.109	0.253	0.000	0.550	0.007	0.320	0.003
1389337_at	AA946032	Transcribed locus	---	0.728	0.109	0.498	0.028	0.859	0.293	0.802	0.104
1375777_at	BF402633	Transcribed locus	---	0.988	0.109	0.999	0.994	0.448	0.065	0.834	0.108
1376267_at	AA859652	Transcribed locus	---	2.588	0.109	1.116	0.346	7.375	0.009	1.522	0.043
1389411_at	AW435329	Transcribed locus	---	0.631	0.109	0.105	0.003	0.485	0.059	0.273	0.001
1390156_a_at	BF283671	Transcribed locus	---	0.491	0.109	0.328	0.047	0.388	0.062	0.552	0.121
1374113_at	BM387384	Transcribed locus	---	1.783	0.109	1.806	0.015	1.423	0.272	2.432	0.057
1377831_at	BF285316	Transcribed locus	---	0.545	0.109	0.966	0.899	0.517	0.018	0.839	0.042
1397583_at	BF394946	Transcribed locus	---	0.627	0.110	0.356	0.014	0.703	0.925	0.357	0.007
1376275_at	BE101108	Transcribed locus	---	0.762	0.110	0.652	0.038	0.571	0.361	0.855	0.107
1382917_at	AI043869	Transcribed locus	---	0.410	0.110	0.247	0.002	0.480	0.084	0.243	0.004
1382611_at	AA945938	Transcribed locus	---	0.594	0.110	0.810	0.760	1.028	0.403	0.975	0.759
1389736_at	BM392358	Transcribed locus	---	1.604	0.110	0.940	0.372	0.919	0.583	0.939	0.301
1374674_at	AW528792	Transcribed locus	---	0.633	0.110	0.506	0.001	0.848	0.200	0.679	0.082
1382573_at	AI233217	Transcribed locus	---	1.651	0.110	1.021	0.929	0.553	0.022	1.054	0.875
1397881_at	AI575768	Transcribed locus	---	1.181	0.110	0.470	0.011	1.502	0.044	0.551	0.040
1378246_at	AW535196	Transcribed locus	---	1.522	0.111	1.619	0.946	1.544	0.326	1.006	0.599
1375673_at	AI102620	Transcribed locus	---	1.307	0.111	2.011	0.017	1.417	0.140	1.536	0.014
1388524_at	BF284328	Transcribed locus	---	1.211	0.111	0.893	0.050	0.891	0.025	0.633	0.032
1389134_at	BF551369	Transcribed locus	---	1.722	0.111	0.627	0.010	1.351	0.185	0.744	0.043
1392501_at	BE120710	Transcribed locus	---	0.718	0.111	0.497	0.000	0.850	0.682	0.769	0.001
1377823_at	AW531363	Transcribed locus	---	1.688	0.112	1.766	0.022	1.735	0.148	1.533	0.000
1385580_at	AI071620	Transcribed locus	---	1.957	0.112	0.905	0.980	3.249	0.014	2.305	0.021
1378232_at	BF417445	Transcribed locus	---	0.531	0.112	1.670	0.036	0.658	0.006	1.506	0.039
1374879_x_at	AI228249	Transcribed locus	---	1.339	0.112	1.091	0.369	0.874	0.410	1.123	0.250
1376999_at	BF389721	Transcribed locus	---	0.750	0.112	0.549	0.004	0.654	0.277	0.552	0.007
1382395_at	AA963192	Transcribed locus	---	2.570	0.112	1.462	0.329	4.398	0.073	2.691	0.011
1385060_at	BF401036	Transcribed locus	---	1.020	0.113	0.257	0.002	1.014	0.962	0.331	0.020
1376620_at	AI137912	Transcribed locus	---	1.327	0.113	1.229	0.059	1.344	0.062	1.061	0.733
1383123_at	BF559503	Transcribed locus	---	1.263	0.113	0.651	0.004	0.940	0.877	0.908	0.023
1383885_at	BF560882	Transcribed locus	---	1.230	0.113	0.956	0.823	1.380	0.193	0.999	0.549
1384743_at	BF418132	Transcribed locus	---	0.365	0.114	0.590	0.070	0.327	0.001	0.528	0.114
1374729_at	BM385616	Transcribed locus	---	1.712	0.114	2.207	0.026	1.710	0.009	2.625	0.005
1373962_at	AI178556	Transcribed locus	---	2.145	0.114	1.570	0.033	1.359	0.422	1.479	0.004
1376283_at	BG378070	Transcribed locus	---	0.538	0.114	0.139	0.007	0.446	0.004	0.116	0.032
1390034_at	BF393945	Transcribed locus	---	0.938	0.115	0.403	0.025	0.838	0.093	0.496	0.060
1377004_at	AA800184	Transcribed locus	---	0.959	0.115	0.884	0.307	0.975	0.886	0.795	0.299
1388383_at	AI412740	Transcribed locus	---	0.725	0.116	0.552	0.000	0.683	0.001	0.711	0.005
1375781_at	BF419844	Transcribed locus	---	1.271	0.116	0.470	0.075	1.273	0.499	0.443	0.070
1388825_at	BE119400	Transcribed locus	---	0.860	0.116	1.076	0.147	0.764	0.049	0.614	0.017

1393736_at	BE116820	Transcribed locus	---	0.770	0.117	0.318	0.001	0.813	0.044	0.501	0.030
1376800_at	AA892496	Transcribed locus	---	1.392	0.117	1.118	0.517	1.006	0.236	1.003	0.841
1374372_at	BF392147	Transcribed locus	---	0.867	0.117	0.881	0.128	1.118	0.696	0.760	0.166
1388317_at	BE110655	Transcribed locus	---	0.791	0.118	0.658	0.027	0.827	0.121	0.796	0.117
1396461_at	BE117448	Transcribed locus	---	1.394	0.118	0.888	0.451	1.046	0.945	1.050	0.373
1396397_at	AW529321	Transcribed locus	---	1.951	0.118	1.389	0.895	1.241	0.275	1.659	0.083
1391499_at	BF551074	Transcribed locus	---	1.190	0.119	0.836	0.945	0.999	0.999	0.977	0.756
1385881_at	BE100612	Transcribed locus	---	0.390	0.119	0.060	0.003	0.410	0.058	0.059	0.002
1395425_at	BE099398	Transcribed locus	---	0.803	0.119	0.809	0.099	0.877	0.476	0.833	0.078
1393930_at	AI029426	Transcribed locus	---	1.463	0.120	0.600	0.094	1.603	0.181	1.143	0.768
1378565_at	AW435439	Transcribed locus	---	0.827	0.120	0.612	0.060	0.788	0.012	0.686	0.111
1384025_at	AA943432	Transcribed locus	---	0.774	0.120	0.340	0.000	0.725	0.367	0.421	0.035
1373072_at	AI170552	Transcribed locus	---	1.731	0.121	4.978	0.000	1.561	0.086	3.629	0.000
1393314_at	BI289840	Transcribed locus	---	2.039	0.121	0.612	0.128	0.905	0.290	0.702	0.112
1398596_at	AA925896	Transcribed locus	---	1.238	0.121	1.274	0.229	1.672	0.039	1.133	0.268
1389784_at	AI177507	Transcribed locus	---	1.232	0.121	0.665	0.005	1.207	0.174	0.630	0.003
1375028_at	AI409635	Transcribed locus	---	3.355	0.121	2.713	0.017	1.778	0.419	1.011	0.415
1376183_at	AI101484	Transcribed locus	---	0.707	0.122	0.207	0.000	0.786	0.437	0.326	0.007
1390538_at	BF414192	Transcribed locus	---	0.557	0.123	0.752	0.106	0.676	0.016	0.924	0.357
1377412_at	AI146237	Transcribed locus	---	0.494	0.123	0.149	0.002	0.645	0.086	0.178	0.009
1385164_at	BE108640	Transcribed locus	---	1.525	0.123	1.783	0.042	1.002	0.397	1.983	0.059
1379913_at	BE100916	Transcribed locus	---	0.667	0.124	0.395	0.090	0.651	0.119	0.400	0.020
1392604_at	AA997187	Transcribed locus	---	0.264	0.124	0.353	0.003	0.425	0.173	0.561	0.078
1367517_at	BG373057	Transcribed locus	---	1.265	0.124	0.807	0.201	1.089	0.641	0.842	0.251
1382524_at	AA850361	Transcribed locus	---	1.174	0.125	0.510	0.002	0.643	0.148	0.537	0.006
1392251_at	BF397284	Transcribed locus	---	1.431	0.125	0.759	0.124	2.269	0.010	0.981	0.596
1372003_at	BI296755	Transcribed locus	---	1.390	0.125	0.779	0.098	1.498	0.038	0.772	0.034
1378499_at	BF405148	Transcribed locus	---	1.709	0.125	1.427	0.045	1.856	0.064	1.363	0.154
1379265_at	BF398764	Transcribed locus	---	1.354	0.125	1.108	0.491	1.099	0.377	1.040	0.754
1382162_at	BG373568	Transcribed locus	---	1.880	0.126	0.993	0.978	1.304	0.461	1.004	0.715
1377725_at	AI575322	Transcribed locus	---	0.702	0.126	0.466	0.015	0.706	0.295	0.445	0.001
1391936_a_at	BI289110	Transcribed locus	---	0.827	0.126	0.185	0.008	0.679	0.890	0.514	0.017
1372885_at	AI230467	Transcribed locus	---	1.599	0.127	1.914	0.002	1.564	0.067	1.906	0.009
1383954_at	BI273721	Transcribed locus	---	0.386	0.127	0.378	0.001	0.761	0.034	0.401	0.009
1385689_at	BI290860	Transcribed locus	---	0.935	0.127	0.805	0.053	0.702	0.055	0.752	0.075
1385873_at	BM388405	Transcribed locus	---	1.444	0.127	0.895	0.162	1.309	0.131	1.115	0.218
1396326_at	BM390873	Transcribed locus	---	0.702	0.127	0.251	0.002	0.723	0.080	0.336	0.037
1384284_at	BI290838	Transcribed locus	---	0.589	0.127	0.266	0.006	0.509	0.145	0.357	0.021
1391361_at	BF411568	Transcribed locus	---	0.600	0.128	0.226	0.014	0.736	0.154	0.238	0.011
1373583_at	BF396317	Transcribed locus	---	1.605	0.129	0.925	0.158	1.473	0.158	1.727	0.036
1380610_at	AI406521	Transcribed locus	---	1.122	0.129	0.548	0.071	1.220	0.095	0.633	0.121
1376194_at	BM384889	Transcribed locus	---	0.801	0.130	0.300	0.001	0.765	0.024	0.635	0.176
1380081_at	AA819551	Transcribed locus	---	1.497	0.130	1.237	0.170	3.680	0.006	1.301	0.062
1383483_at	BE106581	Transcribed locus	---	0.733	0.130	0.952	0.545	0.805	0.926	0.945	0.088
1375879_at	BE111762	Transcribed locus	---	0.769	0.131	0.414	0.002	0.728	0.051	0.446	0.033
1390873_at	BE118616	Transcribed locus	---	1.359	0.131	0.731	0.113	1.220	0.901	0.568	0.004
1374990_at	AI233786	Transcribed locus	---	0.977	0.131	1.387	0.394	0.796	0.051	1.197	0.104
1375088_at	BF404846	Transcribed locus	---	0.842	0.131	1.960	0.069	1.081	0.222	0.902	0.737
1394785_at	BE329290	Transcribed locus	---	1.650	0.132	0.958	0.244	1.150	0.774	0.899	0.501
1390586_at	AA924192	Transcribed locus	---	1.251	0.132	1.097	0.334	0.819	0.513	1.032	0.958
1376206_at	BF398576	Transcribed locus	---	0.596	0.133	1.614	0.023	0.753	0.216	1.620	0.013
1381303_at	BE107070	Transcribed locus	---	3.235	0.133	1.726	0.130	1.794	0.054	1.742	0.192
1383368_at	BF550060	Transcribed locus	---	0.634	0.133	1.183	0.074	0.725	0.056	1.034	0.062
1384000_at	BF560932	Transcribed locus	---	0.750	0.134	0.651	0.450	0.472	0.004	0.716	0.633
1375538_at	AI230737	Transcribed locus	---	1.474	0.134	1.574	0.022	0.884	0.916	1.310	0.024
1379274_at	AW535515	Transcribed locus	---	0.793	0.134	0.499	0.002	0.809	0.048	0.691	0.160
1398481_at	BF402699	Transcribed locus	---	1.293	0.135	0.451	0.003	1.334	0.193	0.758	0.059
1372164_at	AI600255	Transcribed locus	---	1.396	0.135	0.860	0.831	0.978	0.998	0.885	0.980
1384680_at	AA924336	Transcribed locus	---	1.007	0.135	0.824	0.066	0.993	0.811	0.689	0.053
1384607_at	BE120546	Transcribed locus	---	0.699	0.135	1.017	0.821	0.703	0.139	0.997	0.967
1373818_at	AI408351	Transcribed locus	---	0.443	0.136	0.236	0.004	0.181	0.006	0.451	0.017

1372292_at	AI009732	Transcribed locus	---	0.431	0.137	0.240	0.001	0.394	0.000	0.295	0.001
1394029_at	BF283049	Transcribed locus	---	0.460	0.137	0.630	0.032	0.394	0.038	0.686	0.188
1378536_at	AI638960	Transcribed locus	---	0.787	0.137	0.994	0.921	0.813	0.170	1.068	0.639
1373129_at	BF388415	Transcribed locus	---	0.510	0.137	0.641	0.241	1.040	0.247	0.748	0.311
1389049_at	BM382847	Transcribed locus	---	0.706	0.137	0.402	0.061	0.701	0.857	0.543	0.235
1391145_at	BE112120	Transcribed locus	---	0.535	0.137	0.814	0.132	0.602	0.156	0.931	0.425
1389579_at	BI284372	Transcribed locus	---	0.733	0.137	0.727	0.164	0.706	0.114	0.702	0.087
1383338_at	AA875190	Transcribed locus	---	1.272	0.138	1.716	0.001	1.338	0.079	1.850	0.001
1383064_at	AI137878	Transcribed locus	---	0.658	0.138	0.567	0.068	0.851	0.102	0.613	0.001
1378345_at	BF389196	Transcribed locus	---	0.518	0.139	0.521	0.013	0.487	0.015	0.530	0.015
1394993_at	AW531339	Transcribed locus	---	1.327	0.139	1.159	0.570	1.001	0.986	0.849	0.044
1392490_at	BM390676	Transcribed locus	---	0.557	0.139	0.553	0.019	0.518	0.034	0.527	0.004
1385643_at	AI045069	Transcribed locus	---	1.173	0.139	0.896	0.282	0.831	0.856	1.228	0.242
1394153_at	AA858641	Transcribed locus	---	0.512	0.139	0.214	0.030	0.507	0.138	0.480	0.069
1381686_at	BI276419	Transcribed locus	---	1.096	0.140	1.309	0.160	1.202	0.068	1.236	0.985
1392764_at	BE115434	Transcribed locus	---	0.765	0.141	0.681	0.069	0.764	0.227	0.681	0.122
1371999_at	BI303641	Transcribed locus	---	0.374	0.141	0.187	0.005	0.712	0.003	0.196	0.022
1396993_at	BM390929	Transcribed locus	---	1.609	0.141	1.018	0.829	5.123	0.017	1.225	0.091
1383190_at	BE113297	Transcribed locus	---	0.895	0.142	0.828	0.283	0.892	0.036	0.892	0.162
1390512_at	AI170376	Transcribed locus	---	1.324	0.142	0.851	0.327	4.367	0.068	2.531	0.047
1381685_a_at	BI276419	Transcribed locus	---	1.269	0.142	1.692	0.010	1.114	0.306	1.882	0.014
1384648_at	AA963844	Transcribed locus	---	1.163	0.142	0.794	0.095	2.002	0.144	1.042	0.762
1380340_at	BF387865	Transcribed locus	---	2.769	0.142	1.026	0.930	0.918	0.848	1.062	0.394
1379494_at	AI012029	Transcribed locus	---	0.796	0.143	0.753	0.089	0.800	0.244	0.969	0.360
1383963_at	AW521925	Transcribed locus	---	1.333	0.144	1.587	0.015	0.872	0.215	1.122	0.206
1381414_at	AA964872	Transcribed locus	---	1.469	0.144	1.162	0.583	0.834	0.312	0.771	0.509
1390335_at	AW252589	Transcribed locus	---	1.274	0.144	1.807	0.014	1.056	0.746	1.523	0.021
1390475_at	AI412632	Transcribed locus	---	0.613	0.144	0.880	0.569	1.037	0.714	0.708	0.554
1392046_at	BE121124	Transcribed locus	---	0.563	0.144	1.089	0.718	1.096	0.592	1.177	0.971
1378824_at	BF389173	Transcribed locus	---	0.602	0.144	0.399	0.046	0.977	0.874	0.400	0.050
1372524_at	BG378238	Transcribed locus	---	0.851	0.145	0.710	0.014	0.558	0.001	0.817	0.364
1398051_at	BF392993	Transcribed locus	---	0.853	0.145	1.267	0.329	0.854	0.584	1.457	0.254
1376453_at	BF419074	Transcribed locus	---	0.790	0.146	0.996	0.955	0.983	0.138	0.996	0.896
1398935_at	AI009819	Transcribed locus	---	0.871	0.147	0.854	0.185	0.694	0.230	0.830	0.007
1372912_at	AA851280	Transcribed locus	---	1.242	0.147	0.908	0.541	0.886	0.925	1.339	0.011
1396844_at	AI547818	Transcribed locus	---	1.359	0.147	1.367	0.019	1.123	0.820	1.207	0.275
1373825_at	BG373078	Transcribed locus	---	0.829	0.147	1.129	0.184	1.002	0.860	0.880	0.742
1378620_at	BE104164	Transcribed locus	---	0.681	0.147	0.457	0.015	1.024	0.235	0.533	0.051
1399122_at	BI278603	Transcribed locus	---	1.417	0.147	1.091	0.440	2.738	0.023	1.483	0.025
1382317_at	AI408597	Transcribed locus	---	1.476	0.148	2.538	0.004	1.315	0.232	2.479	0.003
1382824_at	AI059884	Transcribed locus	---	1.488	0.148	1.224	0.178	1.009	0.520	1.072	0.137
1376834_at	AI407992	Transcribed locus	---	0.734	0.148	0.882	0.229	0.729	0.550	0.948	0.102
1376686_at	BI279363	Transcribed locus	---	0.453	0.148	1.550	0.009	0.361	0.027	1.223	0.430
1395455_at	AI713082	Transcribed locus	---	0.634	0.148	0.729	0.064	0.620	0.217	0.985	0.699
1382594_at	AI113090	Transcribed locus	---	0.854	0.149	0.245	0.024	0.796	0.378	0.197	0.039
1389486_at	BE108354	Transcribed locus	---	0.645	0.150	0.249	0.002	0.421	0.003	0.326	0.015
1395909_at	BE105118	Transcribed locus	---	1.010	0.150	0.795	0.026	1.001	0.971	0.803	0.008
1388580_at	AI100850	Transcribed locus	---	0.702	0.150	0.627	0.000	0.744	0.102	0.718	0.002
1390916_at	AI407187	Transcribed locus	---	0.848	0.150	0.676	0.211	1.075	0.615	0.851	0.837
1380379_at	AI228000	Transcribed locus	---	0.577	0.150	0.489	0.007	0.623	0.030	0.531	0.011
1383637_at	AA925807	Transcribed locus	---	1.402	0.150	1.084	0.293	1.087	0.059	0.990	0.997
1396077_at	BF554876	Transcribed locus	---	2.723	0.150	0.719	0.165	3.230	0.013	1.039	0.448
1381078_at	BF409999	Transcribed locus	---	0.839	0.151	0.994	0.947	0.843	0.157	0.995	0.998
1380640_at	BM389373	Transcribed locus	---	1.001	0.151	0.983	0.979	0.771	0.080	1.231	0.993
1374833_at	BF290953	Transcribed locus	---	0.639	0.152	0.175	0.002	0.749	0.339	0.222	0.005
1376401_at	AI412569	Transcribed locus	---	1.315	0.152	2.109	0.008	0.910	0.196	1.999	0.009
1395745_at	AI113308	Transcribed locus	---	0.836	0.152	0.308	0.005	0.478	0.151	0.380	0.010
1377165_at	BF420664	Transcribed locus	---	0.469	0.152	0.229	0.001	0.365	0.019	0.401	0.000
1383051_at	AW915925	Transcribed locus	---	1.174	0.153	0.945	0.684	0.667	0.106	0.850	0.127
1393961_at	AA926088	Transcribed locus	---	0.304	0.153	0.829	0.048	0.275	0.093	0.652	0.016
1372750_at	AI102517	Transcribed locus	---	0.547	0.153	0.796	0.195	0.457	0.072	1.265	0.309

1381592_at	AA926244	Transcribed locus	---	0.609	0.153	0.671	0.095	0.924	0.757	0.637	0.109
1390536_at	BF551311	Transcribed locus	---	0.457	0.153	0.264	0.076	0.541	0.159	0.314	0.028
1381575_at	AI638986	Transcribed locus	---	2.761	0.153	2.038	0.159	1.011	0.797	1.761	0.061
1373367_at	AI556297	Transcribed locus	---	0.811	0.154	0.557	0.000	0.752	0.123	0.653	0.000
1375462_at	BE109177	Transcribed locus	---	0.794	0.154	0.845	0.668	0.648	0.110	0.799	0.025
1376679_at	AI556021	Transcribed locus	---	0.754	0.154	0.938	0.241	0.849	0.022	0.907	0.098
1376906_at	BM391974	Transcribed locus	---	2.163	0.154	1.968	0.007	1.765	0.138	1.615	0.057
1392507_at	AI385280	Transcribed locus	---	0.566	0.155	0.896	0.243	0.521	0.079	0.737	0.036
1390983_at	AA956823	Transcribed locus	---	1.158	0.155	1.182	0.432	1.957	0.628	0.734	0.309
1371517_at	BF283627	Transcribed locus	---	1.980	0.155	1.648	0.083	0.700	0.674	0.791	0.436
1395574_at	BE118358	Transcribed locus	---	2.090	0.155	1.125	0.238	1.220	0.506	1.169	0.239
1385261_s_at	BE103057	Transcribed locus	---	1.433	0.156	0.479	0.086	1.283	0.370	0.814	0.208
1383810_at	AA955678	Transcribed locus	---	0.499	0.156	0.630	0.254	0.332	0.076	0.629	0.464
1395953_at	AA955517	Transcribed locus	---	0.354	0.157	0.610	0.095	0.361	0.075	0.683	0.054
1374327_at	AW531530	Transcribed locus	---	1.073	0.157	1.495	0.206	1.459	0.309	1.284	0.156
1372849_at	AI229183	Transcribed locus	---	0.512	0.157	0.251	0.020	0.640	0.026	0.356	0.000
1388734_at	AA894193	Transcribed locus	---	0.750	0.157	0.925	0.419	0.951	0.751	0.944	0.958
1389392_at	BF399468	Transcribed locus	---	1.125	0.157	1.104	0.393	1.090	0.207	0.974	0.703
1374783_at	BI301183	Transcribed locus	---	0.865	0.157	1.192	0.083	0.848	0.119	0.852	0.404
1385773_at	BF416395	Transcribed locus	---	1.175	0.157	0.416	0.066	1.139	0.072	0.376	0.046
1382915_at	AI237079	Transcribed locus	---	1.588	0.157	1.120	0.147	1.618	0.013	1.254	0.006
1382791_at	AI716238	Transcribed locus	---	1.594	0.158	1.379	0.075	1.415	0.411	2.372	0.125
1374093_at	BE108840	Transcribed locus	---	0.808	0.158	0.371	0.014	1.325	0.273	0.550	0.044
1384896_at	AA997660	Transcribed locus	---	1.295	0.158	0.460	0.087	1.470	0.046	1.098	0.420
1394160_at	AI101945	Transcribed locus	---	1.573	0.158	0.784	0.095	2.093	0.037	0.697	0.011
1396023_at	AW522736	Transcribed locus	---	1.549	0.158	1.215	0.232	1.463	0.221	1.432	0.434
1386470_at	H33577	Transcribed locus	---	0.574	0.159	1.046	0.764	1.139	0.300	1.008	0.941
1395904_at	BF388148	Transcribed locus	---	2.498	0.159	0.490	0.191	1.837	0.136	0.563	0.038
1383575_at	BG376561	Transcribed locus	---	0.774	0.159	0.767	0.628	0.554	0.119	0.566	0.034
1382891_at	BE108241	Transcribed locus	---	1.502	0.159	1.099	0.494	1.018	0.929	0.999	0.996
1375349_at	BI295776	Transcribed locus	---	1.623	0.159	1.032	0.182	4.340	0.011	2.162	0.052
1396029_at	BE120584	Transcribed locus	---	1.141	0.159	0.966	0.902	0.318	0.057	1.040	0.823
1371903_at	BM384012	Transcribed locus	---	0.559	0.160	0.940	0.808	0.274	0.026	0.797	0.410
1392509_at	AA925469	Transcribed locus	---	1.248	0.161	1.087	0.156	1.265	0.710	1.366	0.175
1382609_at	AI058451	Transcribed locus	---	1.811	0.161	1.837	0.141	1.319	0.230	1.217	0.486
1381857_at	AA963157	Transcribed locus	---	1.396	0.161	0.688	0.008	0.808	0.864	0.909	0.228
1385467_at	BF388485	Transcribed locus	---	0.704	0.162	1.000	0.510	0.832	0.206	1.107	0.043
1382412_at	BM389786	Transcribed locus	---	1.114	0.162	0.832	0.048	1.274	0.331	0.927	0.337
1382131_at	AW523674	Transcribed locus	---	1.074	0.163	0.886	0.307	1.286	0.032	0.847	0.441
1385868_at	AA875124	Transcribed locus	---	0.676	0.164	0.846	0.540	0.496	0.079	1.047	0.806
1374052_at	AI599270	Transcribed locus	---	1.398	0.164	1.361	0.059	1.410	0.252	1.281	0.076
1382564_at	AI233574	Transcribed locus	---	0.808	0.164	1.360	0.093	0.669	0.062	1.593	0.061
1376242_at	BF402365	Transcribed locus	---	0.548	0.164	0.208	0.000	1.087	0.181	0.257	0.036
1374559_at	AI171211	Transcribed locus	---	0.508	0.164	0.538	0.004	0.354	0.042	0.586	0.019
1392603_at	AI717425	Transcribed locus	---	0.650	0.165	2.487	0.004	0.542	0.254	2.151	0.012
1372414_at	BI281979	Transcribed locus	---	1.027	0.165	1.047	0.522	1.024	0.245	1.072	0.636
1383576_at	AW917643	Transcribed locus	---	1.355	0.165	0.982	0.403	0.934	0.994	1.061	0.768
1373165_at	BF404539	Transcribed locus	---	0.589	0.165	0.057	0.001	0.663	0.863	0.192	0.006
1385732_at	BE115744	Transcribed locus	---	1.276	0.166	0.506	0.066	0.986	0.995	0.535	0.009
1377021_at	BI303908	Transcribed locus	---	0.502	0.166	1.176	0.668	0.685	0.089	1.128	0.778
1380766_a_at	BF389689	Transcribed locus	---	0.939	0.166	0.959	0.703	0.987	0.863	0.995	0.663
1374633_at	BF284700	Transcribed locus	---	0.795	0.166	0.146	0.000	0.393	0.017	0.163	0.016
1382032_at	AI407730	Transcribed locus	---	0.733	0.167	0.228	0.002	0.303	0.040	0.538	0.037
1376153_at	BE102621	Transcribed locus	---	1.098	0.167	0.994	0.944	1.320	0.156	0.955	0.787
1384546_at	AA924204	Transcribed locus	---	1.175	0.167	3.018	0.014	0.668	0.068	3.284	0.015
1395922_at	BF412539	Transcribed locus	---	0.777	0.168	0.662	0.264	0.896	0.671	0.479	0.663
1374421_at	AA850752	Transcribed locus	---	1.072	0.168	1.079	0.496	1.191	0.457	1.034	0.135
1392618_at	BG379597	Transcribed locus	---	1.181	0.168	1.075	0.793	1.904	0.131	1.434	0.118
1393192_at	AW528963	Transcribed locus	---	0.480	0.169	0.229	0.000	0.631	0.142	0.459	0.001
1391407_at	BF392634	Transcribed locus	---	2.440	0.169	1.704	0.242	1.986	0.500	1.200	0.026
1378325_at	BE098737	Transcribed locus	---	2.069	0.169	0.354	0.004	2.618	0.097	0.358	0.005

1391589_at	BM385772	Transcribed locus	---	1.108	0.169	0.718	0.103	1.458	0.018	0.849	0.198
1372079_at	AI410099	Transcribed locus	---	1.116	0.169	0.922	0.035	1.088	0.182	1.037	0.633
1378139_at	AI412468	Transcribed locus	---	1.420	0.169	0.360	0.017	1.211	0.980	0.359	0.012
1373439_at	AI178491	Transcribed locus	---	1.163	0.169	1.736	0.022	1.284	0.255	1.347	0.032
1382651_at	AA998677	Transcribed locus	---	0.303	0.169	0.062	0.014	0.579	0.182	0.068	0.019
1378395_at	BF411826	Transcribed locus	---	0.596	0.170	0.373	0.004	0.512	0.015	0.504	0.073
1371477_at	BG380735	Transcribed locus	---	1.142	0.170	1.333	0.367	1.142	0.352	1.359	0.116
1391923_at	BG376838	Transcribed locus	---	0.373	0.170	0.113	0.000	0.530	0.033	0.170	0.019
1382404_at	BG669741	Transcribed locus	---	2.003	0.170	2.392	0.004	1.597	0.038	1.937	0.019
1397822_at	BF554794	Transcribed locus	---	0.398	0.170	0.865	0.803	1.097	0.225	0.455	0.268
1384708_at	BF400572	Transcribed locus	---	0.471	0.170	0.354	0.010	0.148	0.037	0.123	0.048
1381075_at	AA956937	Transcribed locus	---	0.816	0.170	0.522	0.002	0.951	0.641	0.479	0.007
1384821_at	AI511134	Transcribed locus	---	0.550	0.170	0.984	0.324	1.387	0.108	1.094	0.320
1380466_at	BG670778	Transcribed locus	---	0.748	0.171	1.042	0.233	0.264	0.001	0.725	0.088
1391526_at	AI029006	Transcribed locus	---	1.260	0.171	0.928	0.477	1.025	0.076	0.649	0.187
1383869_at	AI071350	Transcribed locus	---	1.680	0.171	1.232	0.016	1.281	0.297	1.738	0.000
1396676_at	BF394718	Transcribed locus	---	1.862	0.172	1.044	0.779	1.018	0.925	1.074	0.175
1393806_at	BE107400	Transcribed locus	---	1.063	0.172	0.818	0.233	1.195	0.290	1.328	0.479
1382205_at	AW527509	Transcribed locus	---	0.812	0.173	1.926	0.177	0.821	0.618	2.247	0.072
1389790_at	AI410565	Transcribed locus	---	2.638	0.174	1.872	0.008	2.773	0.012	2.444	0.005
1394460_at	BF564428	Transcribed locus	---	1.162	0.175	0.276	0.006	1.720	0.014	0.610	0.018
1396448_at	BE119407	Transcribed locus	---	1.532	0.175	1.354	0.057	1.573	0.045	1.597	0.088
1384690_at	AI071329	Transcribed locus	---	0.473	0.175	1.014	0.328	0.483	0.172	1.316	0.530
1392598_at	AA899326	Transcribed locus	---	1.071	0.176	0.934	0.513	0.754	0.506	1.022	0.119
1391773_at	BM390802	Transcribed locus	---	0.777	0.176	0.433	0.003	0.680	0.033	0.588	0.019
1371867_at	BE120836	Transcribed locus	---	1.324	0.176	0.967	0.961	1.306	0.169	1.077	0.310
1383434_at	AA997640	Transcribed locus	---	0.666	0.177	0.711	0.008	0.636	0.029	0.436	0.065
1385723_at	BE097133	Transcribed locus	---	1.752	0.177	0.512	0.157	1.338	0.256	1.000	0.186
1374820_at	AI598946	Transcribed locus	---	0.679	0.177	1.091	0.639	0.802	0.241	1.391	0.045
1398335_at	BI285665	Transcribed locus	---	0.717	0.177	0.441	0.029	0.785	0.214	0.611	0.058
1385429_at	AA957452	Transcribed locus	---	0.733	0.177	0.815	0.409	0.841	0.426	1.016	0.637
1393342_at	BG380998	Transcribed locus	---	0.636	0.178	0.482	0.004	0.782	0.764	0.605	0.002
1377711_at	BF284137	Transcribed locus	---	0.891	0.178	0.660	0.030	0.470	0.470	0.481	0.015
1379874_at	BE107929	Transcribed locus	---	0.796	0.178	0.476	0.007	0.675	0.209	0.414	0.015
1384875_at	AW529951	Transcribed locus	---	1.547	0.179	0.405	0.177	1.582	0.459	0.494	0.080
1376097_at	BF416935	Transcribed locus	---	1.203	0.179	0.782	0.587	1.814	0.048	0.986	0.274
1396057_at	AW521804	Transcribed locus	---	0.903	0.180	0.548	0.005	0.940	0.099	0.563	0.006
1376173_at	BI292125	Transcribed locus	---	0.662	0.180	1.140	0.064	0.878	0.044	1.129	0.086
1390248_at	AW142935	Transcribed locus	---	1.496	0.180	1.001	0.965	1.011	0.687	0.999	0.992
1396330_at	AW526516	Transcribed locus	---	0.610	0.180	0.969	0.942	1.008	0.247	0.989	0.935
1375841_at	BI282607	Transcribed locus	---	0.750	0.180	0.346	0.000	0.907	0.597	0.576	0.008
1384812_at	AI229409	Transcribed locus	---	0.664	0.181	0.861	0.081	0.796	0.182	0.773	0.169
1389976_at	BE109682	Transcribed locus	---	0.905	0.181	0.783	0.644	0.998	0.193	0.796	0.798
1389297_at	AI146215	Transcribed locus	---	0.469	0.182	1.154	0.974	0.493	0.003	0.958	0.168
1376991_at	BE095620	Transcribed locus	---	1.281	0.182	0.749	0.288	1.040	0.645	0.678	0.125
1385876_at	AA817826	Transcribed locus	---	1.049	0.183	1.612	0.812	0.688	0.035	1.107	0.981
1392101_s_at	AI175670	Transcribed locus	---	0.809	0.183	1.187	0.101	0.978	0.906	1.237	0.015
1393206_at	BM383684	Transcribed locus	---	1.177	0.183	0.735	0.038	1.786	0.032	0.921	0.191
1375484_at	BG376458	Transcribed locus	---	0.669	0.184	0.825	0.364	0.959	0.687	0.642	0.034
1377934_at	BF387289	Transcribed locus	---	0.860	0.184	0.827	0.302	0.601	0.097	0.726	0.189
1373252_at	AI411930	Transcribed locus	---	1.934	0.184	4.219	0.005	2.816	0.118	4.555	0.003
1388495_at	BI303583	Transcribed locus	---	0.877	0.184	0.506	0.013	1.042	0.069	0.464	0.003
1391460_at	BF408186	Transcribed locus	---	1.052	0.186	0.694	0.024	1.248	0.340	0.981	0.549
1378517_at	AI176472	Transcribed locus	---	0.423	0.187	1.179	0.069	1.481	0.405	1.745	0.186
1376428_at	BF412631	Transcribed locus	---	0.902	0.187	1.007	0.926	0.968	0.535	1.229	0.996
1373807_at	AI175732	Transcribed locus	---	1.011	0.187	0.960	0.580	1.095	0.944	1.020	0.174
1385901_at	BE118197	Transcribed locus	---	1.434	0.187	0.512	0.006	1.317	0.284	0.772	0.032
1391725_at	BI289277	Transcribed locus	---	1.168	0.187	0.418	0.023	0.872	0.712	0.539	0.227
1389724_at	BI274507	Transcribed locus	---	1.227	0.187	0.991	0.227	0.726	0.534	0.805	0.078
1376022_at	BI292196	Transcribed locus	---	1.516	0.188	0.913	0.327	3.205	0.013	1.480	0.030
1375016_at	AI406912	Transcribed locus	---	0.854	0.188	0.739	0.080	0.758	0.042	0.850	0.095

1384261_at	AI072173	Transcribed locus	---	0.790	0.188	0.627	0.020	0.933	0.802	0.546	0.010
1391821_at	BF391706	Transcribed locus	---	0.914	0.188	1.090	0.346	1.100	0.544	1.092	0.352
1373218_at	BG381051	Transcribed locus	---	1.502	0.188	1.165	0.615	0.999	0.959	0.859	0.992
1381948_at	AI547876	Transcribed locus	---	1.392	0.188	0.437	0.086	3.282	0.018	0.667	0.102
1389397_at	AI234012	Transcribed locus	---	0.684	0.189	0.800	0.015	0.673	0.014	0.744	0.015
1382347_at	AA850576	Transcribed locus	---	2.073	0.189	0.755	0.092	1.675	0.028	1.113	0.464
1386798_at	BF552068	Transcribed locus	---	1.678	0.189	0.604	0.048	1.963	0.214	0.919	0.149
1373221_at	BI278478	Transcribed locus	---	1.384	0.189	1.485	0.006	1.403	0.220	1.333	0.017
1373285_at	AI406624	Transcribed locus	---	1.591	0.190	0.588	0.024	1.812	0.061	0.999	0.350
1380068_at	AA964641	Transcribed locus	---	0.525	0.190	0.704	0.511	0.828	0.075	0.683	0.012
1376622_at	BM389574	Transcribed locus	---	0.743	0.190	0.361	0.000	0.527	0.004	0.483	0.005
1392887_at	AI575082	Transcribed locus	---	0.585	0.190	0.218	0.022	0.610	0.037	0.360	0.136
1376706_at	BG373822	Transcribed locus	---	1.306	0.191	0.982	0.935	2.914	0.038	0.693	0.158
1372855_at	BF287135	Transcribed locus	---	0.797	0.191	0.237	0.009	0.843	0.424	0.286	0.011
1371986_at	AI576652	Transcribed locus	---	0.965	0.191	0.408	0.002	0.998	0.270	0.498	0.021
1377151_at	AI102833	Transcribed locus	---	1.973	0.191	2.877	0.008	1.861	0.027	5.355	0.013
1382835_at	BM387260	Transcribed locus	---	0.678	0.192	1.374	0.063	0.898	0.103	0.845	0.411
1379761_at	BE104517	Transcribed locus	---	0.586	0.193	2.548	0.007	0.549	0.077	1.152	0.150
1381091_at	BE101556	Transcribed locus	---	0.670	0.193	1.097	0.949	0.639	0.237	0.977	0.942
1383288_at	BE117716	Transcribed locus	---	1.482	0.193	2.811	0.010	1.115	0.550	2.506	0.022
1393959_at	BI293249	Transcribed locus	---	1.151	0.193	0.568	0.021	1.392	0.141	0.482	0.003
1388978_at	BF283704	Transcribed locus	---	0.655	0.193	0.552	0.001	0.830	0.184	0.662	0.001
1372717_at	BI296012	Transcribed locus	---	1.318	0.193	1.755	0.001	0.934	0.467	1.487	0.007
1395382_at	AW522848	Transcribed locus	---	0.745	0.193	0.950	0.175	0.734	0.084	0.877	0.057
1374123_at	BM384680	Transcribed locus	---	0.670	0.194	0.951	0.295	0.841	0.191	0.852	0.044
1393879_at	BF391763	Transcribed locus	---	0.740	0.194	0.363	0.015	0.667	0.111	0.518	0.083
1376584_at	BE116408	Transcribed locus	---	0.747	0.194	0.403	0.001	0.668	0.112	0.464	0.004
1388768_at	BI285601	Transcribed locus	---	1.306	0.194	1.054	0.498	2.062	0.067	1.231	0.449
1376946_at	BG380358	Transcribed locus	---	0.455	0.194	0.309	0.001	0.521	0.046	0.530	0.008
1389867_at	BI281086	Transcribed locus	---	1.099	0.195	0.544	0.005	1.250	0.240	0.703	0.027
1393743_at	AI453930	Transcribed locus	---	0.540	0.195	2.825	0.002	0.390	0.205	3.780	0.014
1398528_at	BE117514	Transcribed locus	---	1.243	0.195	1.040	0.813	1.244	0.169	0.752	0.364
1383280_at	BG669130	Transcribed locus	---	1.692	0.195	0.687	0.006	2.019	0.007	0.686	0.001
1371823_at	BM392158	Transcribed locus	---	0.835	0.195	0.528	0.001	0.800	0.073	0.618	0.004
1389479_at	AI233750	Transcribed locus	---	1.497	0.196	1.143	0.577	0.989	0.787	1.016	0.812
1397394_at	BF412275	Transcribed locus	---	0.866	0.196	1.116	0.608	0.577	0.191	1.185	0.876
1394487_at	AW526344	Transcribed locus	---	1.123	0.196	0.877	0.094	1.091	0.328	0.768	0.026
1377819_at	AA955441	Transcribed locus	---	1.017	0.196	0.730	0.012	1.412	0.263	0.802	0.011
1390889_at	AI102132	Transcribed locus	---	1.090	0.196	0.874	0.236	0.892	0.790	0.869	0.216
1385761_s_at	BF400633	Transcribed locus	---	1.228	0.197	1.220	0.406	1.411	0.172	0.999	0.978
1389707_at	AW251681	Transcribed locus	---	0.390	0.197	0.509	0.008	0.305	0.016	0.590	0.018
1390239_at	BE112417	Transcribed locus	---	2.543	0.197	0.641	0.291	1.828	0.223	0.631	0.619
1382262_at	BE111891	Transcribed locus	---	1.642	0.197	0.951	0.782	1.872	0.158	0.868	0.765
1389776_at	BE105589	Transcribed locus	---	0.878	0.198	1.721	0.019	0.827	0.154	1.203	0.155
1398348_at	AA945604	Transcribed locus	---	1.557	0.198	1.708	0.187	1.975	0.010	0.873	0.862
1376778_at	AI406670	Transcribed locus	---	0.574	0.198	1.003	0.970	0.983	0.192	0.992	0.954
1395207_at	AW527787	Transcribed locus	---	1.687	0.198	0.673	0.235	1.411	0.127	0.828	0.398
1376588_at	BF284632	Transcribed locus	---	1.245	0.199	1.086	0.872	1.523	0.029	0.817	0.764
1389143_at	BF288139	Transcribed locus	---	0.929	0.199	0.846	0.021	1.066	0.964	0.865	0.031
1385891_at	AI101553	Transcribed locus	---	0.632	0.200	0.411	0.012	1.138	0.801	0.288	0.055
1376635_at	BF283341	Transcribed locus	---	0.811	0.200	0.842	0.381	0.331	0.013	0.520	0.099
1381940_at	AW527798	Transcribed locus	---	1.526	0.200	1.492	0.069	0.826	0.653	1.309	0.274
1383084_at	BG671922	Transcribed locus	---	0.652	0.200	0.314	0.003	0.899	0.671	0.423	0.003
1373836_at	AI236582	Transcribed locus	---	0.755	0.200	0.614	0.005	0.751	0.126	0.628	0.011
1375199_at	BG378641	Transcribed locus	---	1.263	0.202	1.401	0.891	1.521	0.149	0.598	0.072
1379408_at	AW916148	Transcribed locus	---	1.482	0.202	1.046	0.839	0.945	0.931	0.835	0.377
1392625_at	AI578406	Transcribed locus	---	0.995	0.203	1.001	0.972	1.000	0.844	1.001	0.780
1373021_at	AI171823	Transcribed locus	---	0.715	0.203	0.384	0.002	0.706	0.042	0.432	0.010
1378801_at	AI599072	Transcribed locus	---	1.931	0.204	1.034	0.937	1.452	0.370	0.927	0.918
1373967_at	AI229311	Transcribed locus	---	0.490	0.204	0.138	0.000	0.499	0.159	0.331	0.018
1388623_at	BI277003	Transcribed locus	---	1.092	0.205	1.211	0.110	0.999	0.996	0.859	0.270

1394488_at	AW524157	Transcribed locus	---	1.341	0.205	0.216	0.003	0.607	0.016	0.342	0.001
1390153_at	BG378721	Transcribed locus	---	0.604	0.205	0.386	0.000	0.503	0.014	0.358	0.021
1397563_at	AW522171	Transcribed locus	---	0.834	0.205	1.004	0.850	0.824	0.429	0.997	0.361
1389732_at	BM386323	Transcribed locus	---	1.522	0.206	3.112	0.006	1.891	0.109	1.952	0.037
1380529_at	AI059721	Transcribed locus	---	1.375	0.206	0.931	0.275	1.673	0.192	0.665	0.052
1393835_s_at	AA900738	Transcribed locus	---	1.010	0.206	1.289	0.389	1.735	0.115	1.419	0.820
1379630_at	AI105051	Transcribed locus	---	1.835	0.206	1.504	0.051	1.671	0.243	1.340	0.062
1384360_at	BI282303	Transcribed locus	---	1.949	0.206	1.352	0.046	2.139	0.057	0.990	0.995
1392999_at	AA819279	Transcribed locus	---	1.050	0.207	0.893	0.467	1.014	0.316	1.236	0.049
1377682_at	AW522708	Transcribed locus	---	1.626	0.207	0.997	0.967	1.803	0.015	1.251	0.898
1383691_at	BF415419	Transcribed locus	---	1.699	0.207	0.998	0.797	1.265	0.484	1.600	0.356
1376982_at	BI295869	Transcribed locus	---	1.371	0.207	0.649	0.013	1.413	0.196	0.924	0.923
1394742_at	AW534107	Transcribed locus	---	0.965	0.207	0.819	0.183	0.906	0.213	0.720	0.610
1381984_at	AI600142	Transcribed locus	---	1.669	0.207	1.698	0.005	2.768	0.037	1.832	0.001
1379252_at	AW522833	Transcribed locus	---	1.165	0.208	0.725	0.014	0.940	0.817	0.644	0.005
1371872_at	BE108905	Transcribed locus	---	0.824	0.208	0.877	0.249	0.833	0.035	0.896	0.082
1392119_at	BF390340	Transcribed locus	---	1.290	0.209	0.652	0.000	1.111	0.706	0.920	0.318
1392775_at	AI136598	Transcribed locus	---	0.785	0.209	1.296	0.695	0.552	0.219	1.334	0.529
1392432_at	AA998022	Transcribed locus	---	1.257	0.209	0.966	0.600	1.144	0.623	1.170	0.819
1389259_at	AA894084	Transcribed locus	---	1.043	0.210	0.971	0.289	0.957	0.944	0.899	0.944
1377287_at	AA957673	Transcribed locus	---	1.128	0.210	2.377	0.009	0.776	0.711	2.021	0.025
1394509_at	BE114001	Transcribed locus	---	0.406	0.211	0.983	0.768	0.406	0.037	0.996	0.903
1388474_at	AI104523	Transcribed locus	---	0.732	0.211	0.341	0.002	0.739	0.605	0.590	0.032
1397184_at	AI574688	Transcribed locus	---	0.740	0.211	0.308	0.001	1.047	0.302	0.365	0.008
1378105_at	BF289201	Transcribed locus	---	0.670	0.212	0.477	0.043	1.023	0.830	1.233	0.387
1377012_at	AI012630	Transcribed locus	---	0.809	0.213	0.384	0.007	1.142	0.178	0.877	0.391
1378182_at	BI288560	Transcribed locus	---	0.638	0.213	0.990	0.283	1.252	0.122	1.024	0.566
1372379_at	AI177706	Transcribed locus	---	1.534	0.214	1.275	0.336	0.701	0.132	1.206	0.627
1393251_at	BM391286	Transcribed locus	---	0.724	0.214	0.693	0.260	0.748	0.168	0.512	0.030
1391431_at	AI712476	Transcribed locus	---	1.080	0.214	0.810	0.035	1.320	0.105	0.939	0.199
1372779_at	BG373352	Transcribed locus	---	0.965	0.215	1.595	0.003	0.611	0.013	1.262	0.020
1385594_at	AW144020	Transcribed locus	---	0.689	0.215	0.556	0.015	0.453	0.118	0.489	0.016
1382557_at	AA946491	Transcribed locus	---	0.689	0.216	1.018	0.667	0.987	0.290	0.774	0.085
1395071_at	AI010512	Transcribed locus	---	1.184	0.217	0.748	0.252	1.281	0.033	1.472	0.748
1395742_at	AW920352	Transcribed locus	---	1.472	0.218	1.886	0.022	2.604	0.021	2.645	0.033
1385955_at	AI029023	Transcribed locus	---	0.708	0.218	0.998	0.952	0.604	0.382	1.000	0.984
1390864_at	BE107335	Transcribed locus	---	0.639	0.219	0.299	0.024	0.971	0.243	0.689	0.072
1398964_at	AI231773	Transcribed locus	---	0.779	0.219	0.530	0.007	0.873	0.062	0.751	0.007
1372594_at	AI233721	Transcribed locus	---	0.680	0.219	0.600	0.017	0.872	0.503	0.702	0.006
1391752_at	BF394182	Transcribed locus	---	1.948	0.220	0.695	0.057	2.132	0.009	0.706	0.271
1390574_at	BE101126	Transcribed locus	---	1.489	0.220	1.062	0.535	1.661	0.013	1.410	0.053
1373612_at	BM391810	Transcribed locus	---	1.539	0.220	0.841	0.055	1.599	0.044	0.765	0.218
1390583_at	AI228169	Transcribed locus	---	0.752	0.221	1.122	0.735	0.773	0.309	0.825	0.330
1380785_at	BF405178	Transcribed locus	---	1.029	0.221	1.255	0.982	0.873	0.545	1.617	0.153
1374941_at	BF397951	Transcribed locus	---	0.911	0.221	0.945	0.236	1.093	0.174	0.922	0.236
1393350_at	BI284396	Transcribed locus	---	0.617	0.222	1.698	0.097	1.405	0.052	1.080	0.293
1379412_at	BF559875	Transcribed locus	---	0.914	0.222	0.748	0.417	1.174	0.371	0.814	0.560
1375011_at	AA818819	Transcribed locus	---	0.661	0.222	0.384	0.000	0.814	0.741	0.476	0.042
1384217_at	BI276341	Transcribed locus	---	1.270	0.223	1.472	0.009	1.049	0.231	1.480	0.027
1383776_at	AW525120	Transcribed locus	---	1.065	0.223	0.494	0.024	0.999	0.995	0.581	0.041
1377092_at	BF389682	Transcribed locus	---	2.219	0.223	1.639	0.028	1.854	0.109	2.403	0.001
1395474_at	AW530415	Transcribed locus	---	1.256	0.224	0.999	0.562	1.460	0.055	1.064	0.041
1381724_at	BF392468	Transcribed locus	---	1.798	0.224	0.856	0.460	1.003	0.095	0.841	0.288
1388874_at	BE113032	Transcribed locus	---	0.844	0.224	0.799	0.306	0.785	0.111	0.898	0.737
1389491_at	BE102814	Transcribed locus	---	0.777	0.225	2.637	0.040	1.897	0.178	1.857	0.010
1374721_at	AI178647	Transcribed locus	---	0.635	0.226	0.363	0.011	0.821	0.419	0.570	0.004
1383404_at	BI295203	Transcribed locus	---	0.486	0.226	0.466	0.005	0.531	0.006	0.409	0.012
1389379_at	AI011967	Transcribed locus	---	1.387	0.226	0.954	0.957	2.184	0.060	0.958	0.996
1381336_at	BF408248	Transcribed locus	---	0.785	0.227	0.205	0.011	0.707	0.284	0.235	0.012
1383982_at	BE112063	Transcribed locus	---	1.514	0.227	1.643	0.043	1.077	0.285	1.393	0.080
1384668_at	AI070299	Transcribed locus	---	1.291	0.227	0.709	0.097	1.020	0.631	0.791	0.098

1390252_at	AI176825	Transcribed locus	---	1.692	0.228	1.073	0.979	2.281	0.160	1.604	0.154
1380522_at	AI060201	Transcribed locus	---	0.953	0.228	1.121	0.074	0.939	0.160	0.989	0.969
1395631_at	BF418465	Transcribed locus	---	0.740	0.228	0.956	0.101	0.830	0.158	0.978	0.577
1391994_at	AI408264	Transcribed locus	---	1.101	0.228	1.035	0.727	1.433	0.121	1.331	0.041
1378010_at	BG662522	Transcribed locus	---	0.652	0.228	0.527	0.000	1.029	0.542	0.764	0.129
1372442_at	BG673216	Transcribed locus	---	1.119	0.229	0.982	0.477	1.495	0.019	1.349	0.011
1383044_at	BM385117	Transcribed locus	---	1.923	0.229	3.638	0.002	0.906	0.932	3.348	0.009
1382223_at	AA874952	Transcribed locus	---	0.940	0.229	0.820	0.025	0.761	0.259	0.894	0.448
1371898_at	BI287946	Transcribed locus	---	1.714	0.229	2.091	0.071	1.013	0.957	1.364	0.409
1389070_at	AI179506	Transcribed locus	---	1.398	0.229	1.554	0.008	1.113	0.716	1.164	0.245
1374192_at	BE105137	Transcribed locus	---	1.423	0.230	1.157	0.216	1.054	0.230	1.269	0.742
1394598_at	AA956038	Transcribed locus	---	0.707	0.230	0.915	0.942	1.123	0.545	1.049	0.592
1373373_at	BI295011	Transcribed locus	---	1.153	0.230	1.085	0.890	1.217	0.044	1.016	0.454
1390990_at	AI409862	Transcribed locus	---	0.558	0.230	0.345	0.004	0.552	0.021	0.442	0.001
1394235_at	AA800639	Transcribed locus	---	0.698	0.230	0.944	0.755	1.071	0.050	0.478	0.113
1375054_at	AI233709	Transcribed locus	---	0.820	0.230	0.958	0.843	0.636	0.093	1.137	0.150
1375194_at	AI231460	Transcribed locus	---	1.171	0.231	0.273	0.005	1.433	0.720	0.405	0.007
1385453_at	AI145167	Transcribed locus	---	4.501	0.232	0.977	0.617	3.203	0.078	1.242	0.694
1379126_at	AI555608	Transcribed locus	---	0.655	0.232	0.333	0.001	0.770	0.163	0.509	0.020
1379817_at	AI227924	Transcribed locus	---	1.286	0.232	2.259	0.047	0.755	0.148	1.000	0.137
1372227_at	AI177863	Transcribed locus	---	0.625	0.232	0.834	0.303	0.918	0.204	0.666	0.161
1385978_at	AI072788	Transcribed locus	---	2.068	0.232	1.016	0.940	1.855	0.018	1.354	0.056
1396274_at	AI111884	Transcribed locus	---	0.698	0.232	0.490	0.068	1.214	0.516	0.757	0.280
1378531_at	AI555775	Transcribed locus	---	1.617	0.232	0.239	0.015	1.009	0.242	0.249	0.012
1398579_at	AA997808	Transcribed locus	---	1.725	0.233	1.083	0.722	1.132	0.208	1.236	0.042
1384505_at	BI294773	Transcribed locus	---	0.859	0.233	1.065	0.569	0.808	0.075	0.760	0.128
1391566_at	AA818977	Transcribed locus	---	0.996	0.234	0.990	0.962	0.974	0.577	0.679	0.158
1381102_at	BF415341	Transcribed locus	---	0.617	0.234	0.846	0.282	0.665	0.228	1.133	0.317
1374939_at	BE112927	Transcribed locus	---	0.942	0.234	0.606	0.003	1.249	0.811	0.674	0.002
1388688_at	BI296599	Transcribed locus	---	1.475	0.234	1.103	0.201	1.929	0.416	1.050	0.151
1374212_at	AI012753	Transcribed locus	---	1.377	0.235	1.301	0.043	1.926	0.369	1.348	0.069
1379859_at	AA964506	Transcribed locus	---	0.916	0.235	0.915	0.267	0.753	0.086	0.728	0.040
1376911_at	BM386385	Transcribed locus	---	0.758	0.235	0.328	0.000	0.762	0.235	0.307	0.010
1398450_at	BI291373	Transcribed locus	---	1.456	0.236	0.675	0.075	1.596	0.001	0.732	0.023
1394594_at	BM383974	Transcribed locus	---	1.175	0.236	1.430	0.027	1.176	0.347	1.323	0.359
1391916_at	BE116043	Transcribed locus	---	1.016	0.236	0.740	0.002	0.569	0.015	0.811	0.090
1384280_at	AA964152	Transcribed locus	---	0.610	0.237	0.468	0.027	0.526	0.288	0.522	0.020
1381470_at	AI454052	Transcribed locus	---	1.260	0.237	1.580	0.016	1.721	0.010	1.526	0.022
1371491_at	BM390614	Transcribed locus	---	1.287	0.238	1.043	0.575	1.643	0.086	1.007	0.985
1392989_at	BI295986	Transcribed locus	---	0.575	0.238	0.371	0.002	0.693	0.140	0.409	0.003
1386008_at	AW914833	Transcribed locus	---	0.857	0.239	0.529	0.016	1.033	0.304	0.547	0.050
1378146_at	BG380860	Transcribed locus	---	0.760	0.239	1.010	0.731	0.759	0.020	1.006	0.772
1383005_at	BM383579	Transcribed locus	---	0.625	0.239	1.301	0.005	0.680	0.352	1.092	0.419
1371588_at	AA686007	Transcribed locus	---	1.232	0.239	0.684	0.009	1.131	0.091	0.748	0.023
1390747_at	BF412714	Transcribed locus	---	1.039	0.240	0.820	0.701	1.008	0.513	1.006	0.750
1380399_at	BF393255	Transcribed locus	---	1.320	0.240	0.771	0.306	1.203	0.490	0.961	0.751
1389111_at	BF396316	Transcribed locus	---	0.691	0.240	0.664	0.012	0.537	0.032	0.604	0.031
1377327_at	AI008151	Transcribed locus	---	1.538	0.240	1.237	0.182	0.823	0.437	1.124	0.221
1392303_at	AA998501	Transcribed locus	---	0.914	0.240	1.002	0.986	0.851	0.984	1.000	0.999
1385506_at	AW530507	Transcribed locus	---	2.103	0.242	0.530	0.530	1.613	0.162	0.901	0.722
1390493_at	AI556256	Transcribed locus	---	0.866	0.242	2.204	0.028	1.083	0.058	3.241	0.014
1380760_at	BF420433	Transcribed locus	---	0.969	0.242	1.001	0.153	0.524	0.076	1.359	0.299
1380116_at	AI146098	Transcribed locus	---	1.207	0.242	1.207	0.021	1.300	0.057	0.942	0.595
1397430_at	BF403977	Transcribed locus	---	0.638	0.243	0.824	0.826	1.278	0.986	0.972	0.358
1376568_at	AI144997	Transcribed locus	---	1.386	0.243	0.705	0.070	1.683	0.096	0.852	0.421
1378592_at	BF396210	Transcribed locus	---	1.388	0.243	3.101	0.001	1.242	0.314	3.764	0.010
1382148_at	AA923980	Transcribed locus	---	1.139	0.243	2.159	0.072	1.077	0.084	1.987	0.019
1377609_at	BE112251	Transcribed locus	---	1.169	0.243	1.001	0.701	1.025	0.810	1.023	0.668
1393382_at	BE096740	Transcribed locus	---	0.669	0.243	1.013	0.626	0.750	0.637	1.404	0.156
1375561_at	BG372234	Transcribed locus	---	1.432	0.245	1.032	0.378	1.500	0.054	0.993	0.340
1375970_at	AI010423	Transcribed locus	---	0.990	0.245	0.628	0.003	1.043	0.776	0.780	0.002

1391981_at	AI639181	Transcribed locus	---	1.209	0.246	1.004	0.974	0.881	0.532	1.009	0.972
1378014_at	BF405144	Transcribed locus	---	0.846	0.246	0.618	0.010	1.365	0.160	0.974	0.838
1397986_at	BF389825	Transcribed locus	---	1.572	0.246	0.581	0.990	1.532	0.049	0.666	0.493
1373482_at	BI303106	Transcribed locus	---	1.234	0.247	1.265	0.160	1.441	0.119	1.367	0.025
1390735_at	BG375163	Transcribed locus	---	0.897	0.247	1.114	0.795	0.608	0.218	1.426	0.057
1381818_at	BF409711	Transcribed locus	---	0.769	0.248	0.923	0.708	1.022	0.762	1.078	0.673
1385117_at	BE101831	Transcribed locus	---	1.285	0.249	1.008	0.913	1.046	0.837	0.927	0.883
1385731_at	BE113552	Transcribed locus	---	0.588	0.249	0.298	0.025	0.462	0.018	0.386	0.030
1389616_at	BF403163	Transcribed locus	---	0.851	0.250	0.960	0.147	0.826	0.508	0.625	0.036
1393178_at	BF551322	Transcribed locus	---	0.496	0.250	0.875	0.965	0.431	0.243	0.700	0.374
1377850_at	AI178231	Transcribed locus	---	1.564	0.250	0.678	0.945	0.935	0.834	0.819	0.173
1397858_at	AI548704	Transcribed locus	---	3.639	0.250	1.179	0.285	2.967	0.082	1.432	0.233
1386027_at	AI409701	Transcribed locus	---	0.635	0.251	0.130	0.005	0.464	0.185	0.254	0.075
1396957_at	BF404490	Transcribed locus	---	0.555	0.251	0.461	0.059	0.630	0.283	0.517	0.129
1395759_at	AI556251	Transcribed locus	---	0.989	0.251	2.963	0.011	1.269	0.435	1.863	0.041
1380789_at	BF416254	Transcribed locus	---	1.896	0.251	1.258	0.301	1.043	0.297	1.401	0.126
1382002_at	AI230621	Transcribed locus	---	1.231	0.252	0.485	0.024	1.102	0.242	0.370	0.118
1378537_at	BI289126	Transcribed locus	---	1.970	0.253	0.989	0.734	1.001	0.998	1.034	0.896
1367539_at	AI170357	Transcribed locus	---	1.388	0.253	0.716	0.079	1.080	0.679	0.853	0.087
1377421_at	BF562337	Transcribed locus	---	0.838	0.253	0.873	0.021	1.003	0.182	0.990	0.300
1377913_at	AI598485	Transcribed locus	---	1.483	0.253	1.559	0.119	1.127	0.676	1.328	0.838
1380978_at	AI044494	Transcribed locus	---	0.694	0.254	0.904	0.027	0.967	0.803	0.763	0.025
1383866_at	BI293248	Transcribed locus	---	1.010	0.254	0.418	0.001	0.565	0.817	0.417	0.113
1373626_at	AI102507	Transcribed locus	---	1.636	0.255	1.077	0.076	1.831	0.183	1.248	0.013
1384463_at	AW523485	Transcribed locus	---	0.647	0.255	0.603	0.089	1.010	0.973	0.780	0.607
1390199_at	BM389647	Transcribed locus	---	0.935	0.256	1.641	0.001	0.760	0.010	1.412	0.045
1397750_at	AI145087	Transcribed locus	---	1.484	0.256	0.668	0.171	1.038	0.876	0.868	0.253
1374116_at	AA964836	Transcribed locus	---	0.895	0.256	0.885	0.314	0.904	0.083	0.855	0.064
1391183_at	BI290796	Transcribed locus	---	0.491	0.256	1.220	0.223	0.889	0.162	0.828	0.635
1376712_at	AI144967	Transcribed locus	---	0.703	0.256	0.546	0.009	0.836	0.329	0.747	0.085
1372509_at	AI172024	Transcribed locus	---	1.013	0.257	0.936	0.449	0.999	0.431	0.775	0.174
1390734_at	BI291369	Transcribed locus	---	1.681	0.257	0.583	0.044	0.919	0.475	0.612	0.060
1383390_at	AI111644	Transcribed locus	---	0.649	0.257	0.493	0.023	0.566	0.145	0.555	0.048
1382177_at	BF415064	Transcribed locus	---	1.314	0.258	0.970	0.104	4.194	0.004	2.560	0.007
1382372_at	AA858521	Transcribed locus	---	2.033	0.258	1.752	0.002	1.734	0.475	1.662	0.014
1379725_at	AW920459	Transcribed locus	---	1.239	0.259	0.836	0.618	0.986	0.456	0.947	0.410
1372774_at	AI170570	Transcribed locus	---	0.682	0.259	1.299	0.022	0.591	0.011	1.098	0.435
1394573_at	BF288475	Transcribed locus	---	0.950	0.260	0.703	0.090	0.903	0.746	0.608	0.001
1384141_at	BI289930	Transcribed locus	---	1.344	0.260	2.147	0.020	0.849	0.417	1.196	0.322
1382079_at	AI511007	Transcribed locus	---	0.653	0.261	1.103	0.420	1.347	0.570	0.821	0.109
1383687_at	AW435306	Transcribed locus	---	0.726	0.261	0.722	0.131	0.865	0.343	0.780	0.083
1382249_at	AI171858	Transcribed locus	---	1.264	0.262	1.022	0.781	1.423	0.186	1.062	0.231
1390799_at	AI177748	Transcribed locus	---	0.579	0.262	1.172	0.587	0.431	0.002	0.965	0.944
1395964_at	BI301241	Transcribed locus	---	1.051	0.263	0.983	0.097	1.074	0.175	0.718	0.258
1391012_at	BF283210	Transcribed locus	---	0.681	0.263	0.992	0.557	0.770	0.199	1.237	0.740
1393580_at	AW531476	Transcribed locus	---	1.125	0.263	1.611	0.645	1.043	0.668	1.290	0.977
1377700_at	BE111648	Transcribed locus	---	0.971	0.263	0.588	0.001	1.187	0.158	0.784	0.049
1375067_at	AI555354	Transcribed locus	---	0.943	0.264	1.405	0.050	0.834	0.040	1.113	0.221
1383498_at	BG373354	Transcribed locus	---	1.677	0.264	1.890	0.002	1.279	0.942	1.201	0.013
1375035_at	AI169627	Transcribed locus	---	1.215	0.264	0.883	0.199	0.979	0.908	0.868	0.289
1392951_at	AW521231	Transcribed locus	---	0.764	0.264	0.545	0.003	0.702	0.273	0.620	0.007
1376168_at	BE100946	Transcribed locus	---	0.614	0.266	1.000	0.996	0.691	0.062	1.089	0.619
1382132_at	AW524858	Transcribed locus	---	0.801	0.266	0.412	0.011	0.997	0.112	0.500	0.057
1389590_at	AA925513	Transcribed locus	---	0.741	0.266	0.996	0.186	0.705	0.305	0.880	0.208
1383778_at	AW917920	Transcribed locus	---	1.268	0.267	1.193	0.642	1.622	0.013	1.194	0.672
1389700_at	H31078	Transcribed locus	---	1.171	0.267	1.462	0.058	1.256	0.274	1.526	0.193
1383493_at	BE102202	Transcribed locus	---	1.355	0.268	0.606	0.024	1.088	0.484	0.620	0.122
1377852_at	BF410258	Transcribed locus	---	1.999	0.269	1.002	0.989	1.804	0.096	1.003	0.997
1388778_at	BF284876	Transcribed locus	---	0.720	0.270	0.324	0.003	1.406	0.614	0.702	0.037
1378314_at	AA956277	Transcribed locus	---	0.921	0.270	1.100	0.110	0.921	0.275	0.997	0.987
1391441_at	AA899943	Transcribed locus	---	1.011	0.271	0.843	0.756	0.841	0.322	0.957	0.118

1394420_at	BF287027	Transcribed locus	---	1.315	0.271	1.341	0.435	0.995	0.937	1.303	0.478
1383515_at	AW143503	Transcribed locus	---	0.816	0.272	0.328	0.015	0.710	0.138	0.480	0.011
1391549_at	BF288456	Transcribed locus	---	0.764	0.272	0.288	0.003	0.842	0.233	0.282	0.036
1389085_at	BI296359	Transcribed locus	---	0.835	0.272	1.034	0.642	0.862	0.930	1.021	0.985
1377911_at	AI029434	Transcribed locus	---	0.657	0.273	0.652	0.026	0.862	0.354	0.819	0.003
1391476_at	BE113113	Transcribed locus	---	1.332	0.273	0.560	0.010	1.584	0.144	0.731	0.010
1371522_at	BI295010	Transcribed locus	---	1.228	0.274	1.946	0.005	0.898	0.581	2.038	0.000
1372771_at	BI279659	Transcribed locus	---	0.590	0.274	0.419	0.013	0.399	0.025	0.517	0.019
1380452_at	AA964564	Transcribed locus	---	1.605	0.274	1.488	0.841	1.975	0.309	1.345	0.850
1394849_at	BF402012	Transcribed locus	---	1.366	0.275	0.983	0.446	2.193	0.001	0.994	0.985
1380402_at	AA818127	Transcribed locus	---	0.895	0.276	1.970	0.009	0.996	0.281	1.443	0.012
1378441_at	AI176859	Transcribed locus	---	0.540	0.277	0.337	0.005	0.562	0.289	0.289	0.014
1389642_at	H35643	Transcribed locus	---	1.373	0.278	0.887	0.070	2.122	0.010	1.382	0.169
1380437_at	BE104421	Transcribed locus	---	1.005	0.278	0.428	0.002	1.067	0.464	0.534	0.009
1395903_at	BF565954	Transcribed locus	---	1.656	0.279	1.575	0.710	1.355	0.251	1.204	0.581
1376837_at	BE109381	Transcribed locus	---	0.965	0.279	1.270	0.097	0.817	0.896	1.420	0.070
1395563_at	AA875586	Transcribed locus	---	0.562	0.280	0.345	0.093	0.537	0.061	0.293	0.040
1380976_at	BF396723	Transcribed locus	---	1.247	0.280	0.319	0.003	1.316	0.101	0.415	0.002
1390639_at	BM387719	Transcribed locus	---	1.146	0.281	1.020	0.959	0.950	0.779	0.935	0.136
1378736_at	BF391862	Transcribed locus	---	0.915	0.281	0.495	0.029	0.986	0.836	0.528	0.093
1389497_at	BF414808	Transcribed locus	---	0.895	0.282	3.648	0.015	0.781	0.078	2.090	0.109
1372146_at	AA851264	Transcribed locus	---	0.534	0.283	0.802	0.012	0.609	0.040	0.776	0.021
1386701_at	BF565038	Transcribed locus	---	1.235	0.283	0.988	0.974	1.074	0.175	0.935	0.354
1371755_at	AA799607	Transcribed locus	---	0.614	0.284	0.431	0.001	0.561	0.016	0.589	0.004
1382193_at	BI294188	Transcribed locus	---	0.460	0.285	0.508	0.001	0.872	0.331	0.555	0.003
1373569_at	AI013005	Transcribed locus	---	0.839	0.286	1.564	0.233	0.738	0.180	1.165	0.920
1373858_at	BE109064	Transcribed locus	---	0.940	0.288	0.583	0.009	0.876	0.051	0.596	0.019
1389149_at	BM389321	Transcribed locus	---	1.208	0.288	1.251	0.264	1.563	0.143	1.130	0.010
1397573_at	BM391779	Transcribed locus	---	0.894	0.288	1.440	0.049	0.778	0.758	1.467	0.241
1372785_at	BG671790	Transcribed locus	---	1.362	0.288	1.127	0.219	1.206	0.203	1.244	0.113
1391580_at	AI234123	Transcribed locus	---	0.672	0.289	0.574	0.053	0.942	0.649	1.038	0.120
1383366_at	BE107954	Transcribed locus	---	1.523	0.289	0.761	0.053	0.885	0.587	0.612	0.100
1373076_at	AI411577	Transcribed locus	---	0.926	0.289	0.321	0.017	0.835	0.618	0.510	0.046
1390724_at	AW253006	Transcribed locus	---	1.315	0.290	1.177	0.161	1.407	0.139	2.010	0.075
1389456_at	BI296591	Transcribed locus	---	0.716	0.291	0.940	0.616	0.756	0.116	0.868	0.700
1379662_a_at	AI011832	Transcribed locus	---	1.712	0.291	1.412	0.012	1.644	0.430	1.427	0.267
1392666_at	BF554555	Transcribed locus	---	0.718	0.291	0.276	0.044	0.898	0.682	0.327	0.250
1385739_at	BE120816	Transcribed locus	---	1.201	0.291	1.150	0.077	1.410	0.030	1.230	0.020
1396156_at	BE120371	Transcribed locus	---	0.986	0.292	0.514	0.167	0.747	0.203	0.927	0.792
1374164_at	BF410020	Transcribed locus	---	0.909	0.292	0.609	0.022	2.349	0.002	1.872	0.018
1378175_at	AW921557	Transcribed locus	---	0.912	0.292	0.378	0.130	1.356	0.262	0.573	0.022
1388862_at	AI412143	Transcribed locus	---	0.694	0.294	0.650	0.012	0.484	0.027	0.657	0.018
1397485_at	BI298636	Transcribed locus	---	0.691	0.294	0.462	0.010	0.549	0.079	0.646	0.037
1385100_at	AI073049	Transcribed locus	---	1.044	0.295	0.489	0.409	0.943	0.037	0.883	0.376
1377749_at	BE112621	Transcribed locus	---	0.792	0.295	0.839	0.359	0.397	0.146	0.795	0.314
1393331_at	AI575856	Transcribed locus	---	1.466	0.295	11.502	0.001	2.905	0.118	8.103	0.001
1383526_at	AA957027	Transcribed locus	---	1.145	0.295	1.006	0.972	1.310	0.286	1.152	0.988
1394948_at	BI303527	Transcribed locus	---	1.147	0.295	2.795	0.129	0.788	0.278	2.175	0.122
1382668_at	AI232529	Transcribed locus	---	0.863	0.296	0.929	0.259	1.260	0.237	0.813	0.571
1395551_at	BG671371	Transcribed locus	---	0.602	0.296	1.037	0.912	0.496	0.323	1.101	0.389
1386745_at	BF523839	Transcribed locus	---	1.392	0.296	0.542	0.003	1.426	0.303	0.701	0.033
1391167_at	AW532567	Transcribed locus	---	1.388	0.297	0.815	0.140	1.391	0.465	1.025	0.796
1398518_at	AW534099	Transcribed locus	---	1.349	0.297	0.997	0.992	0.990	0.873	1.003	0.801
1378570_at	AA849985	Transcribed locus	---	0.694	0.297	0.318	0.003	1.247	0.643	0.548	0.001
1395655_at	BM383435	Transcribed locus	---	1.202	0.297	0.983	0.295	0.800	0.106	1.043	0.168
1390401_at	BF285365	Transcribed locus	---	1.292	0.298	0.752	0.197	1.401	0.092	0.851	0.182
1372216_at	AI010259	Transcribed locus	---	1.395	0.298	1.069	0.732	0.999	0.639	0.938	0.951
1380692_at	BM387127	Transcribed locus	---	0.578	0.298	0.636	0.063	1.165	0.695	0.850	0.492
1381817_at	AI044318	Transcribed locus	---	0.624	0.300	0.290	0.001	0.583	0.066	0.513	0.003
1379562_at	AA858498	Transcribed locus	---	0.841	0.300	0.413	0.006	0.632	0.463	0.292	0.001
1382469_at	AA900787	Transcribed locus	---	0.861	0.301	0.451	0.001	0.797	0.091	0.519	0.001

1383727_at	BF564921	Transcribed locus	---	1.090	0.302	3.916	0.006	1.039	0.778	1.576	0.057
1398451_at	BI296494	Transcribed locus	---	0.662	0.303	2.579	0.316	0.400	0.077	1.367	0.435
1390341_at	BF396709	Transcribed locus	---	1.030	0.303	0.969	0.397	1.343	0.255	1.005	0.928
1374530_at	AI010048	Transcribed locus	---	0.972	0.304	5.959	0.001	1.299	0.044	4.985	0.004
1388764_at	BM387072	Transcribed locus	---	1.289	0.304	1.007	0.254	1.204	0.065	0.947	0.284
1385956_at	BF289086	Transcribed locus	---	0.653	0.305	0.591	0.032	0.633	0.134	0.539	0.036
1379666_at	BF417824	Transcribed locus	---	1.305	0.305	1.360	0.079	1.317	0.470	1.494	0.637
1383714_at	H32348	Transcribed locus	---	1.227	0.306	1.733	0.001	1.253	0.255	1.842	0.037
1384430_at	BF390040	Transcribed locus	---	1.351	0.306	0.826	0.161	1.326	0.158	0.751	0.999
1386176_at	AA892868	Transcribed locus	---	0.898	0.306	0.997	0.225	2.787	0.100	1.144	0.075
1392645_at	AA998765	Transcribed locus	---	0.735	0.307	0.491	0.013	0.403	0.005	0.437	0.063
1381607_at	AI145754	Transcribed locus	---	1.059	0.307	0.556	0.013	0.709	0.370	0.548	0.178
1388899_at	BE098818	Transcribed locus	---	1.260	0.308	0.677	0.011	1.122	0.977	0.755	0.045
1392946_at	AI029194	Transcribed locus	---	0.799	0.308	0.236	0.001	0.739	0.276	0.331	0.007
1372275_at	BI296757	Transcribed locus	---	0.541	0.309	0.630	0.276	0.619	0.053	0.744	0.098
1372530_at	AA944190	Transcribed locus	---	0.841	0.309	0.824	0.123	0.945	0.840	0.973	0.300
1393341_at	AA955466	Transcribed locus	---	0.819	0.309	0.907	0.036	0.684	0.063	0.902	0.110
1392742_at	AI230806	Transcribed locus	---	0.656	0.310	1.079	0.660	0.366	0.137	0.998	0.245
1379879_at	AI411294	Transcribed locus	---	1.302	0.310	0.655	0.286	0.836	0.650	0.617	0.257
1382605_at	AI234026	Transcribed locus	---	0.697	0.311	1.064	0.882	0.736	0.391	0.934	0.981
1385899_at	BE113381	Transcribed locus	---	0.764	0.311	1.283	0.972	1.090	0.705	1.000	1.000
1378602_at	BE098753	Transcribed locus	---	0.763	0.312	0.900	0.241	0.752	0.010	0.637	0.002
1376157_at	AI236782	Transcribed locus	---	0.764	0.312	0.357	0.033	0.856	0.688	0.676	0.008
1378547_at	AI176027	Transcribed locus	---	0.724	0.312	1.088	0.760	0.545	0.109	0.828	0.615
1383523_at	BE110369	Transcribed locus	---	1.677	0.312	1.710	0.001	2.143	0.002	2.083	0.011
1383632_at	BI295105	Transcribed locus	---	0.757	0.312	1.183	0.072	0.575	0.029	1.282	0.003
1394776_at	AA899386	Transcribed locus	---	0.776	0.313	1.001	0.305	0.780	0.316	1.150	0.065
1374149_at	AW144301	Transcribed locus	---	0.664	0.313	0.434	0.013	0.980	0.935	0.690	0.007
1379625_at	BG664461	Transcribed locus	---	1.244	0.313	0.675	0.006	1.978	0.210	0.941	0.367
1371826_at	BM390536	Transcribed locus	---	0.728	0.314	1.056	0.233	0.759	0.046	1.006	0.361
1374453_at	AW917568	Transcribed locus	---	1.090	0.315	1.250	0.371	0.960	0.227	1.056	0.598
1397290_at	AI408310	Transcribed locus	---	0.843	0.315	0.429	0.023	1.009	0.965	0.488	0.015
1398217_at	BE108367	Transcribed locus	---	1.156	0.315	0.645	0.753	1.221	0.797	1.214	0.140
1375946_at	BF415909	Transcribed locus	---	0.931	0.315	0.578	0.004	1.001	0.986	0.624	0.002
1391486_at	BM388409	Transcribed locus	---	0.819	0.315	0.738	0.065	0.877	0.792	1.041	0.337
1378516_at	BF409076	Transcribed locus	---	0.736	0.316	0.432	0.022	1.489	0.819	0.405	0.063
1397889_at	BF402043	Transcribed locus	---	0.716	0.316	0.965	0.525	1.147	0.104	1.042	0.358
1383113_at	AW523077	Transcribed locus	---	1.154	0.317	1.164	0.416	1.042	0.264	0.951	0.729
1390121_at	BM391112	Transcribed locus	---	0.970	0.317	0.998	0.982	0.795	0.490	0.915	0.055
1390368_at	AI716535	Transcribed locus	---	0.804	0.318	0.550	0.036	0.929	0.064	0.575	0.054
1382054_at	BF285731	Transcribed locus	---	0.606	0.318	1.100	0.491	0.980	0.475	1.626	0.774
1383473_at	BF551504	Transcribed locus	---	1.063	0.318	1.041	0.771	1.179	0.745	1.001	0.521
1393284_at	BF567391	Transcribed locus	---	1.263	0.319	0.938	0.927	0.979	0.885	1.003	0.984
1377430_at	BF413556	Transcribed locus	---	1.249	0.319	0.937	0.037	1.484	0.090	1.130	0.822
1372539_at	AA801220	Transcribed locus	---	1.174	0.320	0.430	0.022	1.570	0.164	0.313	0.022
1389376_at	BE113330	Transcribed locus	---	0.954	0.320	0.287	0.000	0.715	0.089	0.381	0.012
1388478_at	BE108225	Transcribed locus	---	1.037	0.320	1.663	0.001	1.436	0.960	1.852	0.002
1373707_at	BM382865	Transcribed locus	---	1.270	0.321	1.593	0.017	1.668	0.452	1.309	0.002
1391594_at	BI295733	Transcribed locus	---	1.583	0.321	1.061	0.676	1.412	0.621	0.886	0.912
1398427_at	AW526160	Transcribed locus	---	2.085	0.321	3.049	0.013	0.814	0.085	2.174	0.056
1372467_at	AA943794	Transcribed locus	---	0.739	0.322	0.522	0.045	0.698	0.197	0.518	0.133
1373892_at	AA945986	Transcribed locus	---	0.776	0.322	0.622	0.016	0.763	0.006	0.779	0.004
1393571_at	AA963158	Transcribed locus	---	1.440	0.322	0.729	0.113	0.639	0.003	0.819	0.231
1389405_at	BG378880	Transcribed locus	---	1.173	0.323	0.502	0.027	1.091	0.260	0.692	0.021
1388872_at	BI290053	Transcribed locus	---	0.459	0.324	0.404	0.006	0.521	0.185	0.381	0.006
1376575_at	BI302686	Transcribed locus	---	1.317	0.324	1.237	0.005	1.853	0.030	1.505	0.001
1377093_at	BE106555	Transcribed locus	---	1.243	0.325	1.199	0.392	1.151	0.476	0.852	0.211
1373229_at	AI407946	Transcribed locus	---	1.572	0.325	0.821	0.088	1.671	0.717	0.732	0.070
1383170_at	AW143788	Transcribed locus	---	0.751	0.326	1.081	0.715	1.177	0.777	1.503	0.574
1377517_at	AA945491	Transcribed locus	---	1.124	0.326	1.029	0.186	0.991	0.959	1.034	0.668
1397764_at	BG379719	Transcribed locus	---	1.686	0.327	1.721	0.045	1.410	0.497	1.499	0.061

1374174_at	AI555195	Transcribed locus	---	1.751	0.328	1.101	0.580	2.119	0.550	0.868	0.319
1381076_at	BF391525	Transcribed locus	---	0.839	0.329	1.395	0.068	0.614	0.030	1.048	0.225
1386089_at	BF548514	Transcribed locus	---	1.709	0.329	1.020	0.557	0.795	0.296	1.024	0.550
1394546_at	AI556229	Transcribed locus	---	0.815	0.330	0.099	0.000	0.592	0.051	0.206	0.008
1393024_at	BI300589	Transcribed locus	---	0.708	0.331	0.395	0.001	0.582	0.094	0.618	0.010
1397480_at	BF548515	Transcribed locus	---	1.062	0.331	0.992	0.808	1.004	0.945	0.996	0.997
1372822_at	BI287226	Transcribed locus	---	0.794	0.331	0.655	0.015	0.979	0.774	0.763	0.010
1391016_at	AI235914	Transcribed locus	---	1.135	0.331	1.357	0.725	0.576	0.084	1.361	0.556
1379797_at	AI229704	Transcribed locus	---	1.441	0.331	1.664	0.094	1.782	0.025	1.081	0.150
1378103_at	AI406799	Transcribed locus	---	1.301	0.332	1.136	0.391	1.093	0.605	1.146	0.838
1397108_at	BE110342	Transcribed locus	---	2.062	0.332	1.159	0.343	1.906	0.028	1.281	0.166
1390526_at	BI289484	Transcribed locus	---	1.131	0.332	0.588	0.005	1.000	0.152	0.560	0.004
1393577_at	AI058546	Transcribed locus	---	1.638	0.332	0.933	0.984	1.568	0.200	0.815	0.076
1377162_at	BF390386	Transcribed locus	---	0.834	0.332	1.369	0.137	0.599	0.107	1.113	0.127
1390117_at	BG372455	Transcribed locus	---	1.136	0.334	0.887	0.545	0.961	0.830	0.648	0.040
1394209_at	AI236275	Transcribed locus	---	0.633	0.334	0.258	0.017	0.679	0.238	0.306	0.017
1381974_at	AI101499	Transcribed locus	---	0.478	0.335	0.594	0.009	0.377	0.015	0.439	0.001
1382969_at	AI029559	Transcribed locus	---	1.501	0.335	0.504	0.016	1.024	0.722	0.393	0.001
1377770_at	AI168965	Transcribed locus	---	0.849	0.335	0.826	0.405	0.639	0.072	0.804	0.425
1376331_at	BI295137	Transcribed locus	---	0.647	0.335	0.389	0.117	0.640	0.054	0.632	0.245
1389692_at	BM391905	Transcribed locus	---	1.004	0.336	0.462	0.065	0.567	0.247	0.467	0.012
1397854_at	BI275309	Transcribed locus	---	0.626	0.336	0.743	0.068	1.072	0.381	0.679	0.043
1375370_at	BE119626	Transcribed locus	---	1.443	0.336	2.012	0.034	1.670	0.278	1.501	0.013
1390499_at	BG380393	Transcribed locus	---	0.696	0.337	0.680	0.028	0.697	0.338	0.683	0.034
1389565_at	BE113491	Transcribed locus	---	0.904	0.337	0.332	0.009	1.482	0.830	0.344	0.060
1374335_at	AA800786	Transcribed locus	---	2.171	0.338	0.791	0.075	2.124	0.373	0.893	0.440
1388437_at	AI103153	Transcribed locus	---	1.123	0.338	0.530	0.005	1.037	0.771	0.491	0.032
1382568_at	BE098457	Transcribed locus	---	1.430	0.338	2.730	0.000	0.833	0.648	1.987	0.009
1376577_at	AI145247	Transcribed locus	---	0.650	0.339	0.220	0.000	0.771	0.386	0.290	0.002
1377185_at	BG667451	Transcribed locus	---	1.542	0.340	0.392	0.024	1.449	0.021	0.658	0.180
1382953_at	AI043711	Transcribed locus	---	1.612	0.341	1.061	0.647	0.941	0.704	1.148	0.873
1399059_at	BI283868	Transcribed locus	---	1.059	0.341	1.229	0.090	0.903	0.106	1.107	0.166
1382636_at	AA899383	Transcribed locus	---	1.296	0.342	0.778	0.069	0.760	0.559	0.863	0.009
1397536_at	BF564825	Transcribed locus	---	1.466	0.342	1.166	0.629	1.506	0.176	1.285	0.248
1373829_at	AI412658	Transcribed locus	---	1.179	0.343	1.065	0.814	0.935	0.345	0.937	0.817
1372175_at	BE112899	Transcribed locus	---	0.833	0.343	0.650	0.000	1.001	0.836	0.664	0.007
1398346_at	BI275581	Transcribed locus	---	0.763	0.343	0.732	0.104	0.525	0.080	0.962	0.431
1378778_a_at	BF394727	Transcribed locus	---	1.459	0.343	1.234	0.349	1.901	0.004	1.082	0.415
1372231_at	AA893532	Transcribed locus	---	0.948	0.343	1.723	0.013	0.921	0.450	1.499	0.038
1377111_at	BI295188	Transcribed locus	---	0.929	0.343	2.743	0.058	0.312	0.136	2.107	0.058
1390985_at	AA956519	Transcribed locus	---	0.855	0.344	0.460	0.018	0.898	0.370	0.610	0.403
1389430_at	AI176172	Transcribed locus	---	0.768	0.344	0.603	0.043	0.534	0.236	0.536	0.017
1383112_at	BF550315	Transcribed locus	---	1.650	0.344	0.731	0.160	1.448	0.071	0.644	0.066
1398392_at	BF405932	Transcribed locus	---	0.650	0.345	0.404	0.009	0.942	0.445	0.793	0.096
1374476_at	AA866267	Transcribed locus	---	0.977	0.346	1.057	0.524	1.354	0.745	1.493	0.066
1380225_at	BF396725	Transcribed locus	---	0.863	0.347	0.975	0.537	1.211	0.429	0.985	0.201
1376627_at	BF550404	Transcribed locus	---	1.065	0.347	1.465	0.248	1.350	0.567	1.604	0.077
1378840_at	BF402541	Transcribed locus	---	0.606	0.347	0.804	0.899	0.968	0.794	0.969	0.881
1383510_at	AI230360	Transcribed locus	---	1.099	0.347	1.049	0.904	0.664	0.043	1.013	0.572
1374609_at	AI011183	Transcribed locus	---	1.032	0.348	0.497	0.001	0.885	0.563	0.624	0.015
1382060_at	BE115085	Transcribed locus	---	1.190	0.348	0.256	0.001	1.037	0.326	0.408	0.101
1382633_at	BE120748	Transcribed locus	---	1.095	0.349	1.130	0.751	1.204	0.533	1.183	0.738
1393153_at	BG663023	Transcribed locus	---	1.175	0.349	0.547	0.014	1.411	0.020	0.508	0.001
1375721_at	BF408438	Transcribed locus	---	1.028	0.349	0.525	0.217	1.004	0.907	0.525	0.171
1382308_at	AI717668	Transcribed locus	---	1.176	0.350	0.504	0.036	1.087	0.907	0.496	0.044
1374880_at	AW251285	Transcribed locus	---	0.886	0.351	1.103	0.169	0.889	0.338	1.510	0.169
1396083_at	BM390018	Transcribed locus	---	0.584	0.352	1.406	0.180	0.616	0.218	0.986	0.198
1374081_at	AI011704	Transcribed locus	---	0.702	0.352	0.540	0.002	0.762	0.284	0.457	0.002
1394569_at	AI549154	Transcribed locus	---	1.716	0.352	0.777	0.214	1.787	0.069	0.732	0.198
1382760_at	AA899481	Transcribed locus	---	0.894	0.353	2.107	0.267	0.766	0.192	2.129	0.027
1384270_at	BG375371	Transcribed locus	---	0.799	0.353	0.940	0.897	0.892	0.653	0.580	0.021

1372354_at	BM389898	Transcribed locus	---	1.602	0.354	6.511	0.002	2.602	0.009	7.278	0.003
1374918_at	BM392219	Transcribed locus	---	0.734	0.354	1.387	0.398	1.004	0.669	1.858	0.079
1373249_at	AA817861	Transcribed locus	---	0.758	0.355	0.712	0.182	0.522	0.298	0.864	0.301
1372763_at	AI407545	Transcribed locus	---	0.445	0.355	0.354	0.004	0.706	0.379	0.469	0.009
1394570_at	BF284360	Transcribed locus	---	0.812	0.355	0.603	0.004	0.708	0.272	0.796	0.014
1375517_at	AI171654	Transcribed locus	---	1.380	0.356	0.669	0.000	1.051	0.863	0.878	0.283
1384926_at	AA964975	Transcribed locus	---	0.496	0.357	0.469	0.041	0.802	0.604	1.089	0.765
1375639_at	AA850881	Transcribed locus	---	0.632	0.357	0.931	0.448	0.603	0.022	1.152	0.463
1390198_at	AW523642	Transcribed locus	---	0.736	0.358	0.236	0.014	0.836	0.178	0.384	0.014
1390129_at	AI177861	Transcribed locus	---	0.991	0.358	1.166	0.166	0.966	0.739	0.952	0.794
1398333_at	AI598434	Transcribed locus	---	0.255	0.359	1.549	0.036	0.159	0.008	0.988	0.953
1375760_at	AI070270	Transcribed locus	---	0.851	0.359	0.966	0.668	0.898	0.189	0.846	0.290
1384745_at	BE111824	Transcribed locus	---	1.647	0.359	1.093	0.839	1.373	0.177	1.406	0.717
1378007_at	BE103359	Transcribed locus	---	0.722	0.360	0.380	0.009	0.958	0.200	0.564	0.153
1397244_at	AI535406	Transcribed locus	---	0.980	0.360	1.107	0.812	1.025	0.925	1.264	0.169
1392413_at	BE111448	Transcribed locus	---	0.892	0.360	1.052	0.734	0.764	0.025	1.019	0.407
1372220_at	BI278846	Transcribed locus	---	1.231	0.360	1.017	0.182	1.228	0.032	1.083	0.152
1376400_at	BG380445	Transcribed locus	---	1.743	0.362	2.424	0.016	1.387	0.438	1.105	0.033
1382343_at	AA999037	Transcribed locus	---	1.281	0.362	1.668	0.021	0.936	0.551	1.585	0.122
1381333_at	BI294382	Transcribed locus	---	1.495	0.362	0.722	0.012	0.980	0.943	1.024	0.961
1397265_at	AW529600	Transcribed locus	---	1.311	0.362	0.654	0.266	1.135	0.181	0.781	0.103
1384907_at	AI411835	Transcribed locus	---	0.606	0.364	0.280	0.004	0.457	0.073	0.373	0.043
1391877_at	BF405044	Transcribed locus	---	1.287	0.365	0.940	0.549	1.286	0.825	0.668	0.053
1389241_at	AA800593	Transcribed locus	---	1.072	0.366	0.730	0.009	1.133	0.093	0.908	0.532
1376318_at	BE113300	Transcribed locus	---	0.950	0.366	0.995	0.480	0.897	0.297	1.002	0.327
1376979_at	BF393959	Transcribed locus	---	0.948	0.366	0.890	0.403	2.419	0.054	0.926	0.815
1394474_at	BF396804	Transcribed locus	---	1.022	0.367	0.982	0.890	0.661	0.980	1.511	0.158
1383577_at	AA859277	Transcribed locus	---	0.819	0.367	0.741	0.013	0.834	0.393	0.521	0.063
1371906_at	BF288092	Transcribed locus	---	1.064	0.369	0.871	0.953	1.331	0.175	0.870	0.289
1372749_at	AI009786	Transcribed locus	---	1.692	0.369	0.895	0.154	1.384	0.198	0.827	0.037
1382306_at	AW919478	Transcribed locus	---	0.798	0.370	0.984	0.988	0.749	0.380	1.007	0.997
1395325_s_at	BF564628	Transcribed locus	---	0.726	0.370	1.111	0.889	0.570	0.100	1.043	0.627
1382795_at	AI228346	Transcribed locus	---	0.789	0.370	0.805	0.116	1.014	0.995	0.971	0.865
1383466_at	BG667930	Transcribed locus	---	0.601	0.370	0.272	0.023	0.717	0.128	0.302	0.012
1396302_at	BM389727	Transcribed locus	---	0.816	0.371	0.904	0.170	0.896	0.473	1.039	0.517
1397225_at	AA875647	Transcribed locus	---	1.252	0.372	0.712	0.312	1.701	0.211	0.771	0.269
1396772_at	BE116581	Transcribed locus	---	0.591	0.373	0.985	0.100	0.677	0.307	1.061	0.944
1392964_at	BF559822	Transcribed locus	---	1.872	0.373	1.947	0.050	1.356	0.580	1.902	0.059
1377782_at	BF402614	Transcribed locus	---	0.807	0.373	1.002	0.986	0.972	0.869	0.947	0.995
1374001_at	AA851818	Transcribed locus	---	0.925	0.374	0.676	0.192	0.937	0.540	0.813	0.129
1373529_at	BE117883	Transcribed locus	---	0.781	0.375	0.696	0.003	0.520	0.004	0.826	0.027
1391880_at	AA893670	Transcribed locus	---	0.839	0.375	0.998	0.978	0.641	0.012	0.952	0.331
1382698_at	AI030699	Transcribed locus	---	1.222	0.375	0.384	0.006	1.208	0.511	0.595	0.062
1371537_at	AI179422	Transcribed locus	---	1.200	0.376	1.553	0.649	4.643	0.046	1.798	0.147
1373180_at	AI227919	Transcribed locus	---	0.741	0.376	0.729	0.001	0.718	0.014	0.809	0.005
1377366_at	BF389753	Transcribed locus	---	0.532	0.377	0.541	0.020	0.395	0.016	0.554	0.026
1374641_at	BF397653	Transcribed locus	---	1.753	0.377	1.943	0.103	1.487	0.229	1.925	0.026
1374946_at	BI296261	Transcribed locus	---	0.647	0.377	1.054	0.863	0.634	0.623	0.818	0.358
1381627_at	AW529790	Transcribed locus	---	1.040	0.377	1.017	0.655	1.092	0.805	1.124	0.407
1385675_at	BG376858	Transcribed locus	---	1.540	0.378	0.983	0.984	0.999	0.989	1.004	0.991
1376341_at	BM388895	Transcribed locus	---	1.553	0.378	0.563	0.151	1.564	0.348	0.774	0.102
1388558_at	AI171802	Transcribed locus	---	1.161	0.379	0.700	0.004	0.866	0.238	0.870	0.048
1381899_at	AW534794	Transcribed locus	---	1.749	0.379	1.236	0.612	2.082	0.056	1.361	0.216
1390921_at	BG373223	Transcribed locus	---	1.119	0.379	0.578	0.025	1.186	0.043	1.167	0.083
1380606_at	BF404346	Transcribed locus	---	1.339	0.381	1.045	0.482	0.755	0.373	1.050	0.753
1377990_at	BF396815	Transcribed locus	---	0.843	0.382	0.926	0.698	0.926	0.914	0.656	0.039
1381476_at	BF416405	Transcribed locus	---	1.067	0.382	0.719	0.978	0.947	0.304	0.856	0.205
1372332_at	AI170687	Transcribed locus	---	1.624	0.384	0.804	0.117	4.965	0.004	1.440	0.290
1393410_at	BG666397	Transcribed locus	---	1.845	0.385	1.695	0.328	1.448	0.323	4.043	0.025
1376744_at	BI289572	Transcribed locus	---	1.001	0.385	0.865	0.234	0.945	0.169	1.014	0.070
1377394_at	BF387305	Transcribed locus	---	1.083	0.386	0.469	0.042	1.123	0.732	0.592	0.051

1390813_at	AI236624	Transcribed locus	---	1.193	0.387	0.681	0.017	1.377	0.146	0.958	0.830
1394643_at	AA819409	Transcribed locus	---	0.969	0.387	1.191	0.152	1.090	0.227	1.188	0.406
1380718_at	AI600021	Transcribed locus	---	1.226	0.388	0.472	0.021	1.008	0.912	0.774	0.018
1372502_at	AI579645	Transcribed locus	---	0.400	0.388	0.312	0.023	0.475	0.011	0.273	0.061
1379272_at	AA963084	Transcribed locus	---	0.816	0.388	0.791	0.061	0.868	0.190	0.663	0.496
1367545_at	AI710043	Transcribed locus	---	1.143	0.389	0.919	0.208	0.604	0.094	0.823	0.361
1377975_at	AI100827	Transcribed locus	---	0.819	0.389	0.562	0.001	1.004	0.853	0.584	0.031
1379785_at	BI275894	Transcribed locus	---	0.846	0.389	1.405	0.008	1.319	0.471	1.412	0.030
1375943_at	BI288873	Transcribed locus	---	0.828	0.389	0.194	0.000	0.940	0.858	0.302	0.001
1372802_at	AI172500	Transcribed locus	---	1.387	0.390	1.656	0.032	0.865	0.971	1.608	0.084
1378790_at	AW535379	Transcribed locus	---	0.815	0.390	1.079	0.979	0.819	0.381	1.012	0.523
1373932_at	BE098739	Transcribed locus	---	1.382	0.390	5.095	0.011	1.766	0.007	2.093	0.016
1389730_at	AI176502	Transcribed locus	---	1.119	0.391	0.515	0.008	0.820	0.576	0.708	0.040
1375005_at	BF403824	Transcribed locus	---	1.248	0.392	0.823	0.943	1.053	0.717	0.561	0.506
1397531_at	BF522208	Transcribed locus	---	0.808	0.392	0.682	0.016	0.874	0.011	0.663	0.002
1391552_at	BM391661	Transcribed locus	---	0.805	0.392	0.503	0.087	0.619	0.140	0.362	0.011
1392091_at	AI043891	Transcribed locus	---	1.001	0.393	1.352	0.189	1.385	0.509	1.101	0.682
1388486_at	BG671315	Transcribed locus	---	0.866	0.393	0.266	0.000	1.273	0.095	0.329	0.032
1388735_at	BF405161	Transcribed locus	---	1.367	0.393	1.059	0.755	1.266	0.294	0.999	0.749
1395294_at	BE106134	Transcribed locus	---	1.358	0.394	0.544	0.241	1.693	0.337	0.752	0.008
1379886_at	AA997880	Transcribed locus	---	1.008	0.394	1.072	0.569	1.092	0.706	1.099	0.427
1374714_at	BI284781	Transcribed locus	---	0.592	0.395	0.578	0.015	0.948	0.888	0.537	0.003
1377333_at	BE114427	Transcribed locus	---	1.187	0.395	0.411	0.072	1.780	0.036	0.326	0.015
1374893_at	BG380384	Transcribed locus	---	0.460	0.395	2.468	0.005	0.213	0.072	2.385	0.017
1391423_at	AA944812	Transcribed locus	---	0.918	0.395	1.328	0.005	0.971	0.897	1.376	0.032
1382336_at	AI236491	Transcribed locus	---	0.941	0.395	0.588	0.004	0.960	0.211	0.660	0.010
1382585_at	AW529128	Transcribed locus	---	1.169	0.395	0.982	0.261	0.813	0.095	0.947	0.860
1384484_at	AI172598	Transcribed locus	---	1.175	0.395	0.666	0.031	1.181	0.223	1.052	0.183
1385677_s_at	BG372143	Transcribed locus	---	0.914	0.396	0.790	0.124	1.024	0.710	1.115	0.452
1397328_at	AI555961	Transcribed locus	---	1.002	0.397	0.952	0.563	0.958	0.202	0.646	0.178
1389039_at	BM386520	Transcribed locus	---	1.228	0.398	0.999	0.983	0.932	0.523	0.960	0.299
1381988_at	AI029833	Transcribed locus	---	0.729	0.398	0.509	0.031	0.324	0.040	0.356	0.011
1383468_at	BM958512	Transcribed locus	---	0.982	0.399	0.537	0.013	0.980	0.707	0.447	0.028
1377932_at	AI556063	Transcribed locus	---	1.589	0.399	0.772	0.255	1.536	0.456	0.834	0.083
1384058_at	AI059089	Transcribed locus	---	1.489	0.399	0.957	0.319	1.303	0.375	1.273	0.643
1393224_at	AW529774	Transcribed locus	---	0.880	0.400	0.712	0.003	0.936	0.449	0.785	0.222
1379468_at	BI281734	Transcribed locus	---	1.407	0.400	0.802	0.385	1.002	0.994	0.794	0.099
1393181_at	BG663084	Transcribed locus	---	0.810	0.401	0.385	0.009	1.555	0.601	1.045	0.580
1390508_at	BI284393	Transcribed locus	---	0.759	0.401	0.940	0.479	0.525	0.094	0.738	0.075
1383661_at	AA926037	Transcribed locus	---	0.980	0.401	1.557	0.119	0.693	0.252	1.024	0.826
1372257_at	BG662579	Transcribed locus	---	1.035	0.401	0.679	0.018	0.815	0.501	0.838	0.017
1378173_at	BF397791	Transcribed locus	---	0.803	0.402	1.024	0.554	0.718	0.005	1.226	0.977
1386310_at	AI412779	Transcribed locus	---	1.302	0.402	1.159	0.603	1.014	0.973	2.262	0.106
1378152_at	AI170349	Transcribed locus	---	0.832	0.402	1.145	0.919	1.785	0.061	1.467	0.077
1371538_at	BF407786	Transcribed locus	---	0.690	0.402	0.453	0.009	0.776	0.369	0.619	0.190
1390247_at	BI275999	Transcribed locus	---	1.195	0.403	0.692	0.849	1.367	0.435	0.817	0.998
1375984_at	BE103689	Transcribed locus	---	1.810	0.403	1.091	0.981	2.393	0.430	1.575	0.581
1396153_at	AI555740	Transcribed locus	---	0.706	0.404	1.120	0.454	1.373	0.066	1.547	0.003
1395819_at	AW526127	Transcribed locus	---	1.885	0.404	1.187	0.754	0.573	0.178	1.009	0.621
1396925_at	BF542680	Transcribed locus	---	1.682	0.405	1.076	0.682	1.410	0.368	1.258	0.449
1376965_at	BM389656	Transcribed locus	---	0.777	0.406	1.010	0.359	0.899	0.022	0.884	0.455
1397719_at	AI716857	Transcribed locus	---	1.010	0.406	2.604	0.038	1.202	0.033	3.162	0.032
1392383_at	BF405619	Transcribed locus	---	2.276	0.407	1.039	0.944	1.714	0.250	1.095	0.414
1392316_at	BI293349	Transcribed locus	---	1.598	0.407	1.675	0.117	1.676	0.055	1.383	0.117
1382042_at	AI137817	Transcribed locus	---	1.158	0.408	0.994	0.245	1.395	0.173	0.689	0.112
1390909_at	AI171480	Transcribed locus	---	1.153	0.408	1.072	0.798	2.400	0.021	1.258	0.286
1374059_at	AI177428	Transcribed locus	---	0.966	0.408	0.807	0.002	1.057	0.841	0.754	0.054
1395552_s_at	BG671371	Transcribed locus	---	1.070	0.409	0.835	0.472	0.838	0.763	0.885	0.301
1395147_at	BE116565	Transcribed locus	---	1.378	0.409	5.019	0.000	1.361	0.279	5.555	0.000
1377188_at	BI296291	Transcribed locus	---	0.772	0.410	1.014	0.664	0.990	0.399	0.980	0.463
1376409_at	AI176677	Transcribed locus	---	1.080	0.410	0.609	0.037	1.031	0.874	0.604	0.017

1392945_at	BE115154	Transcribed locus	---	1.450	0.410	0.978	0.706	0.939	0.787	0.915	0.411
1395654_at	BI278299	Transcribed locus	---	1.807	0.411	0.996	0.999	1.682	0.197	0.826	0.325
1396186_at	BE095907	Transcribed locus	---	1.762	0.412	0.980	0.413	0.961	0.788	1.117	0.193
1381736_at	BF405604	Transcribed locus	---	1.132	0.412	0.966	0.522	1.002	0.991	1.094	0.787
1374521_at	AI230320	Transcribed locus	---	1.241	0.412	0.875	0.356	1.294	0.806	0.777	0.150
1390169_at	AW144331	Transcribed locus	---	1.103	0.412	0.780	0.062	1.351	0.686	0.800	0.034
1377523_at	BE113698	Transcribed locus	---	0.688	0.412	0.221	0.001	1.786	0.348	0.306	0.004
1380664_at	BF416244	Transcribed locus	---	1.232	0.413	1.398	0.988	0.995	0.989	0.980	0.907
1378909_at	BE120180	Transcribed locus	---	0.800	0.413	0.292	0.011	0.455	0.001	0.756	0.102
1376434_at	AI101016	Transcribed locus	---	1.614	0.414	0.666	0.342	2.661	0.098	1.365	0.504
1392636_at	AA964319	Transcribed locus	---	0.658	0.415	0.258	0.004	0.540	0.047	0.213	0.029
1397545_at	BM386640	Transcribed locus	---	1.036	0.416	0.558	0.090	1.693	0.092	0.919	0.996
1392985_at	BF555731	Transcribed locus	---	0.861	0.416	0.983	0.618	1.062	0.828	1.062	0.442
1373855_at	AI171776	Transcribed locus	---	0.597	0.416	1.107	0.078	0.368	0.010	0.990	0.213
1379415_at	AA998194	Transcribed locus	---	1.221	0.417	0.986	0.944	0.904	0.649	1.037	0.136
1395931_at	BF408949	Transcribed locus	---	0.819	0.417	1.220	0.324	0.919	0.143	1.226	0.864
1378785_at	BI288719	Transcribed locus	---	1.054	0.417	1.001	0.912	1.001	0.999	1.278	0.259
1386376_at	AA892173	Transcribed locus	---	0.929	0.417	0.954	0.869	0.968	0.493	0.998	0.955
1385753_at	BF395818	Transcribed locus	---	0.829	0.418	0.900	0.534	0.530	0.270	1.039	0.348
1373039_at	AI600081	Transcribed locus	---	0.684	0.418	1.246	0.252	0.524	0.012	1.075	0.289
1391464_at	BE104324	Transcribed locus	---	1.492	0.418	1.121	0.712	0.997	0.972	0.859	0.677
1381290_at	AI101288	Transcribed locus	---	0.795	0.418	0.404	0.039	0.862	0.115	0.611	0.099
1389669_at	BI296532	Transcribed locus	---	0.789	0.419	0.827	0.463	1.007	0.928	0.946	0.902
1381026_at	BF391155	Transcribed locus	---	1.165	0.419	1.096	0.999	0.923	0.697	1.194	0.997
1376655_at	AA850435	Transcribed locus	---	0.659	0.419	0.793	0.003	0.723	0.101	0.852	0.029
1393268_at	AI071071	Transcribed locus	---	0.639	0.419	0.707	0.286	0.572	0.016	0.615	0.416
1395121_at	BF394559	Transcribed locus	---	1.497	0.421	0.999	0.701	1.893	0.035	0.960	0.276
1389529_at	AI409595	Transcribed locus	---	0.948	0.422	0.917	0.151	1.083	0.751	0.926	0.180
1382423_at	AW920944	Transcribed locus	---	0.792	0.422	1.281	0.147	0.902	0.098	0.926	0.034
1382549_at	AI071736	Transcribed locus	---	0.758	0.423	0.862	0.370	0.848	0.783	0.745	0.025
1398430_at	AW524711	Transcribed locus	---	0.782	0.423	0.341	0.003	1.086	0.969	0.405	0.053
1377924_at	BE113414	Transcribed locus	---	1.347	0.423	1.726	0.343	1.652	0.194	1.267	0.245
1373867_at	BI289360	Transcribed locus	---	1.293	0.424	1.186	0.065	1.135	0.336	1.168	0.022
1392385_at	BF398583	Transcribed locus	---	0.938	0.424	0.855	0.376	1.571	0.053	1.252	0.034
1392293_at	BE113790	Transcribed locus	---	1.366	0.426	0.859	0.319	1.137	0.680	0.427	0.056
1396989_at	BF402350	Transcribed locus	---	1.562	0.426	1.709	0.793	1.838	0.014	1.067	0.957
1377043_at	BF388434	Transcribed locus	---	0.951	0.426	0.774	0.094	0.946	0.313	0.753	0.158
1376149_at	BE100200	Transcribed locus	---	1.137	0.426	1.133	0.029	1.418	0.039	1.150	0.084
1393440_at	AI071835	Transcribed locus	---	1.823	0.426	1.424	0.288	2.907	0.047	2.569	0.093
1388749_at	BI278823	Transcribed locus	---	0.521	0.427	0.424	0.002	0.593	0.007	0.480	0.003
1393495_at	AI043752	Transcribed locus	---	0.862	0.427	0.745	0.013	0.967	0.781	0.950	0.185
1375886_at	AI236778	Transcribed locus	---	0.567	0.427	0.454	0.039	0.387	0.171	0.472	0.001
1375828_at	BF390631	Transcribed locus	---	2.049	0.429	0.808	0.049	1.573	0.397	0.908	0.340
1380125_at	BM384823	Transcribed locus	---	0.845	0.430	0.857	0.441	1.795	0.489	1.455	0.039
1376872_at	BF283556	Transcribed locus	---	2.977	0.430	0.638	0.021	1.351	0.691	0.945	0.546
1383791_at	BG664616	Transcribed locus	---	0.249	0.430	0.608	0.052	0.812	0.668	0.444	0.020
1375090_at	AI579005	Transcribed locus	---	0.958	0.432	1.011	0.136	0.780	0.461	0.938	0.509
1385342_at	AA998932	Transcribed locus	---	1.078	0.432	0.932	0.287	0.834	0.998	0.875	0.437
1385618_at	AA858570	Transcribed locus	---	0.613	0.433	0.852	0.240	1.151	0.048	0.940	0.550
1392580_at	BF282184	Transcribed locus	---	0.606	0.434	0.552	0.093	0.485	0.035	0.719	0.031
1384281_at	BI295209	Transcribed locus	---	1.281	0.434	1.300	0.090	1.744	0.013	1.922	0.107
1385054_at	BE104042	Transcribed locus	---	1.162	0.437	0.784	0.036	2.033	0.034	0.660	0.385
1376214_at	AA850788	Transcribed locus	---	0.947	0.437	1.458	0.064	0.640	0.368	1.225	0.189
1377257_at	BI290077	Transcribed locus	---	0.543	0.438	0.500	0.238	0.442	0.052	0.464	0.089
1383529_at	BF549256	Transcribed locus	---	0.809	0.439	0.609	0.117	0.678	0.130	0.501	0.012
1380713_at	BG376879	Transcribed locus	---	0.881	0.440	1.044	0.809	0.905	0.620	1.042	0.484
1372666_at	BI284861	Transcribed locus	---	0.982	0.443	1.051	0.063	1.003	0.185	1.048	0.149
1389799_at	BG378730	Transcribed locus	---	0.658	0.445	1.230	0.626	0.896	0.028	0.887	0.413
1388553_at	BI290534	Transcribed locus	---	1.026	0.445	0.617	0.017	1.357	0.058	0.706	0.038
1395581_at	BF389197	Transcribed locus	---	0.912	0.446	0.600	0.272	0.929	0.283	0.961	0.191
1392084_at	BE109244	Transcribed locus	---	0.918	0.446	0.899	0.740	0.971	0.806	0.731	0.564

1383884_at	BF409598	Transcribed locus	---	1.356	0.446	0.860	0.002	1.028	0.694	0.981	0.979
1374680_at	AA858731	Transcribed locus	---	0.847	0.446	1.560	0.030	1.029	0.806	1.890	0.010
1375210_at	AW252841	Transcribed locus	---	0.635	0.447	0.779	0.092	0.519	0.143	0.821	0.488
1392917_at	BI302971	Transcribed locus	---	1.122	0.447	1.356	0.001	0.929	0.088	1.257	0.003
1393815_at	BM387050	Transcribed locus	---	0.840	0.450	0.905	0.547	0.787	0.539	1.011	0.900
1372192_at	AI145385	Transcribed locus	---	0.777	0.450	0.602	0.008	0.927	0.239	0.640	0.023
1394410_at	BF393802	Transcribed locus	---	1.254	0.450	0.995	0.962	0.668	0.231	0.887	0.967
1393402_at	BG670858	Transcribed locus	---	0.999	0.450	1.308	0.198	1.235	0.560	1.065	0.467
1386448_at	AI639182	Transcribed locus	---	2.359	0.450	1.492	0.487	0.642	0.473	0.992	0.737
1394449_at	AW524715	Transcribed locus	---	0.493	0.451	0.861	0.630	0.630	0.299	0.742	0.372
1383061_at	AI070680	Transcribed locus	---	0.945	0.451	0.856	0.019	0.904	0.203	0.810	0.090
1381149_at	BI293484	Transcribed locus	---	1.068	0.451	0.502	0.062	0.730	0.139	0.680	0.141
1388505_at	BE109642	Transcribed locus	---	0.874	0.451	0.715	0.068	1.057	0.833	0.722	0.032
1390453_at	AI599873	Transcribed locus	---	0.705	0.451	0.160	0.002	1.099	0.746	0.201	0.006
1381186_at	AW527770	Transcribed locus	---	1.003	0.451	0.997	0.807	1.620	0.092	1.301	0.573
1393666_at	BE101321	Transcribed locus	---	1.191	0.451	0.865	0.122	1.171	0.474	1.061	0.205
1393626_at	BF562507	Transcribed locus	---	0.587	0.452	0.069	0.000	0.818	0.432	0.098	0.005
1382870_at	AI103536	Transcribed locus	---	0.859	0.452	1.229	0.029	0.696	0.244	0.983	0.144
1392934_at	BM384509	Transcribed locus	---	0.874	0.453	0.935	0.519	0.659	0.038	0.923	0.241
1399145_at	BF410891	Transcribed locus	---	1.482	0.453	1.494	0.179	1.772	0.295	1.256	0.068
1386592_at	AI639154	Transcribed locus	---	0.895	0.453	0.999	0.990	1.103	0.963	1.144	0.448
1391799_at	AA899247	Transcribed locus	---	0.666	0.453	1.844	0.016	1.332	0.357	1.030	0.502
1379964_at	BF417011	Transcribed locus	---	0.940	0.455	0.868	0.297	0.887	0.319	0.963	0.340
1386395_at	H31724	Transcribed locus	---	0.999	0.455	1.016	0.981	1.002	0.997	1.013	0.962
1382236_at	BI288538	Transcribed locus	---	1.061	0.455	0.707	0.063	1.213	0.059	0.965	0.787
1385191_at	AA997253	Transcribed locus	---	1.089	0.456	0.650	0.013	1.088	0.507	0.547	0.016
1378797_at	BF394883	Transcribed locus	---	0.883	0.456	0.867	0.681	1.503	0.032	1.173	0.272
1382731_at	AA818685	Transcribed locus	---	0.688	0.457	0.782	0.361	1.523	0.849	0.747	0.808
1376734_at	BI279030	Transcribed locus	---	0.999	0.457	0.926	0.463	1.964	0.085	0.694	0.189
1392660_at	BE119130	Transcribed locus	---	1.314	0.458	0.864	0.381	1.494	0.119	0.911	0.606
1397185_at	BE102060	Transcribed locus	---	0.621	0.458	0.441	0.176	0.427	0.010	0.691	0.066
1374652_at	BF285372	Transcribed locus	---	1.275	0.459	0.770	0.314	0.468	0.011	0.647	0.055
1378253_at	AI555294	Transcribed locus	---	1.061	0.461	0.808	0.007	0.987	0.625	0.763	0.006
1372583_at	AI009094	Transcribed locus	---	0.773	0.461	0.600	0.047	2.174	0.013	0.919	0.886
1391148_at	AA957886	Transcribed locus	---	1.218	0.462	1.643	0.579	1.169	0.444	1.290	0.846
1377197_at	BE108892	Transcribed locus	---	0.986	0.463	0.595	0.019	0.860	0.371	0.640	0.024
1398990_at	BI281754	Transcribed locus	---	0.425	0.463	0.243	0.002	0.204	0.019	0.243	0.023
1398421_at	BM384203	Transcribed locus	---	1.178	0.463	0.641	0.215	1.205	0.242	0.647	0.125
1389072_at	AI412323	Transcribed locus	---	0.960	0.463	1.122	0.538	1.263	0.110	1.129	0.813
1390924_at	BE109165	Transcribed locus	---	0.839	0.464	0.740	0.275	1.008	0.990	0.934	0.183
1383284_at	BG372598	Transcribed locus	---	0.806	0.464	0.959	0.331	0.852	0.493	0.700	0.112
1374927_at	AI714124	Transcribed locus	---	0.680	0.465	0.507	0.001	0.626	0.135	0.558	0.001
1398548_at	BF389746	Transcribed locus	---	1.304	0.466	1.165	0.672	1.558	0.694	0.738	0.979
1394779_at	AI717218	Transcribed locus	---	1.164	0.467	3.146	0.001	2.263	0.015	1.909	0.043
1390442_at	BF284171	Transcribed locus	---	0.749	0.467	1.708	0.093	0.981	0.817	0.761	0.246
1385029_at	BE110921	Transcribed locus	---	1.062	0.467	1.366	0.465	3.282	0.030	1.238	0.159
1388451_at	AA817802	Transcribed locus	---	0.976	0.468	0.417	0.000	1.192	0.270	0.656	0.010
1393414_at	AW142650	Transcribed locus	---	0.925	0.468	0.502	0.010	0.862	0.276	0.857	0.308
1397596_at	H31511	Transcribed locus	---	2.450	0.469	0.823	0.615	1.489	0.197	1.210	0.031
1391001_at	BE112519	Transcribed locus	---	0.821	0.470	0.696	0.100	0.786	0.401	0.507	0.099
1376314_at	AI172148	Transcribed locus	---	0.859	0.470	0.561	0.003	0.396	0.168	0.481	0.009
1385980_at	AI228059	Transcribed locus	---	1.087	0.471	0.813	0.200	0.951	0.905	0.905	0.767
1372490_at	BF283759	Transcribed locus	---	0.820	0.471	0.798	0.097	0.852	0.553	0.733	0.402
1372444_at	AW918352	Transcribed locus	---	1.117	0.471	1.065	0.623	0.848	0.087	1.003	0.979
1394526_at	AI236935	Transcribed locus	---	0.958	0.471	1.837	0.051	1.297	0.601	0.966	0.089
1384387_at	BE110061	Transcribed locus	---	1.178	0.472	0.608	0.119	0.816	0.339	0.758	0.086
1386123_at	BF553538	Transcribed locus	---	1.043	0.472	0.336	0.005	0.997	0.836	0.698	0.106
1383121_at	BM384218	Transcribed locus	---	0.602	0.472	0.610	0.013	0.513	0.018	0.805	0.155
1377751_at	AI233227	Transcribed locus	---	1.363	0.473	0.383	0.000	0.988	0.971	0.472	0.031
1379110_at	AI763769	Transcribed locus	---	0.935	0.473	0.974	0.544	1.177	0.580	1.080	0.825
1397743_at	BF410216	Transcribed locus	---	0.947	0.474	0.477	0.007	0.993	0.690	0.850	0.030

1376683_at	AI175063	Transcribed locus	---	0.512	0.475	0.979	0.149	1.049	0.400	0.769	0.185
1379058_at	AA900904	Transcribed locus	---	0.904	0.476	0.400	0.037	0.958	0.849	0.409	0.044
1393613_at	BE117871	Transcribed locus	---	0.923	0.476	0.394	0.002	0.801	0.183	0.494	0.016
1377740_at	BF284600	Transcribed locus	---	1.222	0.477	0.727	0.070	0.571	0.560	0.522	0.041
1396694_at	BF400272	Transcribed locus	---	0.641	0.477	0.684	0.198	0.626	0.157	0.802	0.193
1393405_at	AA925444	Transcribed locus	---	0.818	0.477	0.985	0.964	0.993	0.623	0.956	0.725
1393977_at	BI288958	Transcribed locus	---	0.778	0.477	0.437	0.039	0.415	0.012	0.454	0.045
1397638_at	BF412682	Transcribed locus	---	0.983	0.478	0.993	0.947	1.715	0.097	0.999	0.995
1373159_at	AI411370	Transcribed locus	---	0.857	0.478	1.023	0.322	0.769	0.030	0.986	0.551
1396321_at	BE120690	Transcribed locus	---	1.308	0.479	1.001	0.991	1.400	0.071	1.023	0.225
1374392_at	BE113385	Transcribed locus	---	1.007	0.481	0.580	0.017	0.954	0.962	0.652	0.010
1373555_at	BM392315	Transcribed locus	---	0.834	0.481	0.658	0.005	1.031	0.550	0.713	0.005
1375298_at	BF408443	Transcribed locus	---	0.878	0.481	0.691	0.127	0.895	0.535	0.614	0.025
1390445_at	BE114154	Transcribed locus	---	1.824	0.482	0.987	0.815	2.205	0.213	0.516	0.222
1397385_at	BM387110	Transcribed locus	---	1.201	0.482	0.946	0.074	1.090	0.713	0.593	0.025
1380253_at	BE102139	Transcribed locus	---	0.850	0.483	0.729	0.230	0.762	0.070	0.999	0.632
1372261_at	AI409067	Transcribed locus	---	0.908	0.483	1.272	0.389	0.699	0.062	1.106	0.541
1378722_at	BF393951	Transcribed locus	---	0.832	0.483	1.011	0.569	0.732	0.471	0.977	0.931
1394647_at	AA819479	Transcribed locus	---	1.957	0.484	1.062	0.316	1.885	0.086	1.040	0.380
1379548_at	BF560252	Transcribed locus	---	0.941	0.484	1.178	0.235	0.283	0.472	0.777	0.876
1393310_at	BG672309	Transcribed locus	---	1.169	0.485	1.028	0.257	0.814	0.704	0.515	0.019
1397650_at	BF403165	Transcribed locus	---	0.916	0.485	0.912	0.021	0.818	0.079	0.966	0.296
1386818_at	AA848601	Transcribed locus	---	0.556	0.486	0.452	0.014	0.369	0.035	0.526	0.010
1391291_at	BF410101	Transcribed locus	---	0.863	0.486	1.279	0.112	1.548	0.211	0.924	0.573
1375699_at	BM389190	Transcribed locus	---	1.241	0.487	3.033	0.075	1.292	0.343	2.338	0.003
1379394_at	BF289573	Transcribed locus	---	0.791	0.488	0.799	0.027	1.156	0.997	0.802	0.183
1393712_at	BF419515	Transcribed locus	---	0.958	0.488	0.549	0.013	0.897	0.104	0.569	0.025
1373220_at	BI296489	Transcribed locus	---	0.814	0.488	0.239	0.006	0.908	0.191	0.167	0.006
1379637_at	BG670537	Transcribed locus	---	0.807	0.489	1.605	0.044	1.060	0.699	1.153	0.083
1385581_at	BF551187	Transcribed locus	---	0.628	0.490	0.210	0.002	0.809	0.430	0.352	0.010
1375308_at	BM383330	Transcribed locus	---	0.728	0.492	1.068	0.862	1.301	0.950	1.470	0.785
1377723_at	AI234810	Transcribed locus	---	0.995	0.493	0.371	0.004	1.144	0.990	0.673	0.078
1383501_at	AI059858	Transcribed locus	---	0.873	0.493	0.608	0.635	0.789	0.450	0.863	0.517
1397554_at	BE108776	Transcribed locus	---	1.015	0.494	1.000	0.616	1.369	0.087	0.896	0.995
1376351_at	BM383716	Transcribed locus	---	0.814	0.494	0.878	0.960	0.822	0.281	0.857	0.280
1393360_at	BE105636	Transcribed locus	---	0.585	0.495	0.328	0.002	0.835	0.257	0.417	0.012
1383069_at	AW144676	Transcribed locus	---	2.001	0.497	0.844	0.551	1.371	0.305	0.806	0.450
1376685_at	AW532489	Transcribed locus	---	1.320	0.497	0.779	0.431	1.631	0.476	0.920	0.763
1379769_at	AW529745	Transcribed locus	---	1.002	0.498	1.000	0.934	0.856	0.096	1.001	0.941
1379433_at	AI059449	Transcribed locus	---	0.923	0.498	0.720	0.007	0.990	0.733	0.644	0.061
1397897_x_at	BI273954	Transcribed locus	---	1.258	0.499	1.371	0.426	1.236	0.030	1.284	0.280
1379043_at	BI284837	Transcribed locus	---	0.851	0.499	2.385	0.002	0.713	0.069	1.541	0.046
1375661_at	BE104180	Transcribed locus	---	1.944	0.500	1.157	0.563	1.818	0.518	4.705	0.045
1384406_at	AW527186	Transcribed locus	---	1.293	0.500	0.985	0.503	1.094	0.377	1.028	0.515
1391976_at	BI286417	Transcribed locus	---	0.656	0.501	0.922	0.148	1.692	0.069	1.743	0.104
1394600_at	AI146026	Transcribed locus	---	0.688	0.501	3.268	0.009	1.084	0.682	2.052	0.029
1399053_at	BM391257	Transcribed locus	---	0.825	0.501	0.703	0.007	0.826	0.449	0.696	0.022
1391943_at	BF393061	Transcribed locus	---	0.944	0.501	0.999	0.974	0.946	0.440	1.000	0.997
1398594_at	AI029767	Transcribed locus	---	1.351	0.501	0.383	0.008	1.811	0.234	0.578	0.120
1397282_at	AW531746	Transcribed locus	---	0.935	0.502	1.002	0.970	0.935	0.506	1.031	0.278
1373981_at	BI299720	Transcribed locus	---	1.001	0.502	1.002	0.464	1.003	0.898	0.923	0.450
1385706_at	BI292758	Transcribed locus	---	0.774	0.502	0.940	0.716	0.895	0.552	0.902	0.455
1394733_at	AW527528	Transcribed locus	---	0.999	0.503	0.811	0.989	1.138	0.209	0.991	0.995
1389536_at	BF281954	Transcribed locus	---	1.805	0.503	1.028	0.958	1.289	0.675	1.292	0.358
1389818_at	AA997712	Transcribed locus	---	0.955	0.504	1.688	0.000	0.774	0.027	1.374	0.008
1385719_at	AW531176	Transcribed locus	---	1.098	0.504	1.042	0.857	0.943	0.685	1.216	0.152
1378087_at	BM387164	Transcribed locus	---	1.239	0.504	0.785	0.895	0.611	0.999	1.467	0.107
1397541_at	BG671148	Transcribed locus	---	1.130	0.504	0.853	0.552	1.956	0.227	1.307	0.099
1397942_at	BF552711	Transcribed locus	---	0.712	0.504	0.681	0.038	0.538	0.045	0.526	0.038
1394026_at	AA875227	Transcribed locus	---	0.968	0.504	1.153	0.540	0.869	0.738	1.189	0.264
1375343_at	BE116572	Transcribed locus	---	1.011	0.506	0.474	0.024	0.707	0.241	0.484	0.005

1397257_at	BE108093	Transcribed locus	---	1.325	0.506	1.286	0.979	1.436	0.292	1.186	0.582
1397371_at	AI577362	Transcribed locus	---	1.348	0.506	1.007	0.900	1.850	0.046	1.001	0.988
1384226_at	AI602005	Transcribed locus	---	0.423	0.507	0.466	0.020	0.954	0.921	0.428	0.157
1380078_at	AW144384	Transcribed locus	---	0.833	0.507	0.374	0.013	1.280	0.566	0.380	0.015
1381506_at	BF417935	Transcribed locus	---	1.203	0.507	1.362	0.147	0.961	0.709	1.424	0.345
1373525_at	AI113011	Transcribed locus	---	0.867	0.508	0.818	0.354	0.767	0.418	0.845	0.113
1386292_at	AI639358	Transcribed locus	---	0.700	0.509	2.024	0.848	1.403	0.329	3.655	0.175
1373511_at	BI296596	Transcribed locus	---	0.753	0.509	0.249	0.013	0.610	0.067	0.237	0.015
1385782_at	AW524067	Transcribed locus	---	0.909	0.511	1.255	0.451	1.748	0.219	0.802	0.227
1395422_at	BF288357	Transcribed locus	---	0.843	0.511	1.209	0.289	0.917	0.716	1.086	0.955
1381681_at	BE110205	Transcribed locus	---	1.499	0.511	1.219	0.416	2.818	0.194	1.204	0.489
1380121_at	BE117215	Transcribed locus	---	1.031	0.512	0.975	0.225	1.104	0.665	0.794	0.321
1389610_at	AW520754	Transcribed locus	---	0.875	0.512	0.960	0.930	0.333	0.003	0.402	0.072
1382978_at	AA955691	Transcribed locus	---	0.653	0.512	0.971	0.704	0.618	0.181	0.975	0.769
1390259_at	AI231279	Transcribed locus	---	0.976	0.512	1.037	0.132	0.845	0.528	0.841	0.766
1383139_at	BM386881	Transcribed locus	---	1.387	0.512	0.426	0.000	1.641	0.037	0.906	0.035
1383751_at	AI555007	Transcribed locus	---	1.197	0.513	3.182	0.005	1.279	0.113	2.041	0.036
1375773_at	BG379365	Transcribed locus	---	0.787	0.513	0.446	0.073	0.734	0.793	0.541	0.057
1394499_at	AI501768	Transcribed locus	---	1.278	0.513	1.295	0.004	1.001	0.821	1.749	0.000
1398693_at	BF289500	Transcribed locus	---	1.034	0.513	0.748	0.260	1.200	0.336	0.689	0.131
1385399_at	AI071789	Transcribed locus	---	1.699	0.514	0.906	0.365	1.659	0.064	0.953	0.749
1380376_at	BI290853	Transcribed locus	---	0.952	0.516	0.474	0.036	0.943	0.770	0.604	0.046
1376773_at	AI406968	Transcribed locus	---	1.120	0.517	0.784	0.048	1.455	0.088	0.781	0.601
1381144_at	AW524106	Transcribed locus	---	0.679	0.517	0.709	0.024	0.669	0.471	0.377	0.010
1385922_at	BM385585	Transcribed locus	---	1.077	0.517	0.730	0.366	1.003	0.991	0.728	0.368
1371675_at	AA893193	Transcribed locus	---	1.022	0.518	1.346	0.088	1.397	0.903	1.492	0.055
1376662_at	BF390141	Transcribed locus	---	1.116	0.518	0.629	0.010	1.036	0.714	0.801	0.043
1372669_at	BF404426	Transcribed locus	---	0.959	0.518	0.287	0.002	1.692	0.092	0.478	0.236
1378627_at	BE120328	Transcribed locus	---	0.883	0.519	1.408	0.764	0.867	0.565	1.227	0.425
1373937_at	AA799661	Transcribed locus	---	1.057	0.519	1.221	0.062	1.711	0.084	1.127	0.277
1373306_at	BM386212	Transcribed locus	---	1.190	0.520	0.812	0.454	0.977	0.295	1.104	0.262
1384916_at	AI717256	Transcribed locus	---	1.219	0.520	0.981	0.401	1.143	0.287	0.983	0.857
1397894_at	BG381542	Transcribed locus	---	0.728	0.521	0.449	0.029	1.085	0.715	1.225	0.591
1393207_at	BF566116	Transcribed locus	---	1.159	0.521	0.998	0.987	1.000	0.999	0.999	0.988
1392044_at	BE117009	Transcribed locus	---	0.987	0.522	0.412	0.020	1.514	0.116	0.556	0.076
1384107_at	AI071397	Transcribed locus	---	1.700	0.522	0.879	0.099	0.787	0.116	1.153	0.057
1380416_at	BF284504	Transcribed locus	---	0.868	0.522	0.826	0.061	0.862	0.131	1.169	0.039
1373184_at	BF410842	Transcribed locus	---	1.292	0.523	0.973	0.924	0.998	0.785	0.999	0.997
1383234_at	BF405850	Transcribed locus	---	1.277	0.523	0.306	0.000	1.124	0.775	0.325	0.001
1392424_at	BF407028	Transcribed locus	---	0.718	0.524	0.849	0.094	0.624	0.121	0.751	0.018
1398496_at	BF390696	Transcribed locus	---	0.555	0.524	0.477	0.006	0.709	0.941	0.520	0.007
1373879_at	AI234961	Transcribed locus	---	0.633	0.525	1.420	0.042	0.465	0.036	1.293	0.477
1395158_at	BF391885	Transcribed locus	---	1.003	0.526	0.986	0.119	1.565	0.212	0.992	0.724
1390427_at	BF397491	Transcribed locus	---	1.008	0.526	0.531	0.131	1.300	0.818	0.532	0.009
1384346_at	AA964754	Transcribed locus	---	1.609	0.527	0.722	0.064	1.399	0.460	0.624	0.007
1375601_at	BF410219	Transcribed locus	---	0.946	0.527	0.634	0.518	0.681	0.180	0.602	0.619
1371328_at	BM986552	Transcribed locus	---	0.912	0.527	1.017	0.799	0.823	0.487	0.908	0.077
1379031_at	BM390697	Transcribed locus	---	0.726	0.527	0.832	0.447	0.929	0.771	0.895	0.047
1389147_at	BE116020	Transcribed locus	---	0.823	0.528	1.328	0.009	0.702	0.009	1.284	0.010
1393582_at	AW529067	Transcribed locus	---	0.968	0.528	0.800	0.024	1.000	0.752	0.743	0.170
1375658_at	AI412317	Transcribed locus	---	1.252	0.529	1.193	0.453	1.588	0.023	1.471	0.167
1378204_at	AI171512	Transcribed locus	---	0.927	0.529	0.911	0.043	0.999	0.392	0.712	0.017
1393772_at	AW523217	Transcribed locus	---	1.131	0.530	0.752	0.029	0.640	0.522	0.948	0.628
1398491_at	BM383434	Transcribed locus	---	0.884	0.531	0.489	0.003	0.720	0.429	0.316	0.002
1376430_at	AA925921	Transcribed locus	---	1.402	0.531	1.113	0.985	1.405	0.846	1.006	0.908
1378506_at	BM385647	Transcribed locus	---	0.529	0.532	0.568	0.012	0.586	0.130	0.553	0.002
1395217_at	AA899394	Transcribed locus	---	1.290	0.532	1.002	0.702	1.366	0.216	0.943	0.704
1385106_at	BE107024	Transcribed locus	---	1.121	0.532	0.562	0.013	0.976	0.915	0.701	0.111
1390028_at	BE096356	Transcribed locus	---	1.069	0.533	1.081	0.283	0.961	0.717	1.148	0.159
1372314_at	AI179677	Transcribed locus	---	0.950	0.533	0.571	0.002	0.933	0.850	0.770	0.028
1376278_at	BI282100	Transcribed locus	---	0.910	0.533	0.755	0.086	1.132	0.058	0.968	0.583

1388522_at	AI170820	Transcribed locus	---	0.820	0.534	1.136	0.320	0.878	0.041	1.119	0.261
1372668_at	BI289676	Transcribed locus	---	1.030	0.535	1.098	0.101	0.798	0.037	0.707	0.242
1384219_at	BF522747	Transcribed locus	---	0.812	0.535	0.654	0.058	1.176	0.727	0.663	0.053
1375932_at	BF284677	Transcribed locus	---	0.801	0.535	0.520	0.021	0.773	0.823	0.611	0.024
1394049_at	BE108839	Transcribed locus	---	1.142	0.536	0.960	0.228	1.000	0.323	0.891	0.424
1389019_at	AI178561	Transcribed locus	---	0.858	0.536	0.443	0.014	0.787	0.099	0.685	0.047
1393006_at	BF282112	Transcribed locus	---	0.886	0.536	0.733	0.006	1.124	0.604	0.754	0.053
1391901_at	AA956085	Transcribed locus	---	0.844	0.537	0.497	0.012	0.670	0.819	0.602	0.029
1396406_at	BE102611	Transcribed locus	---	0.876	0.538	1.005	0.994	0.871	0.478	1.009	0.777
1388888_at	BI274615	Transcribed locus	---	0.755	0.538	0.728	0.010	0.648	0.001	0.690	0.015
1392139_at	BE105731	Transcribed locus	---	0.873	0.538	0.995	0.213	0.876	0.611	1.002	0.093
1386540_at	BG666051	Transcribed locus	---	1.330	0.539	1.110	0.118	2.635	0.735	1.603	0.006
1378381_x_at	BF552442	Transcribed locus	---	1.531	0.539	1.161	0.832	1.134	0.179	0.787	0.405
1392189_at	BE105136	Transcribed locus	---	0.999	0.540	1.197	0.076	0.593	0.022	1.212	0.935
1376782_at	AW915083	Transcribed locus	---	0.483	0.541	0.717	0.153	0.178	0.039	0.709	0.032
1383331_at	BF548234	Transcribed locus	---	1.274	0.541	1.051	0.548	1.506	0.283	1.167	0.478
1395578_at	BF419340	Transcribed locus	---	0.746	0.542	1.522	0.199	1.215	0.716	1.803	0.002
1378685_at	AI235586	Transcribed locus	---	0.935	0.544	0.630	0.108	1.049	0.126	0.738	0.114
1389800_at	BF420629	Transcribed locus	---	1.048	0.544	1.120	0.383	1.049	0.989	1.004	0.812
1378084_at	BF396266	Transcribed locus	---	0.978	0.545	0.642	0.020	0.953	0.827	0.585	0.001
1372727_at	BM384088	Transcribed locus	---	0.567	0.546	0.389	0.118	1.959	0.264	0.139	0.024
1399025_at	AW916140	Transcribed locus	---	1.004	0.546	0.958	0.410	1.083	0.633	1.021	0.960
1373766_at	BF405110	Transcribed locus	---	0.608	0.547	1.158	0.222	0.674	0.331	1.012	0.769
1379828_at	AI113302	Transcribed locus	---	1.002	0.547	0.993	0.953	1.309	0.184	1.000	0.957
1385935_at	AI577552	Transcribed locus	---	1.234	0.548	0.701	0.101	1.279	0.128	0.602	0.086
1381060_at	AI113313	Transcribed locus	---	2.446	0.548	0.872	0.952	1.043	0.784	0.891	0.848
1391523_at	AA955605	Transcribed locus	---	0.999	0.550	1.285	0.185	1.245	0.767	0.900	0.098
1382655_at	AA964534	Transcribed locus	---	1.029	0.551	1.153	0.048	0.906	0.125	1.867	0.053
1397278_at	BE113877	Transcribed locus	---	1.044	0.552	1.186	0.934	1.148	0.595	0.717	0.081
1392796_at	AI231609	Transcribed locus	---	1.233	0.553	0.726	0.091	1.461	0.013	1.083	0.272
1373645_at	BM386246	Transcribed locus	---	0.975	0.553	1.002	0.972	1.103	0.134	1.007	0.923
1379074_at	BE329032	Transcribed locus	---	1.030	0.554	1.200	0.159	0.724	0.118	1.223	0.034
1371901_at	AI176646	Transcribed locus	---	1.124	0.554	0.813	0.013	1.092	0.583	0.793	0.070
1381131_at	AI171441	Transcribed locus	---	1.644	0.555	0.922	0.361	1.579	0.881	0.990	0.322
1373261_at	BF388657	Transcribed locus	---	1.320	0.555	0.561	0.056	1.674	0.061	0.719	0.471
1382692_at	AI045955	Transcribed locus	---	0.987	0.556	1.003	0.992	1.596	0.307	1.284	0.382
1380124_at	BF388563	Transcribed locus	---	1.098	0.556	0.863	0.981	0.872	0.176	0.690	0.514
1374758_at	BM387112	Transcribed locus	---	0.646	0.556	0.322	0.000	0.521	0.018	0.385	0.002
1372805_at	BE328984	Transcribed locus	---	1.194	0.557	0.629	0.058	0.847	0.968	0.746	0.278
1392127_at	BF400081	Transcribed locus	---	0.897	0.557	1.703	0.387	1.329	0.967	1.292	0.301
1372544_at	AI410305	Transcribed locus	---	0.919	0.558	0.468	0.002	1.013	0.260	0.436	0.013
1376933_at	AI170377	Transcribed locus	---	0.857	0.558	0.741	0.176	0.570	0.451	0.438	0.032
1376385_at	BF400806	Transcribed locus	---	0.724	0.558	0.957	0.240	1.010	0.948	0.780	0.466
1383408_at	BI276349	Transcribed locus	---	1.198	0.559	1.029	0.796	0.783	0.005	1.115	0.472
1391039_at	BE115243	Transcribed locus	---	0.999	0.560	0.806	0.030	0.997	0.752	1.222	0.252
1393355_at	AI111659	Transcribed locus	---	1.463	0.561	3.789	0.157	1.027	0.494	1.667	0.107
1381210_at	AI639521	Transcribed locus	---	0.944	0.562	0.870	0.312	0.890	0.651	1.139	0.678
1372681_at	BI294716	Transcribed locus	---	1.041	0.563	0.774	0.735	1.480	0.022	0.755	0.304
1374587_at	AI009750	Transcribed locus	---	0.539	0.564	0.766	0.276	1.258	0.535	0.644	0.033
1384422_at	AI045140	Transcribed locus	---	0.514	0.564	0.095	0.000	0.508	0.019	0.077	0.020
1393916_at	AI044713	Transcribed locus	---	1.040	0.564	0.848	0.079	1.216	0.797	1.074	0.667
1391600_at	BE118049	Transcribed locus	---	1.031	0.564	0.778	0.144	1.481	0.031	0.897	0.007
1383935_at	AW252428	Transcribed locus	---	1.033	0.564	0.941	0.772	1.625	0.128	1.351	0.645
1391492_at	AI103493	Transcribed locus	---	0.998	0.565	1.216	0.501	0.942	0.457	1.028	0.235
1390561_at	BF282191	Transcribed locus	---	1.127	0.565	0.283	0.000	2.088	0.160	0.542	0.007
1380677_at	BF401719	Transcribed locus	---	1.292	0.566	0.848	0.046	1.214	0.604	0.872	0.719
1383167_at	BM392101	Transcribed locus	---	0.574	0.567	0.681	0.006	0.545	0.061	0.813	0.008
1373313_at	BM391570	Transcribed locus	---	0.781	0.568	0.968	0.539	1.059	0.311	1.043	0.724
1385246_at	AI717564	Transcribed locus	---	1.698	0.568	0.901	0.410	1.339	0.117	0.766	0.499
1385087_at	BF406606	Transcribed locus	---	0.988	0.568	0.554	0.009	0.707	0.190	0.519	0.017
1382215_at	AA875331	Transcribed locus	---	1.250	0.569	2.229	0.005	1.773	0.128	2.120	0.047

1374027_at	AI071243	Transcribed locus	---	0.951	0.569	1.303	0.017	1.173	0.343	1.216	0.094
1374888_at	AI317837	Transcribed locus	---	2.281	0.570	1.676	0.053	1.533	0.442	1.439	0.010
1389138_at	AA945574	Transcribed locus	---	0.853	0.571	0.902	0.249	0.791	0.031	0.913	0.039
1381538_at	BF391531	Transcribed locus	---	1.052	0.573	1.226	0.392	1.474	0.217	1.694	0.219
1385003_at	BE099045	Transcribed locus	---	1.328	0.575	0.708	0.008	0.829	0.713	0.726	0.035
1377836_at	AI638997	Transcribed locus	---	1.299	0.577	1.312	0.083	1.543	0.542	1.361	0.049
1382540_at	BI296328	Transcribed locus	---	0.918	0.577	0.754	0.089	0.866	0.148	0.553	0.034
1373183_at	AI229780	Transcribed locus	---	0.682	0.578	0.626	0.030	0.852	0.217	0.638	0.078
1376891_at	AA818282	Transcribed locus	---	0.784	0.579	0.213	0.009	0.733	0.297	0.288	0.010
1395174_at	BI289214	Transcribed locus	---	1.109	0.579	0.325	0.011	1.278	0.352	0.354	0.035
1396062_at	BF290729	Transcribed locus	---	0.784	0.579	0.596	0.112	1.291	0.435	0.544	0.083
1385652_at	AI549246	Transcribed locus	---	1.375	0.580	1.858	0.025	1.004	0.601	1.450	0.173
1378167_at	AI599898	Transcribed locus	---	1.129	0.580	1.097	0.796	1.001	0.969	1.017	0.921
1396760_at	BF405512	Transcribed locus	---	0.756	0.580	1.000	0.296	0.846	0.045	0.927	0.753
1383816_at	BI285419	Transcribed locus	---	1.011	0.581	0.724	0.044	0.944	0.713	0.588	0.056
1385697_at	BI302799	Transcribed locus	---	0.973	0.581	0.661	0.039	1.052	0.236	0.777	0.198
1375237_at	BF404538	Transcribed locus	---	0.825	0.581	0.786	0.032	1.012	0.372	0.759	0.057
1376600_at	BI289616	Transcribed locus	---	0.969	0.582	0.555	0.013	0.853	0.048	0.735	0.028
1385879_at	AA893004	Transcribed locus	---	0.814	0.582	6.279	0.024	1.588	0.958	2.399	0.009
1381848_at	AI228486	Transcribed locus	---	0.909	0.583	1.412	0.663	1.220	0.166	1.347	0.547
1377130_at	AW526352	Transcribed locus	---	1.128	0.584	1.047	0.612	1.323	0.618	1.151	0.207
1383487_at	AW530484	Transcribed locus	---	0.904	0.584	0.666	0.004	0.776	0.190	0.541	0.004
1383854_at	AI715145	Transcribed locus	---	1.005	0.586	1.261	0.545	1.015	0.963	0.935	0.758
1378717_at	BF390952	Transcribed locus	---	1.100	0.586	0.999	0.994	0.992	0.888	1.000	0.962
1373019_at	AI172468	Transcribed locus	---	0.562	0.586	0.526	0.010	0.897	0.220	0.799	0.094
1378097_at	AI599593	Transcribed locus	---	1.130	0.586	0.286	0.036	3.115	0.009	0.657	0.263
1372641_at	AW434261	Transcribed locus	---	1.135	0.587	1.238	0.388	1.290	0.969	1.702	0.127
1395901_at	AW532049	Transcribed locus	---	0.803	0.587	0.948	0.288	0.836	0.010	0.898	0.447
1390684_at	AA892642	Transcribed locus	---	0.898	0.587	0.788	0.087	1.014	0.249	0.957	0.811
1379612_at	BI276164	Transcribed locus	---	1.184	0.588	1.188	0.322	1.005	0.763	0.996	0.958
1379807_at	BE109195	Transcribed locus	---	1.098	0.589	1.857	0.071	0.688	0.106	1.217	0.288
1380860_at	AA819536	Transcribed locus	---	1.020	0.589	0.467	0.015	1.240	0.949	0.635	0.014
1371666_at	BM385852	Transcribed locus	---	1.052	0.589	1.655	0.004	0.903	0.285	1.658	0.004
1381011_at	BF402331	Transcribed locus	---	0.961	0.590	0.587	0.197	0.996	0.799	0.640	0.255
1373513_at	AI012419	Transcribed locus	---	1.205	0.590	0.553	0.000	1.063	0.815	0.608	0.048
1378021_at	AI102035	Transcribed locus	---	1.061	0.591	1.561	0.027	0.919	0.773	1.166	0.236
1383530_at	AA925994	Transcribed locus	---	0.857	0.591	2.090	0.002	0.647	0.029	1.868	0.002
1383747_at	AI578135	Transcribed locus	---	1.308	0.591	0.477	0.043	0.650	0.168	0.494	0.011
1396028_at	BF392616	Transcribed locus	---	1.126	0.591	0.766	0.052	1.237	0.780	0.851	0.038
1377222_at	BF400700	Transcribed locus	---	1.060	0.591	1.144	0.762	0.985	0.325	0.710	0.254
1379912_at	BM392147	Transcribed locus	---	0.972	0.594	0.584	0.007	1.186	0.048	0.621	0.066
1374054_at	BE118605	Transcribed locus	---	0.647	0.594	0.692	0.086	0.726	0.182	0.864	0.044
1378559_at	BF400658	Transcribed locus	---	0.791	0.595	1.117	0.185	1.391	0.212	1.187	0.173
1391649_a_at	AW915522	Transcribed locus	---	1.058	0.595	1.028	0.821	0.456	0.049	1.052	0.968
1377862_at	BI274618	Transcribed locus	---	1.212	0.595	0.688	0.840	0.890	0.857	0.774	0.248
1392155_at	AW523955	Transcribed locus	---	1.286	0.596	1.511	0.769	1.277	0.319	1.245	0.784
1392840_at	AI764605	Transcribed locus	---	0.656	0.597	2.828	0.649	1.799	0.014	2.390	0.363
1384542_at	BE103021	Transcribed locus	---	1.802	0.598	0.778	0.220	1.500	0.611	0.526	0.099
1382226_at	AI502443	Transcribed locus	---	1.343	0.598	1.067	0.813	1.022	0.887	1.144	0.395
1378183_at	AW531387	Transcribed locus	---	1.094	0.600	1.147	0.177	0.713	0.011	0.667	0.119
1373092_at	BE109587	Transcribed locus	---	1.185	0.600	0.411	0.100	0.749	0.574	0.663	0.267
1391023_at	AI548713	Transcribed locus	---	1.388	0.601	1.327	0.308	0.948	0.731	1.294	0.330
1397724_at	BF412617	Transcribed locus	---	1.117	0.601	1.260	0.107	1.005	0.961	0.993	0.009
1390436_at	BI300794	Transcribed locus	---	0.950	0.602	0.980	0.549	0.466	0.180	0.965	0.845
1395052_at	BE118917	Transcribed locus	---	1.136	0.602	0.440	0.024	0.759	0.093	0.492	0.113
1397574_at	BF563598	Transcribed locus	---	0.913	0.602	0.997	0.977	1.277	0.301	0.925	0.992
1383330_at	AW915049	Transcribed locus	---	0.901	0.603	1.698	0.768	0.817	0.410	2.569	0.703
1395306_at	AI502736	Transcribed locus	---	0.878	0.604	0.611	0.029	0.858	0.274	0.720	0.050
1390425_at	BF398716	Transcribed locus	---	1.082	0.604	0.924	0.755	0.670	0.088	0.990	0.653
1384030_at	AI030261	Transcribed locus	---	0.589	0.605	1.491	0.311	0.925	0.715	0.912	0.252
1393093_at	BF522164	Transcribed locus	---	0.905	0.605	0.878	0.268	0.557	0.151	0.988	0.442

1377574_at	BF392065	Transcribed locus	---	1.004	0.605	1.003	0.827	0.791	0.557	1.000	0.754
1398003_at	BF400768	Transcribed locus	---	0.855	0.605	0.978	0.391	0.676	0.166	1.126	0.714
1379522_at	AA956480	Transcribed locus	---	1.212	0.606	1.097	0.588	2.443	0.051	1.000	0.998
1389552_at	BG371715	Transcribed locus	---	0.749	0.606	0.658	0.061	0.568	0.015	0.665	0.114
1390215_at	AI235499	Transcribed locus	---	0.946	0.606	0.461	0.006	0.859	0.214	0.577	0.000
1390387_at	BF396636	Transcribed locus	---	1.135	0.606	1.063	0.562	0.951	0.671	1.529	0.023
1381027_at	BF393571	Transcribed locus	---	0.658	0.607	0.694	0.058	0.566	0.067	0.930	0.190
1373568_at	AI172222	Transcribed locus	---	1.175	0.607	1.242	0.140	1.137	0.299	1.309	0.069
1383552_at	AI071698	Transcribed locus	---	1.008	0.607	0.410	0.028	0.999	0.938	0.407	0.028
1395010_at	AI102173	Transcribed locus	---	1.030	0.608	0.668	0.085	0.994	0.848	0.673	0.072
1390385_at	AA964674	Transcribed locus	---	1.227	0.608	1.758	0.018	1.281	0.757	1.703	0.027
1383352_at	AI029580	Transcribed locus	---	1.082	0.609	0.727	0.178	0.913	0.506	0.864	0.574
1390171_at	AA924717	Transcribed locus	---	0.939	0.609	1.215	0.093	0.896	0.653	1.600	0.007
1376277_at	AI412413	Transcribed locus	---	0.686	0.611	0.958	0.814	0.457	0.032	0.826	0.935
1399017_at	AI234040	Transcribed locus	---	0.916	0.611	0.718	0.039	0.886	0.258	0.779	0.055
1393526_at	AA900633	Transcribed locus	---	0.782	0.612	0.676	0.197	1.689	0.077	0.746	0.221
1375448_at	BM391628	Transcribed locus	---	0.999	0.612	0.929	0.596	1.002	0.290	0.935	0.308
1385486_at	AW534737	Transcribed locus	---	1.313	0.613	0.562	0.183	1.141	0.689	1.565	0.183
1389226_at	BI295219	Transcribed locus	---	0.733	0.613	0.438	0.031	0.520	0.087	0.662	0.068
1394856_at	BM383417	Transcribed locus	---	1.316	0.614	1.187	0.487	1.318	0.691	0.963	0.599
1385505_at	AI072068	Transcribed locus	---	1.660	0.614	0.831	0.569	1.158	0.694	1.122	0.196
1372163_at	BG670246	Transcribed locus	---	0.981	0.614	0.127	0.010	1.404	0.047	0.354	0.049
1380251_at	BM386280	Transcribed locus	---	0.835	0.616	0.849	0.096	0.822	0.572	0.820	0.019
1397073_at	BE117296	Transcribed locus	---	0.873	0.616	1.506	0.406	0.837	0.667	1.358	0.670
1376989_at	BE099568	Transcribed locus	---	0.883	0.617	0.142	0.009	1.235	0.294	0.339	0.097
1382583_at	AA899919	Transcribed locus	---	0.874	0.617	1.213	0.628	0.425	0.813	1.309	0.336
1382938_at	BF386757	Transcribed locus	---	0.737	0.617	1.259	0.531	1.070	0.185	1.887	0.962
1379513_at	BE108949	Transcribed locus	---	2.305	0.618	0.594	0.025	2.359	0.136	0.640	0.310
1390433_at	AI102429	Transcribed locus	---	1.412	0.619	1.274	0.003	1.152	0.273	1.117	0.184
1383278_at	BF558819	Transcribed locus	---	1.160	0.620	2.949	0.004	1.025	0.367	3.056	0.001
1391967_at	BM389832	Transcribed locus	---	0.964	0.620	1.193	0.362	1.660	0.449	1.048	0.687
1390695_at	BM385951	Transcribed locus	---	1.027	0.621	0.392	0.008	1.035	0.703	0.676	0.091
1383835_at	BI303704	Transcribed locus	---	1.148	0.622	1.099	0.268	1.485	0.080	1.094	0.656
1395302_at	BE104435	Transcribed locus	---	1.269	0.622	0.963	0.274	1.582	0.088	0.866	0.766
1391218_at	BI294343	Transcribed locus	---	0.805	0.623	0.532	0.001	0.762	0.184	0.441	0.026
1385393_at	BE099283	Transcribed locus	---	1.088	0.623	2.368	0.014	0.822	0.609	1.438	0.293
1378858_at	BF400182	Transcribed locus	---	1.085	0.623	2.432	0.034	1.839	0.370	1.483	0.553
1377588_at	BI300335	Transcribed locus	---	0.881	0.624	0.990	0.165	0.980	0.113	0.977	0.437
1379980_at	BM386302	Transcribed locus	---	0.708	0.624	1.127	0.432	1.131	0.701	1.203	0.523
1386051_at	H31285	Transcribed locus	---	0.791	0.624	0.955	0.690	0.939	0.246	1.036	0.892
1371606_at	AA819633	Transcribed locus	---	1.063	0.626	0.580	0.014	0.936	0.903	0.693	0.139
1388944_at	BE109016	Transcribed locus	---	1.275	0.626	1.519	0.661	1.049	0.443	1.175	0.339
1372777_at	BM385774	Transcribed locus	---	0.832	0.627	1.497	0.038	1.085	0.119	1.122	0.583
1396045_at	BI299536	Transcribed locus	---	0.728	0.628	0.527	0.101	1.005	0.982	0.878	0.265
1379585_at	AA946230	Transcribed locus	---	0.909	0.628	0.989	0.717	0.907	0.631	0.922	0.709
1397128_at	BF392437	Transcribed locus	---	1.245	0.629	1.068	0.692	1.677	0.129	1.217	0.910
1376204_at	AW531412	Transcribed locus	---	1.936	0.629	0.477	0.012	1.085	0.649	0.650	0.090
1395815_at	BF291198	Transcribed locus	---	1.407	0.629	0.898	0.723	1.216	0.553	0.956	0.191
1377330_at	BF411114	Transcribed locus	---	1.438	0.629	0.926	0.735	1.659	0.451	0.753	0.253
1391676_at	AI511097	Transcribed locus	---	1.151	0.630	0.641	0.007	2.046	0.111	0.901	0.071
1385043_at	AA924649	Transcribed locus	---	0.883	0.631	0.727	0.018	1.097	0.460	0.857	0.114
1396529_at	BF415512	Transcribed locus	---	0.925	0.632	0.695	0.024	1.179	0.223	0.771	0.316
1389225_at	BI296570	Transcribed locus	---	0.860	0.632	0.983	0.963	1.067	0.391	0.857	0.166
1376651_at	AW528774	Transcribed locus	---	0.717	0.632	0.724	0.010	0.688	0.047	0.777	0.005
1386220_at	AA892761	Transcribed locus	---	0.979	0.633	1.014	0.721	0.918	0.158	1.000	0.666
1383130_at	BF555795	Transcribed locus	---	1.149	0.634	0.621	0.194	1.587	0.104	1.086	0.236
1394836_at	AI535155	Transcribed locus	---	0.950	0.634	0.995	0.932	0.988	0.941	0.868	0.854
1379414_at	AA997596	Transcribed locus	---	0.857	0.634	0.502	0.046	0.790	0.626	0.890	0.472
1367528_at	BE103273	Transcribed locus	---	0.631	0.634	1.409	0.071	0.819	0.181	0.907	0.260
1375532_at	AI008792	Transcribed locus	---	1.508	0.635	1.222	0.571	1.932	0.382	1.001	0.999
1393409_at	AW143298	Transcribed locus	---	1.128	0.635	0.812	0.324	0.851	0.484	0.747	0.204

1391331_at	BE106891	Transcribed locus	---	0.822	0.636	0.424	0.003	0.831	0.366	0.561	0.001
1390489_at	BE108860	Transcribed locus	---	0.899	0.636	1.246	0.246	0.935	0.948	1.516	0.013
1398509_at	AI170370	Transcribed locus	---	1.171	0.639	1.090	0.600	1.540	0.977	1.169	0.530
1389050_at	AI170797	Transcribed locus	---	0.925	0.639	1.129	0.776	0.611	0.058	0.688	0.034
1389563_at	BF406562	Transcribed locus	---	0.832	0.639	1.091	0.074	0.794	0.049	1.249	0.012
1384006_at	AI045457	Transcribed locus	---	0.792	0.639	1.575	0.351	0.310	0.016	1.008	0.355
1384120_at	BF386877	Transcribed locus	---	1.428	0.640	0.936	0.406	1.123	0.965	0.895	0.777
1374663_at	AW526756	Transcribed locus	---	0.901	0.641	0.806	0.232	0.464	0.132	0.691	0.033
1383548_at	BI290887	Transcribed locus	---	0.871	0.641	1.333	0.044	1.199	0.498	1.536	0.059
1376095_at	BF401491	Transcribed locus	---	0.911	0.641	1.077	0.738	1.001	0.993	1.003	0.070
1386466_at	H33093	Transcribed locus	---	1.126	0.641	1.096	0.612	0.999	0.746	0.771	0.190
1392792_at	AI071152	Transcribed locus	---	1.555	0.642	0.615	0.012	1.207	0.962	0.495	0.003
1374591_at	AI409042	Transcribed locus	---	1.263	0.642	0.737	0.109	1.806	0.477	0.559	0.204
1374203_at	BM385279	Transcribed locus	---	1.240	0.642	1.357	0.155	0.961	0.766	1.286	0.241
1398028_at	BF399371	Transcribed locus	---	1.134	0.642	1.046	0.968	1.059	0.296	1.000	0.900
1383998_at	BF545601	Transcribed locus	---	0.911	0.643	1.835	0.000	0.851	0.388	1.575	0.003
1392851_at	AI146048	Transcribed locus	---	0.992	0.643	1.277	0.740	1.929	0.024	0.744	0.107
1379720_at	AW528715	Transcribed locus	---	1.018	0.644	0.886	0.407	0.845	0.164	0.847	0.456
1372576_at	AI232347	Transcribed locus	---	1.066	0.645	1.452	0.003	0.821	0.886	1.264	0.015
1393327_at	BG667328	Transcribed locus	---	1.301	0.647	0.648	0.101	1.353	0.813	0.796	0.053
1396430_at	BF410086	Transcribed locus	---	1.199	0.647	0.995	0.933	1.004	0.898	1.005	0.901
1376282_at	BM392087	Transcribed locus	---	0.875	0.647	0.973	0.734	0.870	0.644	0.966	0.655
1397624_at	BI300158	Transcribed locus	---	1.070	0.648	1.241	0.162	1.028	0.789	1.312	0.002
1383111_at	AI058895	Transcribed locus	---	1.003	0.650	0.712	0.328	0.988	0.518	0.711	0.327
1380811_at	BE105756	Transcribed locus	---	0.838	0.650	0.491	0.000	0.616	0.004	0.849	0.018
1373057_at	AI229142	Transcribed locus	---	0.924	0.650	1.165	0.170	0.859	0.633	0.785	0.049
1391447_at	BI299229	Transcribed locus	---	0.853	0.651	0.687	0.252	1.452	0.007	0.586	0.052
1391899_at	BI303858	Transcribed locus	---	1.233	0.652	0.782	0.115	0.948	0.135	0.764	0.033
1380584_at	BE109190	Transcribed locus	---	0.874	0.652	1.106	0.922	0.955	0.152	1.099	0.978
1390960_at	AA893602	Transcribed locus	---	1.146	0.653	1.057	0.797	1.235	0.279	1.258	0.277
1374172_at	AI010883	Transcribed locus	---	1.131	0.655	0.993	0.967	1.020	0.504	0.960	0.626
1378730_at	AW534183	Transcribed locus	---	0.931	0.655	0.588	0.164	0.996	0.275	0.671	0.251
1393527_at	AI501914	Transcribed locus	---	0.811	0.655	1.159	0.143	1.166	0.864	1.285	0.035
1390796_at	AA998424	Transcribed locus	---	1.110	0.656	0.655	0.010	1.655	0.089	0.952	0.233
1396276_at	BG662898	Transcribed locus	---	0.800	0.656	0.084	0.001	0.699	0.190	0.252	0.002
1375086_at	BF393881	Transcribed locus	---	1.197	0.657	1.010	0.502	1.002	0.657	0.778	0.309
1396138_at	BF544511	Transcribed locus	---	1.279	0.660	0.873	0.246	1.622	0.013	1.062	0.097
1372221_at	BM389079	Transcribed locus	---	0.854	0.660	0.683	0.060	1.117	0.731	0.941	0.573
1397078_at	AI111920	Transcribed locus	---	1.041	0.660	0.947	0.827	0.918	0.408	1.034	0.888
1385892_at	AA900322	Transcribed locus	---	0.664	0.660	0.280	0.005	0.788	0.574	0.278	0.093
1389460_at	AI231787	Transcribed locus	---	1.177	0.660	1.267	0.062	0.999	0.378	1.013	0.307
1375925_at	BE113449	Transcribed locus	---	1.533	0.661	3.105	0.088	1.200	0.242	1.903	0.062
1397685_at	BF553180	Transcribed locus	---	0.967	0.661	0.456	0.027	0.993	0.973	0.628	0.079
1372833_at	AW521376	Transcribed locus	---	0.826	0.662	0.808	0.005	0.750	0.155	0.844	0.019
1374038_at	AA799964	Transcribed locus	---	0.870	0.662	0.484	0.001	1.165	0.974	0.526	0.000
1397589_at	BI296502	Transcribed locus	---	0.593	0.663	0.826	0.348	0.520	0.513	1.291	0.922
1396662_at	BF410720	Transcribed locus	---	0.998	0.665	0.988	0.811	0.841	0.081	1.080	0.269
1374130_at	BG373550	Transcribed locus	---	0.864	0.665	0.760	0.018	0.403	0.047	0.690	0.064
1395592_at	AA957981	Transcribed locus	---	1.695	0.665	1.084	0.381	2.614	0.083	1.312	0.052
1385314_at	AA923974	Transcribed locus	---	0.818	0.665	0.795	0.251	0.500	0.086	0.443	0.086
1377389_at	AI145613	Transcribed locus	---	1.145	0.665	0.634	0.111	1.704	0.813	0.893	0.061
1386828_at	BF557642	Transcribed locus	---	1.153	0.667	1.025	0.940	1.273	0.999	0.886	0.177
1382717_at	BF386949	Transcribed locus	---	0.805	0.668	0.737	0.958	1.050	0.065	1.021	0.628
1377224_at	BM391851	Transcribed locus	---	1.320	0.668	0.663	0.020	1.063	0.908	0.691	0.025
1378323_at	AW524892	Transcribed locus	---	1.264	0.669	0.398	0.016	1.326	0.671	0.723	0.140
1379376_at	BG372891	Transcribed locus	---	0.994	0.669	0.910	0.902	1.543	0.037	1.089	0.899
1398074_at	BE109876	Transcribed locus	---	1.154	0.669	0.506	0.422	0.903	0.642	0.707	0.185
1389218_at	AI169490	Transcribed locus	---	0.817	0.669	0.414	0.003	0.951	0.925	0.562	0.003
1375965_at	AI229167	Transcribed locus	---	0.675	0.670	0.226	0.004	1.000	0.295	0.262	0.007
1391584_at	AA850595	Transcribed locus	---	0.814	0.670	0.472	0.062	0.628	0.259	0.504	0.001
1395770_at	BM391695	Transcribed locus	---	1.210	0.670	1.396	0.204	1.561	0.009	1.745	0.835

1392675_at	AI044784	Transcribed locus	---	0.942	0.670	0.686	0.041	1.194	0.384	0.952	0.085
1378063_at	AW524795	Transcribed locus	---	0.652	0.672	0.800	0.044	0.961	0.580	0.958	0.165
1380902_at	BE106303	Transcribed locus	---	0.786	0.672	0.554	0.023	0.753	0.338	0.737	0.120
1391173_at	BF389308	Transcribed locus	---	1.069	0.674	0.882	0.069	0.946	0.689	1.223	0.628
1394601_at	AW526910	Transcribed locus	---	1.281	0.674	0.772	0.043	0.690	0.230	0.813	0.321
1385909_at	BE118035	Transcribed locus	---	0.941	0.675	0.214	0.069	0.646	0.001	0.469	0.013
1392192_at	BF413231	Transcribed locus	---	1.144	0.676	1.115	0.211	1.276	0.044	0.983	0.194
1383877_a_at	AW433647	Transcribed locus	---	1.041	0.677	0.951	0.579	0.790	0.895	1.268	0.075
1372355_at	BE109242	Transcribed locus	---	0.826	0.677	0.855	0.319	0.876	0.068	0.798	0.286
1391215_at	BF386303	Transcribed locus	---	1.145	0.678	1.488	0.172	1.127	0.777	1.195	0.023
1373518_at	AA866231	Transcribed locus	---	0.959	0.679	0.775	0.425	0.963	0.578	0.973	0.818
1389735_at	BE107296	Transcribed locus	---	1.192	0.679	0.323	0.009	2.274	0.017	0.370	0.153
1371859_at	D86655	Transcribed locus	---	1.047	0.679	1.088	0.165	1.202	0.942	0.934	0.331
1388515_at	BE112952	Transcribed locus	---	0.877	0.679	0.945	0.250	0.770	0.319	1.056	0.474
1398406_at	AI102382	Transcribed locus	---	0.855	0.679	0.120	0.002	0.911	0.238	0.084	0.023
1374595_at	BF282323	Transcribed locus	---	1.136	0.680	1.206	0.803	1.306	0.782	0.935	0.570
1398195_at	BF397286	Transcribed locus	---	0.973	0.680	0.997	0.517	1.034	0.596	1.001	0.955
1392641_at	AA957091	Transcribed locus	---	1.129	0.680	0.704	0.007	0.880	0.803	0.662	0.012
1375487_at	BI296529	Transcribed locus	---	1.125	0.681	1.148	0.908	1.014	0.332	1.388	0.999
1391193_at	BI288564	Transcribed locus	---	0.920	0.682	0.872	0.367	1.249	0.173	0.999	0.820
1396021_at	AA999128	Transcribed locus	---	1.072	0.683	0.715	0.023	0.847	0.127	0.697	0.025
1389462_at	BG373049	Transcribed locus	---	0.884	0.683	0.870	0.676	0.941	0.966	0.979	0.206
1385543_at	BF413374	Transcribed locus	---	0.856	0.683	0.538	0.039	1.207	0.337	0.928	0.395
1384446_at	BF402271	Transcribed locus	---	0.922	0.683	0.293	0.061	1.543	0.276	0.295	0.062
1374126_at	BG374261	Transcribed locus	---	1.196	0.684	0.920	0.299	0.597	0.070	1.086	0.301
1390701_at	BG372551	Transcribed locus	---	0.759	0.685	0.868	0.245	1.063	0.738	0.892	0.937
1391928_at	BF418827	Transcribed locus	---	1.022	0.685	2.463	0.017	1.063	0.204	1.852	0.025
1381163_at	AI229248	Transcribed locus	---	0.841	0.685	2.781	0.000	0.610	0.043	1.765	0.003
1384521_at	BE117499	Transcribed locus	---	1.164	0.686	1.047	0.928	0.972	0.048	0.827	0.020
1380961_at	AW526232	Transcribed locus	---	1.115	0.686	1.088	0.357	1.195	0.026	1.130	0.407
1390815_at	BF282870	Transcribed locus	---	1.084	0.687	0.487	0.000	0.760	0.231	0.379	0.010
1394739_at	BE102817	Transcribed locus	---	0.865	0.688	0.936	0.414	0.962	0.559	0.984	0.751
1393131_at	AI112338	Transcribed locus	---	1.166	0.688	1.736	0.040	1.261	0.224	1.740	0.066
1373434_at	AA944179	Transcribed locus	---	1.268	0.689	1.042	0.215	1.020	0.894	1.193	0.406
1380599_at	AI639258	Transcribed locus	---	0.965	0.689	1.132	0.553	0.839	0.136	1.349	0.100
1377611_at	AI145868	Transcribed locus	---	1.247	0.690	1.153	0.117	1.335	0.600	1.557	0.010
1391763_at	BF420184	Transcribed locus	---	0.854	0.690	0.476	0.018	1.429	0.354	0.522	0.026
1383166_at	BE100595	Transcribed locus	---	0.844	0.690	0.853	0.063	0.879	0.316	0.981	0.241
1384958_at	BI279112	Transcribed locus	---	0.741	0.691	0.909	0.089	0.810	0.081	0.901	0.939
1379259_at	AW534671	Transcribed locus	---	0.971	0.691	1.838	0.036	1.059	0.708	1.448	0.219
1390917_at	AI227828	Transcribed locus	---	1.211	0.691	1.247	0.152	1.011	0.538	1.051	0.147
1394577_at	BI279384	Transcribed locus	---	0.883	0.692	0.430	0.025	1.550	0.543	0.595	0.041
1389797_at	AI317854	Transcribed locus	---	0.843	0.693	0.545	0.015	0.886	0.926	0.442	0.126
1374383_at	BE121006	Transcribed locus	---	0.914	0.694	0.995	0.353	0.449	0.184	1.090	0.923
1382520_at	AI008244	Transcribed locus	---	0.862	0.695	1.951	0.352	1.508	0.064	1.002	0.154
1374155_at	BF410502	Transcribed locus	---	0.956	0.696	0.556	0.025	1.256	0.020	0.373	0.020
1395242_at	BF419005	Transcribed locus	---	1.128	0.696	0.996	0.940	0.992	0.151	0.983	0.948
1380520_at	BI295810	Transcribed locus	---	0.973	0.697	0.990	0.974	1.073	0.182	1.163	0.946
1388418_at	BG378875	Transcribed locus	---	0.980	0.697	0.501	0.005	0.830	0.104	0.640	0.025
1377213_at	BI280353	Transcribed locus	---	1.066	0.697	3.443	0.000	0.870	0.227	3.104	0.003
1391406_at	AI169572	Transcribed locus	---	0.939	0.698	0.755	0.038	0.936	0.125	0.721	0.013
1379675_at	BF402435	Transcribed locus	---	1.112	0.699	1.017	0.327	1.111	0.171	0.947	0.997
1377637_at	AW916093	Transcribed locus	---	1.272	0.699	1.531	0.209	1.426	0.012	0.728	0.328
1385597_at	AI709508	Transcribed locus	---	1.904	0.700	0.418	0.026	0.695	0.268	0.468	0.025
1397616_at	BI292232	Transcribed locus	---	0.955	0.700	0.655	0.126	1.084	0.047	0.731	0.147
1379555_at	AI233902	Transcribed locus	---	1.160	0.701	0.898	0.770	1.317	0.397	0.652	0.179
1399085_at	BM384770	Transcribed locus	---	0.995	0.701	0.588	0.004	1.068	0.687	0.690	0.001
1393173_at	BG668164	Transcribed locus	---	1.160	0.701	0.791	0.019	0.955	0.669	0.887	0.803
1396954_at	BM386206	Transcribed locus	---	1.033	0.701	0.954	0.781	1.212	0.703	0.952	0.471
1397134_at	BF414458	Transcribed locus	---	0.923	0.701	1.168	0.676	1.045	0.640	0.903	0.533
1399104_at	BI287258	Transcribed locus	---	1.000	0.702	0.467	0.012	0.833	0.485	0.459	0.067

1379738_at	AI007726	Transcribed locus	---	1.921	0.702	0.719	0.165	1.042	0.483	1.167	0.157
1393252_at	AA996804	Transcribed locus	---	1.038	0.705	1.328	0.781	1.174	0.933	1.014	0.439
1397301_at	BM386743	Transcribed locus	---	0.924	0.705	0.499	0.040	1.551	0.178	0.867	0.186
1374087_at	AI411088	Transcribed locus	---	0.993	0.705	0.962	0.802	0.997	0.253	1.051	0.841
1374613_at	BE100609	Transcribed locus	---	0.868	0.706	0.385	0.001	1.008	0.624	0.577	0.011
1385911_at	AI235281	Transcribed locus	---	1.050	0.706	0.574	0.068	1.134	0.482	0.714	0.090
1390301_at	AW524414	Transcribed locus	---	0.903	0.707	0.858	0.697	0.704	0.285	0.679	0.099
1397422_at	BF390904	Transcribed locus	---	1.252	0.712	1.158	0.580	1.002	0.994	0.714	0.782
1382960_at	BE108047	Transcribed locus	---	0.990	0.713	0.997	0.979	0.978	0.361	1.104	0.680
1390557_at	BF394809	Transcribed locus	---	0.729	0.713	0.837	0.052	0.627	0.214	0.849	0.128
1379208_at	BE113484	Transcribed locus	---	1.185	0.714	1.454	0.075	1.049	0.696	0.954	0.813
1371667_at	BG380728	Transcribed locus	---	0.868	0.715	0.815	0.023	0.891	0.204	0.949	0.247
1399090_at	AA944459	Transcribed locus	---	0.634	0.715	0.875	0.158	0.513	0.080	0.747	0.028
1385877_at	BI294012	Transcribed locus	---	0.911	0.716	0.791	0.897	0.998	0.933	0.789	0.279
1380975_at	AW534466	Transcribed locus	---	1.095	0.716	0.775	0.331	1.118	0.501	0.758	0.314
1373680_at	AA800708	Transcribed locus	---	1.050	0.718	0.751	0.152	1.036	0.802	0.666	0.046
1373505_at	BI287800	Transcribed locus	---	1.058	0.719	1.719	0.005	0.801	0.105	1.361	0.009
1375012_at	BF399627	Transcribed locus	---	0.950	0.719	0.407	0.024	1.494	0.133	0.500	0.010
1385521_at	AI603505	Transcribed locus	---	1.117	0.721	0.998	0.483	1.094	0.256	0.766	0.191
1392968_at	BI300566	Transcribed locus	---	0.848	0.721	0.265	0.002	0.426	0.301	0.376	0.003
1384004_at	AI030360	Transcribed locus	---	0.684	0.725	0.639	0.005	0.562	0.051	0.773	0.052
1395004_at	BF397827	Transcribed locus	---	1.504	0.725	1.068	0.655	1.158	0.837	0.839	0.495
1378673_at	AI071509	Transcribed locus	---	1.077	0.727	1.049	0.506	1.357	0.008	0.999	0.997
1378616_at	BG380791	Transcribed locus	---	0.977	0.727	0.816	0.127	0.997	0.926	0.721	0.116
1386589_at	AW143518	Transcribed locus	---	0.814	0.728	0.547	0.008	0.401	0.028	0.569	0.003
1397698_at	AW917627	Transcribed locus	---	0.796	0.728	0.511	0.059	0.520	0.170	0.634	0.008
1383174_at	AI576562	Transcribed locus	---	1.108	0.729	0.244	0.002	1.030	0.907	0.556	0.007
1374994_at	BF394281	Transcribed locus	---	1.035	0.729	0.403	0.020	1.002	0.991	0.302	0.000
1377875_at	BF400747	Transcribed locus	---	0.514	0.730	0.103	0.001	0.733	0.710	0.208	0.009
1399066_at	AI236763	Transcribed locus	---	0.950	0.730	0.642	0.003	0.907	0.455	0.608	0.005
1378117_at	BF396269	Transcribed locus	---	1.046	0.731	1.075	0.374	0.846	0.377	1.288	0.023
1375705_at	AI103622	Transcribed locus	---	0.907	0.731	0.457	0.022	0.651	0.281	0.479	0.007
1392587_at	BE115141	Transcribed locus	---	1.421	0.733	0.843	0.158	1.034	0.930	1.033	0.100
1392144_at	BF391491	Transcribed locus	---	1.130	0.733	0.837	0.306	0.999	0.389	0.962	0.384
1395944_at	AI548667	Transcribed locus	---	0.942	0.734	0.814	0.225	0.958	0.984	0.816	0.267
1377132_at	AW527797	Transcribed locus	---	0.957	0.734	1.198	0.192	1.153	0.615	1.231	0.111
1385637_at	AI029494	Transcribed locus	---	1.479	0.734	1.029	0.501	1.865	0.053	1.002	0.994
1399119_at	BI282030	Transcribed locus	---	0.932	0.734	2.328	0.016	1.142	0.395	1.658	0.035
1374700_at	BF388903	Transcribed locus	---	1.071	0.735	1.295	0.127	1.156	0.226	1.625	0.129
1376060_at	BF416794	Transcribed locus	---	1.075	0.736	0.673	0.006	1.084	0.139	0.605	0.047
1379915_at	BF393083	Transcribed locus	---	0.836	0.736	1.262	0.714	1.313	0.309	1.404	0.052
1376771_at	BF412303	Transcribed locus	---	1.157	0.737	0.829	0.950	0.800	0.787	0.970	0.320
1390597_at	BF419818	Transcribed locus	---	0.981	0.737	0.962	0.634	0.967	0.739	0.981	0.883
1390952_at	AI144822	Transcribed locus	---	1.207	0.737	1.266	0.127	0.488	0.069	1.033	0.146
1385156_at	BE120415	Transcribed locus	---	0.962	0.738	0.997	0.992	0.994	0.915	1.009	0.967
1391400_at	BI296500	Transcribed locus	---	1.002	0.738	0.843	0.065	1.090	0.480	0.584	0.075
1395085_at	BF386354	Transcribed locus	---	1.058	0.738	1.085	0.576	0.861	0.716	1.518	0.098
1379799_at	BF415056	Transcribed locus	---	0.405	0.738	2.378	0.101	0.670	0.357	0.963	0.996
1383087_at	BF409251	Transcribed locus	---	1.134	0.739	0.848	0.384	1.568	0.018	1.152	0.683
1395499_at	BF392443	Transcribed locus	---	1.117	0.739	1.453	0.080	1.001	0.189	1.000	0.952
1394816_at	AI501478	Transcribed locus	---	0.927	0.739	0.819	0.971	0.886	0.477	0.843	0.996
1391337_at	BE116623	Transcribed locus	---	0.849	0.740	0.419	0.026	0.999	0.986	0.624	0.168
1373792_at	AI228348	Transcribed locus	---	0.884	0.741	0.914	0.431	0.809	0.351	1.020	0.696
1381038_at	BE101442	Transcribed locus	---	1.010	0.743	0.999	0.925	1.018	0.833	0.990	0.967
1381354_at	BF403728	Transcribed locus	---	1.192	0.743	0.562	0.120	0.893	0.974	0.676	0.110
1380714_at	AI600230	Transcribed locus	---	1.103	0.745	0.825	0.510	1.002	0.797	0.673	0.199
1398328_at	BM389797	Transcribed locus	---	1.088	0.745	0.876	0.960	0.572	0.808	0.608	0.100
1384199_at	BF395951	Transcribed locus	---	1.764	0.746	1.470	0.923	1.641	0.220	1.136	0.410
1371711_at	AA800689	Transcribed locus	---	0.816	0.746	0.763	0.069	0.666	0.079	0.721	0.009
1380075_at	BF390843	Transcribed locus	---	1.161	0.749	0.618	0.083	0.958	0.679	0.824	0.149
1382108_at	AA900536	Transcribed locus	---	0.985	0.750	0.903	0.603	0.660	0.026	0.999	0.803

1372285_at	BM389061	Transcribed locus	---	0.810	0.753	0.611	0.056	0.776	0.165	0.864	0.302
1381147_at	BF409065	Transcribed locus	---	0.894	0.754	0.255	0.007	0.706	0.138	0.292	0.032
1379951_at	BE104039	Transcribed locus	---	1.033	0.754	0.893	0.972	0.999	0.995	1.025	0.996
1395457_at	BM387150	Transcribed locus	---	1.406	0.755	1.351	0.720	0.913	0.810	1.027	0.438
1382159_at	BF386740	Transcribed locus	---	1.038	0.755	0.871	0.402	0.986	0.184	0.926	0.234
1389352_at	BF281980	Transcribed locus	---	0.898	0.755	0.470	0.015	1.255	0.089	0.670	0.001
1398235_at	BE097092	Transcribed locus	---	1.049	0.755	0.644	0.617	0.788	0.113	0.885	0.512
1380603_at	AI044853	Transcribed locus	---	1.007	0.756	1.213	0.908	0.930	0.476	1.190	1.000
1381471_at	AI060117	Transcribed locus	---	0.956	0.757	0.782	0.334	1.766	0.001	0.964	0.417
1394979_at	BE101703	Transcribed locus	---	0.998	0.758	0.599	0.046	0.780	0.638	0.628	0.077
1392331_at	BE100256	Transcribed locus	---	1.029	0.758	0.950	0.818	1.264	0.215	0.945	0.759
1379617_at	BF288779	Transcribed locus	---	0.937	0.759	1.626	0.395	1.232	0.885	1.206	0.875
1374493_at	H35017	Transcribed locus	---	1.107	0.759	0.991	0.889	0.783	0.320	0.993	0.552
1376404_at	AI639317	Transcribed locus	---	1.027	0.759	0.736	0.222	0.588	0.051	0.620	0.084
1390517_at	BM392260	Transcribed locus	---	0.890	0.760	0.558	0.045	0.825	0.436	0.782	0.885
1394525_at	BM385125	Transcribed locus	---	1.165	0.761	1.196	0.168	1.444	0.513	1.243	0.188
1386683_at	BF562870	Transcribed locus	---	1.168	0.762	0.371	0.023	0.854	0.100	0.508	0.003
1391496_at	AA819635	Transcribed locus	---	0.933	0.763	0.554	0.014	0.752	0.213	0.616	0.007
1381837_at	AI502137	Transcribed locus	---	0.958	0.764	0.649	0.009	0.963	0.542	0.446	0.008
1396502_at	BF405162	Transcribed locus	---	1.104	0.765	0.924	0.341	1.046	0.882	0.854	0.390
1375562_at	BF408460	Transcribed locus	---	0.963	0.766	1.115	0.770	0.559	0.714	0.962	0.757
1378903_at	AI712467	Transcribed locus	---	1.006	0.767	1.000	0.944	1.159	0.386	1.112	0.973
1391511_at	AA997877	Transcribed locus	---	0.875	0.768	0.855	0.434	1.135	0.773	1.027	0.920
1392768_at	AA900944	Transcribed locus	---	0.983	0.768	0.912	0.293	1.089	0.388	0.783	0.375
1375431_at	AW531861	Transcribed locus	---	0.694	0.768	0.707	0.027	0.425	0.029	0.785	0.076
1386109_at	BF287631	Transcribed locus	---	1.374	0.768	1.115	0.459	1.413	0.219	1.030	0.493
1375235_at	BG378732	Transcribed locus	---	1.305	0.768	0.985	0.956	1.194	0.397	0.993	0.804
1376619_at	AI412803	Transcribed locus	---	0.947	0.770	1.360	0.611	1.255	0.207	1.055	0.920
1384193_at	AI235607	Transcribed locus	---	1.340	0.771	1.113	0.636	1.369	0.460	1.010	0.549
1380387_at	BE105492	Transcribed locus	---	1.967	0.772	0.714	0.514	1.487	0.764	0.922	0.521
1381916_at	AA997234	Transcribed locus	---	1.269	0.772	0.866	0.970	1.009	0.958	0.737	0.125
1375591_at	AI101245	Transcribed locus	---	1.303	0.772	0.496	0.012	1.221	0.970	0.626	0.019
1376378_at	BF393577	Transcribed locus	---	0.957	0.772	1.001	0.430	1.305	0.050	0.941	0.429
1383334_at	AW921244	Transcribed locus	---	0.790	0.772	0.613	0.186	0.908	0.376	0.644	0.016
1379528_at	BI284017	Transcribed locus	---	1.118	0.773	1.104	0.648	1.065	0.504	1.040	0.725
1393200_at	AI500827	Transcribed locus	---	0.981	0.774	0.926	0.419	0.857	0.123	0.820	0.461
1377474_at	AI007668	Transcribed locus	---	0.909	0.774	1.528	0.060	0.722	0.034	1.451	0.250
1384035_at	AW536030	Transcribed locus	---	1.453	0.775	0.599	0.112	1.022	0.991	1.457	0.634
1378036_at	AI029387	Transcribed locus	---	1.004	0.775	0.549	0.000	1.309	0.020	0.700	0.007
1371864_at	AW524563	Transcribed locus	---	1.176	0.775	1.040	0.346	1.180	0.553	0.942	0.202
1372816_at	BE107319	Transcribed locus	---	0.675	0.776	0.542	0.002	0.595	0.051	0.536	0.002
1395366_at	BG669749	Transcribed locus	---	0.684	0.778	1.365	0.040	1.005	0.963	1.451	0.105
1377750_at	AI454536	Transcribed locus	---	0.964	0.778	0.397	0.002	1.609	0.000	0.437	0.001
1389495_at	BF394211	Transcribed locus	---	1.060	0.779	0.999	0.961	1.090	0.150	0.986	0.786
1385734_at	BE118753	Transcribed locus	---	1.063	0.779	0.656	0.014	1.065	0.553	0.903	0.375
1399096_at	AA894279	Transcribed locus	---	1.259	0.779	0.470	0.012	1.101	0.320	0.585	0.271
1378188_at	BE102810	Transcribed locus	---	0.914	0.782	0.983	0.583	1.166	0.650	0.885	0.192
1383521_at	AW915081	Transcribed locus	---	0.958	0.782	1.074	0.352	1.122	0.362	1.110	0.012
1374214_at	AI235359	Transcribed locus	---	1.051	0.786	1.083	0.207	0.693	0.007	1.223	0.252
1395720_at	BE098012	Transcribed locus	---	0.813	0.786	0.405	0.112	0.961	0.651	0.376	0.017
1394395_at	BG668719	Transcribed locus	---	1.095	0.786	0.257	0.003	0.904	0.665	0.395	0.059
1382789_at	BM389812	Transcribed locus	---	1.719	0.786	1.754	0.002	2.233	0.050	1.304	0.291
1397784_at	BI297092	Transcribed locus	---	0.815	0.789	0.409	0.015	0.745	0.733	0.470	0.008
1382086_at	AI235883	Transcribed locus	---	1.034	0.789	1.028	0.631	2.546	0.044	1.012	0.938
1396883_at	AI548898	Transcribed locus	---	0.747	0.791	0.973	0.912	0.898	0.997	1.542	0.178
1395862_at	BF397879	Transcribed locus	---	1.142	0.791	1.135	0.521	1.097	0.627	0.756	0.275
1390431_at	AI111559	Transcribed locus	---	1.020	0.792	0.340	0.016	0.910	0.880	0.415	0.012
1372901_at	BM386850	Transcribed locus	---	0.781	0.792	1.244	0.567	0.623	0.367	1.075	0.590
1385271_at	AI763870	Transcribed locus	---	0.835	0.793	0.470	0.005	0.707	0.142	0.730	0.071
1396044_at	AI706203	Transcribed locus	---	1.198	0.795	1.287	0.571	1.013	0.379	0.868	0.523
1389401_at	BI294956	Transcribed locus	---	0.983	0.795	0.875	0.326	0.532	0.004	0.729	0.071

1378076_at	AA963273	Transcribed locus	---	1.054	0.796	0.532	0.007	1.149	0.677	0.576	0.006
1381549_at	BG376818	Transcribed locus	---	1.048	0.797	1.508	0.031	3.057	0.041	1.209	0.212
1374920_at	AI228955	Transcribed locus	---	0.925	0.798	0.552	0.006	0.931	0.306	0.441	0.008
1379097_at	BF416779	Transcribed locus	---	0.986	0.798	0.700	0.023	0.372	0.087	0.834	0.331
1381146_at	AW434387	Transcribed locus	---	1.326	0.799	1.233	0.345	1.151	0.609	0.942	0.024
1380383_at	AI030650	Transcribed locus	---	0.975	0.799	0.297	0.004	0.729	0.061	0.476	0.008
1379416_at	AW535897	Transcribed locus	---	1.560	0.799	0.609	0.078	1.216	0.501	1.035	0.965
1378258_at	AI716449	Transcribed locus	---	0.856	0.800	0.999	0.969	1.200	0.022	1.003	0.994
1375676_at	AA956897	Transcribed locus	---	1.002	0.801	0.947	0.617	1.243	0.706	1.052	0.201
1374186_at	BE109362	Transcribed locus	---	0.970	0.801	1.268	0.121	0.978	0.194	1.162	0.982
1383509_at	BF551003	Transcribed locus	---	1.207	0.801	1.325	0.008	1.090	0.505	0.971	0.127
1389748_at	BE118122	Transcribed locus	---	1.444	0.803	0.642	0.118	1.338	0.504	1.085	0.757
1383740_at	AI029740	Transcribed locus	---	0.747	0.804	0.927	0.090	0.885	0.537	0.817	0.028
1390631_at	BE107619	Transcribed locus	---	1.303	0.804	3.014	0.005	1.017	0.343	1.877	0.006
1392183_at	AI547389	Transcribed locus	---	1.408	0.805	1.093	0.620	1.293	0.742	1.012	0.435
1378439_at	AI175531	Transcribed locus	---	1.435	0.806	1.244	0.282	1.794	0.240	1.123	0.395
1390173_at	BG377886	Transcribed locus	---	1.105	0.808	0.991	0.451	1.006	0.978	0.999	0.621
1381684_at	BM391296	Transcribed locus	---	1.006	0.809	2.392	0.234	1.518	0.398	1.636	0.086
1394809_at	AW522733	Transcribed locus	---	1.050	0.809	0.854	0.846	0.912	0.718	1.013	0.953
1378921_at	BF407470	Transcribed locus	---	0.981	0.810	0.965	0.999	1.054	0.983	0.817	0.057
1391599_at	AA875010	Transcribed locus	---	1.015	0.811	0.797	0.193	0.653	0.245	0.468	0.057
1392909_at	AT005674	Transcribed locus	---	1.014	0.811	0.512	0.830	1.021	0.062	0.851	0.543
1395307_at	AI409823	Transcribed locus	---	1.300	0.812	0.994	0.934	1.030	0.710	0.999	0.976
1377617_at	BF550438	Transcribed locus	---	0.834	0.812	0.546	0.024	0.846	0.094	0.609	0.022
1386600_at	BF522129	Transcribed locus	---	0.805	0.813	1.535	0.056	0.639	0.238	0.960	0.831
1386286_at	AI639322	Transcribed locus	---	0.935	0.814	0.119	0.010	1.646	0.438	0.386	0.080
1374251_at	AA893192	Transcribed locus	---	1.098	0.814	0.541	0.022	1.146	0.958	0.793	0.195
1392487_at	BI303896	Transcribed locus	---	1.075	0.815	1.505	0.041	0.850	0.785	0.969	0.548
1390615_at	BI281629	Transcribed locus	---	1.382	0.815	1.485	0.235	0.461	0.592	1.845	0.406
1390298_at	BI287856	Transcribed locus	---	0.994	0.815	1.393	0.025	1.093	0.468	1.190	0.780
1383861_at	BF394135	Transcribed locus	---	0.983	0.816	0.751	0.044	0.793	0.383	0.828	0.162
1373851_at	AI171998	Transcribed locus	---	0.661	0.816	0.923	0.039	0.915	0.458	0.928	0.356
1393115_at	BI293687	Transcribed locus	---	1.670	0.817	0.864	0.310	0.998	0.888	0.717	0.138
1382444_at	AA925250	Transcribed locus	---	1.071	0.817	1.624	0.036	1.152	0.769	1.202	0.664
1398382_at	AI175556	Transcribed locus	---	0.887	0.817	1.541	0.005	0.588	0.258	1.229	0.484
1396530_at	BE120509	Transcribed locus	---	1.319	0.817	1.597	0.450	1.710	0.309	1.364	0.318
1389064_at	BE111732	Transcribed locus	---	0.975	0.818	1.284	0.133	0.719	0.304	0.979	0.855
1384366_at	BI283477	Transcribed locus	---	1.130	0.820	0.889	0.386	1.133	0.203	0.583	0.013
1373944_at	AW530292	Transcribed locus	---	1.052	0.820	0.916	0.076	0.939	0.433	0.946	0.365
1390778_at	AI556731	Transcribed locus	---	1.321	0.820	1.204	0.917	0.722	0.193	0.987	0.908
1381071_at	AI112096	Transcribed locus	---	0.732	0.821	0.731	0.114	1.388	0.224	0.929	0.896
1367534_at	BG374688	Transcribed locus	---	0.894	0.822	0.761	0.241	0.654	0.439	0.803	0.197
1397407_at	AI137564	Transcribed locus	---	0.970	0.822	0.777	0.041	1.573	0.100	0.937	0.031
1386065_at	AI169118	Transcribed locus	---	0.931	0.822	5.043	0.000	1.179	0.603	4.564	0.000
1371636_at	BE104321	Transcribed locus	---	0.933	0.822	0.724	0.036	0.950	0.188	0.858	0.150
1376181_at	BG668724	Transcribed locus	---	0.820	0.822	1.390	0.121	1.106	0.011	1.926	0.053
1396000_at	AI704583	Transcribed locus	---	1.037	0.822	0.997	0.977	1.090	0.680	1.468	0.139
1398187_at	BM391924	Transcribed locus	---	1.092	0.822	1.043	0.498	1.229	0.058	0.833	0.502
1395548_at	BG666506	Transcribed locus	---	0.949	0.824	0.529	0.070	1.418	0.164	0.483	0.046
1383716_at	BF556301	Transcribed locus	---	0.818	0.824	0.856	0.231	1.047	0.482	0.897	0.534
1371960_at	AI230548	Transcribed locus	---	0.849	0.825	0.798	0.050	1.142	0.426	0.929	0.537
1378601_at	AI413056	Transcribed locus	---	1.061	0.825	0.966	0.871	1.006	0.925	0.716	0.777
1386474_at	H31753	Transcribed locus	---	0.730	0.825	0.776	0.529	1.002	0.994	1.469	0.301
1373839_at	BG372386	Transcribed locus	---	0.660	0.826	0.943	0.820	0.705	0.578	1.294	0.439
1390373_at	BE107528	Transcribed locus	---	1.183	0.827	2.503	0.005	0.487	0.006	1.613	0.020
1378444_at	AI175473	Transcribed locus	---	1.059	0.827	0.200	0.001	0.927	0.533	0.159	0.032
1396428_at	BF409243	Transcribed locus	---	1.016	0.827	0.949	0.330	1.017	0.858	0.957	0.396
1379934_at	BI285676	Transcribed locus	---	0.763	0.827	0.456	0.008	0.588	0.052	0.509	0.023
1383439_at	BI278550	Transcribed locus	---	0.997	0.827	1.196	0.482	0.892	0.721	0.746	0.075
1378268_at	AI554986	Transcribed locus	---	0.922	0.827	1.005	0.966	0.971	0.981	0.901	0.408
1383843_at	AA945568	Transcribed locus	---	0.666	0.828	0.336	0.042	0.395	0.091	0.509	0.102

1392699_at	BF411888	Transcribed locus	---	1.003	0.828	0.993	0.904	0.967	0.754	1.217	0.215
1394541_at	BM387754	Transcribed locus	---	1.081	0.829	1.188	0.279	1.139	0.086	1.262	0.326
1391723_at	BI291869	Transcribed locus	---	0.950	0.830	0.670	0.005	1.291	0.161	0.849	0.050
1381644_at	BE121056	Transcribed locus	---	2.162	0.830	1.124	0.698	1.823	0.300	0.547	0.093
1389960_at	BF390877	Transcribed locus	---	1.171	0.830	1.385	0.700	0.769	0.156	1.153	0.433
1397028_at	BF389733	Transcribed locus	---	1.100	0.831	0.959	0.352	0.992	0.948	1.171	0.428
1391561_at	BE108893	Transcribed locus	---	1.194	0.831	1.625	0.550	1.020	0.259	1.051	0.856
1397204_s_at	BM385125	Transcribed locus	---	1.225	0.831	1.118	0.073	1.172	0.536	1.043	0.100
1385875_at	AA957617	Transcribed locus	---	1.035	0.832	1.350	0.073	1.123	0.329	0.999	0.969
1389279_at	BM386204	Transcribed locus	---	0.681	0.832	1.238	0.110	0.604	0.200	1.131	0.108
1384243_at	AI111413	Transcribed locus	---	0.999	0.832	0.999	0.163	1.001	0.998	1.008	0.964
1380859_at	AA891931	Transcribed locus	---	1.002	0.834	0.785	0.022	0.654	0.020	0.853	0.289
1397615_at	BG375528	Transcribed locus	---	1.122	0.834	0.863	0.563	0.887	0.926	0.877	0.947
1392619_at	BE118107	Transcribed locus	---	1.083	0.835	0.938	0.991	1.434	0.084	1.179	0.307
1392190_at	BF404047	Transcribed locus	---	0.942	0.836	0.907	0.060	1.020	0.912	0.930	0.040
1392898_at	AF011367	Transcribed locus	---	0.969	0.836	0.777	0.023	0.816	0.409	0.775	0.028
1397178_at	AA899041	Transcribed locus	---	1.087	0.836	2.410	0.003	1.124	0.313	3.073	0.004
1395749_at	BE104663	Transcribed locus	---	1.178	0.837	1.302	0.226	1.488	0.236	1.065	0.809
1374992_at	AI714115	Transcribed locus	---	0.692	0.840	0.573	0.351	0.808	0.193	0.571	0.022
1379690_at	BF420785	Transcribed locus	---	1.261	0.840	0.939	0.713	0.875	0.349	0.473	0.524
1389097_at	BI275857	Transcribed locus	---	0.961	0.841	0.711	0.236	1.005	0.934	0.791	0.738
1371893_at	BE111640	Transcribed locus	---	1.223	0.842	0.612	0.001	1.253	0.051	0.735	0.004
1398731_at	BF410569	Transcribed locus	---	0.987	0.842	0.930	0.057	1.779	0.090	0.923	0.094
1390718_at	BE096865	Transcribed locus	---	0.924	0.843	1.061	0.707	1.028	0.100	1.088	0.257
1391814_at	BI293690	Transcribed locus	---	1.011	0.844	0.896	0.331	1.544	0.950	0.930	0.604
1397800_at	BE106592	Transcribed locus	---	1.153	0.844	1.219	0.681	1.794	0.427	2.347	0.091
1383611_at	AI145497	Transcribed locus	---	0.565	0.844	0.589	0.084	1.664	0.323	0.928	0.180
1396363_at	BF399356	Transcribed locus	---	0.932	0.845	1.147	0.397	3.660	0.003	3.119	0.013
1383518_at	AI137914	Transcribed locus	---	1.297	0.845	1.233	0.415	1.015	0.905	1.095	0.264
1391871_at	AI763550	Transcribed locus	---	1.031	0.845	0.457	0.005	0.792	0.105	0.275	0.025
1381324_at	BM387030	Transcribed locus	---	1.019	0.846	1.418	0.329	1.001	0.993	1.115	0.554
1372081_at	BI299305	Transcribed locus	---	0.930	0.847	0.526	0.018	1.359	0.989	0.687	0.012
1389721_at	BI285940	Transcribed locus	---	1.056	0.848	0.974	0.873	1.056	0.162	0.706	0.914
1396451_at	BF393275	Transcribed locus	---	1.176	0.848	0.527	0.014	1.367	0.829	0.564	0.029
1376141_at	BF394672	Transcribed locus	---	0.891	0.848	0.562	0.112	0.818	0.904	0.665	0.727
1395189_at	BE111371	Transcribed locus	---	0.951	0.850	0.673	0.013	1.739	0.184	0.519	0.007
1381296_at	AA819045	Transcribed locus	---	1.111	0.850	0.738	0.420	1.706	0.099	0.928	0.975
1398507_at	BE108415	Transcribed locus	---	0.983	0.851	0.475	0.023	0.973	0.770	0.506	0.029
1393334_at	AW528448	Transcribed locus	---	2.671	0.851	0.784	0.029	0.803	0.985	0.409	0.045
1375692_at	AI229025	Transcribed locus	---	0.768	0.851	1.042	0.832	0.561	0.156	0.789	0.040
1385905_at	AI178616	Transcribed locus	---	0.839	0.852	0.653	0.024	1.053	0.515	0.697	0.264
1377418_at	AI411724	Transcribed locus	---	0.985	0.852	0.968	0.544	0.997	0.059	1.236	0.026
1393391_at	BF406888	Transcribed locus	---	1.259	0.852	2.502	0.007	1.046	0.198	1.728	0.024
1375928_at	BI285329	Transcribed locus	---	1.213	0.853	1.703	0.006	0.868	0.660	1.615	0.061
1396743_at	BF391580	Transcribed locus	---	2.050	0.853	1.745	0.275	2.297	0.394	1.108	0.812
1395355_at	AI555210	Transcribed locus	---	0.965	0.854	0.317	0.001	1.059	0.745	0.636	0.006
1391851_at	AI548705	Transcribed locus	---	1.050	0.854	0.663	0.085	1.405	0.266	0.703	0.013
1385933_at	AI709424	Transcribed locus	---	1.274	0.855	1.222	0.086	1.026	0.700	0.972	0.861
1384934_at	AA893454	Transcribed locus	---	0.928	0.855	0.715	0.094	1.295	0.051	0.906	0.319
1381216_at	BI294178	Transcribed locus	---	0.945	0.856	1.080	0.301	1.016	0.340	1.115	0.117
1394256_at	BG664811	Transcribed locus	---	0.999	0.857	0.614	0.009	1.006	0.954	0.607	0.047
1395921_at	BE097603	Transcribed locus	---	0.958	0.857	0.462	0.017	0.911	0.696	0.473	0.005
1392615_at	AI454224	Transcribed locus	---	0.972	0.859	1.625	0.043	0.874	0.246	1.655	0.102
1384897_at	AA858696	Transcribed locus	---	0.984	0.860	0.683	0.094	1.031	0.702	0.677	0.318
1392025_x_at	BI303277	Transcribed locus	---	1.080	0.861	1.086	0.225	1.148	0.095	1.095	0.168
1388520_at	BI278854	Transcribed locus	---	1.266	0.861	0.378	0.000	0.813	0.479	0.588	0.003
1378202_at	BE106504	Transcribed locus	---	0.997	0.862	1.010	0.914	0.992	0.984	1.008	0.991
1378315_at	AI045116	Transcribed locus	---	1.436	0.863	1.221	0.403	1.019	0.986	1.429	0.098
1382212_at	AI385201	Transcribed locus	---	1.055	0.863	0.985	0.774	1.224	0.080	0.692	0.613
1374648_at	BM390626	Transcribed locus	---	1.000	0.863	0.093	0.001	0.996	0.918	0.093	0.000
1395381_at	BF542239	Transcribed locus	---	1.016	0.864	1.179	0.106	1.134	0.515	1.072	0.075

1393119_at	BM388725	Transcribed locus	---	1.004	0.864	8.035	0.000	0.545	0.007	6.812	0.004
1373007_at	BF417885	Transcribed locus	---	1.091	0.864	0.933	0.734	1.186	0.414	1.158	0.066
1397080_at	BM390517	Transcribed locus	---	0.897	0.865	0.833	0.085	1.057	0.870	0.664	0.029
1392774_at	BF284310	Transcribed locus	---	0.847	0.865	0.611	0.003	0.845	0.113	0.737	0.064
1392118_at	BE099845	Transcribed locus	---	0.837	0.866	0.426	0.003	0.790	0.400	0.317	0.014
1393025_at	BI297354	Transcribed locus	---	0.988	0.866	0.833	0.346	0.961	0.930	0.820	0.074
1395022_at	AA859303	Transcribed locus	---	1.091	0.866	0.712	0.906	1.340	0.026	1.110	0.606
1379205_at	BG374111	Transcribed locus	---	1.082	0.867	1.581	0.987	1.111	0.704	1.273	0.960
1381335_at	BE349658	Transcribed locus	---	0.928	0.869	0.985	0.068	1.224	0.075	1.075	0.113
1374216_at	BI280277	Transcribed locus	---	0.897	0.869	1.714	0.067	1.264	0.257	0.825	0.113
1376750_at	AA963477	Transcribed locus	---	1.552	0.869	0.601	0.417	1.682	0.266	0.999	0.999
1391514_at	AI575440	Transcribed locus	---	1.130	0.869	0.813	0.378	0.820	0.046	1.094	0.444
1383809_at	BF562237	Transcribed locus	---	0.952	0.871	0.538	0.081	1.143	0.289	0.830	0.076
1382575_at	BE118546	Transcribed locus	---	0.847	0.871	1.101	0.295	0.713	0.739	1.248	0.084
1395674_at	BF408259	Transcribed locus	---	1.155	0.871	0.362	0.005	0.932	0.855	0.451	0.051
1396603_at	BF406214	Transcribed locus	---	1.166	0.872	0.879	0.232	0.936	0.771	1.410	0.969
1397173_at	BE109095	Transcribed locus	---	0.974	0.873	0.320	0.035	0.968	0.860	0.367	0.002
1372851_at	AI412931	Transcribed locus	---	1.052	0.873	0.809	0.476	1.407	0.688	0.447	0.765
1380057_at	BE097091	Transcribed locus	---	1.009	0.873	0.946	0.963	1.009	0.344	1.014	0.871
1383063_a_at	AI137878	Transcribed locus	---	1.012	0.876	0.961	0.236	1.877	0.105	1.174	0.947
1397434_at	BF399188	Transcribed locus	---	1.185	0.877	0.973	0.398	1.274	0.341	0.780	0.580
1378208_at	BE099836	Transcribed locus	---	0.981	0.877	0.999	0.970	0.976	0.368	0.968	0.999
1394990_at	BI301740	Transcribed locus	---	1.152	0.877	1.025	0.149	1.506	0.202	1.271	0.360
1381225_at	BE119934	Transcribed locus	---	1.014	0.877	0.241	0.001	1.000	0.449	0.240	0.000
1377747_at	BE116029	Transcribed locus	---	0.865	0.879	0.791	0.516	1.019	0.261	0.802	0.144
1383293_at	BG669441	Transcribed locus	---	1.075	0.880	0.832	0.170	1.111	0.783	0.830	0.047
1390177_at	AI233857	Transcribed locus	---	1.001	0.880	0.894	0.341	0.780	0.672	1.008	0.406
1381613_at	BI290213	Transcribed locus	---	0.906	0.881	1.083	0.146	1.362	0.800	1.107	0.996
1381402_at	BE108294	Transcribed locus	---	1.108	0.881	0.962	0.843	1.340	0.413	1.038	0.685
1394996_at	BF390127	Transcribed locus	---	0.585	0.881	0.754	0.460	1.051	0.648	0.795	0.192
1373677_at	AI598315	Transcribed locus	---	1.380	0.881	1.458	0.326	1.902	0.072	0.875	0.346
1383201_at	BI289300	Transcribed locus	---	1.071	0.881	0.432	0.003	1.026	0.998	0.475	0.025
1396623_at	BF399568	Transcribed locus	---	0.981	0.881	1.033	0.587	1.083	0.779	1.127	0.510
1384164_at	BF290416	Transcribed locus	---	0.849	0.882	1.265	0.163	1.505	0.048	1.028	0.099
1378009_at	BF282481	Transcribed locus	---	1.063	0.882	1.030	0.788	0.550	0.012	1.113	0.634
1392497_at	BE104938	Transcribed locus	---	0.932	0.882	0.567	0.007	0.998	0.663	0.763	0.042
1391591_at	AW532531	Transcribed locus	---	1.027	0.882	0.845	0.725	1.186	0.186	1.096	0.246
1397195_at	AI110520	Transcribed locus	---	1.092	0.882	0.997	0.678	0.958	0.828	0.629	0.200
1381591_at	BI302903	Transcribed locus	---	0.935	0.882	0.501	0.027	0.465	0.135	0.513	0.064
1382628_at	BE111904	Transcribed locus	---	0.895	0.882	0.484	0.051	0.790	0.432	0.373	0.005
1374336_at	AI409666	Transcribed locus	---	1.128	0.884	1.115	0.473	1.019	0.658	1.128	0.707
1389285_at	AI229933	Transcribed locus	---	1.000	0.884	0.138	0.013	0.992	0.056	0.163	0.004
1374324_at	AA945828	Transcribed locus	---	0.966	0.884	0.686	0.096	0.822	0.189	0.752	0.033
1382983_at	AI136134	Transcribed locus	---	1.185	0.885	0.907	0.777	2.110	0.073	1.220	0.523
1394898_at	BF286853	Transcribed locus	---	0.971	0.885	0.971	0.600	1.710	0.063	0.935	0.441
1383557_at	BG665587	Transcribed locus	---	1.424	0.885	0.644	0.120	1.378	0.740	0.740	0.113
1381990_at	AA963979	Transcribed locus	---	0.937	0.886	0.831	0.524	0.937	0.932	0.776	0.286
1398072_at	BF409833	Transcribed locus	---	3.074	0.886	1.276	0.950	1.545	0.617	1.459	0.817
1392187_at	BG371676	Transcribed locus	---	0.998	0.887	1.002	0.853	1.003	0.999	1.001	0.964
1376433_at	BF400033	Transcribed locus	---	0.764	0.887	0.973	0.924	0.966	0.987	1.036	0.891
1385442_at	AW529552	Transcribed locus	---	1.046	0.887	0.362	0.000	0.803	0.934	0.248	0.055
1384001_at	AW143174	Transcribed locus	---	1.064	0.888	1.656	0.060	0.771	0.450	1.516	0.015
1385584_at	AI111406	Transcribed locus	---	0.970	0.888	1.223	0.901	0.796	0.410	0.821	0.767
1383133_at	BI295765	Transcribed locus	---	0.962	0.888	0.774	0.112	1.033	0.871	0.555	0.017
1389541_at	AI410836	Transcribed locus	---	1.150	0.888	1.181	0.102	0.747	0.092	1.131	0.848
1382477_at	AW532560	Transcribed locus	---	1.010	0.888	1.292	0.012	1.003	0.154	1.068	0.063
1381655_at	BE102083	Transcribed locus	---	0.559	0.889	0.515	0.051	1.492	0.509	0.580	0.234
1392246_at	AA900645	Transcribed locus	---	0.889	0.890	0.695	0.127	0.746	0.329	0.671	0.081
1395390_at	BM384238	Transcribed locus	---	1.029	0.890	0.991	0.944	0.993	0.960	0.994	0.996
1376096_a_at	BE108246	Transcribed locus	---	0.980	0.891	0.990	0.972	1.425	0.043	1.004	0.400
1380935_at	AI179379	Transcribed locus	---	1.003	0.893	1.701	0.085	1.068	0.778	1.071	0.272

1389442_at	AI406804	Transcribed locus	---	0.978	0.894	0.563	0.013	0.612	0.930	0.679	0.085
1385924_at	AI454060	Transcribed locus	---	0.816	0.895	0.443	0.033	0.894	0.417	0.427	0.014
1384093_at	AW523562	Transcribed locus	---	1.033	0.895	1.741	0.358	1.004	0.910	1.259	0.314
1380886_at	AI145907	Transcribed locus	---	0.856	0.895	1.124	0.041	0.717	0.642	0.778	0.295
1375293_at	BE107875	Transcribed locus	---	0.992	0.896	0.991	0.627	1.016	0.993	0.994	0.991
1376266_at	AA819086	Transcribed locus	---	1.002	0.896	1.035	0.881	1.006	0.993	0.934	0.995
1383192_at	BI289990	Transcribed locus	---	1.008	0.897	0.876	0.773	1.014	0.900	0.954	0.506
1374180_at	AI236753	Transcribed locus	---	0.962	0.898	1.755	0.002	0.901	0.580	1.647	0.015
1398369_at	AI599048	Transcribed locus	---	1.001	0.898	0.502	0.006	0.923	0.170	0.799	0.154
1393428_at	BF398638	Transcribed locus	---	1.003	0.898	1.183	0.593	0.975	0.434	0.544	0.078
1383889_at	AI511225	Transcribed locus	---	0.882	0.898	1.811	0.082	0.627	0.030	1.481	0.309
1375953_at	AI012884	Transcribed locus	---	0.980	0.898	1.064	0.898	1.022	0.048	0.993	0.823
1378580_at	AI007848	Transcribed locus	---	1.104	0.898	0.346	0.014	0.974	0.775	0.303	0.000
1396600_at	BF393953	Transcribed locus	---	0.810	0.899	0.719	0.079	0.919	0.250	0.612	0.503
1391479_at	BE107968	Transcribed locus	---	1.032	0.899	0.331	0.042	1.028	0.703	0.347	0.047
1384790_at	BF388025	Transcribed locus	---	0.998	0.899	1.002	0.976	1.011	0.970	0.996	0.997
1393432_a_at	AA899840	Transcribed locus	---	1.006	0.900	0.374	0.000	0.961	0.996	0.510	0.013
1374754_at	BF400833	Transcribed locus	---	0.955	0.900	1.265	0.091	1.220	0.783	0.983	0.437
1377946_at	BF420043	Transcribed locus	---	1.013	0.901	0.999	0.958	0.952	0.682	0.951	0.603
1374537_at	AI406533	Transcribed locus	---	0.959	0.901	0.675	0.109	1.007	0.922	0.527	0.017
1385068_at	BF397283	Transcribed locus	---	0.730	0.902	0.450	0.074	1.002	0.874	0.496	0.044
1383105_at	BI293339	Transcribed locus	---	1.038	0.903	1.108	0.955	1.022	0.804	0.885	0.133
1385798_at	AW533857	Transcribed locus	---	0.987	0.904	0.325	0.004	0.959	0.992	0.585	0.071
1372783_at	BM387109	Transcribed locus	---	0.979	0.904	0.742	0.035	0.905	0.758	0.776	0.001
1383850_at	BF548042	Transcribed locus	---	0.936	0.904	1.559	0.228	0.940	0.878	1.146	0.282
1397472_at	AI454728	Transcribed locus	---	1.290	0.904	1.122	0.399	1.217	0.591	1.054	0.254
1389554_at	AA956784	Transcribed locus	---	1.181	0.905	0.947	0.283	1.060	0.153	1.227	0.132
1393703_at	BI288832	Transcribed locus	---	0.991	0.906	1.019	0.987	0.979	0.833	1.023	0.937
1391708_at	BE096515	Transcribed locus	---	1.045	0.906	1.095	0.428	0.997	0.847	1.118	0.858
1373385_at	BF550271	Transcribed locus	---	1.009	0.906	1.474	0.016	0.996	0.895	1.279	0.143
1380471_at	H31701	Transcribed locus	---	0.838	0.907	0.601	0.088	0.512	0.057	0.486	0.018
1385002_at	AI454867	Transcribed locus	---	0.960	0.907	1.184	0.063	0.963	0.934	1.709	0.072
1379511_at	AA875275	Transcribed locus	---	0.961	0.908	1.035	0.089	1.161	0.595	0.617	0.041
1377781_at	AA899278	Transcribed locus	---	0.960	0.908	0.350	0.018	0.955	0.295	0.419	0.003
1383385_at	AI136674	Transcribed locus	---	0.981	0.908	0.574	0.063	0.997	0.851	0.833	0.329
1375358_at	AA998150	Transcribed locus	---	1.024	0.908	1.684	0.050	0.690	0.068	1.772	0.110
1375698_at	BG372400	Transcribed locus	---	1.066	0.908	1.001	0.960	0.994	0.992	1.020	0.564
1394627_at	AW527508	Transcribed locus	---	0.878	0.908	0.817	0.778	0.998	0.974	0.999	0.777
1381608_at	BF394383	Transcribed locus	---	0.968	0.908	1.091	0.967	0.972	0.900	1.014	0.906
1380997_at	BE103561	Transcribed locus	---	0.990	0.909	1.418	0.122	1.270	0.689	1.115	0.271
1378863_at	BF412077	Transcribed locus	---	0.986	0.909	0.749	0.107	1.514	0.090	0.639	0.073
1393211_at	AW144047	Transcribed locus	---	0.915	0.910	0.775	0.541	1.104	0.793	0.780	0.543
1399015_at	BI281753	Transcribed locus	---	0.719	0.910	0.874	0.014	0.773	0.748	0.784	0.052
1394818_at	AI176867	Transcribed locus	---	1.223	0.910	0.482	0.028	0.916	0.453	0.515	0.003
1371689_at	BE107334	Transcribed locus	---	1.006	0.910	1.071	0.821	0.973	0.497	0.935	0.093
1397930_at	BE104754	Transcribed locus	---	1.015	0.912	1.000	0.924	0.963	0.856	1.471	0.694
1378440_at	BM385137	Transcribed locus	---	1.405	0.912	0.850	0.332	1.350	0.376	1.146	0.472
1382299_at	AW914657	Transcribed locus	---	1.011	0.913	1.120	0.996	1.051	0.985	1.117	0.391
1376031_at	BE099769	Transcribed locus	---	0.739	0.913	1.014	0.807	0.858	0.210	1.187	0.031
1398545_at	BI288876	Transcribed locus	---	1.002	0.913	0.997	0.855	1.013	0.060	0.996	0.733
1389304_at	AI176323	Transcribed locus	---	0.950	0.913	1.729	0.123	1.492	0.704	0.978	0.851
1388656_at	BI294968	Transcribed locus	---	0.947	0.914	0.580	0.009	0.949	0.453	0.727	0.009
1385720_at	AW533911	Transcribed locus	---	1.074	0.915	1.345	0.357	1.555	0.494	1.488	0.189
1372392_at	AI599125	Transcribed locus	---	1.610	0.915	1.512	0.084	0.848	0.689	1.941	0.050
1394390_at	BF394739	Transcribed locus	---	0.840	0.915	0.962	0.753	0.711	0.111	0.951	0.061
1382846_at	AI501459	Transcribed locus	---	0.977	0.915	1.545	0.028	0.655	0.059	1.711	0.138
1376543_at	BF404136	Transcribed locus	---	0.966	0.915	0.883	0.159	1.104	0.593	0.981	0.878
1372489_at	AI172498	Transcribed locus	---	0.910	0.916	0.448	0.010	0.820	0.069	0.669	0.000
1378110_at	AI412190	Transcribed locus	---	0.594	0.916	1.510	0.032	0.586	0.576	1.266	0.061
1388916_at	BE109616	Transcribed locus	---	0.924	0.916	0.556	0.179	2.070	0.074	1.180	0.313
1392668_at	AI235429	Transcribed locus	---	1.870	0.916	1.369	0.483	0.898	0.880	1.111	0.928

1374089_at	BI289692	Transcribed locus	---	1.181	0.917	0.713	0.015	1.152	0.460	0.774	0.065
1390609_at	BI296683	Transcribed locus	---	1.021	0.918	0.621	0.024	0.738	0.583	1.206	0.702
1383470_at	AI548857	Transcribed locus	---	1.064	0.918	0.917	0.978	1.042	0.528	1.039	0.204
1393938_at	AI501880	Transcribed locus	---	0.887	0.919	0.982	0.353	0.881	0.699	0.747	0.032
1373765_at	BG371708	Transcribed locus	---	0.950	0.919	0.410	0.042	0.985	0.943	0.592	0.004
1389649_at	AI411897	Transcribed locus	---	1.056	0.919	0.408	0.015	1.046	0.996	0.395	0.019
1375369_at	Z83035	Transcribed locus	---	1.060	0.922	1.224	0.404	1.069	0.378	1.107	0.207
1383636_at	AA997509	Transcribed locus	---	0.708	0.923	0.697	0.051	0.802	0.313	0.626	0.046
1383027_at	AA900262	Transcribed locus	---	1.256	0.924	1.397	0.881	1.483	0.121	1.740	0.579
1377737_at	BE098874	Transcribed locus	---	0.948	0.925	1.146	0.077	1.133	0.073	1.280	0.066
1388585_at	BF281959	Transcribed locus	---	0.891	0.925	0.944	0.679	1.093	0.819	1.119	0.787
1392529_at	BI294478	Transcribed locus	---	0.749	0.925	1.278	0.109	0.753	0.111	1.027	0.836
1398047_at	BF394787	Transcribed locus	---	0.977	0.926	0.295	0.001	1.541	0.187	0.348	0.014
1392893_a_at	AA926239	Transcribed locus	---	1.070	0.926	0.831	0.613	1.125	0.213	1.065	0.225
1379898_at	AI030607	Transcribed locus	---	0.999	0.926	1.221	0.994	0.781	0.581	1.535	0.143
1381017_at	AA925043	Transcribed locus	---	1.019	0.926	1.254	0.324	0.919	0.942	0.986	0.344
1375233_at	BI296668	Transcribed locus	---	1.010	0.926	1.319	0.084	1.002	0.975	1.084	0.230
1382706_at	AI501895	Transcribed locus	---	1.034	0.927	1.303	0.251	0.762	0.229	1.128	0.663
1395362_at	BG670699	Transcribed locus	---	1.005	0.927	0.468	0.025	1.016	0.973	0.899	0.146
1383164_at	AW524366	Transcribed locus	---	0.986	0.927	0.371	0.005	0.676	0.038	0.431	0.032
1377957_at	AI716128	Transcribed locus	---	0.955	0.927	0.209	0.011	1.031	0.935	0.409	0.073
1374606_at	BF283073	Transcribed locus	---	0.835	0.928	0.736	0.041	0.716	0.313	0.631	0.019
1379680_at	AI030284	Transcribed locus	---	0.783	0.929	1.019	0.971	0.922	0.688	0.809	0.105
1384189_at	AI045368	Transcribed locus	---	0.663	0.929	0.718	0.177	1.184	0.703	0.990	0.120
1377661_at	AW524539	Transcribed locus	---	0.830	0.930	0.832	0.102	0.627	0.036	0.843	0.056
1388737_at	AI410799	Transcribed locus	---	1.000	0.931	0.820	0.029	1.141	0.108	1.080	0.641
1391146_at	BE111632	Transcribed locus	---	1.174	0.931	0.998	0.904	0.805	0.381	0.930	0.976
1385032_at	BE114028	Transcribed locus	---	0.985	0.931	0.694	0.164	1.001	0.995	0.688	0.166
1374144_at	BF402375	Transcribed locus	---	0.868	0.932	0.644	0.060	0.713	0.104	0.711	0.052
1372191_at	BI303656	Transcribed locus	---	0.975	0.933	1.716	0.119	0.918	0.283	1.091	0.163
1392039_at	AI007657	Transcribed locus	---	0.963	0.933	1.259	0.813	1.003	0.244	0.703	0.375
1380069_at	BF389717	Transcribed locus	---	1.066	0.935	0.415	0.001	1.251	0.052	0.474	0.008
1382844_at	AA819037	Transcribed locus	---	0.991	0.935	0.999	0.971	1.111	0.964	0.795	0.998
1374168_at	BE099608	Transcribed locus	---	0.923	0.936	0.496	0.002	1.253	0.039	0.704	0.049
1379149_at	BF404318	Transcribed locus	---	1.019	0.936	0.993	0.675	0.945	0.487	1.000	0.994
1380699_at	BE110761	Transcribed locus	---	1.101	0.936	1.540	0.212	1.472	0.085	1.012	0.982
1380214_at	BE118929	Transcribed locus	---	1.011	0.936	0.979	0.112	1.007	0.877	1.029	0.949
1394636_at	BM385501	Transcribed locus	---	1.009	0.937	0.625	0.183	1.003	0.993	0.983	0.826
1394589_at	AA892134	Transcribed locus	---	1.024	0.937	0.304	0.077	1.706	0.868	1.162	0.562
1380433_at	AI229240	Transcribed locus	---	1.031	0.938	0.977	0.982	0.838	0.385	0.862	0.252
1386178_at	AA799690	Transcribed locus	---	0.994	0.939	0.484	0.028	0.951	0.991	0.415	0.058
1384554_at	AI058725	Transcribed locus	---	1.002	0.939	1.001	0.810	1.004	0.887	1.003	0.982
1374094_at	BF408129	Transcribed locus	---	0.981	0.939	1.028	0.591	1.379	0.115	0.866	0.391
1376295_at	BE119676	Transcribed locus	---	1.049	0.940	1.007	0.991	1.008	0.967	1.314	0.115
1381292_at	BE095785	Transcribed locus	---	0.991	0.940	1.009	0.747	1.027	0.206	1.000	0.920
1381803_at	BE110472	Transcribed locus	---	1.000	0.940	1.000	0.923	0.974	0.988	1.004	0.912
1393574_at	AI103347	Transcribed locus	---	0.981	0.940	1.248	0.314	1.592	0.127	1.081	0.313
1398050_at	BI300450	Transcribed locus	---	0.995	0.941	0.962	0.688	1.636	0.052	0.988	0.990
1380880_at	AA900583	Transcribed locus	---	1.016	0.942	1.132	0.109	1.740	0.162	1.104	0.056
1375972_at	AA851327	Transcribed locus	---	1.203	0.942	1.470	0.080	1.164	0.586	0.954	0.414
1390497_at	AI175594	Transcribed locus	---	0.958	0.942	1.616	0.008	1.039	0.816	1.495	0.064
1376376_at	AI501923	Transcribed locus	---	1.160	0.942	0.606	0.001	1.345	0.137	0.915	0.132
1396968_at	BF404591	Transcribed locus	---	1.044	0.943	1.104	0.986	1.024	0.950	1.138	0.530
1379336_at	BF289150	Transcribed locus	---	1.266	0.943	1.676	0.045	5.082	0.009	3.342	0.002
1393059_at	AI137360	Transcribed locus	---	1.015	0.944	0.901	0.929	0.997	0.993	0.936	0.997
1380588_at	AI511180	Transcribed locus	---	1.002	0.945	0.804	0.134	1.006	0.968	1.372	0.131
1385760_at	BF400633	Transcribed locus	---	1.013	0.945	0.989	0.703	1.030	0.463	1.098	0.431
1379350_at	AI179648	Transcribed locus	---	1.015	0.945	0.955	0.184	0.789	0.663	0.677	0.028
1374395_at	AI102825	Transcribed locus	---	1.019	0.945	1.446	0.016	0.755	0.005	1.508	0.048
1396779_at	BF402702	Transcribed locus	---	0.977	0.945	1.479	0.062	0.869	0.839	0.976	0.942
1389592_at	AI317817	Transcribed locus	---	0.920	0.946	2.678	0.069	0.995	0.886	1.995	0.138

1382681_at	AA899948	Transcribed locus	---	1.027	0.946	1.232	0.651	1.174	0.582	0.802	0.325
1386043_at	BF289242	Transcribed locus	---	1.009	0.948	1.034	0.628	1.012	0.943	0.935	0.500
1397248_at	AI547500	Transcribed locus	---	0.993	0.948	0.985	0.633	0.997	0.993	0.983	0.975
1373396_at	BF283617	Transcribed locus	---	0.789	0.948	1.015	0.150	0.927	0.711	0.872	0.823
1381079_at	BF411725	Transcribed locus	---	1.007	0.949	1.075	0.361	0.997	0.993	1.057	0.906
1379187_at	BF418643	Transcribed locus	---	0.998	0.949	0.997	0.985	1.002	0.980	1.068	0.587
1391563_at	AA963184	Transcribed locus	---	1.415	0.950	0.659	0.161	1.323	0.494	0.442	0.145
1390845_at	AI179288	Transcribed locus	---	1.003	0.950	1.018	0.867	1.004	0.979	1.399	0.012
1374268_at	AA859010	Transcribed locus	---	1.005	0.950	0.487	0.097	0.999	0.969	0.519	0.090
1375000_at	BF415422	Transcribed locus	---	0.865	0.950	0.432	0.000	0.926	0.554	0.476	0.003
1395831_at	BF288661	Transcribed locus	---	0.969	0.950	1.242	0.773	1.002	0.577	3.054	0.419
1397883_at	H33845	Transcribed locus	---	0.980	0.952	1.105	0.163	1.393	0.074	1.290	0.196
1376078_at	BI296274	Transcribed locus	---	0.998	0.952	0.957	0.837	1.542	0.239	0.955	0.670
1383741_at	BE100721	Transcribed locus	---	0.979	0.952	1.005	0.916	1.007	0.971	1.032	0.509
1384595_at	AI030888	Transcribed locus	---	0.959	0.952	0.315	0.005	0.954	0.496	0.512	0.004
1378397_at	BM385449	Transcribed locus	---	0.999	0.952	0.266	0.013	1.296	0.550	0.397	0.026
1382567_at	AI013639	Transcribed locus	---	1.026	0.953	2.885	0.013	0.997	0.958	1.863	0.088
1390229_at	BF284176	Transcribed locus	---	0.952	0.954	0.614	0.099	0.673	0.808	0.742	0.759
1395606_at	BF412220	Transcribed locus	---	1.214	0.954	0.521	0.036	1.504	0.206	0.504	0.039
1379143_at	BF409564	Transcribed locus	---	1.106	0.954	0.884	0.424	1.156	0.551	0.546	0.237
1382391_at	BF397532	Transcribed locus	---	1.247	0.954	0.427	0.004	1.265	0.281	0.655	0.084
1398490_at	BM390414	Transcribed locus	---	0.980	0.955	1.224	0.498	1.018	0.553	1.360	0.942
1396014_at	BM384523	Transcribed locus	---	1.023	0.955	0.995	0.860	1.009	0.814	0.999	0.947
1375649_at	BF396469	Transcribed locus	---	1.115	0.956	1.339	0.616	1.070	0.988	1.654	0.150
1397149_at	BF395834	Transcribed locus	---	1.109	0.956	0.869	0.267	1.010	0.971	0.977	0.379
1382595_at	BF289213	Transcribed locus	---	1.074	0.956	0.641	0.126	1.166	0.038	0.667	0.131
1395151_at	AW527014	Transcribed locus	---	1.110	0.956	0.468	0.035	1.927	0.890	0.536	0.019
1382361_at	BF290407	Transcribed locus	---	0.862	0.957	0.486	0.067	0.713	0.099	0.708	0.127
1389796_at	BI298018	Transcribed locus	---	1.001	0.957	0.904	0.043	1.371	0.110	0.649	0.014
1390595_at	AW527996	Transcribed locus	---	1.002	0.958	1.037	0.041	1.019	0.880	1.034	0.476
1376885_at	BE095660	Transcribed locus	---	1.027	0.958	1.256	0.849	0.789	0.096	0.961	0.201
1398563_at	BE115879	Transcribed locus	---	2.002	0.959	0.884	0.397	2.024	0.100	0.730	0.246
1395743_at	BF522730	Transcribed locus	---	0.999	0.960	0.874	0.082	1.005	0.947	0.895	0.077
1391999_at	BI301720	Transcribed locus	---	1.008	0.960	1.518	0.305	1.325	0.307	1.018	0.583
1381271_at	BF403362	Transcribed locus	---	1.362	0.961	0.916	0.443	1.086	0.732	1.075	0.278
1395715_at	BI288113	Transcribed locus	---	0.994	0.961	0.999	0.721	0.998	0.913	0.997	0.967
1394738_at	AW531516	Transcribed locus	---	0.871	0.962	1.011	0.399	0.906	0.049	0.990	0.352
1383681_at	BI289508	Transcribed locus	---	0.993	0.962	1.057	0.551	1.001	0.990	1.134	0.257
1385046_at	BM387916	Transcribed locus	---	1.003	0.962	0.999	0.872	1.001	0.994	1.001	0.999
1397377_at	AA955664	Transcribed locus	---	0.981	0.963	0.593	0.004	1.250	0.278	0.534	0.002
1381112_at	AI555805	Transcribed locus	---	1.017	0.963	1.278	0.685	1.194	0.115	0.846	0.138
1383767_at	AW524430	Transcribed locus	---	0.932	0.963	1.382	0.660	0.988	0.708	1.300	0.684
1398045_at	BE120285	Transcribed locus	---	0.989	0.964	0.814	0.767	0.875	0.381	0.852	0.817
1373234_at	BI277492	Transcribed locus	---	1.020	0.964	0.505	0.040	1.015	0.625	0.754	0.214
1391985_at	BI288541	Transcribed locus	---	0.971	0.965	1.514	0.027	0.777	0.151	1.371	0.007
1377357_at	BE106428	Transcribed locus	---	0.910	0.965	0.424	0.000	1.202	0.606	0.505	0.026
1397119_at	BF563062	Transcribed locus	---	1.001	0.965	0.495	0.062	0.990	0.991	0.512	0.075
1393605_at	AI145306	Transcribed locus	---	0.792	0.966	0.450	0.016	1.171	0.413	0.773	0.095
1381614_at	BF406227	Transcribed locus	---	1.010	0.966	1.002	0.715	1.314	0.053	1.000	0.952
1384588_at	BI295602	Transcribed locus	---	1.011	0.966	0.886	0.270	1.484	0.103	0.835	0.219
1397787_at	BF416511	Transcribed locus	---	1.540	0.967	1.430	0.525	1.178	0.200	1.129	0.849
1395560_at	BF522151	Transcribed locus	---	1.015	0.967	0.996	0.911	1.138	0.138	0.912	0.229
1379268_at	AA924312	Transcribed locus	---	0.998	0.967	0.599	0.022	1.001	0.948	0.603	0.022
1392142_at	AI764196	Transcribed locus	---	0.997	0.968	1.337	0.057	0.889	0.185	0.919	0.760
1383482_at	AI578183	Transcribed locus	---	0.928	0.968	0.689	0.044	0.622	0.074	0.649	0.050
1378199_at	AI408485	Transcribed locus	---	0.998	0.969	1.417	0.080	0.968	0.400	1.032	0.650
1389864_at	BF405086	Transcribed locus	---	1.048	0.969	0.994	0.891	0.992	0.967	1.015	0.895
1372635_at	BF282163	Transcribed locus	---	1.017	0.970	0.484	0.071	1.294	0.025	0.846	0.088
1382555_at	BF407487	Transcribed locus	---	0.994	0.970	0.939	0.605	1.031	0.984	0.904	0.875
1398007_at	AI713125	Transcribed locus	---	1.178	0.971	1.133	0.562	2.024	0.021	1.126	0.528
1374498_at	AW916866	Transcribed locus	---	0.568	0.971	0.203	0.002	0.989	0.421	0.369	0.065

1378272_at	BF411569	Transcribed locus	---	0.936	0.972	1.281	0.940	0.944	0.452	1.003	0.962
1392941_at	BE103748	Transcribed locus	---	1.011	0.972	0.423	0.053	1.272	0.119	0.426	0.035
1396337_at	AW529811	Transcribed locus	---	0.852	0.972	0.621	0.324	1.592	0.488	1.072	0.261
1379819_at	BF392928	Transcribed locus	---	1.011	0.972	1.100	0.355	1.112	0.087	1.025	0.640
1396488_at	BI291411	Transcribed locus	---	1.233	0.972	1.072	0.748	1.416	0.244	1.005	0.999
1385034_at	AW527447	Transcribed locus	---	0.991	0.973	0.996	0.899	1.053	0.879	1.006	0.954
1383918_at	AI070651	Transcribed locus	---	1.006	0.973	0.495	0.014	1.405	0.048	0.524	0.019
1371569_at	BI294976	Transcribed locus	---	0.892	0.973	0.917	0.571	1.592	0.028	0.875	0.951
1373608_at	AI639277	Transcribed locus	---	0.925	0.973	0.817	0.437	0.856	0.418	0.853	0.434
1394696_at	BF287122	Transcribed locus	---	1.067	0.973	0.576	0.429	1.212	0.103	0.931	0.506
1380651_at	BI296352	Transcribed locus	---	0.845	0.974	0.286	0.039	0.770	0.548	0.519	0.010
1381351_at	AI599264	Transcribed locus	---	0.984	0.974	1.195	0.414	1.137	0.194	1.046	0.549
1374586_at	AI103993	Transcribed locus	---	0.997	0.974	0.507	0.021	0.763	0.439	0.336	0.033
1397138_at	BF396994	Transcribed locus	---	1.109	0.975	1.577	0.631	1.112	0.667	1.040	0.791
1378333_at	BI284174	Transcribed locus	---	1.034	0.975	0.966	0.734	1.035	0.810	0.810	0.221
1397767_at	BG377356	Transcribed locus	---	1.590	0.975	0.886	0.644	1.407	1.000	0.795	0.107
1378931_at	AW523881	Transcribed locus	---	1.000	0.976	0.996	0.981	0.999	0.962	0.997	0.942
1390187_at	AI060043	Transcribed locus	---	0.997	0.976	0.462	0.051	0.995	0.979	0.388	0.023
1395139_at	BM388214	Transcribed locus	---	1.271	0.976	0.997	0.230	0.932	0.165	0.833	0.097
1393303_at	AW918896	Transcribed locus	---	1.019	0.976	0.953	0.995	0.886	0.998	0.863	0.398
1377531_at	BF405592	Transcribed locus	---	1.005	0.976	1.021	0.853	1.001	0.180	1.003	0.989
1374563_at	BI301280	Transcribed locus	---	0.794	0.977	1.051	0.738	0.871	0.072	1.147	0.344
1393661_at	BG381658	Transcribed locus	---	0.984	0.977	1.058	0.881	0.683	0.133	0.751	0.068
1388513_at	BI281612	Transcribed locus	---	0.999	0.977	1.002	0.773	1.356	0.079	0.998	0.571
1395973_at	AI236099	Transcribed locus	---	1.063	0.978	0.756	0.230	1.564	0.460	0.722	0.017
1377318_at	BF415648	Transcribed locus	---	1.204	0.978	1.200	0.809	0.794	0.436	1.271	0.859
1378020_at	AI060205	Transcribed locus	---	0.989	0.978	1.273	0.029	1.174	0.270	1.866	0.129
1373066_at	AI407797	Transcribed locus	---	1.009	0.978	1.003	0.586	6.919	0.002	1.828	0.076
1390235_at	BF410589	Transcribed locus	---	0.998	0.979	0.919	0.939	1.007	0.535	0.930	0.970
1378304_at	BI276118	Transcribed locus	---	1.002	0.979	1.506	0.724	1.035	0.804	1.449	0.045
1398182_at	BF411782	Transcribed locus	---	0.693	0.979	0.596	0.080	1.019	0.031	0.580	0.077
1381191_at	AI145988	Transcribed locus	---	1.011	0.980	0.560	0.007	0.902	0.987	0.509	0.047
1383667_at	AI603411	Transcribed locus	---	0.787	0.980	1.001	0.866	1.679	0.012	1.066	0.841
1380473_at	AW529772	Transcribed locus	---	0.995	0.980	0.987	0.952	1.614	0.088	1.024	0.984
1390626_at	BF398788	Transcribed locus	---	0.883	0.981	0.992	0.839	2.100	0.182	1.625	0.048
1371739_at	AI104605	Transcribed locus	---	0.959	0.981	1.244	0.709	0.920	0.156	1.171	0.910
1391316_at	AI072558	Transcribed locus	---	0.949	0.981	1.002	0.197	1.057	0.467	1.167	0.986
1389710_at	BF558393	Transcribed locus	---	1.007	0.982	2.032	0.047	0.751	0.214	1.181	0.367
1374071_at	BG670800	Transcribed locus	---	0.951	0.982	0.673	0.049	1.007	0.974	0.960	0.842
1376301_at	BE110719	Transcribed locus	---	1.127	0.983	1.218	0.392	1.587	0.035	1.142	0.908
1392569_at	AA955871	Transcribed locus	---	0.990	0.983	1.230	0.196	0.985	0.948	0.992	0.929
1380180_at	AW528635	Transcribed locus	---	0.998	0.984	0.355	0.011	0.999	0.994	0.415	0.012
1391181_at	BF390734	Transcribed locus	---	0.999	0.984	0.675	0.126	0.998	0.273	0.753	0.122
1384654_at	AI113214	Transcribed locus	---	0.909	0.984	0.995	0.982	1.019	0.970	0.999	0.940
1395628_at	AW434310	Transcribed locus	---	0.999	0.984	0.977	0.140	0.998	0.986	0.975	0.104
1392102_at	BE118959	Transcribed locus	---	0.998	0.984	0.939	0.531	0.544	0.009	1.030	0.850
1396288_s_at	BI273954	Transcribed locus	---	1.060	0.984	1.121	0.889	0.930	0.086	1.312	0.774
1379689_at	AI011930	Transcribed locus	---	1.515	0.984	0.911	0.866	0.594	0.160	0.606	0.851
1390553_at	BE104167	Transcribed locus	---	1.003	0.984	1.704	0.119	0.821	0.182	1.219	0.250
1379523_at	AA818187	Transcribed locus	---	0.999	0.984	0.968	0.428	1.347	0.043	1.109	0.821
1372326_at	AA901341	Transcribed locus	---	0.998	0.984	1.009	0.978	1.012	0.912	0.999	0.647
1381095_at	BI302849	Transcribed locus	---	1.032	0.985	0.996	0.586	1.026	0.583	1.001	0.995
1391558_at	BF290997	Transcribed locus	---	1.043	0.985	1.046	0.828	1.339	0.248	0.981	0.931
1380939_at	BE118701	Transcribed locus	---	1.624	0.985	0.672	0.366	1.046	0.917	0.621	0.054
1382910_at	AI072237	Transcribed locus	---	1.010	0.985	1.489	0.637	1.382	0.292	1.108	0.370
1390540_at	BF400717	Transcribed locus	---	0.970	0.986	0.660	0.111	1.010	0.945	0.732	0.071
1383997_at	AA874850	Transcribed locus	---	2.442	0.986	0.984	0.880	1.244	0.519	1.049	0.698
1396283_at	BI293995	Transcribed locus	---	0.998	0.987	1.086	0.962	1.007	0.150	1.083	0.975
1378422_at	BE117312	Transcribed locus	---	1.056	0.987	1.069	0.664	1.191	0.064	0.981	0.901
1383578_at	AI071227	Transcribed locus	---	1.169	0.987	0.739	0.110	1.726	0.198	0.909	0.137
1383590_at	AA963863	Transcribed locus	---	2.382	0.987	1.383	0.102	1.738	0.095	5.014	0.023

1395611_at	BE106061	Transcribed locus	---	1.356	0.987	1.525	0.994	1.452	0.814	1.550	0.991
1385470_at	AI045606	Transcribed locus	---	0.998	0.987	0.672	0.191	0.715	0.218	0.677	0.188
1383720_at	AW527404	Transcribed locus	---	1.062	0.987	1.194	0.705	1.097	0.994	0.973	0.293
1390818_at	BF288088	Transcribed locus	---	0.999	0.988	0.657	0.406	1.000	0.973	0.867	0.336
1374713_at	AI228970	Transcribed locus	---	1.000	0.988	0.854	0.437	1.001	0.995	0.825	0.502
1382298_at	BM385955	Transcribed locus	---	1.002	0.988	1.323	0.305	1.751	0.373	1.295	0.217
1375264_at	BF416264	Transcribed locus	---	1.003	0.988	0.703	0.092	1.003	0.996	0.608	0.176
1397390_at	BF398678	Transcribed locus	---	1.285	0.988	1.047	0.933	1.009	0.628	1.071	0.627
1383909_at	BG376442	Transcribed locus	---	0.988	0.988	0.791	0.037	0.758	0.149	0.886	0.101
1392238_at	AI112241	Transcribed locus	---	1.618	0.989	0.996	0.985	0.983	0.987	0.981	0.995
1375376_at	AA997231	Transcribed locus	---	1.059	0.989	1.035	0.038	0.999	0.993	1.091	0.011
1398428_at	BF410381	Transcribed locus	---	1.156	0.989	1.199	0.409	1.274	0.054	0.978	0.986
1391256_at	AA900781	Transcribed locus	---	1.006	0.989	0.114	0.001	0.999	0.981	0.157	0.000
1386709_at	AW916606	Transcribed locus	---	1.349	0.989	1.058	0.605	1.096	0.697	0.509	0.018
1378269_at	AI112113	Transcribed locus	---	1.086	0.989	0.819	0.383	0.971	0.727	0.804	0.227
1371767_at	BG380270	Transcribed locus	---	1.312	0.990	0.877	0.054	1.020	0.905	0.839	0.006
1376126_at	BE107449	Transcribed locus	---	1.079	0.990	0.944	0.909	1.090	0.907	0.768	0.147
1380774_at	AI227918	Transcribed locus	---	1.339	0.990	1.001	0.978	1.025	0.901	0.985	0.448
1380099_at	BM391357	Transcribed locus	---	1.004	0.991	0.822	0.432	0.926	0.562	0.854	0.806
1391073_at	AA964252	Transcribed locus	---	1.010	0.992	1.216	0.892	1.291	0.063	1.014	0.769
1380543_at	BF564294	Transcribed locus	---	1.011	0.992	0.880	0.874	1.021	0.758	1.033	0.959
1379733_at	BF396474	Transcribed locus	---	0.999	0.992	0.920	0.060	1.004	0.981	0.859	0.071
1377455_at	BE106526	Transcribed locus	---	1.854	0.992	0.994	0.997	1.044	0.893	1.045	0.826
1390898_at	BE111116	Transcribed locus	---	1.369	0.992	1.161	0.500	1.468	0.150	0.931	0.498
1392297_at	BF410297	Transcribed locus	---	1.252	0.992	1.027	0.723	0.973	0.980	1.691	0.167
1392228_at	BI294408	Transcribed locus	---	0.998	0.992	0.612	0.104	1.145	0.397	0.992	0.837
1396785_at	BF419700	Transcribed locus	---	1.148	0.992	0.939	0.821	1.184	0.311	1.110	0.234
1379622_at	BF405145	Transcribed locus	---	1.001	0.992	0.858	0.281	1.007	0.396	0.997	0.952
1389949_at	BI298868	Transcribed locus	---	1.002	0.992	0.884	0.955	1.005	0.995	0.881	0.991
1383452_at	BG670461	Transcribed locus	---	0.998	0.992	1.028	0.876	1.000	0.998	1.000	0.992
1388887_at	AI178222	Transcribed locus	---	1.003	0.993	0.568	0.012	1.144	0.878	0.656	0.011
1386804_at	BF553434	Transcribed locus	---	1.002	0.993	1.042	0.736	1.043	0.813	1.439	0.124
1377059_at	AW533194	Transcribed locus	---	0.998	0.993	1.006	0.692	1.042	0.138	1.146	0.042
1379917_at	AW528106	Transcribed locus	---	1.599	0.993	1.185	0.822	1.434	0.218	0.886	0.096
1395027_at	BI290841	Transcribed locus	---	0.998	0.993	1.259	0.988	1.383	0.253	0.924	0.810
1390030_at	BI284294	Transcribed locus	---	0.999	0.993	1.004	0.890	1.001	0.991	1.000	0.993
1377822_at	AI179605	Transcribed locus	---	1.070	0.993	1.001	0.303	1.114	0.137	0.910	0.485
1390874_at	BE109206	Transcribed locus	---	0.973	0.993	0.379	0.005	1.281	0.609	0.738	0.030
1388942_at	BM390129	Transcribed locus	---	0.767	0.993	0.459	0.002	1.054	0.975	0.378	0.003
1382516_at	AI170660	Transcribed locus	---	1.001	0.994	0.331	0.003	0.687	0.983	0.509	0.003
1383253_at	AI179795	Transcribed locus	---	1.034	0.994	0.802	0.249	0.739	0.090	0.633	0.047
1384574_at	AI502627	Transcribed locus	---	1.105	0.994	0.994	0.950	1.001	0.998	0.996	0.999
1397744_at	BI276183	Transcribed locus	---	1.002	0.994	1.017	0.472	1.007	0.354	0.978	0.700
1378001_at	AI548615	Transcribed locus	---	1.015	0.994	0.975	0.908	1.036	0.602	0.997	0.990
1397564_at	BF286959	Transcribed locus	---	1.117	0.994	1.524	0.869	0.985	0.328	1.306	0.369
1391035_at	BE096618	Transcribed locus	---	0.875	0.994	1.164	0.269	0.992	0.902	0.966	0.925
1394959_at	AI502099	Transcribed locus	---	1.024	0.994	0.997	0.543	0.923	0.097	1.002	0.988
1374960_at	BM390080	Transcribed locus	---	1.002	0.994	0.994	0.022	1.001	0.866	0.991	0.041
1382793_at	BF288344	Transcribed locus	---	0.998	0.994	1.265	0.922	1.000	0.489	0.999	0.996
1391094_at	BM387077	Transcribed locus	---	1.002	0.994	0.883	0.584	1.062	0.660	0.577	0.227
1379712_at	BF408872	Transcribed locus	---	1.003	0.995	1.197	0.066	1.307	0.422	1.123	0.021
1389648_at	AI170382	Transcribed locus	---	1.001	0.995	0.980	0.787	0.778	0.026	0.868	0.015
1380428_at	AI030973	Transcribed locus	---	0.940	0.995	0.763	0.311	0.963	0.549	0.688	0.234
1377966_at	BI275560	Transcribed locus	---	0.995	0.995	1.004	0.951	0.808	0.168	0.814	0.634
1395907_at	BF416753	Transcribed locus	---	1.007	0.995	0.974	0.980	0.999	0.999	0.984	0.725
1378695_at	AI007942	Transcribed locus	---	1.001	0.995	1.194	0.049	1.475	0.236	1.262	0.032
1382640_at	AA944498	Transcribed locus	---	0.919	0.995	1.010	0.938	1.002	0.966	1.000	0.980
1393358_at	AA957379	Transcribed locus	---	1.001	0.995	0.998	0.974	1.001	0.259	1.001	0.995
1398510_at	BI295013	Transcribed locus	---	0.999	0.996	1.278	0.238	0.831	0.486	0.829	0.348
1379060_at	BG378788	Transcribed locus	---	0.895	0.996	0.502	0.244	1.323	0.807	1.525	0.162
1398099_at	AW527241	Transcribed locus	---	1.000	0.996	1.001	0.883	1.077	0.983	1.011	0.992

1397186_at	AW529325	Transcribed locus	---	0.793	0.996	1.012	0.295	1.033	0.268	1.123	0.582
1397189_at	BE108217	Transcribed locus	---	0.822	0.996	0.154	0.000	0.641	0.948	0.128	0.000
1376859_at	BM384750	Transcribed locus	---	1.001	0.996	0.553	0.072	1.347	0.072	0.937	0.210
1395131_at	BF288188	Transcribed locus	---	1.013	0.997	1.106	0.481	1.380	0.003	0.970	0.570
1398702_at	BE117785	Transcribed locus	---	0.998	0.997	0.865	0.934	1.002	0.996	0.926	0.767
1385119_at	AI043832	Transcribed locus	---	0.749	0.997	0.231	0.027	0.685	0.329	0.179	0.025
1398445_at	BF420311	Transcribed locus	---	1.001	0.997	0.564	0.187	1.621	0.114	0.824	0.139
1378234_at	BF524457	Transcribed locus	---	1.455	0.997	0.997	0.988	1.974	0.087	1.035	0.197
1374166_at	AW252076	Transcribed locus	---	1.002	0.997	1.138	0.825	1.005	0.991	1.004	0.998
1377628_at	AW523327	Transcribed locus	---	1.001	0.997	1.379	0.214	1.338	0.690	1.026	0.835
1392652_at	AI060083	Transcribed locus	---	0.986	0.997	0.813	0.125	1.004	0.990	0.996	0.920
1384075_at	BF523960	Transcribed locus	---	1.292	0.997	1.160	0.366	1.716	0.292	0.967	0.371
1393576_at	AA963989	Transcribed locus	---	1.003	0.997	0.998	0.982	1.011	0.778	1.000	0.569
1383006_at	AW528365	Transcribed locus	---	1.000	0.997	1.001	0.983	1.003	1.000	1.000	0.879
1390942_at	AI043817	Transcribed locus	---	1.001	0.998	2.052	0.016	0.957	0.971	1.592	0.206
1381762_at	AW526420	Transcribed locus	---	1.001	0.998	0.894	0.076	1.095	0.223	1.065	0.628
1396704_at	BF394808	Transcribed locus	---	1.011	0.999	0.410	0.001	0.987	0.246	0.560	0.007
1393395_at	BE120797	Transcribed locus	---	1.000	0.999	0.738	0.213	0.724	0.882	0.998	0.985
1391862_at	BG377635	Transcribed locus	---	0.689	0.999	0.327	0.009	1.158	0.880	0.689	0.101
1384829_at	AI454917	Transcribed locus	---	0.884	1.000	0.588	0.051	0.951	0.414	0.551	0.016
1374286_at	AA996836	Transcribed locus	---	1.000	1.000	1.334	0.011	1.091	0.313	1.247	0.021
1375655_at	BE107208	Transcribed locus	---	1.000	1.000	2.040	0.632	1.334	0.253	1.158	0.597
1398220_at	BE121176	Transcribed locus	---	1.000	1.000	0.976	0.019	1.023	1.000	1.137	0.147
1392352_at	AW521481	Transcribed locus	---	1.481	1.000	1.226	0.556	1.078	0.904	1.869	0.186
1377251_at	AW251255	Transcribed locus	---	1.260	1.000	0.788	0.225	1.449	0.172	1.104	0.734
1376939_at	BI284907	Transcribed locus	---	1.000	1.000	0.970	0.588	1.470	0.078	0.931	0.603
1377346_at	AI112098	Transcribed locus, moderately similar to NP_001007591.1 hypothetical protein LOC433886 [Mus musculus]	---	0.954	0.715	1.353	0.044	0.705	0.056	1.272	0.515
1378706_at	BE101875	Transcribed locus, moderately similar to NP_003416.1 zinc finger protein 45 [Homo sapiens]	---	0.999	0.403	0.996	0.927	0.727	0.267	0.982	0.377
1398713_at	BI279821	Transcribed locus, moderately similar to NP_032607.1 melanoma antigen [Mus musculus]	---	0.958	0.596	1.358	0.163	1.256	0.220	1.136	0.324
1389006_at	AI170394	Transcribed locus, moderately similar to NP_035543.1 sex-limited protein [Mus musculus]	---	1.003	0.993	1.032	0.860	5.505	0.002	1.693	0.138
1374682_at	BM383170	Transcribed locus, moderately similar to NP_035569.1 SRY-box 13 [Mus musculus]	---	2.358	0.000	1.549	0.005	2.410	0.001	1.428	0.013
1398396_at	BF281315	Transcribed locus, moderately similar to NP_037116.1 myosin IXb [Rattus norvegicus]	---	1.417	0.338	0.442	0.023	1.401	0.191	0.654	0.011
1394620_at	BI288579	Transcribed locus, moderately similar to NP_038630.1 metallothionein 1 [Mus musculus]	---	0.615	0.006	0.515	0.050	0.516	0.001	0.603	0.037
1384179_at	BI294722	Transcribed locus, moderately similar to NP_038871.1 zinc finger protein 53 [Mus musculus]	---	1.418	0.071	1.032	0.346	1.828	0.017	1.292	0.020
1367474_at	AI231320	Transcribed locus, moderately similar to NP_055637.1 Sec24-related protein D [Homo sapiens]	---	0.855	0.007	0.984	0.702	0.907	0.087	1.105	0.004
1372096_at	BI296062	Transcribed locus, moderately similar to NP_060655.1 hypothetical protein LOC55208 isoform a [Homo sapiens]	---	1.297	0.082	1.218	0.072	1.364	0.016	1.177	0.145
1383377_at	BG372192	Transcribed locus, moderately similar to NP_062289.1 DNA binding protein with his-thr domain [Mus musculus]	---	2.344	0.229	0.830	0.498	1.908	0.161	0.920	0.182
1372479_at	AI175666	Transcribed locus, moderately similar to NP_064456.1 fibrinogen, beta polypeptide [Rattus norvegicus]	---	21.995	0.001	0.995	0.523	18.446	0.000	1.534	0.092
1373643_at	AI177028	Transcribed locus, moderately similar to NP_081983.2 delangin isoform A [Mus musculus]	---	0.747	0.504	1.103	0.279	0.785	0.558	0.832	0.042
1382309_at	BI286390	Transcribed locus, moderately similar to NP_081983.2 delangin isoform A [Mus musculus]	---	0.991	0.783	1.414	0.004	1.069	0.896	1.364	0.023
1391608_at	AI602260	Transcribed locus, moderately similar to NP_083037.1 poly(A)-specific ribonuclease (deadenylation nuclease) [Mus musculus]	---	0.749	0.354	0.776	0.086	0.579	0.074	1.325	0.700
1381416_at	AI029400	Transcribed locus, moderately similar to NP_114131.1 transmembrane protein induced by tumor necrosis factor alpha [Homo sapiens]	---	0.730	0.300	0.132	0.001	0.208	0.007	0.310	0.022
1391477_at	BF396595	Transcribed locus, moderately similar to NP_446319.1 tumor protein, translationally-controlled 1 [Rattus norvegicus]	---	0.540	0.078	0.719	0.738	1.656	0.008	1.211	0.253
1372481_at	AI102873	Transcribed locus, moderately similar to NP_598415.1 CD34 antigen [Mus musculus]	---	1.041	0.933	0.995	0.971	1.005	0.942	0.995	0.813
1374765_at	BI288055	Transcribed locus, moderately similar to NP_598623.1 fibrinogen, gamma polypeptide [Mus musculus]	---	1.019	0.793	1.294	0.269	0.921	0.301	1.775	0.011
1391573_at	AA891842	Transcribed locus, moderately similar to NP_620203.1 podocalyxin-like [Rattus norvegicus]	---	0.370	0.036	1.154	0.236	0.204	0.019	1.059	0.771
1376708_at	BM385170	Transcribed locus, moderately similar to NP_666286.1 hypothetical protein LOC232748 [Mus musculus]	---	11.625	0.005	5.441	0.001	11.736	0.002	9.003	0.000
1392683_at	AW142773	Transcribed locus, moderately similar to NP_766102.1 hypothetical protein LOC213068 [Mus musculus]	---	2.385	0.012	1.202	0.218	6.630	0.001	1.078	0.574
1399069_at	AI234008	Transcribed locus, moderately similar to NP_766286.2 hypothetical protein LOC230648 [Mus musculus]	---	0.549	0.161	0.337	0.000	0.911	0.273	0.388	0.005
1376887_at	AI555799	Transcribed locus, moderately similar to NP_775540.3 zinc finger protein 445 [Mus musculus]	---	0.887	0.409	0.996	0.965	0.925	0.178	1.103	0.728
1380883_at	BF386294	Transcribed locus, moderately similar to NP_941007.1 hypothetical protein LOC219114 [Mus musculus]	---	1.717	0.301	0.445	0.006	0.674	0.318	0.309	0.001
1392772_at	BF285633	Transcribed locus, moderately similar to NP_997554.1 zinc finger protein 318 isoform 1 [Mus musculus]	---	1.431	0.059	0.774	0.311	1.422	0.052	0.923	0.406
1377180_at	BF394102	Transcribed locus, moderately similar to NP_998724.1 superkiller viralicidic activity 2-like [Rattus norvegicus]	---	2.772	0.000	0.979	0.497	0.811	0.773	0.595	0.010
1383713_at	BM389843	Transcribed locus, moderately similar to XP_132808.1 PREDICTED: hypothetical protein LOC70291 isoform 1 [Mus musculus]	---	0.879	0.089	0.707	0.000	1.025	0.311	0.768	0.162
1390228_at	BM384446	Transcribed locus, moderately similar to XP_213925.1 PREDICTED: similar to early quiescence protein-1 [Rattus norvegicus]	---	0.633	0.088	1.233	0.858	0.629	0.091	1.132	0.831

1374056_at	AI236229	Transcribed locus, moderately similar to XP_214446.2 PREDICTED: similar to Autosomal Highly Conserved Protein [Rattus norvegicus]	---	1.225	0.570	0.708	0.221	1.267	0.511	1.001	0.998
1395718_at	BE102746	Transcribed locus, moderately similar to XP_216760.3 PREDICTED: similar to peroxisomal membrane protein-1 like protein [Rattus norvegicus]	---	0.783	0.170	0.500	0.006	0.467	0.024	0.381	0.025
1381384_at	AW530069	Transcribed locus, moderately similar to XP_223005.2 PREDICTED: similar to Mdes protein [Rattus norvegicus]	---	0.782	0.267	0.846	0.834	0.512	0.053	0.433	0.122
1392778_at	AA891634	Transcribed locus, moderately similar to XP_236873.3 PREDICTED: similar to RIKEN cDNA 4930555G01 [Rattus norvegicus]	---	0.992	0.910	0.721	0.166	1.134	0.500	0.555	0.045
1397495_at	BE102358	Transcribed locus, moderately similar to XP_237998.3 PREDICTED: similar to mKIAA0183 protein [Rattus norvegicus]	---	0.994	0.976	1.523	0.059	0.910	0.943	0.999	0.579
1375950_a_at	BI294235	Transcribed locus, moderately similar to XP_343384.2 PREDICTED: similar to KIAA1052 protein [Rattus norvegicus]	---	1.309	0.036	2.217	0.001	1.426	0.358	1.591	0.014
1382536_at	BE109224	Transcribed locus, moderately similar to XP_415884.1 PREDICTED: similar to Thyroid hormone receptor-associated protein complex 240 kDa component (Trap240) (Activator-recruited cofactor 250 kDa component) (ARC250) (Thyroid hormone receptor associated protein 1) [Gallus gallus]	---	0.709	0.343	1.835	0.135	0.475	0.017	1.558	0.204
1383949_at	AI703880	Transcribed locus, moderately similar to XP_415884.1 PREDICTED: similar to Thyroid hormone receptor-associated protein complex 240 kDa component (Trap240) (Activator-recruited cofactor 250 kDa component) (ARC250) (Thyroid hormone receptor associated protein 1) [Gallus gallus]	---	1.078	0.471	0.929	0.047	1.042	0.289	0.880	0.050
1397614_at	BF404116	Transcribed locus, moderately similar to XP_416880.1 PREDICTED: similar to Gamma-aminobutyric-acid receptor alpha-5 subunit precursor (GABA(A) receptor) [Gallus gallus]	---	0.682	0.753	1.074	0.992	1.153	0.487	1.198	0.816
1376994_at	BE098799	Transcribed locus, moderately similar to XP_418823.1 PREDICTED: similar to leucine-rich repeats containing F-box protein FBL3 [Gallus gallus]	---	1.111	0.468	1.665	0.140	1.166	0.252	1.421	0.075
1390981_at	AI028965	Transcribed locus, moderately similar to XP_423294.1 PREDICTED: similar to dolichyl-diphosphooligosaccharide-protein glycotransferase (EC 2.4.1.119) 50k chain - chicken [Gallus gallus]	---	0.756	0.297	0.573	0.046	1.198	0.214	0.645	0.019
1395963_at	BI303658	Transcribed locus, moderately similar to XP_509099.1 PREDICTED: similar to mitogen-activated protein kinase kinase kinase 12; leucine zipper protein kinase; zipper protein kinase; protein kinase MUK; dual leucine zipper kinase DLK [Pan troglodytes]	---	0.896	0.592	1.041	0.159	0.747	0.905	0.904	0.883
1394452_at	BM391487	Transcribed locus, moderately similar to XP_510359.1 PREDICTED: hypothetical protein XP_510359 [Pan troglodytes]	---	0.912	0.268	0.553	0.028	1.113	0.663	1.024	0.165
1375353_at	BI296696	Transcribed locus, moderately similar to XP_512059.1 PREDICTED: similar to Cdk5 and Abl enzyme substrate 1 [Pan troglodytes]	---	0.446	0.149	1.065	0.832	0.455	0.006	0.819	0.068
1393156_at	BI278333	Transcribed locus, moderately similar to XP_514381.1 PREDICTED: similar to mannan-binding lectin serine protease 2 isoform 1 precursor; MBL-associated plasma protein of 19 kD; small MBL-associated protein; MBL-associated protein MAp19 [Pan troglodytes]	---	0.547	0.038	0.456	0.089	0.713	0.096	0.614	0.050
1385893_at	AA874903	Transcribed locus, moderately similar to XP_515015.1 PREDICTED: similar to immunoglobulin lambda light chain [Pan troglodytes]	---	0.979	0.672	1.760	0.064	0.811	0.094	1.464	0.097
1376053_at	BM385144	Transcribed locus, moderately similar to XP_517387.1 PREDICTED: similar to ribosomal protein L34; 60S ribosomal protein L34 [Pan troglodytes]	---	0.925	0.075	1.524	0.021	0.817	0.072	1.291	0.204
1374724_at	BG378232	Transcribed locus, moderately similar to XP_518719.1 PREDICTED: similar to tumor differentially expressed 2 [Pan troglodytes]	---	1.277	0.187	2.205	0.192	1.562	0.160	2.459	0.720
1391194_at	BG377337	Transcribed locus, moderately similar to XP_528650.1 PREDICTED: similar to Superoxide dismutase [Pan troglodytes]	---	1.052	0.761	0.750	0.042	0.870	0.246	1.054	0.652
1382886_at	BE100329	Transcribed locus, moderately similar to XP_528703.1 PREDICTED: similar to chromatin-specific transcription elongation factor large subunit [Pan troglodytes]	---	0.552	0.002	0.476	0.051	0.534	0.030	0.510	0.148
1379410_at	AA925019	Transcribed locus, moderately similar to XP_529790.1 PREDICTED: hypothetical protein XP_529790 [Pan troglodytes]	---	0.638	0.010	0.552	0.033	0.524	0.009	0.704	0.103
1376176_at	AI145586	Transcribed locus, moderately similar to XP_533875.2 PREDICTED: similar to microtubule associated serine/threonine kinase 2 [Canis familiaris]	---	0.347	0.001	0.452	0.120	0.188	0.026	0.611	0.164
1388838_at	AA943752	Transcribed locus, moderately similar to XP_535115.1 PREDICTED: similar to chromatin modifying protein 4C isoform 1 [Canis familiaris]	---	1.130	0.445	1.026	0.852	0.901	0.479	0.740	0.031
1390380_at	BE116633	Transcribed locus, moderately similar to XP_573674.1 PREDICTED: similar to U2 small nuclear ribonucleoprotein auxiliary factor 35 kDa subunit related-protein 1 (U2(RNU2) small nuclear RNA auxillary factor 1-like 1) (SP2) [Rattus norvegicus]	---	1.360	0.021	1.336	0.075	1.319	0.055	1.334	0.009
1375463_at	BG380847	Transcribed locus, moderately similar to XP_573674.1 PREDICTED: similar to U2 small nuclear ribonucleoprotein auxiliary factor 35 kDa subunit related-protein 1 (U2(RNU2) small nuclear RNA auxillary factor 1-like 1) (SP2) [Rattus norvegicus]	---	1.192	0.199	1.282	0.231	0.942	0.867	0.898	0.490
1382802_x_at	AW920828	Transcribed locus, moderately similar to XP_574110.1 PREDICTED: similar to Ab2-143 [Rattus norvegicus]	---	1.327	0.610	1.013	0.385	0.968	0.848	0.822	0.314
1377705_at	BF549971	Transcribed locus, moderately similar to XP_574280.1 PREDICTED: similar to Ab2-143 [Rattus norvegicus]	---	0.889	0.757	1.025	0.206	1.077	0.096	0.958	0.100
1377706_x_at	BF549971	Transcribed locus, moderately similar to XP_574280.1 PREDICTED: similar to Ab2-143 [Rattus norvegicus]	---	0.934	0.858	0.966	0.296	1.055	0.117	0.876	0.204
1391505_x_at	BI275261	Transcribed locus, moderately similar to XP_574280.1 PREDICTED: similar to Ab2-143 [Rattus norvegicus]	---	1.290	0.866	1.373	0.707	1.224	0.137	1.139	0.210
1379497_at	BI275261	Transcribed locus, moderately similar to XP_574280.1 PREDICTED: similar to Ab2-143 [Rattus norvegicus]	---	1.485	0.916	1.307	0.568	1.148	0.200	1.028	0.126

1379735_at	AA850836	Transcribed locus, moderately similar to XP_574686.1 PREDICTED: similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [Rattus norvegicus]	---	1.577	0.042	1.095	0.100	1.080	0.767	1.001	0.950
1394951_at	BE107308	Transcribed locus, moderately similar to XP_575346.1 PREDICTED: similar to Ab1-219 [Rattus norvegicus]	---	1.081	0.862	1.037	0.741	1.169	0.269	1.422	0.105
1396189_at	BI274116	Transcribed locus, moderately similar to XP_575703.1 PREDICTED: similar to LRRGT00139 [Rattus norvegicus]	---	1.374	0.440	0.635	0.069	1.098	0.767	0.570	0.167
1396190_x_at	BI274116	Transcribed locus, moderately similar to XP_575703.1 PREDICTED: similar to LRRGT00139 [Rattus norvegicus]	---	0.971	0.487	0.599	0.064	1.130	0.555	0.673	0.040
1380913_at	BG374053	Transcribed locus, moderately similar to XP_576220.1 PREDICTED: similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [Rattus norvegicus]	---	1.074	0.444	0.755	0.274	1.032	0.769	0.754	0.337
1380662_at	BM389613	Transcribed locus, moderately similar to XP_576260.1 PREDICTED: similar to LRRGT00194 [Rattus norvegicus]	---	0.999	0.995	1.000	0.972	1.004	0.975	0.998	0.305
1390698_at	BF395822	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	2.074	0.002	1.962	0.001	2.041	0.031	2.104	0.002
1379696_at	BI291833	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	8.571	0.003	1.768	0.123	13.135	0.000	2.111	0.027
1384096_at	BI279347	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	0.272	0.010	0.380	0.061	0.292	0.021	0.490	0.083
1377759_at	BG666928	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	6.287	0.013	9.392	0.001	3.478	0.026	4.301	0.019
1389422_at	AI180400	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	0.798	0.138	0.707	0.005	0.934	0.172	0.748	0.016
1392616_at	AI575519	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	0.769	0.223	0.799	0.945	0.876	0.211	0.741	0.058
1382857_at	BE108794	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	1.235	0.237	0.826	0.501	1.305	0.077	1.103	0.030
1396975_at	BI281220	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	2.474	0.267	1.470	0.041	2.685	0.004	1.161	0.990
1374552_at	BF412718	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	0.964	0.393	0.392	0.008	1.903	0.000	0.620	0.006
1380856_at	BE120542	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	0.983	0.425	0.612	0.123	0.973	0.863	0.614	0.124
1372272_at	BF394074	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	0.753	0.497	1.012	0.219	0.662	0.566	0.814	0.479
1382393_at	AI407100	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	1.003	0.505	0.889	0.315	0.920	0.499	0.890	0.320
1379519_at	AI171230	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	0.902	0.641	0.829	0.005	1.066	0.671	0.845	0.292
1380487_at	BE105524	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	1.005	0.666	1.014	0.110	0.707	0.031	0.775	0.125
1396161_at	BI285362	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	0.987	0.911	1.003	0.905	1.121	0.652	1.101	0.782
1392674_at	AI013937	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	0.830	0.935	0.855	0.398	1.082	0.833	0.714	0.172
1384637_at	AW535033	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	1.302	0.959	0.980	0.745	1.344	0.889	1.230	0.877
1393656_at	AA892817	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	1.011	0.971	0.890	0.251	0.937	0.400	0.945	0.527
1396205_at	BI303419	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	1.005	0.980	0.864	0.423	1.641	0.054	0.872	0.300
1375079_at	BE115776	Transcribed locus, moderately similar to XP_576550.1 PREDICTED: similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [Rattus norvegicus]	---	1.294	0.982	1.100	0.161	1.401	0.407	1.235	0.509
1395994_at	BE116471	Transcribed locus, moderately similar to XP_578397.1 PREDICTED: similar to sentrin 17 [Rattus norvegicus]	---	0.862	0.663	0.729	0.024	1.054	0.932	0.617	0.260
1373710_at	BI296600	Transcribed locus, moderately similar to XP_579384.1 PREDICTED: hypothetical protein XP_579384 [Rattus norvegicus]	---	0.543	0.061	0.148	0.001	0.814	0.332	0.280	0.036
1395744_at	BF291140	Transcribed locus, moderately similar to XP_579465.1 PREDICTED: DNA binding protein N5 [Rattus norvegicus]	---	2.625	0.017	1.292	0.242	2.907	0.016	1.888	0.013
1395260_at	BM383147	Transcribed locus, moderately similar to XP_579465.1 PREDICTED: DNA binding protein N5 [Rattus norvegicus]	---	6.921	0.078	1.407	0.122	9.595	0.067	2.325	0.020
1383603_at	BM385552	Transcribed locus, moderately similar to XP_579465.1 PREDICTED: DNA binding protein N5 [Rattus norvegicus]	---	1.927	0.092	1.673	0.036	2.817	0.026	2.053	0.004
1384041_at	BG671630	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.541	0.003	1.180	0.717	1.502	0.092	0.805	0.681
1372911_at	BI281950	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.408	0.004	0.979	0.286	0.483	0.113	0.760	0.430

1376700_at	AI179472	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	3.924	0.004	1.041	0.089	4.312	0.002	1.107	0.025
1381237_at	AW534521	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.666	0.012	1.094	0.017	1.582	0.058	1.313	0.003
1377999_at	BE103242	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.634	0.013	1.045	0.606	2.200	0.000	1.460	0.356
1391613_at	AW534807	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.821	0.023	1.721	0.132	2.384	0.034	1.254	0.448
1383169_at	BF563716	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.374	0.032	0.586	0.003	2.124	0.000	0.665	0.022
1397463_at	BE105818	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.597	0.049	1.448	0.084	1.933	0.096	0.890	0.403
1385569_at	BF559640	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	8.241	0.066	3.953	0.004	13.523	0.052	7.751	0.002
1377556_at	AW535380	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.802	0.084	0.472	0.004	0.664	0.703	0.605	0.020
1394437_at	AI407319	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.922	0.089	1.418	0.461	1.560	0.090	1.082	0.550
1384845_at	AI176044	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	2.144	0.089	1.321	0.490	2.675	0.012	1.328	0.278
1383085_at	BG672648	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	2.283	0.096	0.433	0.081	1.237	0.519	0.274	0.017
1381643_at	AW536050	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.420	0.110	0.998	0.968	1.929	0.112	1.153	0.218
1398409_at	AA850428	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.151	0.147	1.550	0.045	1.222	0.083	1.168	0.110
1379941_at	BM384685	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.487	0.158	0.630	0.236	2.119	0.059	0.739	0.348
1393146_at	BG663116	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.617	0.210	0.555	0.061	0.679	0.062	0.596	0.062
1380477_at	BE112382	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.910	0.213	1.628	0.673	1.709	0.089	1.099	0.897
1376129_at	BE108174	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.211	0.218	0.781	0.056	0.935	0.193	0.776	0.207
1374607_at	AI599854	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.825	0.225	0.445	0.001	0.674	0.240	0.594	0.026
1374278_at	BG381647	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.436	0.265	0.703	0.466	0.242	0.024	0.334	0.093
1373178_at	AA945183	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.583	0.294	0.469	0.003	1.717	0.016	0.598	0.042
1386032_at	BF288135	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.673	0.309	0.891	0.983	1.039	0.980	0.995	0.965
1378231_at	BI300425	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.015	0.318	0.798	0.196	1.708	0.062	0.745	0.105
1382004_at	AI175827	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.999	0.322	0.823	0.344	0.907	0.165	0.732	0.087
1389896_at	AI232217	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.754	0.356	0.328	0.001	1.259	0.078	0.475	0.004
1379825_at	AI112993	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.427	0.359	1.065	0.672	1.277	0.375	1.403	0.724
1374298_at	BG373455	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.293	0.362	0.441	0.015	8.291	0.026	1.734	0.031
1383545_at	BF562608	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.671	0.432	1.003	0.686	0.545	0.056	0.834	0.157
1383142_at	BI289244	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.114	0.511	1.384	0.005	0.660	0.016	1.205	0.405
1386031_at	BF288135	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.149	0.535	0.863	0.508	1.262	0.009	0.989	0.957
1384605_at	BF419162	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.108	0.586	1.074	0.709	1.816	0.493	1.143	0.391

1372187_at	AA945751	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.889	0.617	1.018	0.613	0.769	0.377	1.412	0.037
1383012_at	BE115155	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.130	0.627	1.920	0.001	0.933	0.635	1.322	0.146
1382256_at	AI011445	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.276	0.629	1.460	0.249	0.970	0.602	1.238	0.147
1398454_at	BM389272	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.090	0.633	0.836	0.131	1.032	0.787	0.618	0.038
1374193_at	BI303636	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.579	0.651	1.063	0.133	2.550	0.039	1.406	0.767
1399142_at	BF398045	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.880	0.652	0.483	0.003	0.904	0.214	0.503	0.003
1377310_at	BG374304	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.701	0.662	0.487	0.002	1.245	0.011	0.607	0.060
1374753_at	AI105113	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.988	0.710	0.681	0.047	1.034	0.961	0.712	0.133
1394820_at	AI704849	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.322	0.731	0.759	0.384	1.468	0.243	0.936	0.812
1382703_at	BE099893	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.567	0.734	0.726	0.224	0.836	0.648	0.690	0.036
1383987_at	AI112807	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.048	0.794	0.915	0.168	2.035	0.983	1.481	0.038
1379933_at	AI409737	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.998	0.808	1.002	0.981	0.974	0.982	0.999	0.979
1394773_at	BG378318	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.058	0.908	1.199	0.775	1.016	0.972	1.229	0.825
1397384_at	BM391073	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.251	0.910	0.700	0.017	1.298	0.991	0.753	0.022
1379547_at	AA964652	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.132	0.912	1.007	0.818	1.559	0.074	1.933	0.050
1395220_at	AI556467	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.174	0.928	1.111	0.715	1.594	0.134	0.899	0.896
1398587_at	AA860035	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.831	0.954	0.518	0.000	1.196	0.149	0.560	0.079
1395395_at	BF291053	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.001	0.988	0.844	0.015	1.003	0.983	1.005	0.217
1384359_at	BF407520	Transcribed locus, moderately similar to XP_618803.1 PREDICTED: similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G [Mus musculus]	---	1.030	0.835	0.899	0.189	1.030	0.978	1.000	0.383
1377238_at	BM386889	Transcribed locus, moderately similar to XP_860663.1 PREDICTED: similar to GMP reductase 2 (Guanosine 5-monophosphate oxidoreductase 2) (Guanosine monophosphate reductase 2) isoform 6 [Canis familiaris]	---	0.506	0.076	0.213	0.002	0.683	0.392	0.395	0.010
1372716_at	BF284207	Transcribed locus, moderately similar to XP_866446.1 PREDICTED: similar to chromosome 18 open reading frame 25 isoform b isoform 2 [Canis familiaris]	---	0.896	0.236	1.041	0.862	0.940	0.612	0.999	0.452
1371468_at	BI296378	Transcribed locus, strongly similar to NP_001003955.1 RAB11 family interacting protein 5 (class I) isoform 1 [Mus musculus]	---	1.001	0.990	1.002	0.948	0.999	0.997	1.000	0.997
1383405_at	AW254703	Transcribed locus, strongly similar to NP_001005420.1 hypothetical protein LOC241289 [Mus musculus]	---	0.648	0.321	0.510	0.006	0.436	0.029	0.551	0.082
1382174_at	AI227996	Transcribed locus, strongly similar to NP_006210.1 phosphoinositide-3-kinase, catalytic, beta polypeptide [Homo sapiens]	---	3.081	0.037	1.378	0.032	3.576	0.506	0.790	0.195
1398037_at	BF390325	Transcribed locus, strongly similar to NP_006613.1 polo-like kinase 2 [Homo sapiens]	---	1.553	0.605	1.008	0.208	1.884	0.207	1.271	0.256
1384239_at	AA818474	Transcribed locus, strongly similar to NP_008994.1 TBC1 domain family, member 8 [Homo sapiens]	---	1.021	0.672	1.159	0.045	1.181	0.293	1.015	0.631
1388763_at	AI230762	Transcribed locus, strongly similar to NP_031751.1 calponin 2 [Mus musculus]	---	1.979	0.012	4.957	0.015	2.403	0.055	4.469	0.018
1371981_at	BI294700	Transcribed locus, strongly similar to NP_031860.1 Down syndrome critical region protein A [Mus musculus]	---	1.866	0.009	2.322	0.050	0.835	0.464	1.434	0.070
1373735_at	BG372418	Transcribed locus, strongly similar to NP_031975.2 excision repair cross-complementing rodent repair deficiency, complementation group 2 [Mus musculus]	---	0.680	0.345	0.993	0.985	1.145	0.122	0.767	0.090
1372089_at	AI171222	Transcribed locus, strongly similar to NP_032322.1 heat shock factor 1 [Mus musculus]	---	1.186	0.163	1.185	0.207	1.112	0.270	1.076	0.543
1393836_at	BE097933	Transcribed locus, strongly similar to NP_032627.1 microphthalmia-associated transcription factor [Mus musculus]	---	0.896	0.616	0.724	0.577	2.724	0.021	1.213	0.511
1397872_at	AI577099	Transcribed locus, strongly similar to NP_033413.1 thymidine kinase 1 [Mus musculus]	---	1.138	0.032	0.914	0.722	1.090	0.943	1.527	0.471
1399166_a_at	BF420294	Transcribed locus, strongly similar to NP_033875.1 B-cell CLL/lymphoma 7B [Mus musculus]	---	0.784	0.922	1.625	0.189	0.884	0.492	1.110	0.551
1372484_at	AI176231	Transcribed locus, strongly similar to NP_035242.1 poly (A) polymerase alpha [Mus musculus]	---	0.706	0.047	0.290	0.000	0.952	0.309	0.426	0.018
1382154_at	BI289625	Transcribed locus, strongly similar to NP_035333.2 protein tyrosine phosphatase, non-receptor type 12 [Mus musculus]	---	2.460	0.004	1.791	0.003	2.307	0.004	1.854	0.019

1376101_at	AI228256	Transcribed locus, strongly similar to NP_035543.1 sex-limited protein [Mus musculus]	---	0.918	0.595	0.650	0.023	0.948	0.694	0.750	0.011
1372318_at	AI235528	Transcribed locus, strongly similar to NP_035560.1 synuclein, gamma [Mus musculus]	---	0.077	0.009	0.040	0.006	0.076	0.003	0.034	0.001
1388690_at	AI105439	Transcribed locus, strongly similar to NP_035720.1 translocator of inner mitochondrial membrane 17a [Mus musculus]	---	1.043	0.876	0.473	0.014	0.992	0.768	0.512	0.014
1395532_at	AI137456	Transcribed locus, strongly similar to NP_035873.1 SH3-domain binding protein 3 [Mus musculus]	---	0.799	0.319	0.881	0.133	0.660	0.128	0.743	0.343
1371794_at	BM391449	Transcribed locus, strongly similar to NP_035873.1 SH3-domain binding protein 3 [Mus musculus]	---	0.805	0.817	0.925	0.275	0.907	0.362	0.960	0.510
1381012_at	BI303349	Transcribed locus, strongly similar to NP_035920.1 ariadne homolog 2 [Mus musculus]	---	1.091	0.886	0.688	0.752	1.046	0.685	0.960	0.768
1375172_at	AA850517	Transcribed locus, strongly similar to NP_036061.1 constitutive photomorphogenic protein 1 [Mus musculus]	---	1.166	0.593	0.846	0.873	1.028	0.936	1.059	0.850
1373673_at	BF284593	Transcribed locus, strongly similar to NP_037230.1 glucose-6-phosphatase, catalytic [Rattus norvegicus]	---	0.929	0.810	0.745	0.007	1.035	0.064	0.744	0.055
1396512_at	BF393192	Transcribed locus, strongly similar to NP_062039.1 synaptogyrin 1 [Rattus norvegicus]	---	0.985	0.881	0.258	0.070	0.695	0.286	0.274	0.079
1398617_at	BE098167	Transcribed locus, strongly similar to NP_062613.2 ubiquitin C [Mus musculus]	---	0.982	0.267	1.095	0.502	1.414	0.660	0.686	0.108
1371699_at	BI295739	Transcribed locus, strongly similar to NP_064456.1 fibrinogen, beta polypeptide [Rattus norvegicus]	---	1.988	0.001	1.511	0.006	1.415	0.086	1.060	0.122
1373166_at	BM391823	Transcribed locus, strongly similar to NP_064456.1 fibrinogen, beta polypeptide [Rattus norvegicus]	---	1.664	0.066	1.476	0.137	1.312	0.104	0.883	0.397
1372041_at	BI290059	Transcribed locus, strongly similar to NP_066943.1 synapse-associated protein 102 [Homo sapiens]	---	0.634	0.112	0.279	0.006	0.417	0.065	0.231	0.024
1393184_at	BF420805	Transcribed locus, strongly similar to NP_068778.1 protein phosphatase 1, regulatory (inhibitor) subunit 11 isoform 1 [Homo sapiens]	---	0.902	0.628	0.541	0.033	0.963	0.871	0.454	0.001
1376421_at	BI278838	Transcribed locus, strongly similar to NP_075230.1 nuclear receptor subfamily 1, group I, member 3 [Rattus norvegicus]	---	0.365	0.119	0.372	0.004	0.426	0.044	0.228	0.065
1382087_at	BE109382	Transcribed locus, strongly similar to NP_076005.1 hypoxia-inducible protein 2 [Mus musculus]	---	0.813	0.136	6.674	0.000	1.310	0.079	5.901	0.001
1388692_at	AI411102	Transcribed locus, strongly similar to NP_079814.1 spermatogenesis associated 11 [Mus musculus]	---	0.790	0.964	1.003	0.722	0.954	0.557	1.078	0.308
1374877_at	AI112752	Transcribed locus, strongly similar to NP_079892.1 translocase of inner mitochondrial membrane 50 homolog [Mus musculus]	---	0.616	0.026	1.484	0.069	0.501	0.076	1.217	0.710
1373235_at	AA892370	Transcribed locus, strongly similar to NP_080208.1 synapse associated protein 1 [Mus musculus]	---	0.786	0.741	1.223	0.247	0.896	0.465	1.233	0.010
1386253_at	AA800290	Transcribed locus, strongly similar to NP_080395.1 vitamin D receptor interacting protein [Mus musculus]	---	0.986	0.896	1.795	0.102	0.653	0.949	1.043	0.713
1386180_at	AI178132	Transcribed locus, strongly similar to NP_080601.1 hypothetical protein LOC67706 [Mus musculus]	---	0.987	0.997	0.963	0.461	0.978	0.878	0.999	0.630
1374583_at	BI288131	Transcribed locus, strongly similar to NP_081306.1 histidine triad protein member 5 [Mus musculus]	---	0.789	0.625	0.727	0.124	0.810	0.647	1.125	0.831
1384311_at	BE113314	Transcribed locus, strongly similar to NP_081823.1 PR domain containing 5 [Mus musculus]	---	2.826	0.098	1.717	0.105	1.632	0.084	0.971	0.928
1399100_at	BF396192	Transcribed locus, strongly similar to NP_082675.1 cyclin T2 [Mus musculus]	---	1.355	0.018	1.229	0.380	1.387	0.231	1.150	0.762
1388689_at	AI170755	Transcribed locus, strongly similar to NP_083620.1 acylphosphatase 2, muscle type [Mus musculus]	---	0.885	0.707	0.294	0.013	0.897	0.763	0.465	0.036
1392663_at	AI179925	Transcribed locus, strongly similar to NP_083924.2 hypothetical protein LOC76539 [Mus musculus]	---	0.395	0.057	0.656	0.001	0.417	0.008	0.592	0.027
1374541_at	BM392117	Transcribed locus, strongly similar to NP_109603.2 glycogen synthase 1, muscle [Mus musculus]	---	0.931	0.996	6.471	0.001	1.151	0.784	2.563	0.008
1382649_at	AI030649	Transcribed locus, strongly similar to NP_112381.2 Sjogren syndrome antigen B [Rattus norvegicus]	---	0.964	0.695	0.967	0.187	1.199	0.136	1.100	0.082
1374138_at	BG378169	Transcribed locus, strongly similar to NP_112574.3 ADP-dependent glucokinase [Homo sapiens]	---	0.999	0.934	0.922	0.936	1.014	0.902	0.921	0.999
1371324_at	BG673668	Transcribed locus, strongly similar to NP_112577.1 SF3b10 [Homo sapiens]	---	0.835	0.980	0.573	0.162	0.740	0.753	0.374	0.066
1382422_at	AA956340	Transcribed locus, strongly similar to NP_115833.1 protocadherin 7 isoform c precursor [Homo sapiens]	---	0.802	0.835	0.815	0.037	0.976	0.696	1.143	0.630
1385008_at	AA925373	Transcribed locus, strongly similar to NP_115833.1 protocadherin 7 isoform c precursor [Homo sapiens]	---	1.246	0.998	0.851	0.590	1.538	0.169	1.444	0.081
1379332_at	AI556426	Transcribed locus, strongly similar to NP_361014.1 F-box protein FBW7 isoform 1 [Homo sapiens]	---	0.819	0.507	1.400	0.057	0.786	0.407	1.108	0.367
1373120_at	BM389931	Transcribed locus, strongly similar to NP_446127.3 spermatogenesis associated 2 [Rattus norvegicus]	---	1.322	0.731	1.296	0.233	1.108	0.909	1.117	0.082
1383536_at	AI712541	Transcribed locus, strongly similar to NP_569084.1 dihydrofolate reductase [Rattus norvegicus]	---	1.249	0.934	1.158	0.861	1.006	0.504	1.513	0.773
1374458_at	AI600031	Transcribed locus, strongly similar to NP_573483.1 serum/glucocorticoid regulated kinase 3 [Mus musculus]	---	0.535	0.032	0.396	0.015	0.741	0.222	0.831	0.359
1380148_at	BE118688	Transcribed locus, strongly similar to NP_579890.1 Wolf-Hirschhorn syndrome candidate 1 protein isoform 1 [Homo sapiens]	---	1.020	0.933	1.237	0.097	1.303	0.218	1.029	0.203
1393168_at	BF398450	Transcribed locus, strongly similar to NP_598773.1 mbt domain containing 1 [Mus musculus]	---	1.065	0.911	0.823	0.054	1.684	0.150	0.778	0.054
1386750_at	BF290862	Transcribed locus, strongly similar to NP_666196.1 expressed sequence AW060714 [Mus musculus]	---	1.149	0.050	2.313	0.009	1.057	0.234	2.042	0.007
1373652_at	BG374986	Transcribed locus, strongly similar to NP_666217.2 hypothetical protein LOC226744 [Mus musculus]	---	0.671	0.089	0.559	0.010	0.484	0.057	0.624	0.009
1391623_at	AI706933	Transcribed locus, strongly similar to NP_666224.2 Grb10 interacting GYF protein 2 [Mus musculus]	---	0.942	0.895	0.862	0.351	0.762	0.185	0.801	0.097
1383670_at	BM383134	Transcribed locus, strongly similar to NP_666333.1 zinc finger protein 426 [Mus musculus]	---	0.997	0.057	0.672	0.031	0.888	0.604	0.784	0.129
1389633_at	BI290172	Transcribed locus, strongly similar to NP_683754.1 E2F transcription factor 4 [Mus musculus]	---	0.856	0.454	2.221	0.006	0.791	0.192	1.968	0.010
1372178_at	BM385981	Transcribed locus, strongly similar to NP_695208.1 serine/threonine protein kinase 6 [Rattus norvegicus]	---	2.225	0.018	1.874	0.053	2.747	0.012	1.832	0.005
1398386_at	AW915951	Transcribed locus, strongly similar to NP_705766.2 zinc finger, CCHC domain containing 6 [Mus musculus]	---	1.518	0.549	1.008	0.744	1.344	0.157	1.004	0.786
1382248_at	BI292769	Transcribed locus, strongly similar to NP_705773.1 leucine rich repeat containing 45 [Mus musculus]	---	0.458	0.012	0.648	0.083	0.549	0.755	0.320	0.185
1376021_at	BM384049	Transcribed locus, strongly similar to NP_705773.1 leucine rich repeat containing 45 [Mus musculus]	---	1.545	0.114	1.881	0.005	1.256	0.373	2.005	0.001
1383357_a_at	BF403558	Transcribed locus, strongly similar to NP_722482.1 BCL2-associated transcription factor 1 isoform 2 [Mus musculus]	---	1.659	0.061	1.594	0.001	1.198	0.196	1.524	0.001
1389771_at	AI013885	Transcribed locus, strongly similar to NP_766314.2 hypothetical protein LOC231868 [Mus musculus]	---	0.647	0.027	0.908	0.249	0.729	0.017	0.881	0.580
1373950_at	AI598911	Transcribed locus, strongly similar to NP_766529.2 zinc finger protein 496 [Mus musculus]	---	1.017	0.824	2.850	0.003	1.109	0.983	2.036	0.004
1384517_at	BF420144	Transcribed locus, strongly similar to NP_766529.2 zinc finger protein 496 [Mus musculus]	---	1.005	0.973	1.971	0.133	1.000	0.978	1.093	0.752
1383373_at	AI576635	Transcribed locus, strongly similar to NP_766590.1 ZXD family zinc finger C isoform 2 [Mus musculus]	---	1.377	0.139	0.695	0.127	1.307	0.017	0.887	0.372
1383800_at	AW523537	Transcribed locus, strongly similar to NP_775622.1 transmembrane protein 28 [Mus musculus]	---	0.890	0.917	0.432	0.000	0.980	0.371	0.662	0.015
1394417_at	BF396165	Transcribed locus, strongly similar to NP_786941.1 PC4 and SFRS1 interacting protein 1 [Rattus norvegicus]	---	0.667	0.490	0.546	0.339	0.690	0.378	0.619	0.170
1372690_at	AI137471	Transcribed locus, strongly similar to NP_808376.1 reticulon 4 receptor-like 1 [Mus musculus]	---	0.363	0.004	0.858	0.440	0.477	0.073	0.500	0.022

1393404_at	BF554746	Transcribed locus, strongly similar to NP_808376.1 reticulon 4 receptor-like 1 [Mus musculus]	---	0.420	0.012	0.751	0.724	0.268	0.004	0.752	0.411
1393808_at	AW527783	Transcribed locus, strongly similar to NP_835187.1 fatty acid 2-hydroxylase [Mus musculus]	---	1.008	0.910	1.007	0.861	0.889	0.023	0.968	0.975
1373649_at	AI453889	Transcribed locus, strongly similar to NP_848466.1 COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase [Mus musculus]	---	0.996	0.953	0.969	0.813	0.754	0.969	0.963	0.831
1395285_at	BE108376	Transcribed locus, strongly similar to NP_940969.1 hypothetical protein LOC375484 [Homo sapiens]	---	0.673	0.090	1.257	0.074	0.451	0.004	1.051	0.247
1377002_at	AA946209	Transcribed locus, strongly similar to XP_213649.3 PREDICTED: similar to interferon alpha/beta receptor [Rattus norvegicus]	---	1.314	0.917	0.885	0.676	1.006	0.502	0.710	0.144
1397307_at	BF555100	Transcribed locus, strongly similar to XP_213790.3 PREDICTED: similar to Tescalcin [Rattus norvegicus]	---	1.761	0.212	0.341	0.038	0.895	0.103	0.467	0.485
1380605_at	BM387149	Transcribed locus, strongly similar to XP_213842.2 PREDICTED: similar to Gadd45gip1_predicted protein [Rattus norvegicus]	---	0.997	0.736	1.006	0.945	1.103	0.118	1.000	0.998
1391206_at	AW533313	Transcribed locus, strongly similar to XP_213984.3 PREDICTED: similar to RIKEN cDNA 5730559C18 [Rattus norvegicus]	---	1.995	0.016	1.443	0.677	1.516	0.003	0.886	0.500
1377897_at	AI231330	Transcribed locus, strongly similar to XP_214371.3 PREDICTED: similar to WHSC1L1 protein isoform long [Rattus norvegicus]	---	0.671	0.076	0.884	0.974	0.651	0.308	0.978	0.809
1389172_at	AI179391	Transcribed locus, strongly similar to XP_214403.2 PREDICTED: similar to N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase precursor (Glycosylasparaginase) (Aspartylglucosaminidase) (N4-(N-acetyl-beta-glucosaminyl)-L-asparagine amidase) (AGA) [Rattus norvegicus]	---	1.801	0.137	1.565	0.011	1.986	0.021	1.414	0.140
1376258_at	AI406785	Transcribed locus, strongly similar to XP_214459.3 PREDICTED: similar to serine (or cysteine) proteinase inhibitor, clade B, member 1b [Rattus norvegicus]	---	0.995	0.677	0.992	0.911	0.999	0.970	0.996	0.949
1367518_at	BI274976	Transcribed locus, strongly similar to XP_214652.3 PREDICTED: similar to Fatso [Rattus norvegicus]	---	0.591	0.389	0.906	0.550	0.492	0.008	0.856	0.494
1381248_at	AI763874	Transcribed locus, strongly similar to XP_215477.3 PREDICTED: similar to RIKEN cDNA 1500031M22 [Rattus norvegicus]	---	0.578	0.146	0.712	0.001	0.569	0.136	0.888	0.424
1391680_at	BF410646	Transcribed locus, strongly similar to XP_215614.3 PREDICTED: similar to G patch domain containing 4 [Rattus norvegicus]	---	0.999	0.994	1.026	0.484	0.739	0.298	1.073	0.706
1391250_at	BG374216	Transcribed locus, strongly similar to XP_215812.3 PREDICTED: similar to 53BP1 protein [Rattus norvegicus]	---	0.961	0.338	0.998	0.999	0.947	0.330	1.003	0.971
1383769_at	BF398206	Transcribed locus, strongly similar to XP_217409.3 PREDICTED: bone morphogenic protein receptor, type II (serine/threonine kinase) [Rattus norvegicus]	---	1.032	0.921	1.285	0.002	0.908	0.475	1.114	0.294
1390480_at	AI704806	Transcribed locus, strongly similar to XP_217893.3 PREDICTED: similar to KIF13A [Rattus norvegicus]	---	0.971	0.849	0.766	0.027	0.967	0.807	0.812	0.037
1396191_at	BF395978	Transcribed locus, strongly similar to XP_218162.3 PREDICTED: similar to Eukaryotic translation initiation factor 5B (eIF-5B) (Translation initiation factor IF-2) [Rattus norvegicus]	---	0.763	0.060	0.846	0.394	0.892	0.057	1.256	0.160
1383910_at	BF398220	Transcribed locus, strongly similar to XP_218459.3 PREDICTED: similar to zinc finger protein 574 [Rattus norvegicus]	---	1.714	0.002	1.160	0.239	1.411	0.018	1.062	0.215
1390589_at	AI030995	Transcribed locus, strongly similar to XP_220062.3 PREDICTED: similar to proliferation associated SNF2-like protein [Rattus norvegicus]	---	1.045	0.902	0.760	0.050	0.939	0.525	0.750	0.132
1391187_at	BI303019	Transcribed locus, strongly similar to XP_220174.3 PREDICTED: similar to periplakin [Rattus norvegicus]	---	0.938	0.982	0.898	0.677	0.567	0.311	0.792	0.579
1385439_x_at	BF417541	Transcribed locus, strongly similar to XP_220978.3 PREDICTED: similar to Probable ATP-dependent helicase LGP2 (Protein D11Lgp2) [Rattus norvegicus]	---	15.519	0.000	4.114	0.002	61.098	0.000	11.821	0.001
1383948_at	AA998083	Transcribed locus, strongly similar to XP_222260.3 PREDICTED: similar to OTTHUMP00000028696 [Rattus norvegicus]	---	0.260	0.000	0.101	0.000	0.244	0.006	0.096	0.013
1376610_a_at	BE109163	Transcribed locus, strongly similar to XP_222260.3 PREDICTED: similar to OTTHUMP00000028696 [Rattus norvegicus]	---	0.354	0.046	0.181	0.014	0.548	0.116	0.355	0.014
1386309_at	AI176361	Transcribed locus, strongly similar to XP_222260.3 PREDICTED: similar to OTTHUMP00000028696 [Rattus norvegicus]	---	0.640	0.048	0.332	0.004	0.642	0.006	0.366	0.014
1386805_at	BF554446	Transcribed locus, strongly similar to XP_222260.3 PREDICTED: similar to OTTHUMP00000028696 [Rattus norvegicus]	---	0.653	0.280	0.100	0.002	0.646	0.272	0.100	0.002
1390194_at	BI296401	Transcribed locus, strongly similar to XP_223687.3 PREDICTED: similar to RIKEN cDNA 4933435A13 [Rattus norvegicus]	---	1.100	0.243	0.857	0.180	1.878	0.030	1.109	0.466
1383561_at	BF550555	Transcribed locus, strongly similar to XP_225045.1 PREDICTED: similar to ligase IV, DNA, ATP-dependent [Rattus norvegicus]	---	0.869	0.124	0.666	0.043	1.489	0.456	0.868	0.171
1378676_at	BF406322	Transcribed locus, strongly similar to XP_226159.3 PREDICTED: similar to laminin-5 alpha 3 chain [Rattus norvegicus]	---	1.002	0.742	0.821	0.046	1.713	0.074	1.002	0.999
1397562_at	AW534448	Transcribed locus, strongly similar to XP_226249.3 PREDICTED: similar to amyloid beta precursor protein binding protein 1 [Rattus norvegicus]	---	0.908	0.048	1.006	0.941	0.755	0.083	1.036	0.902
1378454_at	BF405939	Transcribed locus, strongly similar to XP_226608.3 PREDICTED: similar to hypothetical protein FLJ25333 [Rattus norvegicus]	---	1.808	0.208	0.840	0.101	1.775	0.188	1.158	0.310
1390886_at	BE111565	Transcribed locus, strongly similar to XP_227031.3 PREDICTED: similar to hypothetical protein D3Ertd789e [Rattus norvegicus]	---	0.664	0.026	0.511	0.017	0.605	0.106	0.685	0.704
1389632_at	AA799294	Transcribed locus, strongly similar to XP_228131.3 PREDICTED: similar to Rho-related BTB domain-containing protein 1 [Rattus norvegicus]	---	0.479	0.011	0.224	0.000	0.446	0.001	0.305	0.013
1393222_at	AI058449	Transcribed locus, strongly similar to XP_230471.1 PREDICTED: similar to Vps18 protein [Rattus norvegicus]	---	1.005	0.639	1.013	0.947	0.854	0.158	0.991	0.876

1396996_at	BF409811	Transcribed locus, strongly similar to XP_233217.2 PREDICTED: similar to ubiquitin specific protease 1 [Rattus norvegicus]	---	0.766	0.537	1.009	0.175	4.798	0.006	1.132	0.096
1376824_at	AI408131	Transcribed locus, strongly similar to XP_233612.3 PREDICTED: similar to DNA-damage inducible protein 2 [Rattus norvegicus]	---	1.416	0.023	0.768	0.291	1.555	0.011	0.994	0.993
1372987_at	BF393934	Transcribed locus, strongly similar to XP_233741.1 PREDICTED: similar to Non-receptor tyrosine-protein kinase TYK2 [Rattus norvegicus]	---	2.640	0.103	1.262	0.862	2.964	0.011	1.802	0.040
1377741_at	BF389042	Transcribed locus, strongly similar to XP_235292.3 PREDICTED: similar to PHD finger protein 20-like 1 isoform 1 [Rattus norvegicus]	---	1.510	0.034	0.456	0.058	1.652	0.044	0.631	0.015
1376169_at	BE104290	Transcribed locus, strongly similar to XP_235292.3 PREDICTED: similar to PHD finger protein 20-like 1 isoform 1 [Rattus norvegicus]	---	1.353	0.089	0.461	0.000	1.696	0.005	0.606	0.009
1383002_at	AA998043	Transcribed locus, strongly similar to XP_235292.3 PREDICTED: similar to PHD finger protein 20-like 1 isoform 1 [Rattus norvegicus]	---	1.188	0.414	0.417	0.008	1.591	0.010	0.540	0.021
1371716_at	BE107610	Transcribed locus, strongly similar to XP_236644.2 PREDICTED: similar to SWI/SNF related matrix-associated actin-dependent regulator of chromatin subfamily C member 1 (SWI/SNF complex 155 kDa subunit) (BRG1-associated factor 155) (SWI3-related protein) [Rattus norvegicus]	---	0.710	0.612	0.249	0.000	1.644	0.084	0.367	0.035
1381539_at	BI294601	Transcribed locus, strongly similar to XP_236784.3 PREDICTED: similar to sex-determination protein homolog Fem1a [Rattus norvegicus]	---	1.001	0.992	0.873	0.130	1.001	1.000	0.778	0.143
1383310_at	AI030892	Transcribed locus, strongly similar to XP_236988.3 PREDICTED: similar to DNA replication licensing factor MCM3 (DNA polymerase alpha holoenzyme-associated protein P1) (P1-MCM3) [Rattus norvegicus]	---	0.996	0.959	0.666	0.033	0.806	0.506	0.826	0.176
1373459_at	AI103051	Transcribed locus, strongly similar to XP_237307.3 PREDICTED: similar to serine/threonine kinase 11 interacting protein [Rattus norvegicus]	---	0.798	0.397	3.477	0.004	0.828	0.721	2.019	0.017
1390492_a_at	BM391750	Transcribed locus, strongly similar to XP_237371.3 PREDICTED: similar to Ubiquitin carboxyl-terminal hydrolase 40 (Ubiquitin thiolesterase 40) (Ubiquitin-specific processing protease 40) (Deubiquitinating enzyme 40) [Rattus norvegicus]	---	0.933	0.659	0.626	0.035	0.851	0.478	0.638	0.034
1383841_at	BF396378	Transcribed locus, strongly similar to XP_282969.4 PREDICTED: hypothetical protein LOC70802 isoform 1 [Mus musculus]	---	1.027	0.780	0.771	0.248	1.737	0.047	1.106	0.609
1379292_at	AI412288	Transcribed locus, strongly similar to XP_341302.2 PREDICTED: similar to mKIAA1344 protein [Rattus norvegicus]	---	0.727	0.127	0.912	0.527	0.907	0.610	1.134	0.254
1399167_a_at	BI278183	Transcribed locus, strongly similar to XP_341668.2 PREDICTED: similar to Growth factor receptor bound protein 2-associated protein 1 [Rattus norvegicus]	---	3.285	0.019	1.000	0.563	3.586	0.016	1.637	0.054
1376219_at	BI273855	Transcribed locus, strongly similar to XP_342285.2 PREDICTED: similar to ATPase, Class I, type 8B, member 2 isoform a; phospholipid-transporting ATPase ID [Rattus norvegicus]	---	1.273	0.159	1.115	0.545	1.207	0.135	0.698	0.048
1390250_x_at	BI273855	Transcribed locus, strongly similar to XP_342285.2 PREDICTED: similar to ATPase, Class I, type 8B, member 2 isoform a; phospholipid-transporting ATPase ID [Rattus norvegicus]	---	0.798	0.294	1.269	0.094	0.998	0.983	0.890	0.371
1376218_a_at	BI273855	Transcribed locus, strongly similar to XP_342285.2 PREDICTED: similar to ATPase, Class I, type 8B, member 2 isoform a; phospholipid-transporting ATPase ID [Rattus norvegicus]	---	0.812	0.320	1.272	0.845	0.946	0.697	0.932	1.000
1391065_at	BG373309	Transcribed locus, strongly similar to XP_343352.2 PREDICTED: similar to KIAA1731 protein [Rattus norvegicus]	---	0.914	0.723	0.988	0.054	1.365	0.881	1.213	0.077
1373199_at	AA943573	Transcribed locus, strongly similar to XP_343818.1 PREDICTED: similar to Alpha-galactosidase A precursor (Melibiase) (Alpha-D-galactoside galactohydrolase) (Alpha-D-galactosidase A) [Rattus norvegicus]	---	0.638	0.698	0.574	0.012	0.904	0.900	0.614	0.022
1373880_at	AI408513	Transcribed locus, strongly similar to XP_344704.2 PREDICTED: similar to mKIAA1632 protein [Rattus norvegicus]	---	1.201	0.091	1.888	0.004	1.048	0.820	1.396	0.019
1382961_at	AI013305	Transcribed locus, strongly similar to XP_346951.1 PREDICTED: hypothetical protein XP_346950 [Rattus norvegicus]	---	0.988	0.971	1.407	0.904	1.084	0.740	1.332	0.282
1393194_at	BF558732	Transcribed locus, strongly similar to XP_347167.1 PREDICTED: similar to Williams-Beuren syndrome deletion transcript 9 homolog [Rattus norvegicus]	---	1.089	0.232	1.352	0.151	1.047	0.485	1.004	0.569
1382001_at	AI227612	Transcribed locus, strongly similar to XP_418542.1 PREDICTED: similar to Myeloid/lymphoid or mixed-lineage leukemia protein 3 homolog (Histone-lysine N-methyltransferase, H3 lysine-4 specific MLL3) (Homologous to ALR protein) [Gallus gallus]	---	1.136	0.406	0.807	0.004	0.882	0.599	0.937	0.380
1379423_at	AA963364	Transcribed locus, strongly similar to XP_418627.1 PREDICTED: similar to Ras suppressor protein 1 (Rsu-1) (RSP-1) [Gallus gallus]	---	1.183	0.181	1.047	0.253	1.170	0.429	0.867	0.119
1389466_at	BG374280	Transcribed locus, strongly similar to XP_421547.1 PREDICTED: similar to coiled-coil domain containing 6 [Gallus gallus]	---	0.470	0.053	0.893	0.660	0.562	0.012	0.712	0.063
1371776_at	AA819268	Transcribed locus, strongly similar to XP_424759.1 PREDICTED: similar to 3-phosphatidylinositol kinase (EC 2.7.1.-) 85K chain alpha - bovine [Gallus gallus]	---	1.353	0.534	1.410	0.155	1.638	0.901	0.914	0.508
1394463_at	BE097727	Transcribed locus, strongly similar to XP_507983.1 PREDICTED: similar to PRO1933 [Pan troglodytes]	---	1.033	0.852	0.927	0.145	1.659	0.049	0.929	0.219
1398945_at	AA851439	Transcribed locus, strongly similar to XP_508798.1 PREDICTED: similar to probable RNA helicase (EC 3.6.1.-) RCK - human [Pan troglodytes]	---	0.726	0.060	0.475	0.001	0.641	0.123	0.516	0.000
1391031_at	BF389889	Transcribed locus, strongly similar to XP_510753.1 PREDICTED: similar to Transcription elongation factor B polypeptide 2 (RNA polymerase II transcription factor SIII subunit B) (SIII p18) (Elongin B) (EloB) (Elongin 18 kDa subunit) [Pan troglodytes]	---	2.330	0.002	1.538	0.126	1.359	0.037	1.490	0.062

1396638_at	BM382854	Transcribed locus, strongly similar to XP_510927.1 PREDICTED: similar to septin 1 [Pan troglodytes]	---	1.045	0.946	1.362	0.976	1.246	0.208	1.086	0.889
1380921_at	AI548341	Transcribed locus, strongly similar to XP_512522.1 PREDICTED: similar to MEF2B protein [Pan troglodytes]	---	1.001	0.902	0.858	0.247	1.027	0.616	0.998	0.990
1382110_at	AA899630	Transcribed locus, strongly similar to XP_518480.1 PREDICTED: similar to trinucleotide repeat containing 5; expanded repeat domain, CAG/CTG 5; CAG repeat containing [Pan troglodytes]	---	0.596	0.084	1.324	0.264	0.575	0.076	1.374	0.598
1379173_at	BF394515	Transcribed locus, strongly similar to XP_518598.1 PREDICTED: similar to pleckstrin homology domain interacting protein [Pan troglodytes]	---	0.852	0.796	1.224	0.013	0.689	0.172	1.002	0.971
1382142_at	AI029975	Transcribed locus, strongly similar to XP_520163.1 PREDICTED: similar to ATP-binding cassette transporter 1 [Pan troglodytes]	---	1.014	0.091	0.413	0.006	0.954	0.616	0.398	0.012
1382431_at	AI103530	Transcribed locus, strongly similar to XP_520163.1 PREDICTED: similar to ATP-binding cassette transporter 1 [Pan troglodytes]	---	1.076	0.297	0.445	0.002	0.809	0.236	0.442	0.002
1383204_at	BE099804	Transcribed locus, strongly similar to XP_523419.1 PREDICTED: similar to zinc and ring finger protein 1; nerve injury gene 283 [Pan troglodytes]	---	4.598	0.004	3.677	0.001	6.751	0.001	2.748	0.001
1392975_at	AI058938	Transcribed locus, strongly similar to XP_525786.1 PREDICTED: similar to chromosome 2 open reading frame 7 [Pan troglodytes]	---	0.472	0.020	0.763	0.110	0.473	0.014	0.750	0.223
1393841_at	AA859317	Transcribed locus, strongly similar to XP_528581.1 PREDICTED: similar to hypothetical protein FLJ31810 [Pan troglodytes]	---	0.190	0.000	0.124	0.004	0.279	0.005	0.309	0.094
1376324_at	BF406329	Transcribed locus, strongly similar to XP_528965.1 PREDICTED: similar to dJ54B20.4 (novel KRAB box containing C2H2 type zinc finger protein) [Pan troglodytes]	---	0.920	0.802	1.044	0.508	1.582	0.059	0.796	0.213
1379400_at	AI044556	Transcribed locus, strongly similar to XP_531763.2 PREDICTED: similar to aldehyde dehydrogenase 1 family, member L2 [Canis familiaris]	---	0.207	0.002	0.252	0.016	0.273	0.004	0.267	0.025
1389558_at	BF281962	Transcribed locus, strongly similar to XP_532522.2 PREDICTED: similar to CG3570-PA [Canis familiaris]	---	1.481	0.054	1.248	0.056	2.229	0.002	1.345	0.013
1385149_at	AI502063	Transcribed locus, strongly similar to XP_532627.2 PREDICTED: similar to methyltransferase like 3 isoform 1 [Canis familiaris]	---	0.844	0.144	0.878	0.409	1.010	0.281	1.070	0.566
1396247_at	AI453997	Transcribed locus, strongly similar to XP_537630.2 PREDICTED: similar to CG10802-PA [Canis familiaris]	---	0.974	0.160	1.491	0.446	1.369	0.097	1.329	0.918
1390915_at	BI275327	Transcribed locus, strongly similar to XP_538131.2 PREDICTED: similar to MORC family CW-type zinc finger 4 (Zinc finger CW-type coiled-coil domain protein 2) [Canis familiaris]	---	0.969	0.292	1.000	0.775	1.068	0.659	0.949	0.532
1378229_at	BE118073	Transcribed locus, strongly similar to XP_541626.2 PREDICTED: similar to leucine rich repeat and fibronectin type III domain containing 1 [Canis familiaris]	---	1.373	0.363	0.993	0.897	1.500	0.090	0.997	0.930
1397174_at	AW520453	Transcribed locus, strongly similar to XP_547003.2 PREDICTED: similar to Forkhead box protein K1 (Myocyte nuclear factor) (MNF) [Canis familiaris]	---	1.767	0.057	0.843	0.360	1.381	0.124	0.844	0.001
1386744_x_at	BF544149	Transcribed locus, strongly similar to XP_574268.1 PREDICTED: similar to LRRGT00194 [Rattus norvegicus]	---	1.191	0.837	0.804	0.154	0.983	0.924	0.772	0.281
1373872_at	BE096535	Transcribed locus, strongly similar to XP_574462.1 PREDICTED: similar to hypothetical protein C230069C04 [Rattus norvegicus]	---	0.991	0.999	0.663	0.852	0.999	0.991	0.995	0.962
1373703_at	BE113247	Transcribed locus, strongly similar to XP_576199.1 PREDICTED: similar to envelope [Rattus norvegicus]	---	2.326	0.220	1.071	0.075	10.954	0.002	3.250	0.053
1381459_at	BE099644	Transcribed locus, strongly similar to XP_576213.1 PREDICTED: similar to RIKEN cDNA 4933417K05 gene [Rattus norvegicus]	---	0.313	0.002	0.841	0.385	0.428	0.008	1.188	0.260
1398922_at	BM389018	Transcribed locus, strongly similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	0.702	0.071	0.856	0.069	0.704	0.045	1.035	0.198
1373942_at	BF396312	Transcribed locus, strongly similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	0.838	0.384	0.628	0.054	1.321	0.624	1.116	0.745
1385653_at	AA817920	Transcribed locus, strongly similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	1.160	0.482	0.950	0.955	1.525	0.285	0.973	0.543
1395427_at	AW918981	Transcribed locus, strongly similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	0.997	0.986	0.989	0.353	0.930	0.193	1.076	0.269
1390678_at	AA955527	Transcribed locus, strongly similar to XP_578163.1 PREDICTED: similar to hypothetical protein, expressed [Rattus norvegicus]	---	1.579	0.036	1.552	0.183	1.104	0.411	0.935	0.643
1372022_at	BI283822	Transcribed locus, strongly similar to XP_579363.1 PREDICTED: hypothetical protein XP_579363 [Rattus norvegicus]	---	0.586	0.623	0.930	0.071	0.590	0.486	0.921	0.059
1371735_at	AI105202	Transcribed locus, strongly similar to XP_579758.1 PREDICTED: hypothetical protein XP_579758 [Rattus norvegicus]	---	1.262	0.298	2.978	0.004	0.910	0.147	2.819	0.005
1383921_at	AW916957	Transcribed locus, strongly similar to XP_579758.1 PREDICTED: hypothetical protein XP_579758 [Rattus norvegicus]	---	1.044	0.512	1.140	0.787	0.868	0.052	1.394	0.707
1379801_at	AI137954	Transcribed locus, strongly similar to XP_580017.1 PREDICTED: hypothetical protein XP_580017 [Rattus norvegicus]	---	0.954	0.100	0.461	0.091	1.456	0.682	0.755	0.476
1379445_at	BF283378	Transcribed locus, strongly similar to XP_580091.1 PREDICTED: hypothetical protein XP_580091 [Rattus norvegicus]	---	0.838	0.660	0.183	0.002	0.930	0.148	0.309	0.037
1378530_at	BF394061	Transcribed locus, strongly similar to XP_580104.1 PREDICTED: hypothetical protein XP_580104 [Rattus norvegicus]	---	0.659	0.053	0.995	0.927	0.596	0.063	1.000	0.795
1383185_at	BE105131	Transcribed locus, strongly similar to XP_580113.1 PREDICTED: hypothetical protein XP_580113 [Rattus norvegicus]	---	0.918	0.716	0.315	0.003	1.314	0.132	0.282	0.074
1383247_a_at	BI291029	Transcribed locus, strongly similar to XP_848415.1 PREDICTED: similar to spinster-like [Canis familiaris]	---	0.671	0.006	0.947	0.405	0.617	0.063	1.061	0.198

1375939_at	BM391922	Transcribed locus, strongly similar to XP_852159.1 PREDICTED: similar to GC-rich sequence DNA-binding factor homolog [Canis familiaris]	---	1.105	0.598	0.915	0.496	1.217	0.552	1.000	0.998
1375268_at	AA858591	Transcribed locus, strongly similar to XP_853191.1 PREDICTED: similar to 40S ribosomal protein S27-like protein [Canis familiaris]	---	0.959	0.898	2.295	0.008	0.790	0.582	2.631	0.001
1388454_at	AI230759	Transcribed locus, strongly similar to XP_853377.1 PREDICTED: similar to ornithine decarboxylase antizyme 2 [Canis familiaris]	---	0.917	0.892	0.438	0.005	1.197	0.040	0.569	0.012
1374562_at	AI177115	Transcribed locus, strongly similar to XP_860264.1 PREDICTED: similar to CG4699-PA, isoform A isoform 5 [Canis familiaris]	---	1.436	0.035	1.049	0.876	1.290	0.005	0.940	0.179
1378416_at	AA892565	Transcribed locus, strongly similar to XP_868417.1 PREDICTED: similar to tetratricopeptide repeat domain 8 isoform B isoform 2 [Canis familiaris]	---	0.476	0.004	0.265	0.001	0.314	0.018	0.272	0.027
1382140_at	AI012247	Transcribed locus, weakly similar to NP_001003141.1 protein tyrosine kinase fer [Canis familiaris]	---	1.379	0.338	0.766	0.144	1.857	0.984	0.751	0.038
1376464_at	BE102505	Transcribed locus, weakly similar to NP_001007662.1 thymocyte protein thy28 [Rattus norvegicus]	---	0.454	0.025	0.325	0.001	0.562	0.084	0.351	0.003
1394416_at	AI176741	Transcribed locus, weakly similar to NP_006141.2 LIM domain only 6 [Homo sapiens]	---	0.645	0.340	0.302	0.028	0.385	0.233	0.283	0.053
1374178_at	AI103954	Transcribed locus, weakly similar to NP_032303.1 4-hydroxyphenylpyruvic acid dioxygenase [Mus musculus]	---	1.122	0.538	1.332	0.061	1.336	0.065	1.643	0.004
1389414_at	BI285335	Transcribed locus, weakly similar to NP_032607.1 melanoma antigen [Mus musculus]	---	0.309	0.029	1.046	0.691	0.708	0.321	0.780	0.022
1383901_at	BI287446	Transcribed locus, weakly similar to NP_035020.2 neural precursor cell expressed, developmentally down-regulated gene 4 [Mus musculus]	---	1.452	0.128	1.796	0.015	2.824	0.007	1.876	0.009
1380232_at	BE119516	Transcribed locus, weakly similar to NP_035020.2 neural precursor cell expressed, developmentally down-regulated gene 4 [Mus musculus]	---	0.935	0.714	0.583	0.068	1.585	0.016	0.788	0.058
1380233_x_at	BE119516	Transcribed locus, weakly similar to NP_035020.2 neural precursor cell expressed, developmentally down-regulated gene 4 [Mus musculus]	---	0.916	0.728	0.616	0.037	1.467	0.594	0.683	0.023
1374800_at	BI303627	Transcribed locus, weakly similar to NP_035385.1 retinol binding protein 4, plasma [Mus musculus]	---	0.535	0.409	0.354	0.001	0.856	0.433	0.515	0.001
1381124_at	AA819672	Transcribed locus, weakly similar to NP_035385.1 retinol binding protein 4, plasma [Mus musculus]	---	1.059	0.962	0.742	0.155	1.058	0.950	0.761	0.076
1393160_at	AA955879	Transcribed locus, weakly similar to NP_035665.2 T-box 3 protein isoform 1 [Mus musculus]	---	1.222	0.948	0.991	0.981	0.826	0.429	1.241	0.561
1388935_at	AI231814	Transcribed locus, weakly similar to NP_036019.1 septin 3 [Mus musculus]	---	1.112	0.235	1.093	0.690	1.022	0.896	0.998	0.984
1372368_at	AI230431	Transcribed locus, weakly similar to NP_036925.1 guanidinoacetate methyltransferase [Rattus norvegicus]	---	0.709	0.192	0.989	0.555	0.797	0.075	0.959	0.526
1376109_at	BM387711	Transcribed locus, weakly similar to NP_062289.1 DNA binding protein with his-thr domain [Mus musculus]	---	1.423	0.051	0.995	0.941	2.004	0.068	1.486	0.207
1389530_at	BI274313	Transcribed locus, weakly similar to NP_071556.1 L-gulonolactone oxidase [Rattus norvegicus]	---	0.755	0.612	1.781	0.001	0.802	0.025	1.643	0.012
1390823_at	AA924839	Transcribed locus, weakly similar to NP_116026.1 S-phase kinase-associated protein 2 isoform 2 [Homo sapiens]	---	0.665	0.093	0.964	0.920	0.800	0.095	0.994	0.966
1396349_at	BE099657	Transcribed locus, weakly similar to NP_190697.1 unknown protein [Arabidopsis thaliana]	---	1.020	0.142	0.456	0.006	1.846	0.027	0.756	0.097
1383058_at	AI410438	Transcribed locus, weakly similar to NP_198672.1 ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase/ structural constituent of cell wall [Arabidopsis thaliana]	---	1.134	0.294	0.973	0.255	0.978	0.827	1.090	0.693
1383332_at	BI281615	Transcribed locus, weakly similar to NP_473118.2 hypothetical protein [Plasmodium falciparum 3D7]	---	1.252	0.024	0.966	0.700	1.211	0.031	0.933	0.476
1388933_at	AI233748	Transcribed locus, weakly similar to NP_473118.2 hypothetical protein [Plasmodium falciparum 3D7]	---	0.453	0.280	3.245	0.003	0.336	0.036	2.514	0.001
1393003_at	AA899900	Transcribed locus, weakly similar to NP_473118.2 hypothetical protein [Plasmodium falciparum 3D7]	---	0.798	0.465	0.215	0.002	1.301	0.017	0.128	0.018
1379545_at	BG372752	Transcribed locus, weakly similar to NP_473118.2 hypothetical protein [Plasmodium falciparum 3D7]	---	0.814	0.489	0.310	0.012	0.661	0.434	0.328	0.037
1392868_at	AA859495	Transcribed locus, weakly similar to NP_473357.1 FUS interacting protein (serine-arginine rich) 1 isoform 2 [Homo sapiens]	---	1.199	0.147	1.514	0.056	2.268	0.207	1.880	0.001
1373501_at	AA955361	Transcribed locus, weakly similar to NP_542945.1 proteosome (prosome, macropain) subunit, beta type 8 [Rattus norvegicus]	---	1.025	0.954	0.922	0.065	1.633	0.002	1.184	0.248
1380406_at	BE115630	Transcribed locus, weakly similar to NP_570953.1 CAMP [Mus musculus]	---	0.601	0.049	0.590	0.520	0.947	0.731	0.677	0.072
1399031_at	BM391360	Transcribed locus, weakly similar to NP_594758.1 hypothetical protein SPAC4F10.15c [Schizosaccharomyces pombe 972h-]	---	0.784	0.256	0.695	0.658	0.847	0.143	0.998	0.993
1382005_at	BI280285	Transcribed locus, weakly similar to NP_598738.1 transferrin [Mus musculus]	---	1.205	0.314	0.876	0.077	1.448	0.006	1.089	0.020
1390905_at	AW533482	Transcribed locus, weakly similar to NP_608540.1 CG2839-PA [Drosophila melanogaster]	---	1.737	0.003	1.087	0.379	1.283	0.182	1.011	0.608
1377794_at	BF288862	Transcribed locus, weakly similar to NP_659075.1 RIKEN cDNA 4732497O03 [Mus musculus]	---	0.609	0.148	0.900	0.205	0.569	0.011	0.867	0.604
1379471_at	BI275767	Transcribed locus, weakly similar to NP_671483.1 hippyragranin [Rattus norvegicus]	---	0.842	0.133	0.545	0.003	0.775	0.140	0.695	0.033
1394154_at	AI008375	Transcribed locus, weakly similar to NP_671483.1 hippyragranin [Rattus norvegicus]	---	1.020	0.245	0.914	0.717	1.022	0.811	0.974	0.672
1377633_a_at	AW918411	Transcribed locus, weakly similar to NP_671483.1 hippyragranin [Rattus norvegicus]	---	0.970	0.887	0.726	0.997	1.710	0.025	0.910	0.543
1396984_at	BM390248	Transcribed locus, weakly similar to NP_703313.1 hypothetical protein [Plasmodium falciparum 3D7]	---	1.426	0.045	0.649	0.027	1.675	0.090	0.641	0.018
1372471_at	BI283728	Transcribed locus, weakly similar to NP_703313.1 hypothetical protein [Plasmodium falciparum 3D7]	---	0.989	0.973	1.231	0.102	0.959	0.813	0.977	0.764
1384702_at	AI231062	Transcribed locus, weakly similar to NP_704188.1 hypothetical protein [Plasmodium falciparum 3D7]	---	1.509	0.199	0.742	0.110	1.614	0.202	0.901	0.021
1378494_at	BF394109	Transcribed locus, weakly similar to NP_731093.2 CG31483-PA [Drosophila melanogaster]	---	1.001	0.996	1.023	0.754	1.012	0.672	1.004	0.993
1397457_at	BE106796	Transcribed locus, weakly similar to NP_778159.1 hypothetical protein LOC211039 [Mus musculus]	---	1.231	0.784	1.020	0.230	1.783	0.108	1.205	0.159
1384414_at	AI044483	Transcribed locus, weakly similar to NP_778159.1 hypothetical protein LOC211039 [Mus musculus]	---	0.996	0.993	0.867	0.473	1.115	0.674	0.969	0.473
1378786_at	AI228437	Transcribed locus, weakly similar to NP_780607.2 hypothetical protein LOC109050 [Mus musculus]	---	1.011	0.876	0.719	0.029	1.335	0.091	1.505	0.855
1385749_at	BF392886	Transcribed locus, weakly similar to NP_795944.1 hypothetical protein LOC319641 [Mus musculus]	---	1.234	0.171	0.312	0.001	1.891	0.005	0.582	0.026
1390675_at	BE119856	Transcribed locus, weakly similar to NP_796192.1 hypothetical protein LOC320650 [Mus musculus]	---	1.015	0.908	1.003	0.984	1.125	0.153	1.201	0.875
1373316_at	BF409329	Transcribed locus, weakly similar to NP_851783.1 zinc finger protein 120 isoform 1 [Mus musculus]	---	0.679	0.198	0.938	0.862	1.137	0.465	1.063	0.806
1379731_at	BG666613	Transcribed locus, weakly similar to NP_862906.1 CD59b antigen [Mus musculus]	---	1.125	0.534	0.879	0.200	1.473	0.052	0.784	0.027
1373676_at	AI712626	Transcribed locus, weakly similar to NP_937890.1 SERTA domain containing 4 [Mus musculus]	---	0.504	0.042	0.477	0.024	0.442	0.053	0.404	0.013

1383036_at	AI137547	Transcribed locus, weakly similar to XP_125510.6 PREDICTED: hypothetical protein LOC73112 [Mus musculus]	---	1.541	0.067	1.202	0.224	2.052	0.027	1.662	0.167
1392007_at	AI044568	Transcribed locus, weakly similar to XP_214508.3 PREDICTED: similar to mKIAA0019 protein [Rattus norvegicus]	---	0.745	0.567	1.010	0.279	0.610	0.045	1.649	0.073
1398600_at	AW524565	Transcribed locus, weakly similar to XP_215059.1 PREDICTED: similar to erythroid differentiation-related factor [Rattus norvegicus]	---	1.022	0.694	0.617	0.012	0.827	0.164	0.460	0.099
1388577_at	BI274650	Transcribed locus, weakly similar to XP_215184.3 PREDICTED: similar to inner centromere protein [Rattus norvegicus]	---	1.139	0.631	1.693	0.142	0.747	0.361	1.252	0.978
1381065_at	BG379401	Transcribed locus, weakly similar to XP_218469.3 PREDICTED: similar to zinc finger protein 383 [Rattus norvegicus]	---	1.146	0.584	1.119	0.634	1.305	0.882	1.146	0.171
1393746_at	BE117730	Transcribed locus, weakly similar to XP_219319.3 PREDICTED: similar to deleted in malignant brain tumors 1 [Rattus norvegicus]	---	1.610	0.957	0.506	0.074	1.336	0.340	0.955	0.565
1395980_at	BF393243	Transcribed locus, weakly similar to XP_219541.3 PREDICTED: similar to RIKEN cDNA 5730596K20 [Rattus norvegicus]	---	0.879	0.451	0.610	0.616	1.593	0.183	0.916	0.608
1397579_x_at	BI294552	Transcribed locus, weakly similar to XP_220408.3 PREDICTED: similar to m-D/Bsp120I 1-1 [Rattus norvegicus]	---	0.912	0.906	0.318	0.017	1.002	0.997	0.265	0.011
1384468_at	BI283314	Transcribed locus, weakly similar to XP_224414.3 PREDICTED: similar to LRRGT00066 [Rattus norvegicus]	---	0.346	0.044	0.419	0.026	0.387	0.003	0.296	0.061
1396991_at	BF402387	Transcribed locus, weakly similar to XP_228401.3 PREDICTED: similar to LRRGT00152 [Rattus norvegicus]	---	1.143	0.798	1.070	0.306	0.940	0.560	0.982	0.139
1374318_at	BE328978	Transcribed locus, weakly similar to XP_229142.3 PREDICTED: similar to Ac1-163 [Rattus norvegicus]	---	0.700	0.127	0.791	0.066	0.776	0.232	0.813	0.881
1374037_at	BI288699	Transcribed locus, weakly similar to XP_234171.3 PREDICTED: similar to 1110008L16Rik protein [Rattus norvegicus]	---	0.593	0.003	0.716	0.045	0.640	0.036	0.784	0.012
1383187_a_at	AA944136	Transcribed locus, weakly similar to XP_234997.2 PREDICTED: similar to RIKEN cDNA E430026E19 [Rattus norvegicus]	---	1.993	0.036	1.142	0.683	1.752	0.036	0.939	0.512
1386855_at	AA944136	Transcribed locus, weakly similar to XP_234997.2 PREDICTED: similar to RIKEN cDNA E430026E19 [Rattus norvegicus]	---	1.369	0.130	0.896	0.786	1.330	0.019	1.124	0.258
1371878_at	BI294787	Transcribed locus, weakly similar to XP_315986.2 ENSANGP00000010844 [Anopheles gambiae str. PEST]	---	1.343	0.363	0.838	0.822	1.184	0.566	0.847	0.716
1397738_at	BF416112	Transcribed locus, weakly similar to XP_341211.2 PREDICTED: similar to Ac1591 [Rattus norvegicus]	---	0.686	0.344	0.504	0.118	0.990	0.965	0.609	0.192
1378811_at	BF402978	Transcribed locus, weakly similar to XP_341211.2 PREDICTED: similar to Ac1591 [Rattus norvegicus]	---	1.368	0.731	0.988	0.871	1.086	0.748	1.152	0.973
1393371_at	BG378781	Transcribed locus, weakly similar to XP_341767.2 PREDICTED: similar to zinc finger protein 52 [Rattus norvegicus]	---	1.258	0.811	1.200	0.427	0.990	0.975	1.110	0.827
1373919_at	AA943801	Transcribed locus, weakly similar to XP_342574.1 PREDICTED: similar to Csr1 [Rattus norvegicus]	---	1.016	0.271	0.502	0.012	0.882	0.332	0.513	0.010
1373079_at	BI296427	Transcribed locus, weakly similar to XP_342574.1 PREDICTED: similar to Csr1 [Rattus norvegicus]	---	0.645	0.359	0.382	0.000	0.718	0.053	0.349	0.000
1385322_at	AI602154	Transcribed locus, weakly similar to XP_342574.1 PREDICTED: similar to Csr1 [Rattus norvegicus]	---	1.135	0.574	0.899	0.560	1.084	0.371	1.008	0.952
1395277_at	BF396535	Transcribed locus, weakly similar to XP_342574.1 PREDICTED: similar to Csr1 [Rattus norvegicus]	---	1.151	0.610	1.072	0.761	1.662	0.110	1.045	0.337
1391569_at	BF406435	Transcribed locus, weakly similar to XP_342574.1 PREDICTED: similar to Csr1 [Rattus norvegicus]	---	0.889	0.630	0.987	0.986	1.263	0.058	0.971	0.868
1396095_at	BG673600	Transcribed locus, weakly similar to XP_342574.1 PREDICTED: similar to Csr1 [Rattus norvegicus]	---	1.169	0.796	2.250	0.010	1.737	0.114	2.068	0.009
1375593_at	BF401589	Transcribed locus, weakly similar to XP_342574.1 PREDICTED: similar to Csr1 [Rattus norvegicus]	---	0.983	0.960	1.007	0.792	0.900	0.519	1.056	0.734
1391952_at	BE110628	Transcribed locus, weakly similar to XP_342574.1 PREDICTED: similar to Csr1 [Rattus norvegicus]	---	1.772	0.981	0.517	0.004	1.681	0.997	0.652	0.026
1390947_at	AA891255	Transcribed locus, weakly similar to XP_343062.2 PREDICTED: similar to RIKEN cDNA D930036F22 gene [Rattus norvegicus]	---	0.918	0.683	1.230	0.060	1.286	0.133	1.465	0.024
1392447_at	AI073058	Transcribed locus, weakly similar to XP_415605.1 PREDICTED: similar to hypothetical protein FLJ20531 [Gallus gallus]	---	1.085	0.911	1.261	0.513	1.630	0.103	1.384	0.999
1394576_at	AA900572	Transcribed locus, weakly similar to XP_417491.1 PREDICTED: similar to Serine/threonine phosphatase 4 regulatory subunit 1 [Gallus gallus]	---	0.500	0.003	0.619	0.018	0.508	0.017	0.606	0.033
1389083_at	AI411510	Transcribed locus, weakly similar to XP_421321.1 PREDICTED: similar to hypothetical protein FLJ20707 isoform 1 [Gallus gallus]	---	1.072	0.459	0.775	0.144	1.305	0.378	0.914	0.303
1375856_at	AI102258	Transcribed locus, weakly similar to XP_426788.1 PREDICTED: similar to gene 11-1 protein precursor, partial [Gallus gallus]	---	0.265	0.040	0.094	0.001	0.368	0.001	0.186	0.020
1376665_at	BG670208	Transcribed locus, weakly similar to XP_472448.1 OSJNBb0108J11.9 [Oryza sativa (japonica cultivar-group)]	---	2.164	0.026	0.807	0.049	1.235	0.139	1.008	0.236
1380006_at	AW921301	Transcribed locus, weakly similar to XP_486128.1 PREDICTED: hypothetical protein isoform 1 [Mus musculus]	---	0.920	0.729	1.065	0.362	1.105	0.270	1.129	0.757
1389650_at	BI295153	Transcribed locus, weakly similar to XP_512729.1 PREDICTED: hypothetical protein XP_512729 [Pan troglodytes]	---	0.311	0.017	0.415	0.096	0.441	0.143	0.597	0.057
1381061_at	AI058949	Transcribed locus, weakly similar to XP_514364.1 PREDICTED: similar to KIAA1448 protein [Pan troglodytes]	---	1.398	0.052	2.069	0.249	1.090	0.496	0.730	0.310
1393501_at	AI043579	Transcribed locus, weakly similar to XP_517024.1 PREDICTED: similar to putative tumor suppressor [Pan troglodytes]	---	1.123	0.800	0.919	0.210	0.962	0.960	1.099	0.653
1379277_at	AI575341	Transcribed locus, weakly similar to XP_518782.1 PREDICTED: utrophin [Pan troglodytes]	---	0.884	0.654	0.420	0.000	0.742	0.025	0.377	0.000
1384621_at	AA924327	Transcribed locus, weakly similar to XP_519783.1 PREDICTED: similar to hypothetical protein MGC34646 [Pan troglodytes]	---	0.764	0.275	0.369	0.012	0.764	0.587	0.399	0.011
1384232_at	AI709768	Transcribed locus, weakly similar to XP_522550.1 PREDICTED: nuclear receptor co-repressor 2 [Pan troglodytes]	---	2.232	0.011	0.677	0.014	1.465	0.825	0.639	0.042
1384401_at	AI059296	Transcribed locus, weakly similar to XP_524118.1 PREDICTED: similar to zinc finger protein 433 [Pan troglodytes]	---	1.341	0.164	0.853	0.164	1.313	0.034	0.991	0.725

1386633_at	BF549535	Transcribed locus, weakly similar to XP_524118.1 PREDICTED: similar to zinc finger protein 433 [Pan troglodytes]	---	0.907	0.642	0.971	0.228	0.820	0.292	0.770	0.076
1374474_at	BE099085	Transcribed locus, weakly similar to XP_524153.1 PREDICTED: similar to ribosomal protein L18a; 60S ribosomal protein L18a [Pan troglodytes]	---	0.855	0.665	2.593	0.023	0.795	0.354	2.559	0.039
1379217_at	AW141971	Transcribed locus, weakly similar to XP_525946.1 PREDICTED: similar to activin A type I receptor precursor; hydroxyalkyl-protein kinase; activin A receptor, type II-like kinase 2 [Pan troglodytes]	---	1.199	0.133	0.839	0.102	1.051	0.104	0.940	0.144
1392339_at	BF406130	Transcribed locus, weakly similar to XP_526043.1 PREDICTED: phenylalanine-tRNA synthetase-like, beta subunit [Pan troglodytes]	---	0.945	0.874	0.898	0.471	0.999	0.973	1.281	0.567
1383114_at	BI296782	Transcribed locus, weakly similar to XP_529413.1 PREDICTED: hypothetical protein XP_529413 [Pan troglodytes]	---	1.827	0.006	0.930	0.624	1.725	0.037	0.841	0.259
1388541_at	BE116383	Transcribed locus, weakly similar to XP_529532.1 PREDICTED: hypothetical protein XP_529532 [Pan troglodytes]	---	0.499	0.026	0.766	0.045	0.573	0.028	0.798	0.066
1376786_a_at	BF397709	Transcribed locus, weakly similar to XP_529728.1 PREDICTED: hypothetical protein XP_529728 [Pan troglodytes]	---	0.748	0.140	0.734	0.008	0.680	0.099	0.626	0.011
1390468_at	BF397709	Transcribed locus, weakly similar to XP_529728.1 PREDICTED: hypothetical protein XP_529728 [Pan troglodytes]	---	0.930	0.674	0.509	0.084	0.769	0.346	0.471	0.040
1377492_at	BM387395	Transcribed locus, weakly similar to XP_529855.1 PREDICTED: hypothetical protein XP_529855 [Pan troglodytes]	---	0.285	0.037	0.211	0.002	0.254	0.034	0.402	0.023
1384287_at	BI278552	Transcribed locus, weakly similar to XP_529954.1 PREDICTED: hypothetical protein XP_529954 [Pan troglodytes]	---	1.989	0.021	1.329	0.097	2.238	0.001	1.289	0.311
1383744_at	AI146250	Transcribed locus, weakly similar to XP_537771.2 PREDICTED: similar to CG6734-PA [Canis familiaris]	---	0.604	0.118	0.299	0.000	1.079	0.884	0.610	0.093
1389419_at	BI296079	Transcribed locus, weakly similar to XP_541379.2 PREDICTED: similar to zinc finger protein 91 (HPF7, HTF10) [Canis familiaris]	---	1.940	0.048	2.378	0.014	1.852	0.050	1.999	0.034
1393543_at	BF399884	Transcribed locus, weakly similar to XP_541674.2 PREDICTED: similar to zinc finger protein 91 (HPF7, HTF10) isoform 1 [Canis familiaris]	---	0.539	0.025	0.406	0.041	0.565	0.044	0.589	0.010
1380026_at	BF405898	Transcribed locus, weakly similar to XP_573254.1 PREDICTED: similar to putative RNA binding protein 1 [Rattus norvegicus]	---	1.019	0.495	1.060	0.078	1.061	0.857	1.038	0.155
1390270_at	BF400616	Transcribed locus, weakly similar to XP_573661.1 PREDICTED: similar to LRRGT00197 [Rattus norvegicus]	---	1.043	0.656	0.665	0.078	1.174	0.580	0.863	0.026
1396526_at	BF410339	Transcribed locus, weakly similar to XP_573899.1 PREDICTED: similar to Ab1-351 [Rattus norvegicus]	---	1.456	0.430	1.364	0.910	1.175	0.671	1.598	0.904
1379986_at	BM390668	Transcribed locus, weakly similar to XP_574218.1 PREDICTED: similar to LRRGT00194 [Rattus norvegicus]	---	0.899	0.504	0.959	0.479	1.006	0.817	0.999	0.611
1379881_at	BI304043	Transcribed locus, weakly similar to XP_574512.1 PREDICTED: similar to LRRG00121 [Rattus norvegicus]	---	0.647	0.026	0.689	0.011	0.821	0.413	0.846	0.444
1382911_at	BE105150	Transcribed locus, weakly similar to XP_574807.1 PREDICTED: similar to HORMA domain containing 1 [Rattus norvegicus]	---	1.202	0.694	1.254	0.207	1.509	0.039	1.246	0.271
1384496_at	BI274749	Transcribed locus, weakly similar to XP_574871.1 PREDICTED: similar to LRRGT00036 [Rattus norvegicus]	---	0.716	0.457	0.717	0.117	0.997	0.992	0.961	0.068
1393739_at	BE108371	Transcribed locus, weakly similar to XP_574902.1 PREDICTED: similar to LRRGT00194 [Rattus norvegicus]	---	1.144	0.371	0.794	0.029	0.829	0.379	0.706	0.045
1385135_at	BE118923	Transcribed locus, weakly similar to XP_574917.1 PREDICTED: similar to LRRGT00194 [Rattus norvegicus]	---	0.997	0.462	0.987	0.341	0.917	0.728	0.880	0.323
1378890_at	BF408090	Transcribed locus, weakly similar to XP_574992.1 PREDICTED: hypothetical protein XP_574992 [Rattus norvegicus]	---	1.030	0.715	1.362	0.035	1.025	0.905	0.975	0.413
1398183_at	BE101139	Transcribed locus, weakly similar to XP_575026.1 PREDICTED: similar to LRRGT00171 [Rattus norvegicus]	---	1.297	0.431	0.802	0.040	0.901	0.656	0.860	0.091
1378074_at	AI175045	Transcribed locus, weakly similar to XP_575132.1 PREDICTED: similar to LRRGT00012 [Rattus norvegicus]	---	0.995	0.895	1.094	0.182	0.814	0.465	1.817	0.141
1395500_at	BE119104	Transcribed locus, weakly similar to XP_575411.1 PREDICTED: similar to Ac1262 [Rattus norvegicus]	---	0.824	0.099	0.856	0.519	0.759	0.172	1.051	0.799
1385303_at	BI301855	Transcribed locus, weakly similar to XP_575785.1 PREDICTED: similar to LRRGT00194 [Rattus norvegicus]	---	0.939	0.947	0.854	0.411	1.063	0.781	1.090	0.896
1379124_at	BE103417	Transcribed locus, weakly similar to XP_576175.1 PREDICTED: similar to Sfrs7 protein [Rattus norvegicus]	---	1.062	0.920	0.968	0.926	1.093	0.878	0.742	0.485
1394619_at	AI598752	Transcribed locus, weakly similar to XP_576199.1 PREDICTED: similar to envelope [Rattus norvegicus]	---	1.194	0.692	0.685	0.015	1.151	0.491	0.627	0.040
1385172_at	BF389065	Transcribed locus, weakly similar to XP_576359.1 PREDICTED: similar to LRRGT00073 [Rattus norvegicus]	---	1.006	0.708	0.886	0.496	1.112	0.798	0.903	0.266
1394553_at	AI007661	Transcribed locus, weakly similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	0.519	0.017	0.680	0.061	0.574	0.000	0.605	0.000
1395509_at	BG666117	Transcribed locus, weakly similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	0.559	0.175	0.279	0.047	0.393	0.062	0.364	0.003
1394450_at	AI228600	Transcribed locus, weakly similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	0.554	0.187	0.204	0.016	0.630	0.016	0.552	0.098
1378404_at	AW435040	Transcribed locus, weakly similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	1.014	0.238	0.863	0.021	0.695	0.065	1.335	0.126
1389606_at	BI303298	Transcribed locus, weakly similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	0.473	0.321	0.640	0.001	0.589	0.033	0.657	0.018
1397900_at	BG375046	Transcribed locus, weakly similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	0.909	0.779	1.024	0.684	1.093	0.792	1.052	0.696
1372694_at	AI407148	Transcribed locus, weakly similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	0.990	0.940	1.131	0.482	1.062	0.758	1.375	0.158
1390159_at	AA819332	Transcribed locus, weakly similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	1.327	0.984	0.648	0.064	1.519	0.202	1.142	0.895

1378473_at	BE107166	Transcribed locus, weakly similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]	---	0.907	0.989	0.698	0.203	0.908	0.755	0.969	0.656
1373053_at	AI169620	Transcribed locus, weakly similar to XP_576559.1 PREDICTED: similar to Ormdl1 protein [Rattus norvegicus]	---	0.470	0.010	0.924	0.800	0.464	0.014	0.744	0.735
1377774_at	AI029275	Transcribed locus, weakly similar to XP_576559.1 PREDICTED: similar to Ormdl1 protein [Rattus norvegicus]	---	1.070	0.250	0.884	0.289	0.724	0.217	0.884	0.182
1379512_at	BF396579	Transcribed locus, weakly similar to XP_576934.1 PREDICTED: similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [Rattus norvegicus]	---	1.013	0.995	0.968	0.812	1.034	0.860	1.005	0.578
1397755_at	AI575649	Transcribed locus, weakly similar to XP_577160.1 PREDICTED: similar to LRRGT00088 [Rattus norvegicus]	---	1.243	0.811	0.649	0.260	0.959	0.623	1.044	0.774
1385454_at	AW526025	Transcribed locus, weakly similar to XP_577160.1 PREDICTED: similar to LRRGT00088 [Rattus norvegicus]	---	1.211	0.892	0.952	0.819	1.014	0.830	0.994	0.971
1384691_at	BE113194	Transcribed locus, weakly similar to XP_577161.1 PREDICTED: similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [Rattus norvegicus]	---	1.138	0.839	1.139	0.072	1.197	0.545	0.899	0.186
1397570_at	BF410161	Transcribed locus, weakly similar to XP_577194.1 PREDICTED: similar to CG13990-PA [Rattus norvegicus]	---	2.002	0.930	1.597	0.533	1.324	0.456	4.656	0.111
1385267_at	AW433616	Transcribed locus, weakly similar to XP_577796.1 PREDICTED: similar to LRRGT00049 [Rattus norvegicus]	---	0.976	0.610	0.647	0.107	1.031	0.906	0.903	0.353
1395093_at	AI145025	Transcribed locus, weakly similar to XP_578830.1 PREDICTED: similar to LRRGT00191 [Rattus norvegicus]	---	0.649	0.330	1.128	0.109	1.354	0.906	1.324	0.038
1381115_at	AW536039	Transcribed locus, weakly similar to XP_579465.1 PREDICTED: DNA binding protein N5 [Rattus norvegicus]	---	1.011	0.835	0.951	0.375	1.164	0.398	0.951	0.651
1385347_at	BE103484	Transcribed locus, weakly similar to XP_579981.1 PREDICTED: hypothetical protein XP_579981 [Rattus norvegicus]	---	0.778	0.319	0.957	0.177	0.814	0.032	0.920	0.177
1389369_at	BF289017	Transcribed locus, weakly similar to XP_579981.1 PREDICTED: hypothetical protein XP_579981 [Rattus norvegicus]	---	1.049	0.563	0.804	0.024	1.108	0.185	0.939	0.061
1382278_at	BI278180	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	7.560	0.002	13.014	0.002	6.205	0.006	8.721	0.012
1372796_at	AA894188	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.742	0.006	1.629	0.013	1.265	0.954	1.478	0.023
1372121_at	BF284408	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.637	0.014	0.256	0.001	0.741	0.078	0.325	0.007
1381714_at	BE105488	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.973	0.035	1.190	0.522	1.367	0.115	1.321	0.811
1392903_at	BG665185	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.800	0.045	0.739	0.003	0.946	0.251	0.771	0.036
1377462_at	BE111349	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.657	0.073	1.122	0.478	0.543	0.028	1.126	0.991
1383423_at	BI295136	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.377	0.077	0.278	0.006	0.499	0.053	0.387	0.006
1397706_at	BF388794	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	3.445	0.085	0.553	0.089	4.491	0.001	1.633	0.997
1395240_at	BG665321	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.354	0.153	1.001	0.846	1.000	0.163	1.001	0.991
1390504_at	AW524470	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.849	0.190	0.984	0.949	0.731	0.095	1.069	0.790
1379996_at	AI411753	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.704	0.191	0.462	0.001	0.520	0.232	0.584	0.002
1382820_at	AI176342	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.632	0.279	1.559	0.267	0.957	0.864	1.444	0.223
1371595_at	BM384301	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.429	0.362	16.953	0.001	1.286	0.861	9.407	0.004
1392475_at	BE104169	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.230	0.368	1.715	0.006	1.127	0.916	1.376	0.004
1397164_at	AI175779	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.437	0.401	3.751	0.001	1.871	0.080	2.679	0.005
1382510_at	BE105050	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.873	0.424	0.752	0.066	0.670	0.016	0.648	0.121
1377237_at	AI137274	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.121	0.451	0.822	0.058	1.300	0.627	0.584	0.011
1395327_at	AW522341	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.641	0.521	1.758	0.105	1.159	0.161	1.448	0.059
1390276_at	BI296669	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	1.176	0.536	0.898	0.975	1.312	0.007	1.093	0.457
1391553_at	AA956757	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.753	0.553	0.611	0.102	1.001	0.995	0.681	0.021
1371506_at	AA891207	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.822	0.643	0.819	0.236	1.175	0.392	0.981	0.818

1378591_at	AI556452	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	---	0.996	0.951	2.983	0.001	0.599	0.051	2.274	0.003
1378508_at	BE108221	Transcribed locus, weakly similar to XP_580237.1 PREDICTED: hypothetical protein XP_580237 [Rattus norvegicus]	---	2.454	0.048	2.375	0.023	2.503	0.004	1.436	0.018
1373984_at	AA850715	Transcribed locus, weakly similar to XP_849895.1 PREDICTED: similar to Argininosuccinate synthase (Citrulline--aspartate ligase) isoform 3 [Canis familiaris]	---	0.444	0.388	0.598	0.037	0.375	0.012	0.538	0.010
1372733_at	BM391852	Transcribed locus, weakly similar to XP_850062.1 PREDICTED: similar to conserved nuclear protein Nhn1 isoform 3 [Canis familiaris]	---	0.965	0.279	0.981	0.214	0.635	0.236	0.939	0.386
1390300_at	BM383635	Transcribed locus, weakly similar to XP_851979.1 PREDICTED: similar to LINE-1 reverse transcriptase homolog [Canis familiaris]	---	1.198	0.787	0.962	0.166	1.018	0.544	0.847	0.223
1375707_at	AA817993	Transcribed locus, weakly similar to XP_855499.1 PREDICTED: similar to Zinc finger X-linked protein ZXDB [Canis familiaris]	---	1.063	0.890	1.009	0.255	1.360	0.107	1.223	0.128
1383255_at	BE116202	Transcribed locus, weakly similar to XP_862893.1 PREDICTED: similar to LINE-1 reverse transcriptase homolog isoform 2 [Canis familiaris]	---	2.392	0.002	1.129	0.053	4.268	0.002	1.454	0.027
1374845_at	AI176367	Transcribed locus, weakly similar to XP_864243.1 PREDICTED: similar to chaperonin containing TCP1, subunit 3 isoform c isoform 2 [Canis familiaris]	---	0.942	0.639	3.746	0.001	1.357	0.300	1.326	0.180
1394724_at	BE109084	transcription elongation factor A (SII) 1	Tcea1	1.324	0.038	1.650	0.050	1.412	0.000	1.586	0.138
1367485_at	BM388871	transcription elongation factor A (SII) 1 /// similar to transcription elongation factor IIS - mouse	Tcea1 /// LOC498453	1.379	0.100	1.356	0.047	1.721	0.049	1.982	0.014
1388611_at	AW252817	transcription elongation factor A (SII), 3	Tcea3	0.996	0.864	0.753	0.127	1.064	0.047	0.983	0.190
1391212_at	BF418812	transcription elongation factor A (SII)-like 1	Tceal1	0.284	0.006	0.181	0.015	0.465	0.004	0.364	0.002
1375521_at	AI230334	transcription elongation factor A (SII)-like 8	Tceal8	0.401	0.394	0.489	0.039	0.539	0.134	0.552	0.013
1398794_at	NM_022593	transcription elongation factor B (SIII), polypeptide 1	Tceb1	1.209	0.693	1.167	0.752	1.073	0.615	1.186	0.640
1398837_at	NM_031129	transcription elongation factor B (SIII), polypeptide 2	Tceb2	1.026	0.586	1.426	0.045	1.033	0.152	1.288	0.052
1389778_a_at	AI233115	transcription elongation factor B (SIII), polypeptide 3	Tceb3	0.954	0.171	1.416	0.034	1.022	0.036	1.423	0.502
1368997_at	NM_017103	transcription elongation factor B (SIII), polypeptide 3	Tceb3	0.830	0.270	0.786	0.427	0.641	0.067	0.789	0.023
1371787_at	AI231686	Transcription elongation factor B (SIII), polypeptide 3	Tceb3	1.005	0.989	1.126	0.216	0.907	0.832	1.000	0.152
1372151_at	AI317851	transcription elongation regulator 1 (CA150) (predicted)	Tcerg1_predicted	1.511	0.097	2.300	0.002	1.364	0.016	1.756	0.005
1390871_at	BF286230	transcription elongation regulator 1 (CA150) (predicted)	Tcerg1_predicted	1.020	0.627	1.242	0.079	0.858	0.706	0.799	0.159
1369148_at	NM_012669	transcription factor 1	Tcf1	1.275	0.372	2.168	0.008	1.589	0.124	2.116	0.072
1389555_at	BM387190	transcription factor 19	Tcf19	0.617	0.040	0.163	0.039	0.756	0.022	0.609	0.063
1390817_at	BF394639	transcription factor 20 (mapped)	Tcf20_mapped	1.110	0.546	0.458	0.011	0.636	0.385	0.634	0.009
1390390_at	BM386814	transcription factor 20 (mapped)	Tcf20_mapped	1.209	0.829	1.431	0.014	0.458	0.143	1.255	0.037
1384640_at	AA997287	Transcription factor 20 (mapped)	Tcf20_mapped	1.127	0.929	1.370	0.111	1.236	0.998	1.540	0.171
1388782_at	BE113336	transcription factor 21	Tcf21	0.990	0.949	0.999	0.994	0.994	0.951	0.999	0.987
1391992_at	AI639517	Transcription factor 4	Tcf4	0.319	0.048	0.627	0.046	0.398	0.028	0.458	0.023
1396157_at	BF548958	Transcription factor 4	Tcf4	0.798	0.175	0.973	0.813	0.717	0.177	0.991	0.934
1368842_at	BG377130	transcription factor 4	Tcf4	0.909	0.391	0.316	0.000	0.555	0.024	0.466	0.005
1397286_at	AW435211	Transcription factor 4	Tcf4	1.472	0.903	1.284	0.658	1.044	0.268	1.192	0.985
1368841_at	NM_053369	transcription factor 4	Tcf4	1.000	0.999	0.620	0.027	1.352	0.085	0.495	0.028
1376197_at	AW251860	transcription factor 7, T-cell specific (predicted)	Tcf7_predicted	1.021	0.048	0.683	0.960	1.435	0.005	0.664	0.341
1370965_at	BG381660	transcription factor 8	Tcf8	3.660	0.017	6.815	0.000	6.696	0.015	6.057	0.000
1367941_at	NM_031326	transcription factor A, mitochondrial	Tfam	0.649	0.120	1.179	0.022	0.655	0.002	1.063	0.044
1392545_at	AA999089	transcription factor AP-2 beta (predicted)	Tcfap2b_predicted	0.938	0.510	2.409	0.162	0.737	0.830	1.647	0.061
1386435_at	AI101186	transcription factor AP4 (predicted)	Tcfap4_predicted	0.943	0.417	1.621	0.059	0.781	0.059	1.306	0.009
1379949_at	AI010265	transcription factor B1, mitochondrial	Tfb1m	0.766	0.295	1.510	0.699	0.653	0.148	1.085	0.413
1383171_at	BG373674	transcription factor B2, mitochondrial	Tfb2m	0.362	0.013	0.456	0.018	0.656	0.204	0.740	0.043
1378218_at	AW527419	transcription factor CP2 (predicted)	Tcfcp2_predicted	1.567	0.277	2.238	0.069	1.159	0.144	1.342	0.128
1379914_at	AI716050	transcription factor CP2-like 2	Tcfcp2l2	1.562	0.851	1.499	0.211	1.124	0.850	0.998	0.852
1393545_at	AI043906	transcription factor CP2-like 2	Tcfcp2l2	0.821	0.998	3.019	0.000	0.766	0.915	1.293	0.016
1388967_at	AI012945	transcription factor E3 (predicted)	Tcfe3_predicted	1.614	0.051	1.668	0.020	1.565	0.035	1.734	0.007
1373327_at	BE112887	transcription factor EB	Tcfeb	1.056	0.494	1.093	0.965	1.001	0.989	1.163	0.151
1385125_at	BF397140	transcription factor myocardin	Myocd	1.465	0.608	1.083	0.149	1.485	0.334	0.857	0.126
1374205_at	BI284455	transcription factor Pur-beta	pur-beta	1.349	0.080	0.839	0.337	0.876	0.791	1.082	0.533
1393521_at	AI232280	Transcription termination factor, RNA polymerase II (predicted)	Ttf2_predicted	1.525	0.096	1.212	0.337	1.137	0.100	1.017	0.197
1373238_at	AI234844	transcriptional adaptor 1 (HFI1 homolog, yeast) like	Tada1l	1.157	0.113	2.723	0.009	1.930	0.081	2.135	0.009
1397852_at	H32108	transcriptional adaptor 1 (HFI1 homolog, yeast) like	Tada1l	1.022	0.898	1.503	0.237	1.006	0.995	0.999	0.996
1378617_at	BM390846	transcriptional regulating factor 1 (predicted)	Trerf1_predicted	1.246	0.429	1.240	0.496	1.010	0.600	1.041	0.399
1379182_at	BE105382	Transcriptional regulating factor 1 (predicted)	Trerf1_predicted	0.783	0.494	0.360	0.097	1.326	0.287	0.405	0.093
1391498_at	AI072877	transcriptional regulator, SIN3A (yeast) (predicted)	Sin3a_predicted	0.582	0.062	1.049	0.084	0.665	0.061	1.036	0.221
1375677_at	BI275222	transducer of ERBB2, 2	Tob2	0.888	0.968	0.771	0.090	0.919	0.422	1.057	0.911
1368132_at	NM_133317	transducer of ErbB-2.1	Tob1	0.559	0.014	0.698	0.040	0.355	0.045	0.637	0.385

1379469_at	AA955760	transducin (beta)-like 1 X-linked (predicted)	Tbl1x_predicted	1.012	0.361	4.575	0.031	1.006	0.935	3.821	0.048
1393491_at	BF398496	transducin (beta)-like 1 X-linked (predicted)	Tbl1x_predicted	0.990	0.970	0.996	0.954	0.999	0.996	1.001	0.992
1379309_at	AI030742	Transducin (beta)-like 1X-linked receptor 1 (predicted)	Tbl1xr1_predicted	3.265	0.041	1.813	0.068	1.001	0.038	1.655	0.058
1386070_at	AA859701	Transducin (beta)-like 1X-linked receptor 1 (predicted)	Tbl1xr1_predicted	2.469	0.058	1.181	0.102	0.991	0.905	1.067	0.201
1372661_at	AI406314	transducin (beta)-like 3	Tbl3	0.758	0.032	1.063	0.975	0.549	0.065	1.624	0.973
1374425_at	BG380534	transducin-like enhancer of split 1, homolog of Drosophila E(spl) (predicted)	Tle1_predicted	1.061	0.625	0.505	0.052	1.378	0.703	0.338	0.026
1387169_at	NM_053400	transducin-like enhancer of split 3, E(spl) homolog (Drosophila)	Tle3	3.573	0.001	2.665	0.001	2.224	0.019	2.286	0.001
1388750_at	BF417032	transferrin receptor	Tfrc	0.533	0.133	2.423	0.000	0.662	0.047	2.555	0.002
1371113_a_at	M58040	transferrin receptor	Tfrc	0.389	0.201	5.692	0.000	0.415	0.208	4.251	0.000
1374788_at	AI235252	transformation related protein 53 binding protein 1 (predicted)	Trp53bp1_predicted	1.063	0.687	1.037	0.250	1.227	0.574	1.121	0.274
1384140_at	BF288836	Transformation related protein 53 binding protein 1 (predicted)	Trp53bp1_predicted	0.945	0.739	1.005	0.976	0.906	0.729	0.877	0.938
1383981_at	BE102377	transformation related protein 53 binding protein 2 (predicted)	Trp53bp2_predicted	1.477	0.055	1.260	0.454	1.487	0.451	0.763	0.747
1369108_at	NM_019221	transformation related protein 63	Trp63	1.008	0.672	0.796	0.138	1.226	0.452	0.858	0.857
1384427_at	BI296301	transformed mouse 3T3 cell double minute 2 homolog (mouse) (predicted)	Mdm2_predicted	2.589	0.033	8.044	0.002	1.480	0.036	5.358	0.006
1383485_at	BF548539	transformed mouse 3T3 cell double minute 2 homolog (mouse) (predicted)	Mdm2_predicted	1.007	0.884	1.658	0.389	1.022	0.917	2.137	0.107
1382417_at	AI236886	transformed mouse 3T3 cell double minute 4	Mdm4	1.501	0.002	2.552	0.021	1.053	0.978	1.538	0.146
1377973_at	BF402062	Transformed mouse 3T3 cell double minute 4	Mdm4	0.992	0.879	1.167	0.633	1.106	0.762	1.884	0.223
1381449_s_at	BG670310	transforming growth factor alpha	Tgfa	0.725	0.234	0.516	0.371	0.478	0.012	0.613	0.021
1378081_at	BI285065	Transforming growth factor beta 1 induced transcript 4	Tgfb1i4	0.279	0.004	0.778	0.040	0.093	0.001	0.642	0.033
1398759_at	NM_013043	transforming growth factor beta 1 induced transcript 4	Tgfb1i4	1.074	0.230	0.928	0.136	0.966	0.623	0.879	0.287
1371509_at	BG666773	transforming growth factor beta regulated gene 1	Tbrg1	1.207	0.350	1.690	0.007	1.232	0.125	2.081	0.007
1374577_at	AW254561	transforming growth factor beta regulated gene 4	Tbrg4	0.553	0.189	1.812	0.014	0.447	0.086	1.397	0.052
1387172_a_at	NM_031131	transforming growth factor, beta 2	Tgfb2	0.721	0.004	0.251	0.009	0.667	0.005	0.450	0.016
1378963_at	AA963004	Transforming growth factor, beta 2	Tgfb2	0.597	0.027	0.329	0.002	0.607	0.160	0.296	0.011
1376425_at	BF420705	Transforming growth factor, beta 2	Tgfb2	0.924	0.128	0.164	0.000	0.759	0.126	0.161	0.006
1392382_at	BE117736	Transforming growth factor, beta 2	Tgfb2	0.498	0.409	0.366	0.016	1.093	0.765	0.496	0.024
1367859_at	NM_013174	transforming growth factor, beta 3	Tgfb3	0.955	0.728	0.994	0.929	0.882	0.387	0.999	0.923
1371913_at	BG379319	transforming growth factor, beta induced	Tgfbi	1.523	0.140	1.140	0.009	1.004	0.974	1.084	0.440
1376636_at	BE111972	transforming growth factor, beta receptor 1	Tgfbr1	0.903	0.196	1.060	0.199	0.688	0.147	1.016	0.073
1369504_at	NM_012775	transforming growth factor, beta receptor 1	Tgfbr1	1.001	0.861	1.093	0.131	1.001	0.955	1.008	0.970
1390149_at	BI286164	transforming, acidic coiled-coil containing protein 2	Tacc2	1.201	0.117	2.162	0.013	1.305	0.026	2.854	0.009
1388335_at	BI285865	transgelin 2	Tagln2	1.152	0.245	1.217	0.027	1.153	0.087	1.138	0.020
1387529_a_at	NM_031676	transgelin 3	Tagln3	0.258	0.043	0.051	0.000	0.253	0.034	0.170	0.000
1389965_at	AA799818	trans-golgi network protein 2	Tgoln2	0.772	0.215	0.512	0.003	0.833	0.456	0.575	0.004
1371028_at	AW917192	trans-golgi network protein 2	Tgoln2	1.026	0.894	0.273	0.006	0.990	0.978	0.340	0.008
1370411_at	AF061266	transient receptor potential cation channel, subfamily C, member 1	Trpc1	1.149	0.806	0.361	0.000	1.121	0.229	0.425	0.004
1371584_at	BM390843	transient receptor potential cation channel, subfamily C, member 4 associated protein	Trpc4ap	1.028	0.877	1.276	0.028	1.061	0.532	1.588	0.074
1398279_at	NM_053787	transient receptor potential cation channel, subfamily V, member 5	Trpv5	1.475	0.519	1.021	0.210	1.407	0.352	0.728	0.031
1398355_at	AI232142	Transient receptor potential-related protein, ChaK	Trpm7	1.135	0.419	1.346	0.088	1.182	0.216	1.119	0.070
1369059_at	NM_053705	transient receptor potential-related protein, ChaK	Trpm7	0.998	0.990	0.930	0.269	0.950	0.498	0.572	0.332
1386859_at	NM_022592	transketolase	Tkt	0.557	0.251	1.555	0.005	0.438	0.002	1.271	0.055
1367728_at	NM_021762	translin	Tsn	1.220	0.570	1.061	0.966	1.982	0.805	0.998	0.656
1387653_at	BI283853	translin-associated factor X	Tsnax	0.800	0.040	0.667	0.009	0.867	0.256	0.872	0.144
1398823_at	AF262357	translin-associated factor X	Tsnax	0.843	0.522	0.526	0.123	0.801	0.434	0.595	0.130
1370366_at	AF150091	translocase of inner mitochondrial membrane 10 homolog (yeast)	Timm10	0.720	0.722	2.940	0.006	0.572	0.170	3.141	0.002
1398868_at	AI408157	translocase of inner mitochondrial membrane 13 homolog (yeast)	Timm13	0.824	0.836	2.320	0.018	0.582	0.017	1.969	0.012
1375565_at	BF420723	translocase of inner mitochondrial membrane 22 homolog (yeast)	Timm22	0.539	0.014	0.873	0.351	0.564	0.012	0.882	0.364
1370353_at	AF223951	translocase of inner mitochondrial membrane 22 homolog (yeast)	Timm22	0.585	0.042	1.089	0.771	0.449	0.003	0.827	0.173
1398763_at	NM_019352	translocase of inner mitochondrial membrane 23 homolog (yeast) /// similar to Translocase of inner mitochondrial membrane 23 homolog (predicted)	Timm23 /// RGD1559672_predicted	0.993	0.863	1.488	0.026	1.208	0.354	1.431	0.019
1368400_at	NM_053370	translocase of inner mitochondrial membrane 8 homolog a (yeast)	Timm8a	1.229	0.041	1.700	0.125	0.885	0.982	1.342	0.027
1390237_at	BF558361	translocase of inner mitochondrial membrane 8 homolog a (yeast)	Timm8a	0.681	0.277	1.973	0.001	0.921	0.174	2.584	0.005
1367808_at	NM_022541	translocase of inner mitochondrial membrane 8 homolog b (yeast)	Timm8b	0.597	0.355	0.777	0.056	0.567	0.003	0.709	0.050
1388136_at	BF282660	translocase of inner mitochondrial membrane 9 homolog (yeast)	Timm9	0.361	0.032	0.800	0.306	0.257	0.004	0.797	0.159
1398870_at	AI177295	translocase of outer mitochondrial membrane 20 homolog (yeast)	Tomm20	0.735	0.077	1.162	0.050	0.673	0.009	1.011	0.181
1370785_s_at	D63411	translocase of outer mitochondrial membrane 20 homolog (yeast)	Tomm20	0.571	0.273	1.061	0.559	0.536	0.027	0.926	0.517
1367473_at	BI284237	translocase of outer mitochondrial membrane 22 homolog (yeast)	Tomm22	0.608	0.292	0.784	0.022	0.891	0.647	0.876	0.029
1389471_at	AI412736	Translocase of outer mitochondrial membrane 34 (predicted)	Tomm34_predicted	0.513	0.406	0.586	0.017	0.748	0.158	0.665	0.007
1379186_at	BF414701	translocase of outer mitochondrial membrane 70 homolog A (yeast)	Tomm70a	0.716	0.197	2.233	0.001	0.640	0.033	2.120	0.001
1371695_at	AI230732	translocated promoter region	Tpr	0.899	0.559	1.044	0.323	1.137	0.880	1.078	0.573
1382939_at	BE118639	translocated promoter region	Tpr	0.939	0.882	1.461	0.100	0.849	0.529	1.204	0.067

1394814_at	BF398127	translocated promoter region	Tpr	0.927	0.896	1.553	0.211	0.724	0.352	1.056	0.793
1371688_at	AI178493	translocation associated membrane protein 1	Tram1	0.454	0.101	0.373	0.000	0.594	0.044	0.477	0.001
1390077_at	AA956421	Translocation associated membrane protein 1	Tram1	0.412	0.242	0.839	0.107	0.466	0.088	0.634	0.075
1374188_at	AI103194	translocation protein 1	Tloc1	0.730	0.019	0.604	0.051	0.684	0.003	0.596	0.092
1398970_at	BI303004	translocation protein 1	Tloc1	0.840	0.151	0.725	0.001	0.749	0.138	0.776	0.002
1370304_at	AB006450	translocator of inner mitochondrial membrane 17a /// similar to translocator of inner mitochondrial membrane 17a (predicted)	Timm17a /// RGD1560665_predicted	0.404	0.082	0.838	0.166	0.291	0.006	0.782	0.137
1372455_at	AI410264	transmembrane 4 superfamily member 12	Tm4sf12	0.518	0.076	0.568	0.002	0.683	0.116	0.332	0.008
1377630_at	AI408602	transmembrane 4 superfamily member 13 /// similar to transmembrane 4 superfamily member 13	Tm4sf13 /// LOC500643	0.831	0.078	0.762	0.005	0.781	0.048	0.608	0.015
1371702_at	AI234044	transmembrane 4 superfamily member 2 (mapped)	Tm4sf2_mapped	1.121	0.138	0.668	0.004	1.406	0.039	0.808	0.048
1368706_at	NM_053785	transmembrane 4 superfamily member 4	Tm4sf4	0.411	0.003	0.263	0.000	0.383	0.001	0.269	0.016
1374151_at	BI289940	Transmembrane 6 superfamily member 1 (predicted)	Tm6sf1_predicted	1.237	0.696	0.827	0.382	0.558	0.069	0.800	0.182
1379482_at	BI283829	transmembrane 6 superfamily member 1 (predicted)	Tm6sf1_predicted	0.996	0.977	0.582	0.187	1.061	0.719	0.588	0.183
1389725_at	BM390364	transmembrane 7 superfamily member 2	Tm7sf2	0.919	0.952	0.344	0.017	0.532	0.105	0.253	0.020
1389609_at	BG378884	transmembrane 7 superfamily member 3	Tm7sf3	0.796	0.278	0.812	0.050	0.847	0.045	0.913	0.029
1390125_at	BE098998	transmembrane 9 superfamily member 1	Tm9sf1	0.769	0.501	0.996	0.949	0.921	0.315	1.043	0.759
1367496_at	AI179901	transmembrane 9 superfamily member 2	Tm9sf2	0.675	0.094	0.601	0.002	0.711	0.074	0.733	0.139
1396531_at	BF416287	Transmembrane 9 superfamily protein member 4	Tm9sf4	1.016	0.131	1.186	0.408	1.002	0.998	1.001	0.959
1378075_at	BI275978	transmembrane 9 superfamily protein member 4	Tm9sf4	0.673	0.564	0.958	0.707	0.740	0.251	0.784	0.131
1378052_at	AW253907	Transmembrane 9 superfamily protein member 4	Tm9sf4	1.090	0.831	0.492	0.011	0.905	0.831	0.422	0.025
1373391_at	BM390343	transmembrane and coiled-coil domains 1	Tmco1	0.568	0.333	0.812	0.166	0.615	0.078	0.937	0.037
1391134_at	BF404933	transmembrane and coiled-coil domains 3 (predicted)	Tmco3_predicted	0.524	0.050	0.411	0.005	0.519	0.069	0.445	0.007
1396212_at	BE114358	Transmembrane and tetratricopeptide repeat containing 2 (predicted)	Tmtc2_predicted	0.846	0.620	0.414	0.021	1.192	0.856	0.754	0.162
1394937_at	BE112859	Transmembrane and tetratricopeptide repeat containing 2 (predicted)	Tmtc2_predicted	1.011	0.974	1.083	0.848	0.776	0.443	0.995	0.559
1376102_at	BI292351	transmembrane BAX inhibitor motif containing 1	Tmbim1	15.425	0.007	20.507	0.002	4.685	0.014	5.317	0.003
1371968_at	AI013781	transmembrane BAX inhibitor motif containing 4	Tmbim4	3.283	0.008	3.081	0.004	3.475	0.000	4.420	0.014
1393845_a_at	AI556940	transmembrane channel-like gene family 4	Tmc4	1.719	0.010	0.788	0.267	2.597	0.018	1.837	0.036
1385714_at	BF545988	transmembrane channel-like gene family 4	Tmc4	1.968	0.224	0.981	0.466	4.825	0.006	1.619	0.011
1385436_at	AI556940	transmembrane channel-like gene family 4	Tmc4	1.770	0.476	0.998	0.759	3.242	0.018	1.523	0.014
1388628_at	BI284430	transmembrane emp24 domain containing 3	Tmed3	0.532	0.423	0.599	0.025	0.530	0.050	0.595	0.004
1389940_at	AI178934	transmembrane emp24 domain trafficking protein 2	Tmed2	0.719	0.256	0.832	0.136	0.725	0.284	0.859	0.200
1398824_at	NM_031722	transmembrane emp24 domain trafficking protein 2	Tmed2	1.058	0.744	1.262	0.820	1.052	0.385	1.151	0.930
1373056_at	AI409861	transmembrane emp24 protein transport domain containing 4 (predicted)	Tmed4_predicted	0.794	0.255	0.558	0.008	1.174	0.251	0.799	0.020
1376161_at	AI235294	transmembrane emp24 protein transport domain containing 4 (predicted)	Tmed4_predicted	0.926	0.735	1.002	0.993	0.857	0.931	1.184	0.161
1375904_at	AI011285	Transmembrane emp24 protein transport domain containing 5	Tmed5	0.962	0.458	1.596	0.024	1.502	0.019	1.743	0.009
1398553_at	AI137113	transmembrane emp24 protein transport domain containing 5	Tmed5	1.001	0.732	0.996	0.663	1.196	0.336	1.305	0.433
1379429_at	AI045807	Transmembrane emp24 protein transport domain containing 5	Tmed5	0.709	0.742	1.369	0.879	1.786	0.193	1.339	0.061
1388369_at	BM385547	transmembrane emp24 protein transport domain containing 9	Tmed9	0.905	0.165	1.556	0.004	0.834	0.967	1.371	0.030
1384388_at	H34273	transmembrane emp24 protein transport domain containing 9	Tmed9	0.695	0.823	1.479	0.018	0.672	0.604	1.223	0.131
1398796_at	NM_053467	transmembrane emp24-like trafficking protein 10 (yeast)	Tmed10	0.804	0.350	1.349	0.007	0.897	0.025	1.168	0.034
1373329_at	AI412136	transmembrane protease, serine 2	Tmprss2	0.491	0.022	0.671	0.225	0.866	0.068	0.504	0.086
1378952_at	H31535	transmembrane protein 101	Tmem101	0.677	0.481	0.656	0.013	0.646	0.071	0.445	0.001
1372689_at	BG381479	transmembrane protein 103 (predicted)	Tmem103_predicted	0.424	0.088	1.204	0.479	0.425	0.018	1.018	0.938
1374948_at	BI275815	transmembrane protein 106A	Tmem106a	8.079	0.010	6.024	0.001	14.117	0.000	6.508	0.000
1383731_at	AA818065	Transmembrane protein 106B	Tmem106b	0.274	0.036	0.382	0.007	0.493	0.121	0.504	0.037
1392486_at	AW433977	transmembrane protein 106B	Tmem106b	0.536	0.147	1.158	0.031	0.261	0.050	1.365	0.014
1395920_at	AI547931	transmembrane protein 106B	Tmem106b	0.993	0.956	1.021	0.485	0.929	0.971	1.066	0.982
1372657_at	BM391494	transmembrane protein 106C	Tmem106c	0.488	0.044	0.190	0.000	0.300	0.034	0.197	0.019
1372369_at	AI172075	transmembrane protein 109	Tmem109	0.737	0.860	1.711	0.030	0.745	0.465	1.682	0.123
1372591_at	AI410700	transmembrane protein 11 (predicted)	Tmem11_predicted	0.768	0.474	1.649	0.043	0.635	0.035	1.328	0.001
1371865_at	BI283821	transmembrane protein 111	Tmem111	0.743	0.970	1.319	0.002	1.000	1.000	1.090	0.417
1372894_at	BI284179	transmembrane protein 115 (predicted)	Tmem115_predicted	0.504	0.178	1.080	0.504	0.328	0.033	1.071	0.588
1388930_at	AI171651	transmembrane protein 123	Tmem123	0.477	0.014	0.351	0.000	1.100	0.525	0.529	0.003
1378243_at	AA923937	transmembrane protein 17	Tmem17	2.399	0.131	5.010	0.002	0.927	0.758	2.067	0.017
1382065_at	BM388726	Transmembrane protein 18	Tmem18	1.016	0.946	0.648	0.009	0.848	0.261	0.787	0.005
1394842_at	BF289172	transmembrane protein 19	Tmem19	2.700	0.005	1.427	0.003	3.442	0.001	2.119	0.001
1386346_at	BI275715	transmembrane protein 19	Tmem19	1.647	0.076	1.133	0.083	2.409	0.004	1.870	0.003
1383262_at	BG378159	Transmembrane protein 19	Tmem19	0.970	0.646	0.884	0.070	1.093	0.777	0.811	0.242
1392045_at	BE110277	transmembrane protein 22	Tmem22	0.596	0.136	0.435	0.002	0.463	0.045	0.458	0.018
1384106_at	AW141276	transmembrane protein 23	Tmem23	6.489	0.064	5.634	0.000	9.096	0.000	8.594	0.010
1380566_at	BI279622	transmembrane protein 24	Tmem24	0.838	0.037	0.742	0.195	0.951	0.036	0.940	0.995

1390854_at	BG378195	transmembrane protein 24	Tmem24	0.543	0.602	0.591	0.060	0.854	0.440	0.564	0.044
1377812_a_at	BG378195	transmembrane protein 24	Tmem24	0.861	0.621	0.662	0.009	0.999	0.196	0.842	0.036
1387013_at	NM_020976	transmembrane protein 27	Tmem27	0.696	0.559	0.280	0.002	0.700	0.110	0.458	0.004
1373058_at	AI409051	transmembrane protein 30A	Tmem30a	0.538	0.391	0.463	0.000	0.625	0.057	0.569	0.003
1394992_at	BF389891	Transmembrane protein 33	Tmem33	1.055	0.773	1.001	0.960	1.083	0.600	1.015	0.811
1369076_at	NM_021671	transmembrane protein 33	Tmem33	0.853	0.876	1.295	0.568	0.725	0.259	0.934	0.426
1380438_at	BF390276	Transmembrane protein 33	Tmem33	0.855	0.934	0.620	0.050	0.999	0.976	0.523	0.039
1399082_at	AI176581	Transmembrane protein 33	Tmem33	1.027	0.953	1.123	0.911	0.904	0.511	1.109	0.666
1379419_at	AA962979	transmembrane protein 34	Tmem34	0.266	0.005	0.310	0.000	0.449	0.108	0.508	0.044
1397227_at	BE120895	transmembrane protein 35	Tmem35	0.472	0.005	0.247	0.016	0.712	0.033	0.369	0.049
1389171_at	AI104326	transmembrane protein 38a (predicted)	Tmem38a_predicted	0.253	0.002	0.114	0.001	0.119	0.000	0.116	0.014
1374484_at	AI230318	transmembrane protein 39a	Tmem39a	0.712	0.791	1.812	0.007	0.628	0.035	1.249	0.099
1399092_at	BG378899	transmembrane protein 39b	Tmem39b	0.848	0.683	1.332	0.047	1.003	0.993	0.798	0.308
1376571_at	BI285997	transmembrane protein 42 (predicted)	Tmem42_predicted	0.942	0.651	0.588	0.018	0.659	0.233	0.870	0.275
1373595_at	BM385463	transmembrane protein 43	Tmem43	1.557	0.055	2.038	0.004	1.999	0.039	1.962	0.001
1370807_at	AF411216	transmembrane protein 49	Tmem49	1.670	0.550	2.629	0.002	2.035	0.548	2.641	0.004
1395443_at	BF396088	Transmembrane protein 49	Tmem49	0.984	0.944	0.966	0.053	1.003	0.947	1.586	0.139
1376450_at	BG375242	transmembrane protein 5	Tmem5	0.574	0.034	1.315	0.371	0.337	0.039	0.832	0.994
1372100_at	BI283746	transmembrane protein 50A (predicted)	Tmem50a_predicted	1.586	0.157	1.197	0.148	1.552	0.017	1.734	0.011
1397345_at	AI011553	Transmembrane protein 50A (predicted)	Tmem50a_predicted	0.986	0.973	1.223	0.343	1.062	0.867	0.993	0.088
1371347_at	BI279371	transmembrane protein 50B	Tmem50b	1.073	0.609	0.260	0.002	1.213	0.229	0.277	0.001
1372780_at	BM391310	transmembrane protein 53 (predicted)	Tmem53_predicted	0.722	0.023	0.221	0.004	1.011	0.523	0.324	0.014
1383375_at	BI293584	transmembrane protein 55A	Tmem55a	0.468	0.113	1.613	0.000	0.424	0.002	1.926	0.000
1386632_at	BF547901	transmembrane protein 55A	Tmem55a	0.604	0.232	1.626	0.008	0.406	0.026	1.827	0.000
1392697_at	AI230361	Transmembrane protein 55A	Tmem55a	1.128	0.754	2.635	0.070	0.785	0.542	2.813	0.019
1373486_at	BG375421	transmembrane protein 58 (predicted)	Tmem58_predicted	1.000	0.994	1.504	0.141	1.963	0.098	1.257	0.311
1379595_at	AI171745	transmembrane protein 60 (predicted)	Tmem60_predicted	0.692	0.424	0.688	0.040	0.256	0.034	0.752	0.069
1390330_at	AI236259	Transmembrane protein 60 (predicted)	Tmem60_predicted	0.918	0.970	0.889	0.084	1.133	0.054	0.876	0.026
1377102_at	BI288335	transmembrane protein 63a (predicted)	Tmem63a_predicted	1.099	0.104	0.580	0.024	0.960	0.568	0.603	0.018
1398879_at	BE329031	transmembrane protein 66	Tmem66	0.899	0.219	1.306	0.014	0.821	0.047	1.290	0.040
1390893_at	BF284878	transmembrane protein 69	Tmem69	0.777	0.814	0.945	0.883	0.439	0.044	1.175	0.153
1382371_at	AI172475	transmembrane protein 77	Tmem77	1.312	0.109	1.016	0.897	1.027	0.270	0.995	0.936
1374518_at	AA818113	transmembrane protein 77	Tmem77	1.027	0.116	1.327	0.441	1.253	0.120	1.120	0.479
1390292_at	AW527467	transmembrane protein 8 (five membrane-spanning domains) (predicted)	Tmem8_predicted	0.874	0.375	0.477	0.019	0.698	0.397	0.629	0.053
1372139_at	BI289656	transmembrane protein 80	Tmem80	0.689	0.068	0.285	0.040	0.739	0.041	0.616	0.042
1371454_at	BI285673	transmembrane protein 93 (predicted)	Tmem93_predicted	0.658	0.072	1.664	0.013	0.613	0.005	1.391	0.026
1372156_at	BF414018	transmembrane protein 97	Tmem97	0.445	0.728	1.326	0.013	0.710	0.517	1.089	0.255
1396086_at	H31931	transmembrane protein 97	Tmem97	0.646	0.802	0.890	0.916	0.418	0.127	0.792	0.277
1373161_at	BM386009	transmembrane protein 98	Tmem98	0.329	0.084	0.236	0.002	0.470	0.009	0.279	0.004
1392534_at	BI274101	transmembrane, prostate androgen induced RNA (predicted)	Tmepai_predicted	0.971	0.906	1.082	0.983	1.046	0.789	0.986	0.924
1388149_at	X57523	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	Tap1	201.494	0.001	130.820	0.000	217.327	0.000	158.146	0.000
1368732_at	NM_032056	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	Tap2	60.684	0.001	45.620	0.002	70.000	0.000	38.298	0.003
1381364_at	BE116070	transportin 1	Tnpo1	1.028	0.802	1.194	0.156	1.032	0.202	1.277	0.061
1394440_at	BI293863	transportin 1	Tnpo1	1.332	0.900	1.170	0.098	1.162	0.858	0.751	0.271
1389979_at	BI274235	transportin 3	Tnpo3	0.985	0.860	1.063	0.598	1.255	0.115	1.006	0.932
1380596_at	BE098869	Transthyretin	Ttr	0.824	0.304	0.994	0.489	0.967	0.208	1.291	0.262
1389537_at	AI502399	Treacher Collins Franceschetti syndrome 1, homolog (predicted)	Tcof1_predicted	1.001	0.981	1.626	0.036	1.004	0.356	1.234	0.056
1387218_at	NM_013042	trefoil factor 3	Tff3	0.776	0.005	0.473	0.064	0.399	0.014	0.716	0.512
1372451_at	AI598346	Trf (TATA binding protein-related factor)-proximal protein homolog (Drosophila) /// similar to Ubiquitin specific protease homolog 49 (TRF-proximal protein homolog)	Trfp /// LOC501098	0.602	0.457	0.567	0.068	0.569	0.185	0.647	0.046
1371138_at	AJ243303	triadin	Trdn	1.340	0.231	0.978	0.979	0.791	0.998	1.043	0.999
1371019_at	BM387324	tribbles homolog 1 (Drosophila)	Trib1	0.963	0.795	0.897	0.311	0.963	0.829	0.848	0.280
1386321_s_at	H31287	tribbles homolog 3 (Drosophila)	Trib3	2.123	0.053	14.661	0.000	1.301	0.140	10.473	0.001
1370694_at	AB020967	tribbles homolog 3 (Drosophila)	Trib3	1.940	0.062	9.759	0.000	1.162	0.892	7.805	0.001
1370695_s_at	AB020967	tribbles homolog 3 (Drosophila)	Trib3	1.877	0.151	8.150	0.003	0.878	0.120	7.744	0.003
1376802_at	AW915558	Trichoplein, keratin filament binding (predicted)	Tchp_predicted	0.689	0.158	1.131	0.992	0.653	0.132	0.994	0.948
1377798_at	AW915594	trichoplein, keratin filament binding (predicted)	Tchp_predicted	0.981	0.299	1.022	0.966	0.821	0.537	0.992	0.896
1385227_at	BF398245	trichorhinophalangeal syndrome I (predicted)	Trps1_predicted	1.003	0.834	0.989	0.488	1.013	0.962	0.976	0.061
1375664_at	BI294732	Trinucleotide repeat containing 6 (predicted)	Tnrc6_predicted	1.392	0.031	1.109	0.807	1.582	0.007	1.028	0.204
1397608_at	BE107197	Trinucleotide repeat containing 6 (predicted)	Tnrc6_predicted	1.061	0.858	0.847	0.247	1.118	0.831	1.065	0.705
1382579_at	BE107165	trinucleotide repeat containing 9 (predicted)	Tnrc9_predicted	2.732	0.001	1.536	0.005	1.034	0.344	1.242	0.023

1379751_at	BF554367	trinucleotide repeat containing 9 (predicted)	Tnrc9_predicted	2.480	0.066	1.115	0.282	0.949	0.130	1.061	0.947
1377582_at	BE095938	Trinucleotide repeat containing 9 (predicted)	Tnrc9_predicted	2.749	0.149	1.615	0.054	0.758	0.492	1.358	0.087
1380650_at	AA892317	TRIO and F-actin binding protein	Triobp	4.070	0.027	1.390	0.409	2.560	0.041	2.829	0.234
1367603_at	NM_022922	triosephosphate isomerase 1	Tpi1	0.509	0.247	1.628	0.081	0.370	0.018	1.560	0.098
1373550_at	BI280318	Tripartite motif protein 11 (predicted)	Trim11_predicted	0.699	0.008	0.678	0.177	0.531	0.001	0.990	0.140
1377726_at	BI293740	tripartite motif protein 25 (mapped)	Trim25_mapped	6.233	0.039	1.964	0.025	7.725	0.001	2.479	0.084
1383369_at	AI028875	tripartite motif protein 26	Trim26	3.592	0.008	8.916	0.000	3.071	0.020	8.603	0.002
1378293_at	AI556246	tripartite motif protein 26	Trim26	4.892	0.093	4.732	0.002	3.899	0.000	2.635	0.018
1377234_at	BI294862	Tripartite motif protein 27 (predicted)	Trim27_predicted	0.684	0.054	1.746	0.156	0.593	0.028	1.846	0.163
1371737_at	BI281720	tripartite motif protein 27 (predicted)	Trim27_predicted	0.798	0.121	1.531	0.030	0.692	0.005	1.323	0.021
1395822_at	BE098563	tripartite motif protein 28	Trim28	0.920	0.118	1.212	0.044	1.067	0.708	0.844	0.243
1372155_at	BI283697	tripartite motif protein 28	Trim28	0.790	0.194	1.541	0.020	0.739	0.027	1.241	0.037
1389163_at	BG372673	tripartite motif protein 32	Trim32	0.670	0.840	0.339	0.001	0.449	0.019	0.619	0.014
1379927_at	AI113197	Tripartite motif protein 33 (predicted)	Trim33_predicted	0.993	0.963	0.907	0.320	0.913	0.796	0.984	0.366
1385252_at	BI280655	Tripartite motif protein 34 (predicted)	Trim34_predicted	13.794	0.005	3.656	0.012	26.340	0.000	7.853	0.002
1371786_at	BE111791	tripartite motif protein 35	Trim35	0.470	0.003	0.314	0.002	0.462	0.000	0.363	0.002
1373398_at	BI275184	Tripartite motif protein 37 (predicted)	Trim37_predicted	0.491	0.003	1.128	0.228	0.506	0.005	1.133	0.341
1385335_at	BF415953	tripartite motif protein 39	Trim39	0.909	0.052	1.002	0.735	0.837	0.261	0.869	0.462
1397222_at	AW528473	Tripartite motif protein 39	Trim39	1.316	0.123	2.000	0.113	1.109	0.553	0.922	0.592
1373395_at	AI044721	tripartite motif protein 41 (predicted)	Trim41_predicted	0.692	0.017	0.764	0.013	0.883	0.150	0.804	0.161
1390973_at	BI294747	tripartite motif protein 45 (predicted)	Trim45_predicted	3.127	0.289	0.695	0.808	3.074	0.027	1.313	0.193
1373031_at	BI275757	tripartite motif protein 8 (predicted)	Trim8_predicted	1.150	0.376	0.858	0.446	1.032	0.198	0.777	0.143
1368215_at	NM_031357	tripeptidyl peptidase I	Tpp1	0.811	0.488	1.185	0.006	0.700	0.072	1.185	0.034
1367976_at	NM_031137	tripeptidyl peptidase II	Tpp2	0.815	0.033	0.616	0.003	0.877	0.157	0.760	0.047
1374464_at	BI287875	Trk-fused gene	Tfg	0.851	0.411	1.131	0.179	0.798	0.039	1.075	0.361
1389056_at	BF394168	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	Trmt1	0.914	0.482	1.911	0.001	0.828	0.783	1.557	0.045
1399120_at	BF407592	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae) (predicted)	Trmt5_predicted	0.680	0.144	0.534	0.010	0.719	0.129	0.594	0.034
1374133_at	BG373110	tRNA isopentenyltransferase 1 (predicted)	Trit1_predicted	1.487	0.273	2.144	0.001	1.317	0.976	2.233	0.003
1385296_at	AA963783	tRNA methyltranferase 12 homolog (S. cerevisiae)	Trmt12	0.418	0.037	0.914	0.497	0.400	0.044	0.785	0.217
1383144_at	AI454550	tRNA nucleotidyl transferase, CCA-adding, 1	Trnt1	0.639	0.024	0.840	0.105	0.676	0.014	0.866	0.150
1384879_at	AI045958	tRNA phosphotransferase 1 (predicted)	Trpt1_predicted	0.932	0.732	0.968	0.717	1.120	0.649	1.307	0.149
1369975_at	NM_023027	tRNA selenocysteine associated protein	Secp43	0.555	0.474	1.124	0.127	1.023	0.908	1.265	0.131
1383430_at	BF414509	tRNA splicing endonuclease 2 homolog (S. cerevisiae)	Tsen2	0.487	0.002	0.760	0.306	0.362	0.013	0.706	0.134
1397270_at	AI502769	TRNA splicing endonuclease 2 homolog (S. cerevisiae)	Tsen2	0.456	0.071	1.387	0.116	0.984	0.410	1.248	0.931
1371612_at	AI177656	tRNA splicing endonuclease 34 homolog	TSEN34	0.757	0.041	0.848	0.048	0.820	0.038	0.818	0.040
1395568_at	BF398797	TRNA splicing endonuclease 34 homolog	TSEN34	1.137	0.416	0.828	0.909	1.248	0.630	1.032	0.845
1368540_at	NM_031807	trophoblast glycoprotein	Tpbg	14.726	0.005	3.571	0.004	1.776	0.592	2.076	0.020
1388718_at	AI104913	tropomodulin 1	Tmod1	0.770	0.175	1.585	0.062	0.564	0.002	1.513	0.059
1390482_at	BF285511	Tropomodulin 2	Tmod2	0.564	0.056	1.473	0.024	0.598	0.025	0.830	0.501
1393418_at	BF567833	tropomodulin 2	Tmod2	0.571	0.487	0.622	0.981	0.363	0.022	0.517	0.251
1396504_at	BE120185	Tropomodulin 2	Tmod2	2.604	0.898	0.921	0.736	1.485	0.995	0.651	0.095
1369541_at	NM_031613	tropomodulin 2	Tmod2	0.990	0.957	0.575	0.051	0.425	0.047	0.525	0.053
1372500_at	BG378269	tropomodulin 3	Tmod3	1.499	0.072	2.280	0.002	1.712	0.004	1.939	0.016
1370288_a_at	AF372216	tropomyosin 1, alpha	Tpm1	2.149	0.001	3.070	0.046	1.158	0.337	1.057	0.999
1395794_at	BF395218	tropomyosin 1, alpha	Tpm1	2.041	0.016	4.394	0.004	1.931	0.082	1.718	0.127
1370287_a_at	M23764	tropomyosin 1, alpha	Tpm1	2.319	0.019	1.677	0.004	1.142	0.518	1.038	0.153
1390471_at	BM383411	Tropomyosin 1, alpha	Tpm1	2.397	0.099	1.495	0.187	3.256	0.044	0.945	0.987
1370513_at	M34135	tropomyosin 1, alpha	Tpm1	1.305	0.185	1.115	0.774	0.639	0.041	0.987	0.693
1368724_a_at	NM_019131	tropomyosin 1, alpha	Tpm1	1.507	0.218	1.567	0.123	0.884	0.167	0.883	0.527
1395350_at	AW919190	Tropomyosin 1, alpha	Tpm1	1.005	0.621	2.068	0.187	1.006	0.878	0.992	0.671
1391841_at	BE103537	Tropomyosin 1, alpha	Tpm1	1.048	0.820	1.111	0.777	1.645	0.126	0.796	0.797
1379936_at	AA875132	Tropomyosin 1, alpha	Tpm1	1.000	0.994	1.111	0.599	1.443	0.094	1.015	0.882
1383986_at	AI071098	tropomyosin 3, gamma	Tpm3	1.552	0.019	2.234	0.003	1.901	0.018	2.032	0.002
1371239_s_at	AF053361	tropomyosin 3, gamma	Tpm3	1.160	0.092	1.750	0.246	1.191	0.139	1.267	0.271
1370339_at	L24775	tropomyosin 3, gamma	Tpm3	1.239	0.102	2.007	0.000	1.576	0.025	2.422	0.007
1370340_x_at	BI295970	tropomyosin 3, gamma	Tpm3	1.008	0.411	1.262	0.072	1.052	0.221	1.188	0.047
1388268_at	AF053361	tropomyosin 3, gamma	Tpm3	0.723	0.443	1.033	0.763	0.771	0.071	0.844	0.776
1389846_at	BE104273	Tropomyosin 3, gamma	Tpm3	1.247	0.529	1.631	0.011	1.261	0.055	2.087	0.011
1387617_at	NM_057208	tropomyosin 3, gamma	Tpm3	0.967	0.705	0.811	0.287	0.977	0.343	0.784	0.478
1368838_at	NM_012678	tropomyosin 4	Tpm4	2.034	0.189	2.331	0.242	1.312	0.962	0.880	0.236
1371354_at	AI710682	troponin C type 1 (slow)	Tnnc1	0.997	0.897	0.962	0.043	1.004	0.876	0.961	0.130

1392496_at	AI178581	Trypsin V-A	LOC312273	1.150	0.456	0.093	0.007	1.043	0.829	0.162	0.062
1392647_at	BF282318	Tryptophan hydroxylase 1	Tph1	4.904	0.010	5.874	0.003	2.533	0.079	2.801	0.009
1389222_at	BI282847	Tryptophan hydroxylase 1	Tph1	1.919	0.059	1.437	0.049	1.474	0.152	1.504	0.005
1373034_at	AI177128	tryptophan rich basic protein	Wrb	0.464	0.040	0.727	0.063	0.398	0.001	0.582	0.087
1379959_at	BI280216	tryptophan rich basic protein	Wrb	0.412	0.093	1.921	0.061	0.195	0.001	1.216	0.314
1388574_at	BG670966	tryptophanyl-tRNA synthetase	Wars	4.076	0.002	4.106	0.000	4.750	0.001	6.148	0.008
1395124_at	BE101688	tryptophanyl-tRNA synthetase	Wars	15.251	0.018	7.196	0.011	14.346	0.001	5.566	0.004
1367771_at	NM_031345	TSC22 domain family 3	Tsc22d3	0.715	0.210	0.585	0.085	0.626	0.265	0.455	0.047
1390097_at	BI281738	TSPY-like 4	Tspyl4	0.349	0.032	0.189	0.000	0.342	0.025	0.235	0.002
1371962_at	AI412102	Tu translation elongation factor, mitochondrial (predicted)	Tufm_predicted	0.564	0.247	1.001	0.994	0.352	0.003	1.149	0.431
1369362_at	NM_021854	tuberous sclerosis 1	Tsc1	1.002	0.958	2.512	0.043	0.995	0.810	1.125	0.169
1368056_at	U24150	tuberous sclerosis 2	Tsc2	0.763	0.300	1.211	0.105	1.011	0.710	1.180	0.232
1373408_at	BI282062	tubulin cofactor a	Tbca	0.911	0.530	1.471	0.539	0.973	0.908	1.537	0.111
1390311_at	AW528602	Tubulin tyrosine ligase	Ttl	0.498	0.044	0.723	0.105	0.469	0.023	0.750	0.064
1388959_at	BI297049	tubulin tyrosine ligase-like family, member 12 (predicted)	Ttll12_predicted	0.559	0.010	1.848	0.001	0.589	0.161	1.650	0.004
1367579_a_at	BI285434	tubulin, alpha 1 /// tubulin, alpha 6 /// similar to Tubulin alpha-2 chain (Alpha-tubulin 2) (predicted)	Tuba1 /// Tuba6 /// RGD1565476_predicted	1.044	0.358	1.104	0.022	0.882	0.660	0.924	0.539
1371542_at	BI284599	tubulin, alpha 4	Tuba4	0.598	0.143	0.916	0.348	0.559	0.010	0.933	0.878
1388131_at	X03369	Tubulin, beta 2b	Tubb2b	6.680	0.002	14.434	0.006	2.020	0.094	2.845	0.058
1371390_at	AA892044	tubulin, beta 2c	Tubb2c	0.664	0.223	1.107	0.107	0.451	0.002	0.822	0.168
1371618_s_at	AI229029	tubulin, beta 3	Tubb3	1.425	0.307	1.854	0.001	1.109	0.335	1.570	0.012
1387892_at	BI285440	tubulin, beta 5	Tubb5	1.296	0.109	2.806	0.001	0.883	0.590	1.695	0.012
1370290_at	AB011679	tubulin, beta 5	Tubb5	1.107	0.265	1.896	0.111	0.875	0.613	1.312	0.317
1376100_at	BI274903	tubulin, beta 6	Tubb6	0.814	0.158	15.134	0.011	0.664	0.442	11.748	0.010
1381855_at	AA851436	Tubulin, epsilon 1 (predicted)	Tube1_predicted	1.202	0.118	2.342	0.030	1.753	0.025	1.458	0.201
1383568_at	BF523441	tubulin, epsilon 1 (predicted)	Tube1_predicted	1.235	0.428	1.074	0.686	1.159	0.786	1.004	0.952
1372660_at	AI180420	tubulin, gamma complex associated protein 3	Tubgcp3	1.780	0.005	0.893	0.379	1.083	0.234	1.257	0.099
1384220_at	BE120941	tubulin-specific chaperone c (predicted)	Tbcc_predicted	0.745	0.455	1.418	0.016	0.378	0.021	1.098	0.146
1388869_at	BF281319	tubulin-specific chaperone e	Tbce	1.051	0.902	1.320	0.007	0.842	0.432	1.503	0.004
1398401_at	AI412183	tudor domain containing 3	Tdrd3	0.971	0.619	1.869	0.163	0.870	0.695	1.274	0.662
1370351_at	AB030644	tudor domain containing 7	Tdrd7	1.552	0.150	1.909	0.002	2.549	0.007	2.618	0.001
1384143_at	BE114778	Tuftelin 1 (predicted)	Tuft1_predicted	3.446	0.001	1.324	0.028	2.953	0.002	1.036	0.458
1378343_at	BF405132	tuftelin interacting protein 11	Tfip11	0.655	0.162	3.735	0.039	0.353	0.009	1.275	0.412
1376335_at	BI282368	tuftelin interacting protein 11	Tfip11	1.226	0.597	2.312	0.000	0.715	0.201	1.580	0.005
1377353_a_at	AA800814	tumor necrosis factor (ligand) superfamily, member 13	Tnfsf13	1.026	0.700	1.179	0.755	1.000	0.998	1.739	0.110
1391384_at	AA819227	tumor necrosis factor (TNF superfamily, member 2)	Tnf	56.918	0.004	1.511	0.029	33.129	0.010	1.757	0.022
1372503_at	BF283688	tumor necrosis factor ligand superfamily member 12	Tnfsf12	1.030	0.893	0.752	0.062	1.099	0.560	0.614	0.047
1369407_at	NM_012870	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	Tnfrsf11b	6.927	0.015	1.207	0.244	5.225	0.038	0.716	0.127
1371785_at	BI303379	tumor necrosis factor receptor superfamily, member 12a	Tnfrsf12a	4.303	0.004	7.708	0.031	5.009	0.014	4.125	0.045
1376327_at	AI169601	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)	Tnfrsf14	4.172	0.020	2.290	0.048	71.650	0.000	46.186	0.003
1367715_at	NM_013091	tumor necrosis factor receptor superfamily, member 1a	Tnfrsf1a	1.555	0.250	1.759	0.002	1.514	0.004	1.997	0.002
1377698_at	AW433947	tumor necrosis factor receptor superfamily, member 5	Tnfrsf5	625.638	0.004	98.062	0.002	947.693	0.003	47.619	0.000
1384842_s_at	AI231531	Tumor necrosis factor receptor superfamily, member 6	Tnfrsf6	5.873	0.000	5.428	0.009	7.650	0.009	3.634	0.030
1368635_at	NM_019135	tumor necrosis factor receptor superfamily, member 8	Tnfrsf8	1.002	0.822	0.818	0.439	0.636	0.024	0.558	0.175
1371876_at	BM387084	tumor necrosis factor superfamily, member 5-induced protein 1 (predicted)	Tnfsf5ip1_predicted	0.456	0.039	2.761	0.000	0.602	0.028	2.381	0.000
1372436_at	BG668434	tumor protein D52-like 2	Tpd52l2	1.240	0.199	3.814	0.002	1.555	0.457	2.862	0.002
1367831_at	NM_030989	tumor protein p53	Tp53	1.584	0.003	1.593	0.033	2.787	0.002	2.864	0.003
1367830_a_at	NM_030989	tumor protein p53	Tp53	1.303	0.154	1.760	0.065	1.453	0.067	1.454	0.015
1370752_a_at	AY009504	tumor protein p53	Tp53	1.005	0.562	1.152	0.725	1.289	0.142	1.193	0.465
1375420_at	AI170535	tumor protein p53 inducible protein 11 (predicted)	Tp53i11_predicted	1.326	0.515	1.166	0.139	1.018	0.750	1.535	0.005
1388812_at	AI230362	tumor protein p53 inducible protein 13 (predicted)	Trp53i13_predicted	0.789	0.005	0.480	0.019	0.763	0.015	0.476	0.011
1367583_at	NM_053867	tumor protein, translationally-controlled 1	Tpt1	0.891	0.865	0.985	0.536	0.884	0.892	0.990	0.813
1388331_at	BG057543	tumor rejection antigen gp96 (predicted)	Tra1_predicted	0.833	0.332	0.842	0.003	1.084	0.609	0.762	0.002
1379385_at	AW534879	tumor suppressing subtransferable candidate 1	Tssc1	0.544	0.045	0.943	0.576	0.510	0.007	0.941	0.746
1375858_at	BI285715	tumor suppressor candidate 4	Tusc4	0.474	0.039	0.947	0.850	0.637	0.265	0.860	0.595
1372122_at	AI234654	tumor susceptibility gene 101	Tsg101	0.946	0.898	1.284	0.013	0.776	0.186	1.098	0.059
1388199_at	BG376410	tumor-associated calcium signal transducer 1	Tacstd1	0.835	0.529	1.177	0.047	0.712	0.049	1.017	0.506
1390279_at	BI282086	tumor-suppressing subchromosomal transferable fragment 4	Tssc4	1.421	0.027	0.730	0.032	1.211	0.220	1.001	0.988
1376340_a_at	BI282086	tumor-suppressing subchromosomal transferable fragment 4	Tssc4	0.845	0.558	0.521	0.046	1.437	0.191	0.871	0.043
1375905_at	AI412746	tweety homolog 1 (Drosophila) (predicted)	Ttyh1_predicted	1.596	0.001	1.070	0.782	0.959	0.349	0.655	0.133
1377842_at	AW533281	TWIST neighbor (predicted)	Twistnb_predicted	0.841	0.080	1.289	0.101	0.696	0.020	1.354	0.057

1370358_at	AB018253	two pore channel 1	Tpcn1	1.842	0.005	0.775	0.110	1.109	0.544	0.563	0.021
1376313_at	BI296463	two pore segment channel 2 (predicted)	Tpcn2_predicted	2.210	0.001	1.519	0.008	1.291	0.472	1.194	0.320
1387149_at	NM_030836	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator	Arts1	11.170	0.001	1.576	0.136	4.056	0.009	1.873	0.049
1368356_a_at	NM_030836	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator	Arts1	2.116	0.014	2.274	0.005	2.428	0.001	3.038	0.004
1399161_a_at	AF148323	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator	Arts1	1.814	0.039	2.054	0.002	2.133	0.013	2.777	0.005
1373842_at	BM390718	Type II keratin Kb1	Kb1	0.646	0.102	0.513	0.001	0.733	0.111	0.615	0.009
1386999_at	BG380730	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	Ywhab	0.738	0.690	0.880	0.106	0.622	0.162	0.814	0.089
1398800_at	NM_019377	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	Ywhab	1.020	0.982	0.591	0.007	1.081	0.092	0.651	0.008
1398504_at	BF391867	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	Ywhae	3.190	0.411	1.418	0.405	1.099	0.902	1.108	0.420
1398851_at	AA892351	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	Ywhae	1.000	0.765	0.988	0.087	1.009	0.407	1.145	0.079
1367693_at	NM_013052	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	Ywhah	1.684	0.001	1.496	0.001	1.909	0.002	1.428	0.005
1386866_at	NM_019376	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	Ywhag	0.842	0.320	1.012	0.939	0.876	0.012	1.000	0.996
1387862_at	BF281342	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	Ywhaq	0.693	0.245	0.915	0.059	0.710	0.042	0.957	0.232
1370168_at	BI277793	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	Ywhaq	0.596	0.582	0.830	0.427	0.451	0.167	0.882	0.561
1387774_at	D17615	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	Ywhaz	1.114	0.766	0.914	0.067	0.889	0.755	0.740	0.029
1373443_a_at	AI228292	tyrosine hydroxylase	Th	0.981	0.769	0.834	0.252	1.096	0.558	1.384	0.684
1372692_at	AI406490	tyrosine kinase, non-receptor, 2	Tnk2	0.919	0.421	0.999	0.981	0.968	0.848	0.823	0.029
1382672_a_at	AW918207	tyrosine protein kinase FLK	Flk	0.620	0.027	1.448	0.036	0.564	0.036	1.765	0.188
1377137_at	BG379860	tyrosyl-DNA phosphodiesterase 1	Tdp1	0.889	0.797	1.494	0.178	0.845	0.279	0.869	0.623
1379007_at	AI712659	Tyrosylprotein sulfotransferase 1	Tpst1	1.003	0.998	0.762	0.119	1.006	0.962	0.651	0.126
1398994_at	BI301193	tyrosylprotein sulfotransferase 2	Tpst2	0.456	0.004	0.398	0.000	0.322	0.001	0.412	0.008
1372009_at	AI407490	tyrosyl-tRNA synthetase	Yars	1.310	0.070	2.207	0.003	1.124	0.003	2.209	0.004
1393033_at	BG669575	tyrosyl-tRNA synthetase 2 (mitochondrial)	Yars2	0.574	0.322	1.102	0.581	0.568	0.032	1.447	0.071
1371486_at	BG380657	U1 small nuclear ribonucleoprotein 1C (predicted)	Snrp1c_predicted	0.741	0.156	1.469	0.005	0.753	0.142	1.223	0.077
1384375_at	BE100151	U1 small nuclear ribonucleoprotein polypeptide A (predicted)	Snrp70_predicted	1.422	0.008	1.934	0.093	1.036	0.575	1.314	0.092
1371742_at	BE102265	U1 small nuclear ribonucleoprotein polypeptide A (predicted)	Snrp70_predicted	0.665	0.063	0.913	0.320	1.633	0.479	0.721	0.346
1388797_at	AI232163	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 2	U2af2	0.830	0.003	1.566	0.010	0.860	0.354	1.232	0.066
1389576_at	AA944322	U2 small nuclear ribonucleoprotein B (predicted)	Snrpb2_predicted	1.011	0.921	1.170	0.641	0.789	0.083	1.376	0.075
1373205_at	BM391897	U2 small nuclear RNA auxiliary factor 1-like 4	U2af1l4	0.555	0.250	1.082	0.972	0.813	0.403	1.085	0.838
1395143_at	BF389774	U2AF homology motif (UHM) kinase 1	Uhmk1	1.163	0.173	0.926	0.998	2.379	0.014	1.087	0.638
1387406_at	NM_017293	U2AF homology motif (UHM) kinase 1	Uhmk1	0.986	0.790	1.545	0.062	1.509	0.134	1.640	0.026
1370525_at	U13176	ubc2e ubiquitin conjugating enzyme	Ubc2e	0.698	0.544	0.934	0.290	0.687	0.522	0.733	0.004
1370523_a_at	AW142720	ubc2e ubiquitin conjugating enzyme	Ubc2e	1.048	0.759	1.360	0.058	0.800	0.773	1.097	0.530
1381238_at	BE102046	UbiA prenyltransferase domain containing 1 (predicted)	Ubiad1_predicted	1.280	0.534	1.073	0.810	1.326	0.086	0.889	0.549
1373598_at	BE116948	ubinuclein 1 (predicted)	Ubn1_predicted	1.431	0.204	1.087	0.120	0.989	0.579	0.910	0.720
1381878_at	AI578566	ubinuclein 1 (predicted)	Ubn1_predicted	1.282	0.771	2.084	0.094	0.864	0.305	1.044	0.350
1388719_at	BI279735	Ubiquilin 1	Ubqln1	0.662	0.106	0.577	0.003	0.637	0.049	0.686	0.004
1387041_at	NM_053747	ubiquilin 1	Ubqln1	0.985	0.887	2.395	0.003	0.884	0.171	2.409	0.000
1372131_at	BF398140	ubiquilin 2 (predicted)	Ubqln2_predicted	0.663	0.137	0.624	0.000	0.845	0.069	0.840	0.012
1388691_at	AI177410	ubiquilin 4 (predicted)	Ubqln4_predicted	1.222	0.052	1.860	0.007	1.121	0.404	1.892	0.045
1373362_at	BI296109	ubiquinol cytochrome c reductase core protein 2	Uqcrc2	0.542	0.035	0.754	0.101	0.614	0.183	0.719	0.005
1382280_at	BF290998	ubiquinol cytochrome c reductase core protein 2	Uqcrc2	0.663	0.307	0.797	0.023	0.829	0.341	0.455	0.044
1374426_at	BG670074	ubiquinol-cytochrome c reductase binding protein (predicted)	Uqcrb_predicted	0.996	0.772	1.052	0.822	0.821	0.037	0.932	0.478
1388301_at	BI287993	ubiquinol-cytochrome c reductase core protein 1	Uqcrc1	0.684	0.041	1.282	0.005	0.677	0.001	1.194	0.027
1371415_at	BI279016	ubiquinol-cytochrome c reductase hinge protein	Uqcrh	0.763	0.369	0.956	0.516	0.670	0.053	0.916	0.466
1371254_at	AI179382	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	Uqcrfs1	0.638	0.481	0.794	0.082	0.552	0.149	0.712	0.045
1398754_at	NM_031687	ubiquitin A-52 residue ribosomal protein fusion product 1	Uba52	0.881	0.945	1.254	0.032	0.831	0.104	1.119	0.087
1388387_at	BI275880	ubiquitin associated domain containing 1	Ubadc1	0.915	0.318	1.310	0.018	0.583	0.104	1.084	0.493
1398767_at	NM_017314	ubiquitin C	Ubc	1.242	0.048	1.922	0.002	1.223	0.102	1.567	0.003
1370554_at	AB043959	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) /// similar to ubiqutin carboxyl-terminal hydrolase l3	Uchl3 /// LOC498560	2.031	0.048	1.096	0.563	1.170	0.380	0.894	0.120
1391724_at	AI102641	Ubiquitin carboxyl-terminal hydrolase L5	Uchl5	0.788	0.015	0.984	0.874	0.872	0.045	0.956	0.278
1383477_at	BG668115	ubiquitin carboxyl-terminal hydrolase L5	Uchl5	0.960	0.918	1.036	0.827	0.791	0.084	0.719	0.133
1369977_at	NM_017237	ubiquitin carboxy-terminal hydrolase L1	Uchl1	0.762	0.758	0.997	0.418	0.826	0.081	0.913	0.949
1368762_at	NM_053299	ubiquitin D	Ubd	285.958	0.015	94.664	0.019	551.605	0.014	128.556	0.017
1388696_at	BI291922	ubiquitin fusion degradation 1-like	Ufd1l	0.769	0.093	1.227	0.449	0.669	0.019	1.148	0.988
1368665_at	NM_053418	ubiquitin fusion degradation 1-like	Ufd1l	0.559	0.577	1.159	0.619	0.400	0.019	1.113	0.947
1382741_at	BI285961	ubiquitin protein ligase E3A (predicted)	Ube3a_predicted	1.057	0.423	1.083	0.118	0.761	0.034	0.894	0.469
1391393_at	BE117623	ubiquitin protein ligase E3A (predicted)	Ube3a_predicted	1.074	0.955	1.369	0.190	1.100	0.941	1.012	0.917
1373538_at	AW525342	ubiquitin specific peptdiase 1	Usp1	0.877	0.043	1.859	0.053	1.163	0.411	1.572	0.538
1376687_at	AI010241	ubiquitin specific peptdiase 1	Usp1	0.438	0.255	2.125	0.010	0.376	0.035	1.398	0.054

1370460_at	AF106657	ubiquitin specific peptidase 15	Usp15	1.351	0.102	2.171	0.002	1.406	0.130	2.156	0.010
1389034_at	BI295179	ubiquitin specific peptidase 18	Usp18	9.255	0.000	8.298	0.001	18.394	0.000	22.054	0.004
1389091_at	AI411205	ubiquitin specific peptidase 3	Usp3	3.778	0.002	3.509	0.005	2.045	0.008	2.013	0.018
1388896_at	BF404603	ubiquitin specific peptidase 33	Usp33	0.810	0.007	0.858	0.039	0.660	0.006	0.843	0.092
1391770_at	BE108244	Ubiquitin specific peptidase 33	Usp33	0.819	0.395	1.021	0.609	0.752	0.031	0.740	0.176
1389316_at	AW914946	Ubiquitin specific peptidase 9, X chromosome (predicted)	Usp9x_predicted	0.814	0.225	0.404	0.001	0.924	0.235	0.468	0.000
1372150_at	AI229488	ubiquitin specific protease 10	Usp10	0.647	0.071	1.683	0.022	0.623	0.002	1.186	0.093
1376171_at	AA851303	ubiquitin specific protease 11	Usp11	0.720	0.589	1.303	0.119	1.104	0.417	1.227	0.166
1385035_at	AI639241	ubiquitin specific protease 12 (predicted)	Usp12_predicted	0.548	0.395	0.770	0.105	0.720	0.636	1.118	0.515
1381605_at	AW521619	ubiquitin specific protease 13 (isopeptidase T-3) (predicted)	Usp13_predicted	0.417	0.000	0.608	0.008	0.351	0.022	0.506	0.017
1385663_at	BF567505	ubiquitin specific protease 13 (isopeptidase T-3) (predicted)	Usp13_predicted	0.393	0.096	0.338	0.008	0.268	0.014	0.334	0.005
1383073_at	BG666028	ubiquitin specific protease 14	Usp14	0.854	0.323	0.777	0.001	0.827	0.170	0.857	0.027
1399038_at	AA893224	ubiquitin specific protease 19	Usp19	1.167	0.486	1.427	0.150	1.172	0.368	1.003	0.996
1371874_at	AI175026	ubiquitin specific protease 19	Usp19	0.966	0.786	0.892	0.098	1.175	0.285	0.902	0.097
1378309_at	AW434880	ubiquitin specific protease 20 (predicted)	Usp20_predicted	0.682	0.034	1.127	0.887	0.758	0.236	0.812	0.999
1376656_at	BI274796	ubiquitin specific protease 20 (predicted)	Usp20_predicted	0.613	0.065	0.614	0.053	0.590	0.106	0.758	0.135
1386338_at	AI704873	Ubiquitin specific protease 22 (predicted)	Usp22_predicted	1.138	0.595	1.218	0.038	1.026	0.861	1.053	0.086
1394078_at	AW921158	ubiquitin specific protease 22 (predicted)	Usp22_predicted	1.145	0.608	0.982	0.183	1.176	0.705	1.008	0.441
1384456_at	BE118916	Ubiquitin specific protease 24 (predicted)	Usp24_predicted	1.367	0.080	3.495	0.013	1.709	0.146	2.017	0.020
1378679_at	BG372484	Ubiquitin specific protease 25 (predicted)	Usp25_predicted	8.431	0.000	2.612	0.009	12.593	0.000	4.419	0.000
1373163_at	BI287702	Ubiquitin specific protease 28 (predicted)	Usp28_predicted	1.241	0.434	1.003	0.979	1.475	0.678	1.271	0.056
1395054_at	BF416262	ubiquitin specific protease 29 (predicted)	Usp29_predicted	1.650	0.519	0.488	0.184	0.448	0.274	0.489	0.185
1372570_at	AI145892	ubiquitin specific protease 30 (predicted)	Usp30_predicted	0.726	0.081	1.051	0.912	0.796	0.110	1.045	0.592
1390486_at	AI231505	ubiquitin specific protease 32 (predicted)	Usp32_predicted	1.927	0.055	1.074	0.145	1.416	0.195	1.609	0.024
1395019_at	AI101440	ubiquitin specific protease 38 (predicted)	Usp38_predicted	0.672	0.113	0.772	0.208	0.793	0.178	0.650	0.147
1389344_at	BE109258	ubiquitin specific protease 39 (predicted)	Usp39_predicted	0.723	0.172	2.003	0.030	0.951	0.272	2.147	0.027
1394958_at	BF402345	Ubiquitin specific protease 40	Usp40	0.914	0.249	1.189	0.080	0.476	0.061	1.162	0.922
1381420_at	BF397624	Ubiquitin specific protease 47 (predicted)	Usp47_predicted	1.211	0.066	1.724	0.075	1.480	0.059	1.536	0.127
1373157_at	AI407830	ubiquitin specific protease 47 (predicted)	Usp47_predicted	1.048	0.323	1.419	0.367	0.782	0.021	1.017	0.916
1399036_at	AA964374	ubiquitin specific protease 47 (predicted)	Usp47_predicted	0.898	0.683	1.694	0.014	0.954	0.560	1.816	0.029
1399029_at	BI285965	ubiquitin specific protease 48	Usp48	0.518	0.042	0.360	0.002	0.604	0.021	0.463	0.052
1376849_at	BM384872	ubiquitin specific protease 48	Usp48	0.717	0.456	2.400	0.001	1.050	0.998	2.284	0.003
1388938_at	AI411387	ubiquitin specific protease 5 (isopeptidase T) (predicted)	Usp5_predicted	1.011	0.715	0.985	0.399	0.939	0.481	0.904	0.314
1394393_at	BE114562	ubiquitin specific protease 7 (herpes virus-associated)	Usp7	1.262	0.367	2.196	0.004	0.753	0.189	1.972	0.031
1393042_at	BI288780	Ubiquitin specific protease 7 (herpes virus-associated)	Usp7	0.861	0.497	0.865	0.046	0.958	0.487	0.937	0.929
1398351_at	AI175593	Ubiquitin specific protease 7 (herpes virus-associated)	Usp7	0.783	0.948	0.728	0.052	1.024	0.566	0.815	0.407
1383609_at	BI276086	Ubiquitin specific protease 7 (herpes virus-associated)	Usp7	0.953	0.972	0.629	0.055	1.001	0.327	0.602	0.048
1397621_at	AI502942	Ubiquitin specific protease 8 (predicted)	Usp8_predicted	1.053	0.853	0.518	0.018	0.985	0.639	1.167	0.487
1390027_at	AI137190	ubiquitin specific protease 8 (predicted)	Usp8_predicted	0.683	0.986	0.640	0.054	1.772	0.354	0.929	0.592
1398813_at	NM_057205	ubiquitin-activating enzyme E1C	Ube1c	0.900	0.768	1.045	0.037	1.089	0.355	1.020	0.790
1372120_at	AI408025	ubiquitin-activating enzyme E1-domain containing 1	Ube1dc1	0.767	0.070	1.168	0.071	1.058	0.113	1.092	0.352
1372119_at	BM389270	ubiquitin-activating enzyme E1-domain containing 1	Ube1dc1	0.985	0.955	2.709	0.005	0.969	0.825	2.321	0.000
1379633_a_at	BE096453	ubiquitin-activating enzyme E1-like (predicted)	Ube1l_predicted	5.171	0.011	4.433	0.004	12.740	0.002	8.056	0.000
1386277_at	AI177396	ubiquitin-activating enzyme E1-like (predicted)	Ube1l_predicted	3.048	0.036	1.302	0.139	10.641	0.000	3.163	0.033
1379634_at	AW921187	ubiquitin-activating enzyme E1-like (predicted)	Ube1l_predicted	1.144	0.255	1.076	0.033	1.639	0.010	1.008	0.213
1388677_at	BI275991	ubiquitin-associated protein 1	Ubap1	2.180	0.122	3.794	0.011	1.465	0.402	2.934	0.072
1372127_at	BI275824	ubiquitin-associated protein 2 (predicted)	Ubap2_predicted	0.939	0.072	1.417	0.046	1.449	0.227	1.476	0.071
1372888_at	BI294856	ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)	Ube4a	0.600	0.022	0.438	0.000	0.714	0.036	0.501	0.000
1385615_at	BF550268	ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)	Ube4a	0.722	0.159	1.545	0.094	0.999	0.569	0.999	0.989
1384053_at	BF556415	ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)	Ube4a	1.003	0.997	0.963	0.040	1.018	0.927	0.928	0.222
1376862_at	BI296848	ubiquitination factor E4B, UFD2 homolog (S. cerevisiae) (predicted)	Ube4b_predicted	0.463	0.003	0.364	0.000	0.680	0.064	0.543	0.006
1374507_at	BE096671	ubiquitination factor E4B, UFD2 homolog (S. cerevisiae) (predicted)	Ube4b_predicted	0.810	0.077	1.032	0.132	0.669	0.087	0.891	0.430
1398897_at	AI411988	ubiquitin-conjugating enzyme E2 variant 1 (predicted)	Ube2v1_predicted	1.560	0.002	1.346	0.072	1.503	0.003	1.238	0.103
1372143_at	AA849958	ubiquitin-conjugating enzyme E2 variant 2	Ube2v2	0.752	0.044	1.080	0.422	0.723	0.015	1.039	0.266
1373495_at	AW915822	ubiquitin-conjugating enzyme E2, J1 (predicted)	Ube2j1_predicted	1.128	0.366	4.657	0.000	0.731	0.231	3.786	0.000
1392573_at	BF284538	ubiquitin-conjugating enzyme E2A, RAD6 homolog (S. cerevisiae)	Ube2a	1.134	0.442	1.045	0.618	1.253	0.322	1.228	0.135
1388863_at	BE111651	ubiquitin-conjugating enzyme E2A, RAD6 homolog (S. cerevisiae)	Ube2a	0.952	0.836	0.894	0.078	0.995	0.934	0.862	0.333
1380087_at	BE119409	Ubiquitin-conjugating enzyme E2B, RAD6 homolog (S. cerevisiae)	Ube2b	2.289	0.094	0.958	0.146	1.172	0.495	0.817	0.241
1375642_at	AA892795	ubiquitin-conjugating enzyme E2B, RAD6 homolog (S. cerevisiae)	Ube2b	0.809	0.466	0.638	0.006	0.761	0.169	0.627	0.002
1386923_at	M62388	ubiquitin-conjugating enzyme E2B, RAD6 homolog (S. cerevisiae)	Ube2b	1.050	0.936	1.174	0.065	1.092	0.574	1.077	0.879
1374890_at	AW533905	Ubiquitin-conjugating enzyme E2D 2	Ube2d2	0.711	0.439	0.530	0.066	0.524	0.134	0.653	0.001

1399160_a_at	U13177	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	Ube2d3	1.903	0.021	3.795	0.000	1.436	0.125	3.308	0.001
1372586_at	AI411995	Ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	Ube2d3	1.289	0.224	0.943	0.268	1.302	0.083	1.094	0.516
1367456_at	NM_031237	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	Ube2d3	1.387	0.245	1.299	0.030	1.352	0.139	1.257	0.003
1398802_at	AW435034	Ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	Ube2d3	1.266	0.281	1.214	0.037	1.160	0.190	1.182	0.032
1388798_at	AW921519	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	Ube2e2	1.149	0.137	2.176	0.010	1.334	0.037	4.743	0.019
1376438_at	BF416513	Ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	Ube2e2	1.018	0.728	1.133	0.972	1.278	0.452	0.914	0.903
1384121_at	AI058309	Ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	Ube2e2	0.833	0.756	0.970	0.277	0.833	0.554	0.928	0.651
1367484_at	BM391175	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast) /// similar to Ubiquitin-conjugating enzyme E2 E1 (Ubiquitin-protein ligase E1) (predicted)	Ube2e2 /// RGD1561054_predicted	0.995	0.406	0.896	0.060	1.458	0.041	1.003	0.971
1389534_at	BF282336	ubiquitin-conjugating enzyme E2E 3, UBC4/5 homolog (yeast) (predicted)	Ube2e3_predicted	0.926	0.716	0.701	0.176	0.929	0.512	0.804	0.111
1375663_at	AI232346	ubiquitin-conjugating enzyme E2F (putative)	Ube2f	1.114	0.741	2.150	0.001	0.871	0.264	1.686	0.014
1398864_at	BM389287	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)	Ube2g1	0.750	0.364	1.437	0.049	0.843	0.030	1.553	0.067
1370501_at	AF099093	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)	Ube2g1	0.998	0.965	1.258	0.360	1.002	0.970	1.112	0.578
1371814_at	BI282191	ubiquitin-conjugating enzyme E2G 2 (predicted)	Ube2g2_predicted	1.478	0.257	1.590	0.130	1.618	0.028	1.270	0.810
1370250_at	AA799453	ubiquitin-conjugating enzyme E2I /// similar to RIKEN cDNA A930001M12 gene (predicted)	Ube2i /// RGD1562567_predicted	0.823	0.144	1.319	0.101	0.841	0.182	0.967	0.938
1371945_at	AI407788	ubiquitin-conjugating enzyme E2L 3 (predicted)	Ube2l3_predicted	0.777	0.718	0.642	0.017	0.648	0.869	0.751	0.025
1371944_at	BF282658	ubiquitin-conjugating enzyme E2L 3 (predicted)	Ube2l3_predicted	0.857	0.793	1.365	0.029	0.716	0.140	1.374	0.050
1373037_at	BI279216	ubiquitin-conjugating enzyme E2L 6	Ube2l6	12.825	0.005	15.099	0.002	18.341	0.000	17.630	0.001
1388559_at	BG378098	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast) (predicted)	Ube2m_predicted	0.585	0.306	1.187	0.413	0.412	0.224	0.864	0.048
1369617_at	NM_053928	ubiquitin-conjugating enzyme E2N	Ube2n	0.757	0.050	0.908	0.074	0.559	0.111	0.601	0.076
1376213_at	AI007838	Ubiquitin-conjugating enzyme E2N	Ube2n	0.554	0.136	0.602	0.583	0.444	0.305	0.694	0.196
1399143_at	BI294702	ubiquitin-conjugating enzyme E2N	Ube2n	0.814	0.470	1.093	0.457	0.730	0.171	0.984	0.903
1372788_at	AI144725	ubiquitin-conjugating enzyme E2Q (putative) (predicted)	Ube2q_predicted	0.830	0.038	0.596	0.002	0.802	0.053	0.641	0.008
1375162_at	AA800501	ubiquitin-conjugating enzyme E2Q (putative) (predicted)	Ube2q_predicted	0.771	0.410	1.143	0.182	0.736	0.030	1.046	0.618
1393072_at	H32128	ubiquitin-conjugating enzyme E2Q (putative) 2 (predicted)	Ube2q2_predicted	0.822	0.322	1.234	0.194	0.507	0.023	0.847	0.123
1372703_at	BG380680	ubiquitin-conjugating enzyme E2R 2 (predicted)	Ube2r2_predicted	0.856	0.069	1.315	0.035	0.742	0.133	1.130	0.533
1377677_a_at	AA900692	Ubiquitin-conjugating enzyme E2R 2 (predicted)	Ube2r2_predicted	1.391	0.522	1.031	0.858	1.416	0.229	1.041	0.783
1371365_at	BI279788	ubiquitin-conjugating enzyme E2S (predicted)	Ube2s_predicted	0.498	0.283	0.781	0.085	0.472	0.006	0.780	0.156
1388787_at	BM383736	ubiquitin-conjugating enzyme E2Z (putative)	Ube2z	1.437	0.135	1.485	0.010	1.133	0.808	1.489	0.008
1371830_at	BM986263	ubiquitin-like 1 (sentrin) activating enzyme E1A	Uble1a	0.678	0.320	1.007	0.366	0.673	0.034	1.121	0.424
1376212_at	AI102437	ubiquitin-like 1 (sentrin) activating enzyme E1B	Uble1b	1.714	0.034	4.465	0.002	0.747	0.463	3.076	0.005
1371657_at	AA799692	ubiquitin-like 1 (sentrin) activating enzyme E1B	Uble1b	0.752	0.255	0.910	0.121	0.750	0.080	0.870	0.083
1374413_at	BM386522	ubiquitin-like 3	Ubl3	0.908	0.912	1.080	0.057	0.901	0.861	1.115	0.092
1383223_at	BG672206	ubiquitin-like 3	Ubl3	1.374	0.921	0.956	0.662	1.113	0.577	0.676	0.746
1392906_at	AW528860	ubiquitin-like 4a (predicted)	Ubl4a_predicted	0.596	0.224	3.173	0.012	0.319	0.011	2.311	0.097
1371590_s_at	BM386159	Ubiquitin-Like 5 Protein	LOC500954	1.107	0.774	0.761	0.083	1.042	0.176	0.699	0.315
1371589_at	BM386159	Ubiquitin-Like 5 Protein	LOC500954	1.018	0.846	0.989	0.569	1.033	0.616	0.757	0.133
1372540_at	BG671872	ubiquitin-like domain containing CTD phosphatase 1	Ublcp1	0.850	0.051	0.507	0.002	1.134	0.485	0.734	0.057
1373117_at	BI275765	ubiquitin-like, containing PHD and RING finger domains 2 (predicted)	Uhrf2_predicted	1.054	0.796	0.974	0.779	0.839	0.198	1.142	0.102
1374465_at	AI237098	ubiquitously expressed transcript	Uxt	0.505	0.121	0.826	0.379	0.739	0.116	0.717	0.292
1388444_at	BI291633	UBX domain containing 2	Ubxd2	0.778	0.023	1.738	0.000	0.754	0.014	1.355	0.001
1381542_at	AI704885	UBX domain containing 2	Ubxd2	0.579	0.201	1.970	0.127	0.514	0.039	1.338	0.889
1396102_at	BF406574	UBX domain containing 2	Ubxd2	1.543	0.355	1.755	0.034	1.390	0.819	1.383	0.096
1396059_at	BF289251	UBX domain containing 2	Ubxd2	0.662	0.761	2.821	0.017	0.634	0.389	1.515	0.145
1382067_at	AW434917	UBX domain containing 4 (predicted)	Ubxd4_predicted	1.300	0.353	1.875	0.025	0.878	0.773	1.620	0.038
1390785_at	AI232339	UBX domain containing 4 (predicted)	Ubxd4_predicted	0.777	0.383	1.285	0.018	0.736	0.010	1.346	0.018
1397349_at	BF394199	UBX domain containing 6 (predicted)	Ubxd6_predicted	1.342	0.462	2.581	0.077	0.874	0.696	2.146	0.007
1383070_at	AA925934	UBX domain containing 8	Ubxd8	0.680	0.383	0.526	0.004	0.918	0.996	0.545	0.078
1380555_at	BI293042	UBX domain containing 8	Ubxd8	0.455	0.429	0.461	0.004	1.074	0.744	0.494	0.074
1383267_at	BF554347	UBX domain containing 8	Ubxd8	0.730	0.459	0.425	0.000	0.973	0.796	0.702	0.010
1368858_at	L21698	UDP galactosyltransferase 8	Ugt8	0.271	0.003	0.194	0.007	0.342	0.008	0.232	0.005
1369850_at	NM_022228	UDP glucuronosyltransferase 2 family, polypeptide A1	Ugt2a1	1.014	0.938	0.999	0.608	0.999	0.802	1.002	0.713
1387759_s_at	J02612	UDP glycosyltransferase 1 family, polypeptide A1 /// UDP glycosyltransferase 1 family, polypeptide A6 /// UDP glycosyltransferase 1 family, polypeptide A7 /// UDP glycosyltransferase 1 family, polypeptide A8 /// UDP glycosyltransferase 1 family polypeptide A2 /// UDP glycosyltransferase 1 family polypeptide A3 /// UDP glycosyltransferase 1 family polypeptide A10 /// UDP glycosyltransferase 1 family, polypeptide A5	Ugt1a1 /// Ugt1a6 /// Ugt1a7 /// Ugt1a8 /// Ugt1a2 /// Ugt1a3 /// Ugt1a10 /// Ugt1a5	0.725	0.008	1.067	0.274	0.594	0.021	0.998	0.928
1370613_s_at	AF461738	UDP glycosyltransferase 1 family, polypeptide A1 /// UDP glycosyltransferase 1 family, polypeptide A6 /// UDP glycosyltransferase 1 family, polypeptide A7 /// UDP glycosyltransferase 1 family, polypeptide A8 /// UDP glycosyltransferase 1 family polypeptide A2 /// UDP glycosyltransferase 1 family polypeptide A3 /// UDP glycosyltransferase 1 family polypeptide A10 /// UDP glycosyltransferase 1 family, polypeptide A5	Ugt1a1 /// Ugt1a6 /// Ugt1a7 /// Ugt1a8 /// Ugt1a2 /// Ugt1a3 /// Ugt1a10 /// Ugt1a5	0.723	0.014	1.366	0.077	0.516	0.001	0.913	0.288

1398373_at	AA799400	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 3	B3galt3	2.339	0.001	3.444	0.002	1.295	0.074	2.030	0.023
1368346_at	NM_133553	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	B3galt4	0.407	0.058	0.559	0.033	0.744	0.363	0.476	0.014
1371073_at	BI286141	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1 (mapped)	B4galt1_mapped	1.141	0.367	1.148	0.279	1.322	0.097	1.102	0.302
1367487_at	BG378610	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	B4galt3	0.796	0.771	0.933	0.110	1.017	0.936	0.847	0.235
1383689_at	BM382871	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4	B4galt4	1.170	0.354	1.968	0.249	0.712	0.340	0.764	0.666
1387206_at	NM_031740	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	B4galt6	1.638	0.011	0.397	0.000	1.864	0.017	0.392	0.009
1381877_at	AI113234	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	B4galt6	0.908	0.158	1.000	0.987	1.953	0.196	1.048	0.756
1376202_at	BF416236	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (predicted)	B3gnt6_predicted	0.209	0.001	0.290	0.009	0.087	0.008	0.504	0.488
1384083_at	AW532159	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1	B3gntl1	0.614	0.065	0.691	0.150	0.477	0.053	0.694	0.137
1387975_at	AF047707	UDP-glucose ceramide glucosyltransferase	Ugcg	1.068	0.311	0.764	0.064	1.107	0.481	0.796	0.094
1368953_at	NM_133596	UDP-glucose ceramide glucosyltransferase-like 1	Ugcgl1	0.891	0.822	0.991	0.116	0.882	0.329	0.751	0.049
1367938_at	NM_031325	UDP-glucose dehydrogenase	Ugdh	2.108	0.001	4.470	0.000	2.136	0.003	3.727	0.000
1388410_at	AI170679	UDP-glucose pyrophosphorylase 2	Ugp2	1.300	0.483	1.818	0.003	1.069	0.769	1.936	0.004
1376262_at	BM385390	UDP-glucuronate decarboxylase 1	Uxs1	0.945	0.483	0.877	0.067	0.690	0.063	0.902	0.433
1369269_at	NM_024373	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1	Galnt1	1.014	0.861	0.946	0.523	0.998	0.907	0.845	0.391
1383374_at	BE111170	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1	Galnt1	0.931	0.875	0.866	0.998	1.149	0.635	0.656	0.192
1399045_at	AI236745	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1	Galnt1	0.737	0.965	0.832	0.724	0.947	0.797	0.559	0.094
1374624_at	AI179979	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11 (GalNAc-T11)	Galnt11	0.765	0.087	0.827	0.271	0.893	0.582	0.743	0.072
1383021_at	AI103845	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13	Galnt13	0.960	0.943	1.448	0.100	1.341	0.149	1.240	0.061
1382355_at	BM386420	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4)	Galnt4	0.990	0.879	0.378	0.240	0.972	0.726	0.930	0.825
1387554_at	NM_031796	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5	Galnt5	0.528	0.099	0.248	0.001	1.000	1.000	0.306	0.004
1397406_at	BF411788	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1 (predicted)	Uap1l1_predicted	0.701	0.392	1.929	0.045	0.627	0.007	0.953	0.968
1381982_at	BF403568	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1 (predicted)	Uap1l1_predicted	0.479	0.512	8.860	0.004	0.261	0.018	3.758	0.016
1371758_at	BM986259	Ufm1-conjugating enzyme 1	Ufc1	0.718	0.103	1.061	0.768	0.769	0.070	1.007	0.922
1375572_at	BE100602	Ultraviolet B radiation-activated UV98 mRNA, partial sequence	---	0.853	0.352	0.888	0.582	0.854	0.330	0.974	0.579
1372679_at	BI296209	unc-45 homolog A (C. elegans)	Unc45a	1.143	0.028	1.346	0.002	1.370	0.048	1.262	0.058
1393799_at	BI303989	Unc-5 homolog B (C. elegans)	Unc5b	0.974	0.993	1.312	0.142	0.999	0.997	1.013	0.924
1384506_at	H33706	unc-5 homolog C (C. elegans)	Unc5c	7.759	0.001	1.790	0.166	8.699	0.008	4.038	0.036
1382201_at	AA926250	unc-5 homolog C (C. elegans)	Unc5c	1.489	0.416	0.330	0.003	2.824	0.049	0.738	0.368
1398865_at	U96638	unc-50 homolog (C. elegans)	Unc50	0.504	0.288	0.483	0.014	0.554	0.051	0.546	0.014
1382671_at	AW920165	Unc-51 like kinase 2 (C. elegans) (predicted)	Ulk2_predicted	1.233	0.406	0.929	0.679	1.101	0.321	0.995	0.738
1375869_at	AI603439	unc-51-like kinase 1 (mapped)	Ulk1_mapped	0.579	0.048	0.216	0.047	0.798	0.107	0.370	0.042
1375814_at	BG380887	Unc-84 homolog A (C. elegans)	Unc84a	2.410	0.003	0.510	0.706	2.149	0.004	0.493	0.914
1382043_at	AI234533	unc-93 homolog B1 (C. elegans)	Unc93b1	1.259	0.124	1.037	0.693	3.960	0.003	1.516	0.190
1398962_at	BM388453	uncharacterized protein family UPF0227 member RGD1359682	RGD1359682	0.541	0.117	1.125	0.063	0.297	0.057	1.037	0.209
1368669_at	NM_019354	uncoupling protein 2 (mitochondrial, proton carrier)	Ucp2	0.661	0.256	0.370	0.001	0.406	0.007	0.367	0.011
1387681_at	U92069	uncoupling protein 3 (mitochondrial, proton carrier)	Ucp3	1.169	0.709	0.928	0.964	1.068	0.579	0.995	0.935
1388980_at	BG381728	Unknown (protein for MGC:72560)	MGC72560	0.997	0.978	2.657	0.013	0.732	0.242	2.169	0.006
1372961_at	BE101165	Unknown (protein for MGC:72996)	MGC72996	0.703	0.825	1.353	0.093	0.687	0.123	1.026	0.878
1372541_at	BG374849	Unknown (protein for MGC:73003)	MGC73003	0.962	0.229	0.997	0.983	0.967	0.275	0.828	0.092
1371652_at	BF550566	Unknown mRNA sequence	---	1.500	0.057	0.987	0.855	2.082	0.054	1.157	0.734
1371091_at	BE118080	unknown protein	LOC207125	0.296	0.028	0.908	0.492	0.205	0.011	0.735	0.097
1378275_at	BG377170	UPF3 regulator of nonsense transcripts homolog A (yeast)	Upf3a	0.910	0.464	0.971	0.931	0.741	0.205	0.722	0.060
1376298_at	AW525099	UPF3 regulator of nonsense transcripts homolog B (yeast) (predicted)	Upf3b_predicted	0.753	0.038	0.637	0.032	1.037	0.360	0.650	0.050
1371131_a_at	U30789	upregulated by 1,25-dihydroxyvitamin D-3	Txnip	0.232	0.006	0.201	0.018	0.297	0.024	0.388	0.074
1370238_at	AA891707	upregulated during skeletal muscle growth 5	Usmg5	0.989	0.784	1.168	0.189	0.756	0.130	1.154	0.542
1395298_at	AI070708	upstream binding protein 1 (predicted)	Ubp1_predicted	0.955	0.687	0.905	0.734	1.004	0.410	0.660	0.204
1389098_at	AI407261	Upstream binding protein 1 (predicted)	Ubp1_predicted	1.028	0.918	0.971	0.528	1.676	0.193	1.088	0.066
1371187_a_at	M61726	upstream binding transcription factor, RNA polymerase I	Ubtf	1.151	0.618	1.216	0.074	0.724	0.094	0.951	0.991
1389830_at	AI105117	upstream binding transcription factor, RNA polymerase I	Ubtf	1.001	0.983	1.151	0.977	0.999	0.985	1.054	0.986
1397961_x_at	AI010663	upstream of NRAS	Unr	1.383	0.259	0.945	0.034	1.012	0.820	0.707	0.006
1370169_at	BI289608	upstream of NRAS	Unr	0.979	0.262	2.154	0.001	0.716	0.550	1.830	0.022
1387863_at	BE099415	upstream of NRAS	Unr	0.990	0.910	1.098	0.166	0.996	0.346	1.000	0.997
1376954_at	BF406210	Upstream transcription factor 2	Usf2	1.000	0.139	1.478	0.114	1.001	0.994	1.006	0.752
1388088_a_at	AB035650	upstream transcription factor 2	Usf2	0.992	0.850	1.999	0.096	0.995	0.959	1.403	0.368
1368591_at	NM_031139	upstream transcription factor 2	Usf2	0.982	0.873	1.282	0.126	1.129	0.486	1.320	0.036
1389738_at	AA848420	uracil-DNA glycosylase	Ung	0.771	0.019	2.382	0.002	0.748	0.045	1.455	0.014
1368245_at	NM_053845	ureidopropionase, beta	Upb1	0.703	0.015	0.115	0.001	0.907	0.143	0.229	0.009
1383945_at	AA859827	uridine monophosphate kinase (predicted)	Umpk_predicted	0.869	0.133	9.546	0.006	0.375	0.038	6.390	0.025
1389587_at	BM384966	uridine monophosphate synthetase	Umps	0.457	0.011	1.568	0.003	0.352	0.001	1.068	0.516
1391109_x_at	BE108349	Urinary protein 2	Rup2	1.228	0.987	0.795	0.138	1.310	0.322	1.052	0.171

1370878_at	Y00350	uroporphyrinogen decarboxylase	Urod	0.458	0.191	0.524	0.011	0.417	0.012	0.473	0.088
1383214_at	AI555989	USP6 N-terminal like (predicted)	Usp6nl_predicted	1.278	0.588	3.182	0.014	1.817	0.663	1.050	0.440
1383250_at	BE105819	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)	Utp14a	0.970	0.618	2.024	0.067	0.763	0.248	1.726	0.163
1377377_at	BF415808	Utrophin	Utrn	0.886	0.380	0.565	0.036	0.647	0.052	0.525	0.017
1387716_at	NM_013070	utrophin	Utrn	1.012	0.528	0.999	0.980	0.745	0.100	0.975	0.789
1371713_at	BF408884	v-abl Abelson murine leukemia viral oncogene homolog 1 (mapped)	Abl1_mapped	0.878	0.083	1.326	0.276	0.796	0.140	0.819	0.309
1389041_at	BF408597	Vac14 homolog (S. cerevisiae)	Vac14	1.326	0.285	2.772	0.001	1.227	0.059	1.828	0.032
1372419_at	BG380296	vaccinia related kinase 3	Vrk3	1.194	0.114	0.850	0.089	1.618	0.039	1.262	0.069
1379730_at	AA942681	vacuolar ATPase subunit H	Atp6v1h	0.653	0.271	0.826	0.036	0.711	0.046	0.780	0.014
1373498_at	BI295924	vacuolar protein sorting 11 (yeast) (predicted)	Vps11_predicted	0.952	0.712	1.896	0.007	1.127	0.500	1.903	0.011
1388934_at	BI285570	vacuolar protein sorting 16 (yeast)	Vps16	0.863	0.562	1.929	0.002	0.990	0.967	1.395	0.004
1371705_at	BI285508	Vacuolar protein sorting 26 (yeast)	Vps26	1.120	0.135	1.741	0.007	1.256	0.126	1.241	0.007
1382099_at	BI289595	vacuolar protein sorting 26 (yeast)	Vps26	1.317	0.441	1.796	0.005	1.967	0.008	1.717	0.014
1367481_at	BI278301	vacuolar protein sorting 28 (yeast) (predicted)	Vps28_predicted	0.809	0.788	1.066	0.716	0.926	0.597	0.816	0.423
1371639_at	BF291006	vacuolar protein sorting 29 (S. pombe) (predicted)	Vps29_predicted	0.715	0.025	0.739	0.095	0.717	0.005	0.812	0.338
1387557_s_at	NM_022961	vacuolar protein sorting 33A (yeast)	Vps33a	0.898	0.219	0.570	0.041	0.642	0.035	0.665	0.062
1370521_at	U35245	vacuolar protein sorting 33B (yeast)	Vps33b	0.651	0.040	0.607	0.026	0.810	0.452	0.664	0.011
1372806_at	AA955295	vacuolar protein sorting 35 (mapped)	Vps35_mapped	0.752	0.580	1.144	0.093	0.655	0.212	1.107	0.551
1389191_at	AA858649	vacuolar protein sorting 36 (yeast) (predicted)	Vps36_predicted	0.542	0.026	1.193	0.090	1.384	0.842	1.346	0.643
1374068_at	BG673672	vacuolar protein sorting 39 (yeast)	Vps39	0.796	0.595	1.083	0.138	0.940	0.236	0.844	0.784
1370549_at	U81160	vacuolar protein sorting 45 (yeast)	Vps45	0.807	0.153	0.824	0.160	0.787	0.095	0.742	0.101
1372834_at	BI304063	vacuolar protein sorting 4b (yeast)	Vps4b	0.793	0.669	1.002	0.786	0.581	0.100	0.899	0.029
1374824_at	BG373086	vacuolar protein sorting 53 (yeast) (predicted)	Vps53_predicted	1.095	0.716	1.124	0.658	0.937	0.684	1.281	0.047
1370974_at	AJ010392	vacuolar protein sorting 54 (yeast)	Vps54	2.347	0.006	0.919	0.472	4.345	0.001	1.353	0.082
1395193_at	BM384656	Vacuolar protein sorting 54 (yeast)	Vps54	2.351	0.078	2.310	0.133	7.351	0.002	2.490	0.178
1371673_at	AI413005	vacuolar protein sorting 72 (yeast) (predicted)	Vps72_predicted	0.931	0.541	1.221	0.020	0.878	0.589	1.006	0.358
1377849_at	BI284363	valosin containing protein (p97)/p47 complex interacting protein 1	Vcpip1	1.861	0.013	1.830	0.073	2.465	0.007	1.650	0.131
1390858_at	BM383657	valosin containing protein (p97)/p47 complex interacting protein 1	Vcpip1	1.301	0.068	1.179	0.529	1.410	0.030	1.053	0.647
1367455_at	NM_053864	valosin-containing protein	Vcp	0.608	0.280	0.779	0.011	0.890	0.386	0.880	0.057
1372578_at	AI704469	valyl-tRNA synthetase 2	Vars2	1.829	0.025	2.923	0.000	1.887	0.019	2.381	0.001
1385661_at	BG057536	valyl-tRNA synthetase 2	Vars2	0.897	0.050	1.040	0.439	0.698	0.054	1.094	0.122
1389689_at	BI276974	valyl-tRNA synthetase 2-like	Vars2l	2.044	0.244	1.207	0.066	2.252	0.702	0.994	0.982
1394435_at	AI703874	vang, van gogh-like 1 (Drosophila) (predicted)	Vangl1_predicted	1.277	0.180	10.610	0.001	0.792	0.750	10.233	0.001
1392667_at	AI070793	vang-like 2 (van gogh, Drosophila) (predicted)	Vangl2_predicted	0.308	0.028	0.251	0.007	0.719	0.092	0.303	0.006
1375493_at	BE104373	vang-like 2 (van gogh, Drosophila) (predicted)	Vangl2_predicted	0.967	0.969	0.188	0.041	0.925	0.993	0.227	0.042
1389253_at	BI289085	vanin 1	Vnn1	0.622	0.097	0.348	0.217	0.608	0.054	0.356	0.008
1368474_at	NM_012889	vascular cell adhesion molecule 1	Vcam1	3.130	0.038	2.498	0.027	34.831	0.000	28.369	0.000
1370081_a_at	AF080594	vascular endothelial growth factor A	Vegfa	0.851	0.773	4.375	0.045	0.317	0.067	2.682	0.267
1396934_at	AI410280	Vascular endothelial growth factor B	Vegfb	0.960	0.695	1.853	0.035	0.930	0.043	0.946	0.275
1371581_at	BM388899	Vascular endothelial zinc finger 1 (predicted)	Vezf1_predicted	0.615	0.003	1.040	0.244	0.694	0.016	1.025	0.410
1374072_at	AI010272	Vascular endothelial zinc finger 1 (predicted)	Vezf1_predicted	0.682	0.034	0.466	0.034	0.875	0.093	0.768	0.105
1377806_at	BF556273	vascular endothelial zinc finger 1 (predicted)	Vezf1_predicted	1.730	0.060	0.829	0.045	1.235	0.064	0.941	0.144
1393784_at	BI284190	vascular endothelial zinc finger 1 (predicted)	Vezf1_predicted	1.781	0.115	0.336	0.159	1.932	0.281	0.779	0.805
1376594_at	AW524517	vascular endothelial zinc finger 1 (predicted)	Vezf1_predicted	1.731	0.145	3.160	0.004	1.450	0.051	3.436	0.020
1383537_at	BF522715	Vascular endothelial zinc finger 1 (predicted)	Vezf1_predicted	1.840	0.235	1.675	0.006	1.787	0.031	1.796	0.009
1395103_at	BF397372	Vascular endothelial zinc finger 1 (predicted)	Vezf1_predicted	1.116	0.976	1.194	0.253	1.119	0.996	1.068	0.689
1387177_at	NM_017238	vasoactive intestinal peptide receptor 2	Vipr2	0.349	0.002	0.132	0.002	0.360	0.052	0.111	0.003
1372459_at	AW520792	vasodilator-stimulated phosphoprotein (predicted)	Vasp_predicted	1.396	0.019	1.268	0.006	1.090	0.020	1.200	0.010
1395605_at	BM384452	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	Crkl	0.989	0.968	4.107	0.012	0.995	0.987	3.118	0.096
1394539_at	BF413362	Ventral anterior homeobox 2	Vax2	1.092	0.976	0.495	0.060	1.064	0.956	0.669	0.081
1369098_at	NM_013155	very low density lipoprotein receptor	Vldlr	1.074	0.337	2.097	0.010	0.657	0.093	1.699	0.038
1387455_a_at	NM_013155	very low density lipoprotein receptor	Vldlr	0.631	0.362	2.786	0.000	0.498	0.004	2.345	0.002
1371432_at	BI284849	vesicle amine transport protein 1 homolog (T californica)	Vat1	1.054	0.619	2.265	0.003	0.807	0.009	1.472	0.036
1367730_at	NM_019379	vesicle docking protein	Vdp	0.579	0.038	0.899	0.083	0.750	0.027	0.931	0.079
1368889_at	NM_023101	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	Vti1a	1.061	0.645	3.068	0.092	0.840	0.054	1.679	0.127
1373510_at	BF281373	vesicle-associated membrane protein 1	Vamp1	0.592	0.088	0.623	0.024	0.600	0.094	0.645	0.040
1369974_at	NM_012663	vesicle-associated membrane protein 2	Vamp2	0.307	0.140	0.345	0.009	0.327	0.069	0.263	0.001
1399159_a_at	NM_057097	vesicle-associated membrane protein 3	Vamp3	1.261	0.234	0.767	0.028	1.581	0.032	1.014	0.526
1391494_at	AW527503	vesicle-associated membrane protein 4 (predicted)	Vamp4_predicted	0.486	0.237	0.745	0.023	0.571	0.093	0.828	0.116
1384034_at	D86817	vesicle-associated membrane protein 4 (predicted)	Vamp4_predicted	0.907	0.766	0.677	0.051	0.863	0.655	0.620	0.066
1398840_at	NM_053555	vesicle-associated membrane protein 5	Vamp5	1.001	0.954	1.009	0.930	1.040	0.520	1.002	0.970

1369970_at	NM_031827	vesicle-associated membrane protein 8	Vamp8	1.907	0.114	2.123	0.011	1.414	0.002	1.466	0.032
1398843_at	AI411103	vesicle-associated membrane protein, associated protein a	Vapa	0.839	0.175	1.519	0.001	0.800	0.030	1.370	0.001
1397977_at	AI548601	Vesicle-associated membrane protein, associated protein a	Vapa	0.953	0.458	1.215	0.407	1.038	0.989	1.122	0.174
1390257_at	BG376956	vesicle-associated membrane protein, associated protein B and C	Vapb	0.392	0.033	0.775	0.116	0.468	0.030	0.632	0.029
1376893_at	AI406821	Vesicular membrane protein p24 (predicted)	Vmp_predicted	1.240	0.043	4.899	0.001	0.687	0.005	1.530	0.157
1375533_at	BI289645	vestigial like 4 (Drosophila)	Vgll4	1.041	0.402	0.841	0.099	1.033	0.856	0.771	0.038
1374589_at	AI235367	vezatin, adherens junctions transmembrane protein	Vezt	2.258	0.016	1.889	0.102	1.565	0.889	1.299	0.167
1368359_a_at	NM_030997	VGF nerve growth factor inducible	Vgf	1.941	0.009	1.615	0.085	1.900	0.004	2.016	0.034
1379393_at	AI231564	villin 1 (predicted)	Vil1_predicted	1.134	0.478	0.447	0.001	0.658	0.094	0.367	0.034
1370875_at	AA851304	villin 2	Vil2	5.759	0.006	7.296	0.001	9.216	0.000	9.800	0.000
1367574_at	NM_031140	vimentin	Vim	3.782	0.002	1.759	0.025	2.506	0.043	1.676	0.038
1373338_at	AI175767	Vimentin-type intermediate filament associated coiled-coil protein	Vmac	0.274	0.034	0.104	0.001	0.198	0.004	0.158	0.025
1368854_at	AI227991	visinin-like 1	Vsnl1	0.098	0.000	0.094	0.003	0.078	0.019	0.120	0.020
1368853_at	NM_012686	visinin-like 1	Vsnl1	0.506	0.286	0.039	0.001	0.684	0.385	0.059	0.001
1388330_at	BM384958	vitamin K epoxide reductase complex, subunit 1	Vkorc1	0.644	0.328	0.474	0.011	0.666	0.015	0.441	0.020
1393621_at	AA956405	vitamin K epoxide reductase complex, subunit 1-like 1	Vkorc1l1	0.800	0.755	1.684	0.111	0.528	0.036	1.954	0.117
1370035_at	NM_031515	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	Kras	0.935	0.806	1.146	0.400	1.013	0.921	1.058	0.468
1387947_at	U56241	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)	Mafb	1.043	0.868	1.628	0.056	0.883	0.985	0.991	0.949
1372211_at	BI284461	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian)	Mafk	2.872	0.006	4.491	0.001	2.883	0.003	4.190	0.004
1385243_at	AI180340	V-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	Maf	1.495	0.364	0.998	0.554	2.057	0.034	1.365	0.282
1392566_at	AA957811	V-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	Maf	0.498	0.434	1.240	0.592	1.022	0.517	1.079	0.158
1367706_at	NM_031353	voltage-dependent anion channel 1	Vdac1	0.763	0.013	0.860	0.013	0.668	0.000	0.890	0.116
1386909_a_at	AF268467	voltage-dependent anion channel 1	Vdac1	0.670	0.128	0.621	0.255	0.254	0.133	0.556	0.438
1380782_at	AW528654	Voltage-dependent anion channel 1	Vdac1	1.022	0.813	1.163	0.167	1.051	0.680	1.075	0.810
1369933_at	AF268468	voltage-dependent anion channel 2	Vdac2	0.962	0.879	1.252	0.027	0.800	0.049	0.986	0.774
1386902_at	NM_031355	voltage-dependent anion channel 3	Vdac3	0.816	0.271	1.133	0.123	0.710	0.009	1.087	0.872
1368076_at	NM_052801	von Hippel-Lindau syndrome homolog	Vhl	2.414	0.042	2.575	0.000	1.981	0.046	2.374	0.003
1379093_at	BF404377	V-raf murine sarcoma 3611 viral oncogene homolog	Araf	0.752	0.025	0.759	0.914	0.757	0.360	0.945	0.845
1368390_at	NM_022532	v-raf murine sarcoma 3611 viral oncogene homolog	Araf	0.803	0.255	0.847	0.124	1.164	0.923	1.032	0.405
1388305_at	AI176666	v-raf murine sarcoma 3611 viral oncogene homolog	Araf	0.799	0.368	0.761	0.016	0.835	0.279	0.854	0.007
1388818_at	AA946074	V-raf murine sarcoma 3611 viral oncogene homolog	Araf	0.890	0.468	1.220	0.674	1.164	0.548	0.822	0.167
1381099_at	AI236843	V-raf murine sarcoma 3611 viral oncogene homolog	Araf	1.090	0.994	1.027	0.858	1.368	0.220	1.029	0.857
1395554_at	BF405684	V-raf-1 murine leukemia viral oncogene homolog 1	Raf1	0.993	0.469	0.867	0.018	0.980	0.504	0.853	0.013
1369932_a_at	NM_012639	v-raf-1 murine leukemia viral oncogene homolog 1	Raf1	0.951	0.999	1.464	0.003	0.885	0.696	1.109	0.168
1368405_at	NM_031093	v-ral simian leukemia viral oncogene homolog A (ras related)	Rala	1.544	0.288	4.162	0.000	1.173	0.048	3.669	0.000
1374285_at	AW531275	V-ral simian leukemia viral oncogene homolog A (ras related)	Rala	1.002	0.996	0.611	0.004	0.998	0.244	0.768	0.039
1387001_at	NM_053821	v-ral simian leukemia viral oncogene homolog B	Ralb	1.054	0.819	2.336	0.002	1.042	0.928	2.034	0.010
1372853_at	BF283772	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	Rela	2.322	0.016	2.407	0.000	3.094	0.010	2.531	0.006
1368432_a_at	NM_012874	v-ros UR2 sarcoma virus oncogene homolog 1 (avian)	Ros1	1.068	0.825	0.499	0.193	0.811	0.866	0.852	0.710
1392974_at	BI295427	WAS protein family, member 1	Wasf1	0.584	0.255	0.630	0.026	0.664	0.247	0.910	0.050
1394935_at	AI175684	WAS protein family, member 2	Wasf2	1.003	0.328	5.107	0.051	1.007	0.713	1.878	0.066
1376256_at	BE108131	WD repeat and FYVE domain containing 1	Wdfy1	3.432	0.068	4.272	0.009	2.122	0.516	2.411	0.090
1376448_at	AI575081	WD repeat and FYVE domain containing 1	Wdfy1	1.270	0.258	3.906	0.012	1.407	0.872	3.022	0.018
1392710_at	AI101727	WD repeat and FYVE domain containing 1	Wdfy1	0.984	0.371	2.251	0.000	1.022	0.593	1.853	0.007
1372837_at	BI277033	WD repeat and FYVE domain containing 2 (predicted)	Wdfy2_predicted	0.823	0.044	0.850	0.399	0.385	0.178	0.811	0.274
1389128_at	AI146179	WD repeat and FYVE domain containing 3 (predicted)	Wdfy3_predicted	1.207	0.495	0.713	0.013	0.941	0.302	0.671	0.003
1374204_at	BM388946	WD repeat and SOCS box-containing 1	Wsb1	1.572	0.027	2.229	0.004	1.877	0.010	1.966	0.013
1372218_at	BM384448	WD repeat domain 12	Wdr12	0.594	0.042	1.399	0.021	0.567	0.016	1.199	0.046
1372373_at	AI713206	WD repeat domain 13 (predicted)	Wdr13_predicted	0.720	0.131	0.576	0.035	1.236	0.980	0.695	0.477
1375439_at	BF417010	WD repeat domain 18	Wdr18	0.966	0.979	1.216	0.978	1.072	0.788	1.213	0.987
1373084_at	BI300912	WD repeat domain 20	Wdr20	0.767	0.094	0.687	0.374	0.713	0.469	1.526	0.072
1390661_at	BE115928	WD repeat domain 20	Wdr20	1.211	0.507	1.961	0.076	0.701	0.635	1.560	0.051
1397061_at	BF394045	WD repeat domain 22	Wdr22	1.395	0.320	0.829	0.111	1.408	0.808	0.559	0.017
1379084_at	AW533710	WD repeat domain 22	Wdr22	1.161	0.362	2.155	0.046	0.834	0.109	1.400	0.486
1389335_at	BM387479	WD repeat domain 22	Wdr22	1.001	0.674	1.068	0.414	1.025	0.522	1.419	0.086
1371549_at	AI228630	WD repeat domain 23	Wdr23	0.785	0.248	1.326	0.041	1.112	0.608	1.165	0.020
1373938_at	BF284753	WD repeat domain 24	Wdr24	0.453	0.079	1.242	0.068	0.789	0.549	1.353	0.240
1374793_at	BE113663	WD repeat domain 3 (predicted)	Wdr3_predicted	0.389	0.009	1.919	0.008	0.823	0.131	1.583	0.007
1389993_at	BI299095	WD repeat domain 33 (predicted)	Wdr33_predicted	1.183	0.174	1.150	0.330	0.897	0.771	1.251	0.048
1385240_at	AW523099	WD repeat domain 33 (predicted)	Wdr33_predicted	0.780	0.677	1.065	0.830	1.990	0.252	0.943	0.668
1377619_at	AI407932	WD repeat domain 36 (predicted)	Wdr36_predicted	0.674	0.104	0.775	0.209	0.339	0.040	0.951	0.188

1385804_x_at	AA956841	WD repeat domain 36 (predicted)	Wdr36_predicted	0.788	0.628	1.567	0.053	0.594	0.011	1.186	0.200
1390788_a_at	AI407932	WD repeat domain 36 (predicted)	Wdr36_predicted	0.978	0.933	1.440	0.056	0.708	0.018	1.289	0.043
1390784_at	BG662814	WD repeat domain 37 (predicted)	Wdr37_predicted	0.420	0.013	1.431	0.554	0.480	0.032	0.806	0.480
1380131_at	BE116354	WD repeat domain 37 (predicted)	Wdr37_predicted	0.907	0.276	0.930	0.390	0.821	0.068	1.135	0.344
1372245_at	AA894272	WD repeat domain 39	Wdr39	0.563	0.102	0.555	0.001	0.462	0.053	0.657	0.002
1395065_at	AW521367	WD repeat domain 41 (predicted)	Wdr41_predicted	0.710	0.061	0.860	0.387	1.318	0.709	0.844	0.350
1390451_at	BM390195	WD repeat domain 41 (predicted)	Wdr41_predicted	1.523	0.113	1.030	0.370	1.544	0.334	0.938	0.229
1397843_at	BG663841	WD repeat domain 44	Wdr44	0.887	0.054	0.994	0.523	0.862	0.047	0.980	0.844
1393955_at	BI293101	WD repeat domain 44	Wdr44	1.376	0.103	0.603	0.023	0.962	0.075	0.748	0.026
1399030_at	AA800682	WD repeat domain 45	Wdr45	0.932	0.655	1.138	0.121	0.796	0.411	1.147	0.160
1374152_at	BF290018	WD repeat domain 46	Wdr46	0.744	0.304	0.989	0.938	1.131	0.719	1.006	0.950
1372781_at	BG378912	WD repeat domain 47	Wdr47	0.876	0.447	0.305	0.004	0.859	0.548	0.546	0.018
1384152_at	BE101118	WD repeat domain 48 (predicted)	Wdr48_predicted	1.074	0.037	1.743	0.146	1.160	0.146	0.901	0.391
1372388_at	AI227930	WD repeat domain 48 (predicted)	Wdr48_predicted	1.142	0.126	0.745	0.008	0.923	0.622	0.769	0.086
1388897_at	BI282734	WD repeat domain 5	Wdr5	1.045	0.540	1.369	0.140	0.674	0.127	1.108	0.495
1383297_at	BI275422	WD repeat domain 5	Wdr5	1.062	0.994	1.890	0.020	0.772	0.026	1.443	0.038
1393043_at	BM391844	WD repeat domain 50 (predicted)	Wdr50_predicted	0.712	0.059	1.054	0.778	0.557	0.045	0.987	0.351
1397157_at	BF411716	WD repeat domain 59	Wdr59	3.575	0.022	1.994	0.062	2.675	0.058	1.146	0.027
1389232_at	BI296464	WD repeat domain 5B	Wdr5b	0.858	0.274	0.839	0.212	0.932	0.717	0.687	0.286
1373399_at	BI291997	WD repeat domain 6	Wdr6	0.386	0.001	0.252	0.001	0.398	0.004	0.344	0.019
1389323_at	BF282629	WD repeat domain 61	Wdr61	0.497	0.142	0.714	0.002	0.605	0.041	0.715	0.000
1373548_at	BE107518	WD repeat domain 68 (predicted)	Wdr68_predicted	0.687	0.324	0.677	0.039	0.794	0.042	0.752	0.646
1397017_at	BF400853	WD repeat domain 7	Wdr7	0.887	0.833	1.137	0.644	0.745	0.702	0.840	0.652
1395058_at	AI556441	WD repeat domain 75	Wdr75	0.709	0.048	0.851	0.865	0.845	0.068	0.660	0.188
1391432_at	BM385275	WD repeat domain 75	Wdr75	0.692	0.074	1.078	0.765	0.961	0.135	1.063	0.688
1388560_at	AI412580	WD repeat domain 77	Wdr77	0.683	0.080	1.832	0.002	0.604	0.007	1.742	0.002
1373694_at	H33486	WD repeat domain 79	Wdr79	0.644	0.096	1.007	0.960	0.637	0.051	0.721	0.739
1373270_at	AI233288	WD repeat domain, phosphoinositide interacting 1 (predicted)	Wipi1_predicted	1.783	0.097	0.795	0.313	1.686	0.209	0.690	0.086
1389068_at	BI288819	WD repeat domain, phosphoinositide interacting 2	Wipi2	1.418	0.756	3.951	0.015	1.018	0.943	1.897	0.078
1389520_at	BI285874	WD repeat protein 1	Wdr1	1.486	0.028	1.351	0.045	1.281	0.040	1.046	0.178
1392399_at	BG377835	WD repeats and SOF domain containing 1 (predicted)	Wdsof1_predicted	0.913	0.194	1.202	0.018	0.932	0.606	1.078	0.015
1383651_a_at	AA964509	Wdr45 like (predicted)	Wdr45l_predicted	0.948	0.636	1.505	0.002	1.101	0.242	1.329	0.009
1397409_s_at	BE113999	wee 1 homolog (S. pombe)	Wee1	0.983	0.250	1.887	0.019	0.543	0.017	1.884	0.029
1370663_at	D31838	wee 1 homolog (S. pombe)	Wee1	1.181	0.719	1.870	0.027	0.641	0.049	1.739	0.011
1389090_at	BI284350	Werner helicase interacting protein 1	Wrnip1	0.929	0.675	1.441	0.010	1.007	0.700	1.620	0.110
1389643_at	H31790	widely-interspaced zinc finger motifs (predicted)	Wiz_predicted	1.170	0.464	1.913	0.025	1.219	0.651	1.829	0.002
1387021_at	NM_022548	wild-type p53-induced gene 1	Wig1	0.933	0.233	0.782	0.270	1.369	0.426	0.960	0.626
1399083_at	BF283000	Williams Beuren syndrome chromosome region 21 /// similar to Williams-Beuren syndrome critical region protein 21	Wbscr21 /// LOC368083	0.729	0.376	0.993	0.872	0.692	0.132	0.982	0.739
1367531_at	BG666846	Williams-Beuren syndrome chromosome region 1 homolog (human)	Wbscr1	1.108	0.668	1.283	0.049	1.016	0.872	1.370	0.146
1368614_at	NM_133552	Williams-Beuren syndrome chromosome region 14 homolog (human)	Wbscr14	1.233	0.155	0.447	0.000	1.679	0.128	0.410	0.082
1377223_at	AI599621	Wilms tumor 1	Wt1	0.954	0.591	1.000	0.986	1.000	0.612	0.989	0.961
1368641_at	NM_053402	wingless-related MMTV integration site 4	Wnt4	0.671	0.422	0.569	0.650	0.580	0.304	0.320	0.075
1376063_at	AI599019	wingless-related MMTV integration site 6 (predicted)	Wnt6_predicted	1.001	0.386	0.986	0.685	0.849	0.342	0.988	0.258
1369263_at	NM_022631	wingless-type MMTV integration site 5A	Wnt5a	1.375	0.674	1.046	0.980	0.778	0.377	0.677	0.294
1385385_at	BE116745	Wingless-type MMTV integration site 5A	Wnt5a	0.997	0.890	0.997	0.377	2.012	0.000	0.995	0.994
1387227_at	NM_057192	Wiskott-Aldrich syndrome protein interacting protein	Waspip	1.738	0.288	1.002	0.708	0.852	0.672	0.868	0.403
1376124_at	BG375480	Wiskott-Aldrich syndrome-like (human)	Wasl	2.402	0.038	1.526	0.051	2.394	0.049	1.373	0.004
1384549_at	BI292428	Within bgcn homolog (Drosophila) (predicted)	Wibg_predicted	1.337	0.811	0.865	0.275	0.999	0.114	0.620	0.616
1369203_at	NM_053738	Wnt inhibitory factor 1	Wif1	0.845	0.375	0.315	0.007	0.624	0.162	0.557	0.019
1392806_at	AI234807	Wolf-Hirschhorn syndrome candidate 1-like 1 (predicted)	Whsc1l1_predicted	1.917	0.089	2.082	0.000	1.084	0.812	1.747	0.010
1378114_at	BF415965	Wolf-Hirschhorn syndrome candidate 1-like 1 (predicted)	Whsc1l1_predicted	0.958	0.794	0.681	0.102	0.889	0.513	0.461	0.029
1385941_at	BI295778	Wolf-Hirschhorn syndrome candidate 1-like 1 (predicted)	Whsc1l1_predicted	1.002	0.981	0.979	0.940	1.420	0.007	1.013	0.904
1389175_at	AA956953	Wolf-Hirschhorn syndrome candidate 2 (human)	Whsc2	0.684	0.973	0.846	0.048	0.941	0.675	0.944	0.125
1368839_at	AI407433	Wolfram syndrome 1 homolog (human)	Wfs1	0.481	0.014	1.026	0.776	0.572	0.004	0.989	0.766
1387356_at	NM_031823	Wolfram syndrome 1 homolog (human)	Wfs1	0.996	0.918	0.937	0.291	0.998	0.926	0.935	0.276
1372232_at	AI170808	WW domain binding protein 1	Wbp1	0.512	0.127	0.425	0.000	0.698	0.255	0.381	0.047
1380108_at	BI289053	WW domain binding protein 1	Wbp1	0.997	0.817	1.035	0.588	1.000	0.997	1.037	0.739
1372575_at	AA892364	WW domain binding protein 11	Wbp11	0.984	0.847	1.446	0.062	0.848	0.400	1.294	0.018
1384154_at	BF554739	WW domain binding protein 4	Wbp4	1.208	0.181	0.946	0.342	1.534	0.033	0.926	0.310
1396170_at	BG663444	WW domain binding protein 4	Wbp4	0.762	0.277	1.009	0.894	0.995	0.472	1.115	0.091

1389857_at	BG378874	WW domain binding protein 5 (predicted)	Wbp5_predicted	0.567	0.326	0.578	0.023	0.561	0.055	0.620	0.006
1395268_at	BM383223	WW domain containing E3 ubiquitin protein ligase 1	Wwp1	1.432	0.319	2.656	0.029	1.780	0.044	2.496	0.034
1374256_at	BM384248	WW domain containing E3 ubiquitin protein ligase 2 (predicted)	Wwp2_predicted	1.189	0.385	2.744	0.034	0.998	0.757	1.266	0.931
1379922_at	BM389053	WW domain containing E3 ubiquitin protein ligase 2 (predicted)	Wwp2_predicted	1.000	0.862	2.020	0.059	1.610	0.129	1.304	0.138
1379321_at	AI180133	X Kell blood group precursor related family member 6 homolog	Xkr6	0.621	0.009	0.586	0.001	0.710	0.087	0.539	0.075
1371249_at	BF417262	X-box binding protein 1	Xbp1	0.703	0.122	0.927	0.062	0.627	0.080	0.942	0.208
1375846_at	BE113490	Xenotropic and polytropic retrovirus receptor 1 (predicted)	Xpr1_predicted	2.057	0.007	1.467	0.055	1.895	0.004	1.267	0.096
1384029_at	BF554085	xeroderma pigmentosum, complementation group A (predicted)	Xpa_predicted	1.839	0.184	1.696	0.111	0.640	0.043	1.172	0.655
1390381_at	BG379358	xeroderma pigmentosum, complementation group C (predicted)	Xpc_predicted	1.290	0.324	1.270	0.040	1.437	0.072	1.466	0.011
1394928_at	BG669146	XK-related protein 4	XRG4	1.580	0.496	1.737	0.088	0.999	0.987	1.419	0.157
1382025_at	BG668084	X-linked myotubular myopathy gene 1	Mtm1	0.736	0.035	0.677	0.117	0.766	0.050	0.692	0.105
1370343_at	AF277899	XPA binding protein 2	Xab2	1.009	0.418	1.666	0.126	0.999	0.256	1.606	0.032
1370160_at	AI178742	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	Xpnpep1	0.845	0.158	0.915	0.068	0.808	0.373	0.985	0.574
1374304_at	AW526081	X-ray repair complementing defective repair in Chinese hamster cells 4	Xrcc4	1.476	0.168	0.864	0.750	1.025	0.516	1.055	0.053
1370931_at	AA893188	X-ray repair complementing defective repair in Chinese hamster cells 5	Xrcc5	0.984	0.978	0.465	0.071	1.342	0.981	0.753	0.175
1370537_at	AB066102	X-ray repair complementing defective repair in Chinese hamster cells 6	Xrcc6	0.481	0.045	1.019	0.692	0.282	0.053	1.498	0.404
1390857_at	BI279844	xylulokinase homolog (H. influenzae)	Xylb	0.676	0.025	1.234	0.113	0.694	0.045	0.958	0.998
1370213_at	BI282111	Y box protein 1 related, pseudogene 3 /// similar to nuclease sensitive element binding protein 1 (predicted) /// Y box protein 1	Ybx1-ps3 /// RGD1560265_predicted /// Ybx1	0.891	0.515	1.039	0.259	0.914	0.360	0.960	0.582
1387277_at	NM_030857	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog	Lyn	1.170	0.281	0.980	0.927	1.425	0.894	0.737	0.103
1378100_at	BG380660	YEATS domain containing 4 (predicted)	Yeats4_predicted	1.469	0.366	0.944	0.948	1.213	0.352	1.050	0.208
1372893_at	BI284198	Yip1 domain family, member 1	Yipf1	0.826	0.685	0.555	0.005	0.528	0.198	0.567	0.004
1376670_at	AW434026	Yip1 domain family, member 2	Yipf2	0.657	0.468	0.680	0.029	0.725	0.162	0.689	0.098
1389035_at	BF284830	Yip1 domain family, member 3	Yipf3	0.542	0.299	0.280	0.002	0.546	0.040	0.323	0.051
1394414_at	BF386706	Yip1 domain family, member 4	Yipf4	0.688	0.073	0.555	0.001	0.892	0.048	0.610	0.031
1376727_at	BF283348	Yip1 domain family, member 4	Yipf4	0.779	0.561	0.923	0.464	0.720	0.833	0.921	0.723
1371843_at	AI234128	Yip1 domain family, member 5	Yipf5	0.641	0.038	1.113	0.094	0.579	0.012	1.029	0.153
1370305_at	U96490	Yip1 interacting factor homolog (S. cerevisiae)	Yif1	0.479	0.278	0.978	0.346	0.356	0.019	0.950	0.702
1389715_at	BG381499	yippee-like 4	Ypel4	1.364	0.535	0.443	0.005	2.008	0.028	0.598	0.224
1371729_at	AI169150	yippee-like 5 (Drosophila)	Ypel5	0.919	0.383	1.649	0.015	0.892	0.231	1.574	0.049
1373826_at	AI170754	yippee-like 5 (Drosophila)	Ypel5	1.195	0.402	2.125	0.001	1.010	0.953	1.765	0.002
1368843_at	NM_053682	YME1-like 1 (S. cerevisiae)	Yme1l1	1.014	0.285	1.172	0.414	1.131	0.142	0.986	0.882
1385999_at	AA849923	YME1-like 1 (S. cerevisiae)	Yme1l1	0.942	0.627	0.712	0.060	1.043	0.365	0.698	0.003
1394059_s_at	AA849923	YME1-like 1 (S. cerevisiae)	Yme1l1	0.904	0.862	0.648	0.012	0.909	0.715	0.783	0.089
1367498_at	AI177873	YTH domain family 1	Ythdf1	0.770	0.004	0.675	0.003	1.122	0.153	0.782	0.009
1385699_at	BI283897	YTH domain family 1	Ythdf1	1.003	0.966	1.498	0.019	1.232	0.812	1.442	0.044
1389524_at	AA997881	YTH domain family 3 (predicted)	Ythdf3_predicted	0.806	0.695	0.699	0.068	0.827	0.294	0.695	0.024
1375122_at	AI233235	YY1 associated factor 2 (predicted)	Yaf2_predicted	1.674	0.086	1.832	0.076	1.504	0.011	1.408	0.100
1375903_a_at	AI012344	YY1 associated factor 2 (predicted)	Yaf2_predicted	0.972	0.923	1.198	0.881	0.983	0.393	0.837	0.902
1392677_at	AA924705	Zic family member 4 (predicted)	Zic4_predicted	1.131	0.688	0.943	0.829	2.560	0.025	0.705	0.217
1379264_at	BE109004	zinc and ring finger 1 (predicted)	Znrf1_predicted	1.077	0.611	0.596	0.027	0.869	0.342	0.694	0.069
1377844_at	AI411520	zinc binding alcohol dehydrogenase, domain containing 1	Zadh1	0.819	0.548	0.864	0.411	0.966	0.293	1.356	0.895
1388731_at	AA850919	zinc binding alcohol dehydrogenase, domain containing 2 (predicted)	Zadh2_predicted	0.427	0.318	0.221	0.006	0.511	0.048	0.221	0.031
1393652_at	BF398438	zinc finger and BTB domain containing 1	Zbtb1	2.040	0.091	1.337	0.261	2.585	0.089	1.310	0.001
1385217_at	BM385870	Zinc finger and BTB domain containing 10	Zbtb10	2.790	0.006	6.073	0.019	2.060	0.022	3.315	0.002
1379578_at	BF415114	zinc finger and BTB domain containing 20 (predicted)	Zbtb20_predicted	0.728	0.366	0.635	0.034	1.100	0.729	0.813	0.039
1375867_at	AW524493	zinc finger and BTB domain containing 4 (predicted)	Zbtb4_predicted	0.645	0.012	0.472	0.003	0.533	0.014	0.530	0.006
1375302_at	BM384146	zinc finger and BTB domain containing 4 (predicted)	Zbtb4_predicted	1.301	0.429	0.646	0.015	0.740	0.641	0.629	0.030
1394675_at	AI178470	Zinc finger and BTB domain containing 40 (predicted)	Zbtb40_predicted	1.080	0.759	0.994	0.911	1.003	1.000	1.029	0.057
1387107_at	NM_054002	zinc finger and BTB domain containing 7a	Zbtb7a	1.355	0.338	2.105	0.011	1.619	0.983	1.857	0.012
1389907_at	AI169317	zinc finger and BTB domain containing 8 opposite strand (predicted)	Zbtb8os_predicted	0.475	0.239	0.610	0.115	0.252	0.009	0.650	0.096
1377454_at	AW524041	zinc finger and BTB domain containing 9	Zbtb9	0.812	0.180	1.198	0.310	0.701	0.044	1.211	0.631
1379971_at	BE102241	zinc finger CCCH type containing 6 (predicted)	Zc3h6_predicted	1.315	0.393	0.796	0.243	0.916	0.522	0.748	0.162
1374208_at	BE116569	zinc finger CCCH type containing 7 A (predicted)	Zc3h7a_predicted	2.029	0.000	2.455	0.000	2.751	0.009	1.987	0.001
1378119_at	BG381574	zinc finger CCCH type containing 8	Zc3h8	1.250	0.401	1.672	0.005	0.854	0.180	1.447	0.114
1388409_at	AW142595	zinc finger CCCH-type containing 7B (predicted)	Zc3h7b_predicted	0.965	0.370	1.094	0.327	0.911	0.737	0.976	0.709
1371624_at	BI279282	zinc finger CCCH-type containing 7B (predicted)	Zc3h7b_predicted	0.811	0.861	0.684	0.097	1.373	0.321	0.805	0.305
1392629_a_at	BF386158	zinc finger CCHC-type and RNA binding motif 1	Zcrb1	0.837	0.889	1.136	0.383	1.111	0.012	1.261	0.006
1375582_at	AW531902	zinc finger homeodomain 4 (predicted)	Zfhx4_predicted	1.122	0.955	1.165	0.166	1.892	0.223	0.737	0.309
1384282_at	BG379149	zinc finger proliferation 1	Zipro1	1.440	0.332	2.122	0.026	1.026	0.921	1.839	0.049

1370984_at	AF151710	Zinc finger protein (pMLZ-4) mRNA, 3' untranslated region	---	0.897	0.568	1.021	0.083	0.862	0.814	1.465	0.069
1399086_at	AI179640	zinc finger protein 105	Zfp105	0.719	0.427	0.822	0.975	0.567	0.035	1.190	0.282
1372593_at	AI137283	zinc finger protein 110	Zfp110	0.793	0.589	0.711	0.051	0.637	0.139	0.881	0.287
1395418_at	BE110637	zinc finger protein 131	Zfp131	0.780	0.382	1.098	0.226	1.000	0.840	1.349	0.164
1393780_at	AA924380	zinc finger protein 131	Zfp131	0.840	0.661	1.247	0.144	1.152	0.055	1.225	0.095
1395839_at	BF561078	Zinc finger protein 142 (clone pHZ-49) (predicted)	Znf142_predicted	1.299	0.258	0.799	0.168	1.265	0.372	0.874	0.032
1379164_at	BE117672	Zinc finger protein 142 (clone pHZ-49) (predicted)	Znf142_predicted	1.927	0.277	1.539	0.068	1.485	0.236	1.415	0.048
1379704_at	BM383283	zinc finger protein 143	Zfp143	1.238	0.012	1.562	0.087	1.143	0.201	1.282	0.211
1378405_at	AI170262	zinc finger protein 143	Zfp143	1.811	0.104	1.581	0.042	2.698	0.051	1.018	0.976
1381998_at	AW519820	Zinc finger protein 148	Zfp148	0.930	0.071	0.842	0.009	0.632	0.006	0.913	0.041
1368067_at	NM_031615	zinc finger protein 148	Zfp148	0.599	0.213	0.428	0.063	0.633	0.139	0.554	0.011
1384783_at	BI289823	zinc finger protein 161	Zfp161	0.995	0.314	0.936	0.102	1.100	0.579	0.894	0.476
1380106_at	BF283079	zinc finger protein 162	Zfp162	0.853	0.788	0.664	0.060	0.897	0.275	0.565	0.049
1398339_at	BE109605	zinc finger protein 162	Zfp162	1.078	0.904	1.109	0.891	0.878	0.536	0.976	0.203
1387962_at	U41164	zinc finger protein 180	Zfp180	0.816	0.370	1.907	0.102	0.842	0.685	0.947	0.527
1388779_at	BG381516	zinc finger protein 180	Zfp180	0.878	0.931	1.237	0.016	0.633	0.020	1.488	0.038
1377837_at	AI231532	zinc finger protein 183 (RING finger, C3HC4 type)	Znf183	0.446	0.026	0.483	0.010	0.596	0.005	0.772	0.025
1383445_at	BG667490	zinc finger protein 191	Zfp191	1.005	0.957	0.830	0.168	0.803	0.106	0.713	0.157
1397132_at	BF390612	Zinc finger protein 207	Zfp207	1.178	0.027	1.397	0.229	0.876	0.337	0.954	0.981
1394591_at	AI411280	zinc finger protein 207	Zfp207	1.449	0.495	1.209	0.063	1.213	0.095	1.153	0.588
1385145_at	BE119870	Zinc finger protein 212	Zfp212	1.115	0.156	1.269	0.338	1.212	0.342	0.879	0.102
1380094_a_at	AI178375	Zinc finger protein 212	Zfp212	1.186	0.204	1.099	0.885	0.643	0.078	0.996	0.469
1386424_at	AI178375	Zinc finger protein 212	Zfp212	1.219	0.273	1.187	0.670	0.735	0.049	0.879	0.043
1383905_at	BF401729	Zinc finger protein 216 (predicted)	Zfp216_predicted	1.169	0.157	0.343	0.032	0.968	0.375	0.531	0.008
1388868_at	AI172425	zinc finger protein 216 (predicted)	Zfp216_predicted	1.474	0.659	0.970	0.760	1.072	0.826	1.174	0.047
1374189_at	BG668883	zinc finger protein 219	Zfp219	2.344	0.025	2.080	0.005	2.903	0.041	2.043	0.005
1389252_at	AI102190	Zinc finger protein 238	Zfp238	1.814	0.031	1.335	0.005	2.080	0.039	1.590	0.037
1393940_at	AI070444	Zinc finger protein 251 (predicted)	Znf251_predicted	0.824	0.063	0.829	0.235	0.530	0.030	0.972	0.916
1372817_at	BI291616	zinc finger protein 260	Zfp260	0.979	0.623	0.778	0.169	1.353	0.065	1.175	0.129
1368228_at	NM_031616	zinc finger protein 265	Zfp265	0.543	0.003	0.819	0.031	0.717	0.016	0.769	0.011
1387117_at	AF013965	zinc finger protein 265	Zfp265	0.581	0.190	1.250	0.754	0.760	0.163	0.987	0.685
1372205_at	AI713121	zinc finger protein 278	Zfp278	0.892	0.124	0.436	0.006	0.975	0.449	0.581	0.221
1382642_at	BI291753	zinc finger protein 281	Zfp281	0.961	0.109	1.088	0.376	1.089	0.982	0.972	0.128
1385869_at	AI408878	Zinc finger protein 281	Zfp281	0.932	0.148	0.751	0.091	0.881	0.937	0.838	0.217
1385870_at	AA997980	Zinc finger protein 281	Zfp281	0.883	0.768	1.005	0.538	0.825	0.394	1.005	0.980
1367486_at	BM386412	zinc finger protein 289	Zfp289	0.651	0.113	0.713	0.119	0.307	0.105	0.577	0.057
1371520_at	BI296732	zinc finger protein 291	Znf291	1.051	0.315	1.010	0.889	1.116	0.510	0.938	0.661
1390945_at	BI294878	zinc finger protein 292	Znf292	1.360	0.018	3.399	0.005	1.680	0.064	2.737	0.004
1376917_at	BF388585	zinc finger protein 292	Znf292	1.545	0.171	2.165	0.003	2.025	0.103	1.443	0.704
1379441_at	AA965092	zinc finger protein 294	Zfp294	0.610	0.014	0.390	0.001	0.705	0.019	0.702	0.049
1383462_at	BF566263	zinc finger protein 294	Zfp294	0.894	0.410	1.070	0.063	1.144	0.775	0.940	0.326
1399110_at	AW921218	zinc finger protein 297	Zfp297	1.173	0.039	0.956	0.133	0.700	0.955	0.872	0.202
1373763_at	AI013512	zinc finger protein 297B	Zfp297b	1.647	0.042	1.951	0.002	1.566	0.067	1.628	0.000
1398573_at	BE098868	zinc finger protein 307	Zfp307	1.269	0.021	0.746	0.035	0.939	0.711	0.877	0.215
1382744_at	H33694	zinc finger protein 307	Zfp307	1.073	0.533	0.894	0.475	0.907	0.550	0.800	0.990
1395198_at	BE099956	Zinc finger protein 313	Zfp313	1.823	0.049	1.452	0.367	2.567	0.027	1.683	0.542
1375955_at	BI289415	zinc finger protein 313	Zfp313	3.095	0.060	2.087	0.004	3.583	0.000	3.216	0.000
1386093_at	BI274863	zinc finger protein 324 (predicted)	Znf324_predicted	0.458	0.043	0.989	0.786	0.459	0.041	1.005	0.999
1389531_at	AW523471	zinc finger protein 330 (predicted)	Zfp330_predicted	0.782	0.454	2.123	0.002	0.824	0.007	1.506	0.024
1381609_at	AI710364	zinc finger protein 335	Zfp335	1.379	0.196	2.096	0.031	0.956	0.437	1.520	0.042
1390641_at	BE111799	Zinc finger protein 346 (predicted)	Zfp346_predicted	1.378	0.181	0.984	0.671	0.956	0.791	0.945	0.096
1381283_at	BE105217	Zinc finger protein 346 (predicted)	Zfp346_predicted	0.950	0.875	0.800	0.361	1.053	0.178	0.824	0.351
1368726_a_at	AB047638	zinc finger protein 347	Zfp347	1.222	0.146	1.668	0.058	1.159	0.530	1.687	0.000
1368877_at	NM_052798	zinc finger protein 354A	Zfp354a	1.951	0.466	1.715	0.032	1.682	0.593	2.388	0.018
1393127_at	AI707002	zinc finger protein 358 (predicted)	Zfp358_predicted	1.052	0.510	1.075	0.333	0.789	0.115	1.274	0.052
1387870_at	AB025017	zinc finger protein 36	Zfp36	11.336	0.031	4.636	0.001	19.573	0.016	9.877	0.001
1369959_at	NM_017172	zinc finger protein 36, C3H type-like 1	Zfp36l1	1.040	0.674	1.276	0.037	1.368	0.037	2.478	0.025
1373106_at	AI178069	zinc finger protein 36, C3H type-like 2	Zfp36l2	2.706	0.000	3.616	0.001	1.539	0.004	3.017	0.000
1375344_at	BF418884	Zinc finger protein 36, C3H type-like 2	Zfp36l2	1.001	0.490	1.123	0.457	1.001	0.911	0.999	0.260
1372865_at	AI171206	zinc finger protein 364 (predicted)	Zfp364_predicted	2.907	0.044	3.390	0.000	4.105	0.001	4.374	0.001
1384272_at	BG378837	Zinc finger protein 365	Zfp365	1.003	0.974	1.030	0.959	3.756	0.037	1.192	0.119

1379967_at	AI501039	zinc finger protein 367	Zfp367	0.897	0.739	0.848	0.266	0.998	0.987	0.602	0.052
1381166_at	AA944650	Zinc finger protein 383 (predicted)	Znf383_predicted	1.109	0.088	1.373	0.002	1.004	0.300	0.997	0.061
1370175_a_at	AI177799	zinc finger protein 384	Zfp384	1.262	0.082	1.562	0.004	1.110	0.258	1.484	0.014
1368712_at	NM_019620	zinc finger protein 386 (Kruppel-like)	Znf386	1.192	0.339	1.091	0.857	1.324	0.521	0.916	0.833
1390148_a_at	BM388100	Zinc finger protein 395 (predicted)	Zfp395_predicted	0.158	0.001	0.926	0.228	0.167	0.001	0.620	0.023
1372201_at	AI233698	zinc finger protein 403	Zfp403	1.299	0.020	2.212	0.018	1.368	0.013	2.002	0.010
1382721_at	BI280928	zinc finger protein 403	Zfp403	1.023	0.827	1.655	0.007	0.845	0.285	1.158	0.439
1392966_at	BF396256	zinc finger protein 410 (predicted)	Zfp410_predicted	1.378	0.179	1.967	0.014	1.368	0.174	1.296	0.142
1387105_at	NM_133579	zinc finger protein 422 /// zinc finger protein 422 (predicted)	Zfp422 /// Zfp422_predicted	0.792	0.119	0.587	0.052	0.785	0.039	0.646	0.014
1372985_at	BG378167	zinc finger protein 444 (predicted)	Zfp444_predicted	0.776	0.010	1.258	0.024	0.669	0.020	1.014	0.862
1384901_at	BF523017	Zinc finger protein 451	Zfp451	0.463	0.060	0.742	0.075	0.468	0.049	0.873	0.611
1382242_at	BE105280	zinc finger protein 451	Zfp451	1.080	0.248	0.640	0.000	1.566	0.883	0.672	0.003
1372480_at	BE117893	zinc finger protein 462 (predicted)	Zfp462_predicted	1.086	0.152	0.672	0.040	0.770	0.132	0.605	0.012
1372483_at	AI230979	zinc finger protein 469 (predicted)	Zfp469_predicted	1.608	0.065	0.639	0.007	0.782	0.917	0.474	0.027
1393311_at	AI044549	Zinc finger protein 469 (predicted)	Zfp469_predicted	1.290	0.081	2.443	0.089	1.136	0.537	1.654	0.116
1378609_at	AI113031	Zinc finger protein 5 (AZF5)	---	0.673	0.267	0.834	0.489	0.786	0.460	0.735	0.048
1386721_at	BF560938	zinc finger protein 503 (predicted)	Zfp503_predicted	0.965	0.811	1.767	0.038	1.470	0.103	1.082	0.555
1391216_at	BE114482	zinc finger protein 509 (predicted)	Zfp509_predicted	0.952	0.221	0.528	0.053	0.953	0.250	0.529	0.053
1379657_a_at	BM386837	zinc finger protein 511 (predicted)	Znf511_predicted	1.967	0.045	1.135	0.550	0.642	0.416	1.918	0.470
1372346_at	AI230729	zinc finger protein 513	Zfp513	1.370	0.032	1.058	0.821	1.585	0.065	1.242	0.618
1381831_at	AI112536	Zinc finger protein 532 (predicted)	Znf532_predicted	1.139	0.967	1.131	0.179	1.157	0.892	0.928	0.462
1391478_at	BI281649	zinc finger protein 532 (predicted)	Znf532_predicted	1.004	0.992	0.981	0.880	1.024	0.127	1.038	0.862
1390554_at	AA818377	zinc finger protein 533 (predicted)	Zfp533_predicted	3.743	0.021	1.783	0.028	1.331	0.092	1.073	0.686
1374127_at	BM392050	zinc finger protein 535	Zfp535	0.989	0.976	1.137	0.585	0.589	0.116	0.971	0.572
1390003_at	BE103960	zinc finger protein 57	Zfp57	0.463	0.152	0.733	0.003	0.797	0.339	0.931	0.362
1390357_at	AW525082	zinc finger protein 574	Zfp574	0.864	0.217	0.987	0.127	0.956	0.641	1.159	0.062
1383196_at	BI289677	zinc finger protein 579 (predicted)	Znf579_predicted	0.919	0.406	0.769	0.896	1.342	0.255	0.936	0.261
1377433_at	BG376195	zinc finger protein 580 (predicted)	Zfp580_predicted	0.989	0.765	0.891	0.553	1.124	0.815	0.998	0.851
1367524_at	AW533822	zinc finger protein 592 (predicted)	Zfp592_predicted	2.009	0.040	2.368	0.000	1.796	0.083	1.473	0.000
1393292_at	BE114251	zinc finger protein 592 (predicted)	Zfp592_predicted	1.717	0.055	5.251	0.000	0.949	0.403	3.415	0.013
1393572_at	AI229129	Zinc finger protein 592 (predicted)	Zfp592_predicted	1.267	0.360	1.121	0.080	1.622	0.059	1.352	0.105
1389523_at	BM386127	zinc finger protein 598 (predicted)	Zfp598_predicted	2.443	0.005	3.240	0.002	3.248	0.000	1.837	0.012
1395007_at	BE120572	Zinc finger protein 612 (predicted)	Zfp612_predicted	0.616	0.037	0.310	0.003	0.658	0.036	0.399	0.006
1373647_at	BM392399	zinc finger protein 622	Zfp622	0.847	0.815	1.663	0.018	0.649	0.039	1.236	0.031
1380717_at	BF397758	Zinc finger protein 626 (predicted)	Znf626_predicted	0.954	0.504	0.590	0.010	1.052	0.757	0.747	0.084
1377571_at	BI276518	zinc finger protein 628 (predicted)	Zfp628_predicted	2.464	0.068	2.467	0.028	3.484	0.210	3.451	0.029
1372789_at	BF397881	zinc finger protein 637	Zfp637	0.446	0.043	0.264	0.021	0.463	0.017	0.549	0.146
1385977_at	BF557320	Zinc finger protein 644 (predicted)	Zfp644_predicted	1.503	0.028	0.936	0.030	1.444	0.533	0.879	0.056
1367505_at	AW916491	Zinc finger protein 644 (predicted)	Zfp644_predicted	1.249	0.462	0.769	0.057	1.049	0.196	0.833	0.009
1383634_at	BI298546	zinc finger protein 653 (predicted)	Zfp653_predicted	0.654	0.292	1.069	0.954	0.915	0.407	1.015	0.909
1376840_at	AI103040	Zinc finger protein 655	Zfp655	1.151	0.150	1.499	0.040	1.596	0.132	1.526	0.167
1389685_at	AI009613	zinc finger protein 655	Zfp655	0.922	0.884	0.725	0.001	0.748	0.096	0.689	0.047
1398377_at	AI172116	zinc finger protein 672	Zfp672	0.926	0.780	0.773	0.075	0.651	0.185	0.891	0.338
1392835_at	AI705060	zinc finger protein 68 (predicted)	Zfp68_predicted	0.882	0.125	1.002	0.593	0.693	0.031	0.872	0.088
1385153_at	AI555743	zinc finger protein 68 (predicted)	Zfp68_predicted	0.831	0.576	3.263	0.000	0.951	0.887	1.945	0.003
1385236_at	AA875617	zinc finger protein 687 (predicted)	Zfp687_predicted	1.083	0.546	1.421	0.314	1.218	0.533	1.233	0.091
1389445_at	AI406571	zinc finger protein 688 (predicted)	Zfp688_predicted	0.990	0.631	1.053	0.737	0.846	0.851	1.244	0.766
1374944_at	BI275829	zinc finger protein 691 (predicted)	Zfp691_predicted	0.999	0.991	1.155	0.989	0.970	0.975	1.153	0.787
1379342_at	BI297113	zinc finger protein 692 (predicted)	Zfp692_predicted	0.452	0.020	0.441	0.009	0.591	0.044	0.609	0.007
1392913_at	AA964151	zinc finger protein 710 (predicted)	Zfp710_predicted	1.679	0.048	1.085	0.524	1.694	0.017	1.102	0.915
1399044_at	AA819804	Zinc finger protein 91	Zfp91	1.439	0.165	1.809	0.002	1.413	0.128	1.748	0.000
1383463_at	AW918514	Zinc finger protein 91	Zfp91	1.622	0.527	1.936	0.066	0.545	0.483	2.005	0.166
1377244_at	BM390979	Zinc finger protein 95 (predicted)	Zfp95_predicted	0.563	0.062	0.558	0.013	0.492	0.315	0.592	0.226
1384432_at	AW531684	zinc finger protein 96	Zfp96	0.850	0.310	0.919	0.197	0.696	0.384	1.315	0.008
1385078_at	AA957582	Zinc finger protein of the cerebellum 5 (predicted)	Zic5_predicted	1.466	0.278	1.096	0.781	0.834	0.799	1.476	0.204
1381633_at	BE116563	Zinc finger protein X-linked (predicted)	Zfx_predicted	2.732	0.105	0.980	0.493	1.000	0.999	0.747	0.305
1394218_s_at	AI175842	zinc finger protein, multitype 2 (predicted)	Zfpm2_predicted	1.584	0.063	2.190	0.033	2.131	0.205	1.269	0.068
1386550_at	BF563739	Zinc finger protein, subfamily 1A, 5 (predicted)	Zfpn1a5_predicted	1.626	0.513	1.536	0.031	0.656	0.076	1.464	0.349
1393080_at	BF389264	zinc finger RNA binding protein	Zfr	1.173	0.096	2.388	0.001	0.788	0.204	2.686	0.002
1372878_at	BG668247	zinc finger RNA binding protein	Zfr	0.753	0.181	0.823	0.026	0.702	0.017	0.960	0.418

1371464_at	BI295799	zinc finger, A20 domain containing 3	Za20d3	0.850	0.099	0.984	0.948	1.056	0.355	1.225	0.053
1373606_at	AI411964	zinc finger, AN1 type domain 2B	Zfand2b	0.911	0.960	1.439	0.179	1.000	0.996	1.257	0.375
1373767_at	AI406908	zinc finger, AN1-type domain 2A	Zfand2a	1.793	0.010	6.701	0.000	1.162	0.701	4.938	0.000
1376432_at	BM383785	zinc finger, AN1-type domain 3	Zfand3	1.661	0.101	4.083	0.003	1.305	0.131	3.802	0.010
1398918_at	BG380742	zinc finger, AN1-type domain 3	Zfand3	0.742	0.703	1.700	0.078	0.988	0.093	1.924	0.003
1373264_at	BE110658	zinc finger, BED domain containing 3	Zbed3	0.609	0.045	1.475	0.016	0.478	0.003	1.218	0.026
1389237_at	BM383698	zinc finger, C3HC-type 1 (predicted)	Zc3hc1_predicted	0.983	0.958	1.334	0.232	0.949	0.715	1.169	0.128
1374147_at	BF420306	zinc finger, CCCH-type with G patch domain	Zgpat	1.001	0.990	2.632	0.008	0.916	0.639	0.998	0.994
1376597_at	AI100951	zinc finger, CCHC domain containing 10	Zcchc10	0.800	0.037	1.269	0.043	0.934	0.222	1.243	0.013
1390820_at	BE108198	zinc finger, CCHC domain containing 11 (predicted)	Zcchc11_predicted	2.238	0.065	1.156	0.289	2.650	0.022	2.176	0.015
1373891_at	AI101009	zinc finger, CCHC domain containing 12	Zcchc12	0.775	0.087	0.412	0.010	0.835	0.639	0.452	0.002
1383239_at	BF406915	zinc finger, CCHC domain containing 7 (predicted)	Zcchc7_predicted	1.040	0.247	1.843	0.000	1.086	0.513	1.697	0.015
1384452_at	AA924571	zinc finger, CCHC domain containing 7 (predicted)	Zcchc7_predicted	1.321	0.440	1.701	0.000	1.179	0.269	1.705	0.001
1384380_at	AI535316	Zinc finger, CCHC domain containing 7 (predicted)	Zcchc7_predicted	1.533	0.832	1.273	0.046	1.321	0.793	1.246	0.131
1385007_at	BI303672	zinc finger, CCHC domain containing 9	Zcchc9	0.986	0.120	1.001	0.992	0.886	0.060	1.085	0.644
1394293_at	BG664973	Zinc finger, CSL-type containing 3 (predicted)	Zcsl3_predicted	0.601	0.008	0.863	0.040	0.516	0.001	0.614	0.008
1390168_a_at	BI289564	zinc finger, CSL-type containing 3 (predicted)	Zcsl3_predicted	0.690	0.013	1.013	0.516	0.568	0.017	0.794	0.012
1389357_at	AW532663	zinc finger, CW-type with coiled-coil domain 1 (predicted)	Zcwcc1_predicted	1.076	0.752	1.177	0.232	0.421	0.020	0.985	0.219
1398455_at	BG379973	zinc finger, DHHC domain containing 13	Zdhhc13	0.900	0.634	1.388	0.211	1.724	0.050	1.468	0.079
1374306_at	BF394933	zinc finger, DHHC domain containing 18	Zdhhc18	0.971	0.484	0.726	0.081	1.571	0.028	0.968	0.662
1370828_at	AF228917	zinc finger, DHHC domain containing 2	Zdhhc2	0.898	0.777	0.575	0.130	0.779	0.769	0.479	0.018
1390607_at	BG380706	zinc finger, DHHC domain containing 23	Zdhhc23	0.630	0.015	1.120	0.941	0.791	0.333	1.323	0.189
1393388_at	BM387780	Zinc finger, DHHC domain containing 3	Zdhhc3	0.728	0.321	0.687	0.153	0.657	0.023	0.736	0.049
1390039_at	AA800535	zinc finger, DHHC domain containing 3	Zdhhc3	1.046	0.463	1.128	0.207	1.044	0.533	0.893	0.504
1374461_at	AA893686	zinc finger, DHHC domain containing 4	Zdhhc4	1.012	0.402	1.911	0.056	0.641	0.085	1.137	0.561
1383572_at	BF414797	zinc finger, DHHC domain containing 6	Zdhhc6	0.827	0.134	0.607	0.026	0.820	0.111	1.031	0.932
1368152_at	NM_133394	zinc finger, DHHC domain containing 7	Zdhhc7	0.607	0.710	1.109	0.429	0.429	0.023	1.417	0.005
1373335_at	BE349808	Zinc finger, DHHC domain containing 9	Zdhhc9	0.705	0.884	0.659	0.306	1.045	0.566	0.451	0.008
1381708_at	BE097099	Zinc finger, FYVE domain containing 1 (predicted)	Zfyve1_predicted	1.841	0.419	1.137	0.575	1.284	0.173	1.004	0.732
1375622_at	BF402692	zinc finger, FYVE domain containing 20 (predicted)	Zfyve20_predicted	0.778	0.865	1.841	0.243	0.981	0.602	0.678	0.496
1389152_at	AI412984	zinc finger, FYVE domain containing 27	Zfyve27	0.353	0.025	0.260	0.000	0.358	0.010	0.342	0.008
1381049_at	BG375951	zinc finger, FYVE domain containing 9 (predicted)	Zfyve9_predicted	0.885	0.648	1.173	0.389	0.928	0.636	0.901	0.981
1371660_at	AA945153	zinc finger, HIT domain containing 1 (predicted)	Znhit1_predicted	0.669	0.489	1.056	0.619	0.804	0.087	1.000	0.304
1378050_at	AI058960	zinc finger, matrin type 2 /// similar to Histidyl-tRNA synthetase-like	Zmat2 /// LOC498842	0.983	0.848	1.004	0.667	1.061	0.984	1.003	0.966
1384795_at	BE116205	zinc finger, matrin-like (predicted)	Zfml_predicted	1.074	0.320	0.695	0.217	1.600	0.844	0.636	0.013
1394975_at	BF396896	zinc finger, matrin-like (predicted)	Zfml_predicted	1.085	0.604	1.014	0.152	0.760	0.661	0.714	0.047
1373764_at	AI235272	zinc finger, matrin-like (predicted)	Zfml_predicted	1.037	0.820	0.975	0.388	1.005	0.746	0.947	0.191
1376189_at	AA849377	zinc finger, MYM domain containing 1 (predicted)	Zmym1_predicted	0.879	0.121	0.691	0.061	0.902	0.277	0.960	0.923
1380517_at	BI288315	zinc finger, MYM-type 3	Zmym3	0.472	0.134	0.666	0.184	0.884	0.646	0.784	0.823
1392846_at	AA944574	Zinc finger, MYND domain containing 11	Zmynd11	1.068	0.816	1.623	0.075	0.954	0.864	0.851	0.280
1372068_at	BI289543	zinc finger, MYND domain containing 11	Zmynd11	1.065	0.873	0.797	0.048	1.054	0.624	0.902	0.018
1391255_at	BE110035	zinc finger, MYND domain containing 15 (predicted)	Zmynd15_predicted	25.486	0.000	6.618	0.000	70.103	0.001	11.635	0.002
1389436_at	AI236615	zinc finger, MYND domain containing 17 (predicted)	Zmynd17_predicted	2.655	0.045	0.934	0.271	2.706	0.046	1.416	0.150
1391014_at	AW530427	zinc finger, MYND domain containing 19	Zmynd19	1.012	0.416	1.073	0.851	0.766	0.115	0.990	0.697
1382416_at	AI112428	zinc finger, RAN-binding domain containing 1 (predicted)	Zranb1_predicted	1.886	0.038	0.956	0.579	2.182	0.021	1.101	0.636
1393430_at	BG668387	zinc finger, RAN-binding domain containing 1 (predicted)	Zranb1_predicted	1.118	0.154	1.340	0.059	1.039	0.949	1.042	0.797
1377816_at	BG374857	Zinc finger, RAN-binding domain containing 1 (predicted)	Zranb1_predicted	0.828	0.348	1.754	0.023	1.453	0.257	1.540	0.626
1394087_at	BF561962	Zinc finger, RAN-binding domain containing 1 (predicted)	Zranb1_predicted	1.239	0.455	1.533	0.115	1.486	0.057	1.463	0.142
1380755_at	AW533897	Zinc finger, RAN-binding domain containing 1 (predicted)	Zranb1_predicted	1.627	0.855	1.691	0.043	1.306	0.951	1.286	0.160
1376113_at	BI279683	zinc finger, SWIM domain containing 1 (predicted)	Zswim1_predicted	0.806	0.149	0.957	0.590	0.602	0.397	0.790	0.509
1391972_a_at	BE108410	zinc finger, SWIM domain containing 4 (predicted)	Zswim4_predicted	11.987	0.001	6.875	0.003	13.228	0.000	5.345	0.001
1380453_at	AW530611	zinc finger, SWIM domain containing 5 (predicted)	Zswim5_predicted	1.393	0.052	1.759	0.089	1.413	0.017	1.163	0.190
1384571_at	BF398835	zinc finger, SWIM domain containing 5 (predicted)	Zswim5_predicted	1.048	0.776	2.450	0.058	0.374	0.045	1.115	0.645
1385903_at	AA859627	Zinc finger, SWIM domain containing 6	Zswim6	1.129	0.319	1.120	0.711	1.184	0.873	1.284	0.015
1394012_at	BI303933	zinc finger, SWIM domain containing 6	Zswim6	1.600	0.797	1.007	0.771	1.636	0.215	1.200	0.103
1390205_at	BE108876	zinc finger, SWIM domain containing 6	Zswim6	1.064	0.968	1.307	0.247	1.774	0.030	0.809	0.164
1375571_at	AW251798	Zinc finger, ZZ-type with EF hand domain 1 (predicted)	Zzef1_predicted	0.989	0.052	1.254	0.107	0.991	0.424	1.002	0.963
1389703_at	BI295225	Zinc finger, ZZ-type with EF hand domain 1 (predicted)	Zzef1_predicted	1.336	0.650	1.112	0.566	0.885	0.922	0.967	0.958
1394508_at	AW523707	Zinc fingers and homeoboxes 3	Zhx3	1.007	0.752	0.999	0.987	0.999	0.075	0.999	0.504
1389080_at	AI233457	zinc responsive protein ZD7	LOC474154	0.684	0.069	0.873	0.451	0.851	0.146	1.147	0.615
1374549_at	AI317860	zinc responsive protein ZD7	LOC474154	0.853	0.144	1.078	0.676	0.960	0.045	0.959	0.833

1388590_at	AI010455	zinc ribbon domain containing, 1	Znrd1	1.481	0.470	2.539	0.017	1.136	0.136	1.941	0.007
1368175_at	NM_133620	zinc-fingers and homeoboxes 1	Zhx1	0.842	0.891	0.412	0.002	1.138	0.330	0.718	0.010
1399063_at	BE105565	ZUBR1	Rbaf600	0.748	0.169	0.597	0.099	0.969	0.200	0.771	0.098
1379025_at	BF392966	ZUBR1	Rbaf600	0.716	0.285	0.709	0.018	0.624	0.049	0.446	0.018
1374938_at	BI295067	ZW10 homolog, centromere/kinetochore protein (Drosophila)	Zw10	1.156	0.164	1.948	0.002	1.113	0.177	1.229	0.055
1370803_at	AF439397	ZW10 interactor	Zwint	0.807	0.010	1.072	0.065	0.789	0.034	1.142	0.037
1383389_at	BM388790	zyg-11 homolog B (C. elegans)-like	Zyg11bl	0.788	0.886	0.371	0.012	1.463	0.289	0.495	0.002
1396137_at	BF567873	zyg-11 homolog B (C. elegans)-like	Zyg11bl	0.998	0.920	0.735	0.074	0.987	0.633	0.737	0.087
1388130_at	AA943537	zyxin	Zyx	5.324	0.002	4.776	0.011	1.191	0.642	2.188	0.029
1397304_at	AW525366	---	---	171.646	0.000	60.305	0.000	217.642	0.000	98.658	0.000
1380110_at	AI229643	---	---	12.280	0.000	7.266	0.000	14.905	0.000	9.558	0.003
1383448_at	AI029121	---	---	12.176	0.000	10.219	0.000	11.565	0.000	13.755	0.000
1393140_at	AI574699	---	---	47.380	0.000	22.729	0.008	6.742	0.094	3.922	0.048
1376151_a_at	AI407953	---	---	26.907	0.000	10.468	0.001	49.288	0.000	16.071	0.004
1396209_at	BE117343	---	---	0.214	0.000	0.146	0.000	0.495	0.111	0.289	0.032
1371951_at	AA800031	---	---	37.149	0.000	28.617	0.000	5.449	0.077	7.047	0.003
1385641_at	AI070558	---	---	55.437	0.000	14.615	0.001	124.365	0.000	15.875	0.000
1378032_at	AI176265	---	---	12.908	0.000	13.480	0.002	9.856	0.001	10.708	0.002
1373672_at	BM384419	---	---	6.647	0.000	2.197	0.019	11.533	0.008	5.957	0.001
1384765_at	BI289371	---	---	13.233	0.000	15.381	0.000	12.908	0.000	12.985	0.000
1392978_at	BE117086	---	---	4.192	0.000	4.264	0.000	5.511	0.000	4.388	0.009
1393957_at	AI548358	---	---	34.087	0.000	25.305	0.000	34.492	0.001	26.803	0.002
1380570_at	AI145593	---	---	0.285	0.000	0.308	0.001	0.200	0.004	0.352	0.008
1384391_at	BE096510	---	---	14.839	0.000	8.153	0.004	15.984	0.001	3.707	0.002
1374615_at	AI175668	---	---	0.476	0.000	0.559	0.000	0.439	0.050	0.647	0.018
1389412_at	AA800693	---	---	0.281	0.000	0.203	0.002	0.156	0.000	0.184	0.015
1383650_at	BI291080	---	---	0.219	0.000	0.195	0.001	0.321	0.010	0.205	0.005
1372229_at	AI179119	---	---	0.209	0.000	0.089	0.005	0.542	0.130	0.486	0.082
1377626_at	AA924350	---	---	389.403	0.000	319.964	0.000	512.073	0.000	489.690	0.000
1378867_at	BG374639	---	---	12.083	0.000	1.690	0.108	3.346	0.138	1.045	0.803
1393469_at	BE102340	---	---	16.154	0.001	5.250	0.002	7.356	0.002	1.600	0.340
1373519_at	AI412601	---	---	0.282	0.001	0.463	0.000	0.538	0.056	0.413	0.020
1378927_at	BE329364	---	---	1.368	0.001	0.645	0.000	1.078	0.073	0.659	0.034
1384439_at	BM385726	---	---	0.799	0.001	2.145	0.028	0.411	0.013	1.670	0.002
1391280_at	AW529333	---	---	0.391	0.001	0.696	0.041	0.277	0.001	0.943	0.190
1380297_at	AW915533	---	---	2.358	0.001	1.001	0.174	4.838	0.002	1.364	0.182
1382143_at	AA964898	---	---	3.709	0.001	1.388	0.020	4.716	0.001	2.104	0.002
1373403_at	AI230625	---	---	13.423	0.001	21.660	0.007	56.055	0.002	78.351	0.005
1378980_at	AI044779	---	---	3.549	0.001	2.614	0.005	3.546	0.011	3.534	0.003
1396327_at	BG374493	---	---	43.482	0.001	12.579	0.003	38.832	0.005	25.192	0.004
1379541_at	BE329099	---	---	0.276	0.001	0.193	0.000	0.228	0.007	0.271	0.007
1390181_at	BE115041	---	---	0.426	0.001	0.483	0.149	0.417	0.058	0.790	0.461
1373864_at	BM388810	---	---	1.613	0.001	1.392	0.053	1.496	0.006	1.177	0.350
1382426_at	AA997406	---	---	0.587	0.002	1.088	0.396	0.710	0.082	0.861	0.329
1388464_at	AI598527	---	---	0.284	0.002	0.586	0.059	0.352	0.025	0.540	0.040
1393431_at	AI500737	---	---	0.753	0.002	1.124	0.185	0.709	0.141	0.993	0.409
1371871_at	AI409731	---	---	1.994	0.002	1.389	0.005	2.115	0.000	1.916	0.004
1373740_at	AA851385	---	---	0.070	0.002	0.172	0.004	0.084	0.000	0.107	0.003
1390432_at	AA997338	---	---	0.323	0.002	0.158	0.000	0.414	0.008	0.171	0.008
1390932_at	AA875255	---	---	0.759	0.002	0.988	0.853	0.767	0.004	0.998	0.958
1397375_at	BM384537	---	---	0.381	0.002	0.525	0.064	0.417	0.021	0.471	0.067
1372826_at	BI285718	---	---	6.837	0.002	4.913	0.000	5.067	0.000	3.238	0.020
1376880_at	AI639447	---	---	2.222	0.002	1.858	0.016	2.657	0.000	1.753	0.014
1374157_at	AA858930	---	---	4.851	0.002	1.849	0.042	3.515	0.059	1.449	0.022
1371736_at	AI411283	---	---	0.353	0.002	0.349	0.001	0.486	0.000	0.349	0.005
1383254_at	BF403169	---	---	0.232	0.002	0.205	0.000	0.546	0.005	0.182	0.005
1377117_at	BF387780	---	---	3.157	0.003	2.032	0.003	3.045	0.001	2.018	0.003
1389155_at	AA943139	---	---	0.422	0.003	0.668	0.005	0.627	0.028	0.751	0.051
1374592_at	BI282671	---	---	0.295	0.003	0.479	0.004	0.347	0.050	0.626	0.081
1379724_at	BE103244	---	---	0.260	0.003	0.255	0.001	0.329	0.011	0.244	0.005
1372812_at	H33148	---	---	1.826	0.003	1.693	0.022	1.421	0.028	1.374	0.023

1377380_at	AI060045	---	---	2.610	0.003	0.950	0.405	3.690	0.000	1.898	0.239
1386114_at	BF550033	---	---	0.216	0.003	0.085	0.001	0.385	0.108	0.121	0.035
1374432_at	BE118251	---	---	1.565	0.004	0.574	0.014	1.734	0.001	0.564	0.000
1398625_at	BG673169	---	---	0.561	0.004	0.572	0.000	0.477	0.025	0.887	0.195
1391560_at	AI237082	---	---	1.801	0.004	1.807	0.016	1.970	0.003	1.579	0.015
1396252_at	BE117174	---	---	0.591	0.004	0.340	0.004	0.447	0.005	0.232	0.045
1374526_at	BF396420	---	---	2.426	0.004	1.332	0.004	2.769	0.003	1.833	0.001
1390851_at	AA799676	---	---	0.685	0.004	0.609	0.001	0.796	0.007	0.914	0.132
1382277_at	AA894336	---	---	5.708	0.004	4.674	0.000	4.848	0.010	4.541	0.016
1383150_at	BE114751	---	---	0.531	0.004	0.618	0.027	0.475	0.008	0.739	0.086
1374522_at	BG670847	---	---	0.547	0.004	0.591	0.004	0.658	0.029	0.688	0.021
1386695_at	BF565756	---	---	6.290	0.004	3.953	0.178	19.899	0.003	16.401	0.020
1376618_at	AI236218	---	---	1.553	0.004	2.188	0.020	2.199	0.001	1.944	0.011
1393365_at	AW433625	---	---	2.382	0.005	1.238	0.069	6.193	0.007	1.484	0.014
1389913_at	BI276990	---	---	3.239	0.005	2.172	0.091	3.658	0.003	2.316	0.068
1397703_at	BF288942	---	---	2.755	0.005	0.822	0.271	4.037	0.000	1.325	0.190
1383642_at	BG374114	---	---	0.435	0.005	0.411	0.029	0.408	0.008	0.600	0.065
1378501_at	BE113386	---	---	1.459	0.005	1.140	0.084	1.193	0.138	1.271	0.943
1385210_at	BF389450	---	---	4.714	0.005	11.737	0.000	2.500	0.007	9.680	0.005
1399140_at	AA965202	---	---	1.582	0.005	2.453	0.017	1.359	0.032	2.975	0.000
1389053_at	AI171280	---	---	1.684	0.005	2.733	0.009	3.686	0.002	3.773	0.001
1389022_at	AI102760	---	---	2.672	0.006	2.513	0.016	3.088	0.001	2.755	0.010
1385577_at	AW531898	---	---	0.363	0.006	0.431	0.005	0.368	0.027	0.423	0.032
1371972_at	BM388888	---	---	3.288	0.006	4.356	0.001	2.949	0.008	3.006	0.001
1383533_at	AI715743	---	---	2.107	0.006	1.102	0.167	1.843	0.045	0.795	0.573
1381190_at	AI598833	---	---	0.373	0.006	0.758	0.030	0.523	0.132	0.777	0.022
1373638_at	BG380827	---	---	0.417	0.006	0.360	0.009	0.398	0.018	0.380	0.021
1389261_at	BI290739	---	---	3.246	0.006	1.085	0.406	1.212	0.993	1.365	0.282
1374300_at	AA997139	---	---	0.498	0.006	0.756	0.129	0.507	0.026	0.561	0.030
1371990_at	AI012242	---	---	0.184	0.007	0.060	0.021	0.466	0.117	0.305	0.066
1391574_at	AW253369	---	---	2.512	0.007	1.024	0.352	3.133	0.001	1.322	0.084
1386669_at	BF565188	---	---	0.474	0.007	1.546	0.030	0.456	0.004	1.356	0.069
1374940_at	BM388945	---	---	0.530	0.007	0.636	0.006	0.518	0.008	0.658	0.008
1374002_at	AI045904	---	---	0.769	0.007	0.368	0.094	0.623	0.022	0.439	0.157
1389306_at	BM387419	---	---	0.320	0.007	0.103	0.001	0.472	0.098	0.156	0.001
1376136_at	BI296118	---	---	0.390	0.007	0.513	0.003	0.464	0.071	0.957	0.732
1372456_at	AI171229	---	---	0.796	0.008	0.957	0.835	0.996	0.119	1.027	0.242
1377856_at	BE113045	---	---	0.488	0.008	0.246	0.001	0.332	0.001	0.310	0.003
1393952_at	BI278833	---	---	0.145	0.008	0.044	0.000	0.241	0.003	0.055	0.006
1386140_at	AI235950	---	---	0.463	0.008	0.548	0.055	0.565	0.037	0.428	0.037
1388509_at	BI274303	---	---	2.068	0.008	4.189	0.008	1.163	0.335	3.158	0.004
1378302_at	BF403965	---	---	8.078	0.009	1.820	0.004	18.099	0.005	3.291	0.005
1376108_at	AI030915	---	---	0.551	0.009	1.019	0.667	0.841	0.052	1.419	0.149
1385107_at	AI137961	---	---	7.155	0.009	1.402	0.048	1.413	0.526	1.075	0.684
1383649_a_at	BI291080	---	---	0.085	0.009	0.132	0.012	0.450	0.105	0.246	0.002
1382094_at	BI285519	---	---	1.757	0.009	0.751	0.022	1.829	0.001	0.947	0.813
1371333_at	AI180251	---	---	0.765	0.009	0.541	0.005	0.765	0.163	0.496	0.016
1396755_at	BF399394	---	---	9.697	0.009	2.749	0.004	13.653	0.012	3.851	0.005
1395544_at	BG666601	---	---	0.469	0.009	0.924	0.211	0.696	0.043	0.769	0.129
1376625_at	BI296015	---	---	1.905	0.009	2.219	0.143	1.760	0.032	1.466	0.199
1374740_at	BF408740	---	---	1.240	0.010	0.929	0.543	1.780	0.027	1.018	0.939
1388781_at	AW434329	---	---	1.503	0.010	0.699	0.106	1.535	0.013	0.913	0.576
1372104_at	BF289002	---	---	0.397	0.010	0.426	0.019	0.444	0.014	0.421	0.010
1389015_at	AI171982	---	---	0.348	0.010	0.919	0.363	0.436	0.029	0.663	0.152
1391305_at	AI576233	---	---	0.345	0.010	0.543	0.033	0.303	0.011	0.434	0.014
1373494_at	BE120831	---	---	2.633	0.011	3.090	0.004	2.407	0.000	3.445	0.000
1389500_at	BM383122	---	---	4.414	0.011	7.338	0.000	2.515	0.010	3.624	0.002
1378203_at	BE102273	---	---	1.258	0.011	1.454	0.032	1.062	0.229	1.129	0.116
1372719_at	BF283702	---	---	3.400	0.011	1.707	0.005	3.085	0.004	1.469	0.025
1385218_at	AI044551	---	---	2.773	0.011	2.247	0.506	2.143	0.009	1.223	0.484
1391546_at	AI412209	---	---	0.224	0.011	0.142	0.001	0.311	0.021	0.221	0.011

1372955_at	BI282720	---	---	1.250	0.011	1.777	0.064	1.086	0.204	1.120	0.391
1383675_at	BG371620	---	---	0.442	0.011	1.977	0.274	0.493	0.009	1.185	0.528
1383285_at	BG671375	---	---	5.581	0.012	12.434	0.001	1.680	0.275	1.833	0.031
1397828_at	BF387796	---	---	1.575	0.012	0.501	0.044	2.772	0.011	0.796	0.629
1393234_at	BI285850	---	---	10.758	0.012	7.973	0.000	7.271	0.002	6.700	0.006
1373921_at	AI169007	---	---	0.284	0.012	0.664	0.120	0.892	0.127	1.101	0.237
1389511_s_at	BF403383	---	---	0.417	0.012	0.549	0.040	0.482	0.042	0.731	0.048
1390465_at	AW534554	---	---	0.660	0.013	0.861	0.101	0.801	0.025	0.755	0.037
1370899_at	AI599699	---	---	0.418	0.013	0.403	0.009	0.477	0.004	0.302	0.066
1374100_at	AI102771	---	---	0.711	0.013	0.513	0.002	1.250	0.378	0.884	0.192
1372141_at	BI289500	---	---	0.814	0.013	1.391	0.084	0.863	0.481	1.291	0.152
1373300_at	BI296249	---	---	0.536	0.013	0.356	0.001	0.479	0.007	0.348	0.003
1375672_at	BG380279	---	---	0.324	0.013	0.482	0.008	0.865	0.249	0.747	0.061
1383025_at	BE097791	---	---	2.691	0.013	11.017	0.000	0.850	0.195	9.593	0.000
1388204_at	M60616	---	---	14.992	0.013	22.555	0.016	4.363	0.014	7.489	0.058
1372905_at	AW433888	---	---	1.521	0.013	1.652	0.002	0.851	0.779	1.371	0.025
1373936_at	AI407107	---	---	1.419	0.013	1.220	0.358	1.391	0.043	1.312	0.153
1384116_at	AA924216	---	---	10.630	0.014	3.654	0.010	7.753	0.000	3.370	0.001
1373788_at	BE097533	---	---	0.572	0.014	1.345	0.184	0.405	0.076	1.371	0.356
1383173_at	BI281630	---	---	0.391	0.014	0.143	0.000	0.617	0.037	0.306	0.001
1371963_at	BF395042	---	---	0.662	0.015	0.609	0.040	0.704	0.096	0.648	0.008
1373506_at	AA944568	---	---	1.682	0.015	0.339	0.000	1.677	0.012	0.357	0.014
1393000_at	AI045970	---	---	0.251	0.015	0.357	0.000	0.382	0.034	0.498	0.028
1390070_at	BI296990	---	---	0.492	0.015	1.156	0.190	0.553	0.123	0.862	0.459
1389596_at	BM389642	---	---	0.605	0.015	1.428	0.019	0.587	0.120	1.290	0.049
1374811_at	AA858705	---	---	0.455	0.015	1.371	0.015	0.703	0.012	1.106	0.024
1384288_at	BI292470	---	---	1.362	0.015	0.820	0.174	1.994	0.038	1.144	0.060
1392347_at	AW527765	---	---	0.679	0.016	0.995	0.956	0.743	0.118	1.001	0.973
1396386_at	BF408665	---	---	3.881	0.016	9.502	0.007	3.541	0.006	4.885	0.004
1377124_at	AA964824	---	---	2.067	0.017	1.323	0.010	1.896	0.003	1.425	0.001
1388271_at	BM383531	---	---	5.782	0.017	58.245	0.005	8.619	0.029	65.868	0.006
1379854_at	AA996933	---	---	2.948	0.017	10.954	0.001	1.402	0.028	5.296	0.016
1389003_at	BI282008	---	---	0.208	0.018	0.244	0.032	0.457	0.164	0.230	0.031
1379546_at	AA875623	---	---	1.884	0.018	2.210	0.454	1.188	0.095	1.398	0.473
1390204_at	AI227856	---	---	2.186	0.018	1.001	0.292	3.630	0.002	0.965	0.913
1383215_at	BF557467	---	---	0.335	0.018	0.114	0.000	0.336	0.027	0.098	0.001
1390103_at	BE095970	---	---	1.497	0.018	1.502	0.091	1.914	0.010	1.159	0.146
1391454_at	BF286105	---	---	0.702	0.018	0.613	0.015	1.118	0.521	0.751	0.014
1384634_at	AI235340	---	---	0.867	0.019	0.937	0.963	0.941	0.390	0.978	0.887
1395623_at	AW521959	---	---	0.366	0.019	0.788	0.112	0.846	0.480	0.751	0.776
1378582_at	BM383666	---	---	0.489	0.019	0.371	0.000	0.772	0.099	0.418	0.008
1374696_at	AI170182	---	---	2.130	0.019	2.340	0.004	3.655	0.011	3.743	0.008
1373379_at	BF396350	---	---	0.655	0.019	1.034	0.214	0.607	0.029	0.997	0.746
1379316_at	BG373832	---	---	1.845	0.019	1.041	0.995	2.843	0.006	1.587	0.086
1373422_at	BE108280	---	---	1.513	0.019	1.846	0.005	1.485	0.039	2.038	0.008
1383326_a_at	AI576297	---	---	0.552	0.020	0.444	0.000	0.603	0.030	0.457	0.046
1383011_at	AI501182	---	---	1.623	0.020	1.865	0.013	1.618	0.037	1.697	0.000
1375417_at	BM391419	---	---	1.618	0.020	0.699	0.169	1.225	0.099	0.778	0.879
1393048_at	BF561277	---	---	0.261	0.020	0.071	0.000	0.166	0.005	0.094	0.060
1381525_at	BF419130	---	---	2.983	0.020	1.577	0.005	2.734	0.010	1.658	0.011
1385940_at	AI102967	---	---	0.657	0.020	0.959	0.939	0.795	0.118	0.971	0.851
1379453_a_at	AI072423	---	---	1.774	0.020	0.846	0.300	1.113	0.337	0.750	0.468
1376680_at	BG379765	---	---	2.767	0.021	7.866	0.003	3.737	0.007	4.886	0.001
1381234_at	BF398454	---	---	5.080	0.021	1.396	0.128	3.265	0.015	1.491	0.207
1380796_at	AW521390	---	---	1.480	0.021	1.010	0.110	2.047	0.024	1.145	0.155
1373610_at	AI232694	---	---	0.453	0.021	0.525	0.011	0.591	0.092	0.634	0.004
1373216_at	AI236521	---	---	0.522	0.021	0.292	0.008	0.332	0.005	0.677	0.065
1372322_at	BF398016	---	---	0.552	0.021	0.533	0.014	0.572	0.025	0.665	0.014
1383753_at	BF401106	---	---	0.607	0.021	0.656	0.074	0.722	0.179	0.556	0.028
1397953_at	AI113261	---	---	1.881	0.021	1.995	0.022	2.894	0.015	2.517	0.008
1374690_at	AI599770	---	---	3.595	0.021	1.643	0.007	4.958	0.009	1.991	0.003

1373254_at	BI282479	---	---	0.313	0.022	0.920	0.542	1.114	0.833	0.992	0.929
1385800_at	AW531915	---	---	2.443	0.022	2.093	0.013	1.853	0.148	1.374	0.400
1393095_at	BI276113	---	---	2.722	0.022	1.165	0.352	3.685	0.001	1.375	0.060
1389427_at	BM386487	---	---	3.811	0.022	2.243	0.081	2.288	0.015	1.537	0.036
1374044_at	AA850698	---	---	0.718	0.022	0.809	0.027	0.760	0.009	0.992	0.095
1376825_at	BF557258	---	---	0.479	0.022	0.377	0.001	0.873	0.349	0.391	0.002
1379763_at	BE111542	---	---	1.968	0.022	1.413	0.029	2.311	0.029	1.439	0.028
1394047_at	BE107848	---	---	4.373	0.022	1.618	0.029	3.486	0.035	1.295	0.019
1382022_at	BF285121	---	---	2.968	0.023	1.059	0.274	3.142	0.023	1.344	0.065
1393905_at	AI145446	---	---	2.181	0.023	0.901	0.615	1.022	0.836	0.998	0.840
1373193_at	BE108670	---	---	0.694	0.024	0.492	0.011	0.604	0.024	0.569	0.033
1388401_at	BI296155	---	---	2.009	0.024	1.706	0.102	1.801	0.372	1.507	0.033
1371731_at	AI408151	---	---	0.097	0.024	0.414	0.012	0.049	0.001	0.468	0.027
1377249_at	AW526060	---	---	0.263	0.024	0.265	0.002	0.260	0.016	0.471	0.018
1369094_a_at	NM_019140	---	---	0.792	0.024	0.403	0.001	0.823	0.004	0.411	0.005
1391682_at	AI169812	---	---	1.970	0.025	1.224	0.559	1.004	0.471	1.713	0.484
1374390_at	AI716420	---	---	0.579	0.026	0.967	0.792	0.441	0.088	0.638	0.561
1389418_at	AI410452	---	---	2.573	0.026	0.602	0.007	2.932	0.002	1.402	0.014
1389429_at	AA925367	---	---	0.784	0.026	0.273	0.015	1.122	0.170	0.621	0.055
1374499_at	BM383402	---	---	2.989	0.027	1.680	0.006	4.914	0.001	2.610	0.004
1372770_at	BF281357	---	---	1.743	0.028	1.749	0.085	4.127	0.033	3.141	0.007
1382020_at	BE105500	---	---	1.795	0.028	1.349	0.233	1.501	0.015	0.899	0.914
1392368_at	BE117273	---	---	1.869	0.028	1.669	0.298	1.515	0.061	1.705	0.434
1392584_at	BF415201	---	---	0.679	0.028	0.982	0.241	0.665	0.044	1.000	0.987
1371806_at	BI283794	---	---	0.584	0.029	0.465	0.024	0.772	0.113	0.536	0.195
1370176_at	BG378620	---	---	0.506	0.029	0.470	0.006	0.423	0.029	0.458	0.012
1377980_at	AI549077	---	---	0.308	0.029	0.186	0.004	0.549	0.023	0.309	0.009
1390154_at	BI299824	---	---	3.199	0.029	1.606	0.130	1.651	0.149	1.421	0.974
1371842_at	AI227747	---	---	0.898	0.029	0.891	0.092	0.627	0.002	0.880	0.734
1399037_at	AI227962	---	---	0.586	0.030	0.930	0.651	0.518	0.001	0.567	0.243
1384227_at	AI044031	---	---	0.598	0.030	0.681	0.000	0.855	0.248	0.681	0.048
1394793_at	AI715674	---	---	0.601	0.030	0.262	0.001	0.872	0.424	0.318	0.004
1371717_at	AA943135	---	---	1.367	0.030	2.062	0.003	1.543	0.002	2.224	0.003
1371911_at	BM390023	---	---	1.854	0.031	1.316	0.003	1.606	0.002	1.327	0.050
1382989_at	BE116242	---	---	0.737	0.031	0.302	0.000	0.810	0.062	0.286	0.004
1390151_at	BM392146	---	---	0.447	0.031	0.274	0.001	0.617	0.014	0.497	0.002
1383384_at	BG381725	---	---	0.803	0.031	0.453	0.002	1.022	0.200	0.572	0.037
1373419_at	AI556884	---	---	2.493	0.032	0.703	0.633	2.090	0.017	1.212	0.554
1373755_at	AI717543	---	---	1.390	0.032	1.087	0.469	1.006	0.394	0.562	0.033
1388982_at	BM389066	---	---	0.623	0.033	0.474	0.000	0.540	0.010	0.461	0.005
1385219_a_at	AI071110	---	---	0.960	0.033	0.977	0.924	0.750	0.037	1.549	0.065
1394909_at	BF387551	---	---	2.146	0.033	1.091	0.814	1.040	0.909	0.867	0.549
1389439_at	AI172618	---	---	1.499	0.034	3.264	0.000	1.318	0.036	2.020	0.023
1391643_at	BI290758	---	---	1.469	0.034	0.704	0.017	1.004	0.986	0.549	0.050
1384659_at	AI058540	---	---	1.537	0.034	0.849	0.914	0.985	0.601	1.196	0.183
1383382_at	BI294931	---	---	0.803	0.034	0.330	0.001	0.914	0.083	0.436	0.029
1391333_at	AI602218	---	---	0.986	0.034	1.596	0.032	0.746	0.024	1.094	0.109
1395287_at	BE119914	---	---	0.774	0.034	1.002	0.987	0.797	0.057	0.992	0.416
1377283_at	BI274486	---	---	0.552	0.034	0.299	0.004	0.531	0.062	0.316	0.007
1379651_at	BE109884	---	---	2.596	0.034	0.967	0.574	1.881	0.121	0.749	0.290
1384169_a_at	AA900477	---	---	1.243	0.035	0.512	0.005	1.066	0.576	0.462	0.005
1382255_at	BE110785	---	---	3.725	0.035	2.333	0.006	5.422	0.000	2.214	0.002
1372345_at	AA894210	---	---	0.247	0.035	0.221	0.013	0.169	0.003	0.184	0.002
1383879_at	BG377332	---	---	0.696	0.035	0.809	0.979	0.633	0.113	0.811	0.543
1388254_a_at	AJ243338	---	---	1.841	0.035	1.367	0.989	1.822	0.035	1.884	0.107
1378663_at	BF401737	---	---	2.502	0.035	1.363	0.043	1.021	0.847	1.283	0.054
1388540_at	BM390828	---	---	0.694	0.036	0.849	0.442	0.656	0.007	0.733	0.132
1371793_at	AI008697	---	---	0.408	0.036	0.464	0.016	0.281	0.028	0.553	0.019
1373450_at	AI409857	---	---	0.486	0.036	0.535	0.013	0.577	0.143	0.623	0.042
1381918_at	AI144776	---	---	1.002	0.037	0.999	0.984	1.016	0.539	0.999	0.986
1375453_at	BM392052	---	---	0.639	0.037	0.887	0.194	0.732	0.382	0.867	0.666

1378191_at	AI549102	---	---	0.404	0.037	0.545	0.031	0.354	0.047	0.498	0.132
1399131_at	AI703580	---	---	0.450	0.037	0.634	0.056	0.539	0.001	0.666	0.025
1392312_at	BG375255	---	---	1.330	0.038	1.050	0.609	2.490	0.157	1.131	0.644
1390592_at	BM389412	---	---	0.747	0.038	1.825	0.084	0.702	0.094	0.962	0.646
1384183_at	AA996869	---	---	0.394	0.038	0.766	0.715	0.425	0.071	0.751	0.045
1373491_at	BI276464	---	---	0.684	0.038	0.766	0.044	0.812	0.161	0.524	0.014
1382374_at	AA875017	---	---	0.588	0.038	0.494	0.109	0.552	0.026	0.687	0.311
1381224_at	AI502861	---	---	0.735	0.038	1.024	0.506	0.746	0.031	0.942	0.798
1384275_at	BI300393	---	---	0.472	0.038	0.292	0.000	0.474	0.048	0.293	0.002
1391632_at	AA964568	---	---	0.744	0.038	2.208	0.002	0.598	0.003	1.742	0.035
1388501_at	AW916335	---	---	2.453	0.039	1.751	0.004	3.045	0.014	2.571	0.000
1393330_at	AI137898	---	---	0.486	0.039	0.479	0.047	0.697	0.043	1.000	0.157
1384455_at	AA817831	---	---	0.620	0.039	1.277	0.055	0.792	0.247	1.365	0.037
1391532_at	AI535169	---	---	1.719	0.039	1.417	0.161	0.980	0.698	0.903	0.735
1396239_at	AI502035	---	---	2.158	0.039	2.694	0.000	1.452	0.015	1.881	0.003
1388668_at	BM384972	---	---	0.702	0.040	2.399	0.007	0.648	0.041	1.887	0.035
1382038_at	BE113064	---	---	0.542	0.040	1.118	0.752	0.640	0.050	0.870	0.471
1378037_at	BM390078	---	---	0.473	0.040	0.757	0.743	1.060	0.093	0.550	0.101
1388895_at	AI175791	---	---	1.608	0.040	3.248	0.004	1.282	0.152	2.635	0.004
1386507_at	AA799858	---	---	0.355	0.041	0.944	0.634	0.315	0.047	0.710	0.123
1389217_at	AI599568	---	---	0.389	0.041	0.777	0.198	0.426	0.000	0.506	0.002
1392756_at	AI237628	---	---	0.519	0.041	0.841	0.812	0.938	0.144	1.135	0.582
1391202_at	AW252232	---	---	0.541	0.043	0.213	0.007	0.603	0.062	0.385	0.060
1383988_at	AI028887	---	---	0.694	0.043	0.331	0.021	0.665	0.079	0.581	0.384
1383066_at	BG379237	---	---	0.504	0.043	0.334	0.037	0.380	0.029	0.341	0.012
1395966_at	BI282914	---	---	0.372	0.043	0.988	0.033	0.304	0.038	1.016	0.962
1383531_at	AA901061	---	---	1.855	0.044	4.364	0.006	1.621	0.048	4.531	0.026
1398408_at	AI948410	---	---	4.256	0.044	3.586	0.036	9.915	0.011	19.371	0.007
1373770_at	AI105345	---	---	0.501	0.044	1.218	0.004	0.488	0.028	1.195	0.025
1372167_at	AW525656	---	---	0.800	0.044	1.784	0.000	0.596	0.013	1.211	0.047
1373557_at	AI145081	---	---	0.659	0.045	1.177	0.199	0.613	0.048	0.997	0.916
1377733_at	AA944531	---	---	0.491	0.045	0.824	0.749	0.366	0.005	0.640	0.004
1391205_at	AA818139	---	---	0.503	0.045	1.195	0.139	0.531	0.027	1.171	0.256
1372664_at	BM384229	---	---	2.037	0.046	1.579	0.076	2.269	0.026	1.094	0.213
1392829_at	BI289495	---	---	0.862	0.046	1.658	0.679	0.857	0.264	1.168	0.877
1391211_at	AI144936	---	---	2.536	0.046	0.633	0.146	6.757	0.021	0.948	0.800
1392277_at	BI303053	---	---	1.767	0.046	4.100	0.022	1.499	0.009	5.045	0.032
1390389_at	BM385936	---	---	0.663	0.046	0.431	0.022	0.634	0.048	0.474	0.023
1383295_at	AA901194	---	---	1.731	0.046	2.401	0.023	2.322	0.002	2.252	0.014
1390369_at	BI293026	---	---	0.789	0.046	0.949	0.834	0.822	0.036	0.964	0.976
1374030_at	BE100868	---	---	0.556	0.046	0.281	0.000	0.637	0.198	0.402	0.012
1373576_at	BE107337	---	---	0.558	0.046	0.271	0.005	0.637	0.019	0.643	0.009
1378925_at	AW529408	---	---	0.346	0.047	0.679	0.337	0.557	0.005	0.788	0.091
1398624_x_at	AA957044	---	---	0.883	0.047	0.429	0.040	0.944	0.739	0.578	0.061
1388490_at	AI104451	---	---	0.698	0.047	0.990	0.650	0.793	0.023	0.832	0.238
1373559_at	AI228623	---	---	5.969	0.047	0.771	0.801	1.007	0.979	0.968	0.790
1377668_at	BI276788	---	---	1.310	0.048	3.148	0.000	1.349	0.239	2.817	0.001
1377297_at	BE118384	---	---	1.184	0.048	0.992	0.579	1.023	0.030	0.995	0.641
1392650_at	AI059349	---	---	1.106	0.048	2.118	0.018	1.641	0.024	0.915	0.867
1390711_at	AW535406	---	---	2.407	0.048	0.738	0.167	1.066	0.822	0.575	0.227
1392289_at	BI276179	---	---	1.136	0.049	1.393	0.072	1.948	0.036	1.536	0.081
1389617_at	BM392135	---	---	0.484	0.049	0.701	0.067	0.466	0.031	0.977	0.520
1388956_at	BI285945	---	---	0.741	0.050	0.927	0.276	0.879	0.449	0.928	0.605
1396315_at	BF408941	---	---	1.363	0.050	2.961	0.002	1.149	0.417	3.111	0.003
1391564_at	AW526015	---	---	0.637	0.051	0.488	0.128	1.012	0.121	0.568	0.151
1380475_at	BE096160	---	---	0.651	0.051	1.262	0.292	0.737	0.067	1.071	0.125
1383328_x_at	AI576297	---	---	0.544	0.051	0.218	0.006	0.578	0.037	0.224	0.005
1391418_at	AI072641	---	---	2.371	0.052	0.489	0.023	1.043	0.783	0.671	0.098
1393114_at	AI136684	---	---	2.156	0.052	1.391	0.034	2.269	0.005	1.727	0.029
1393349_x_at	BI288992	---	---	1.265	0.052	0.503	0.005	0.913	0.554	0.477	0.002
1398598_at	BF549679	---	---	1.410	0.053	0.725	0.012	1.317	0.067	0.748	0.011

1381750_at	AW251098	---	---	1.850	0.053	1.105	0.614	3.316	0.037	1.049	0.053
1392473_at	AW525353	---	---	0.357	0.054	0.187	0.002	0.416	0.000	0.234	0.000
1372754_at	BG666424	---	---	0.756	0.054	0.836	0.132	0.764	0.332	0.762	0.134
1373109_at	BI294813	---	---	1.342	0.054	1.251	0.008	1.173	0.670	1.245	0.174
1396344_at	AI548117	---	---	0.514	0.055	0.521	0.003	0.538	0.033	0.425	0.004
1370194_at	AA945699	---	---	1.376	0.055	2.160	0.014	0.878	0.568	1.659	0.015
1376640_at	BF285466	---	---	0.631	0.055	0.667	0.021	0.765	0.018	0.769	0.034
1389185_at	BI281183	---	---	0.440	0.056	0.429	0.052	0.317	0.077	0.244	0.059
1382009_at	AA955721	---	---	2.501	0.056	1.804	0.005	3.142	0.040	1.222	0.428
1396323_at	AI709444	---	---	0.748	0.057	1.473	0.227	0.821	0.347	1.770	0.088
1389890_at	BI288731	---	---	1.500	0.057	3.422	0.006	1.379	0.134	1.951	0.032
1374637_at	BE109510	---	---	0.524	0.057	0.664	0.066	0.740	0.405	0.680	0.058
1390805_at	BM390762	---	---	0.232	0.057	0.458	0.007	0.236	0.024	0.279	0.025
1392880_at	BG665051	---	---	0.476	0.058	0.262	0.054	0.511	0.060	0.319	0.195
1389560_at	BF284702	---	---	0.735	0.058	0.676	0.092	0.720	0.092	0.721	0.067
1373298_at	BI288011	---	---	0.570	0.058	0.549	0.024	0.704	0.004	0.641	0.129
1393130_at	BI288617	---	---	1.331	0.058	1.243	0.183	1.450	0.088	1.424	0.066
1376416_at	BI296287	---	---	0.630	0.058	0.723	0.075	0.741	0.096	0.713	0.129
1390111_at	BI285224	---	---	0.606	0.059	1.043	0.535	0.644	0.027	1.114	0.124
1383915_at	AI059630	---	---	1.698	0.059	1.044	0.055	3.235	0.103	1.140	0.621
1373893_at	BI291309	---	---	0.696	0.060	0.714	0.007	0.902	0.545	0.677	0.037
1374751_at	BM383668	---	---	2.000	0.060	0.997	0.983	3.318	0.000	1.617	0.003
1392499_at	H32997	---	---	0.820	0.060	1.181	0.018	0.639	0.011	0.926	0.379
1391190_at	BE117521	---	---	1.692	0.060	1.083	0.084	2.021	0.061	1.398	0.035
1378068_at	AW529368	---	---	0.279	0.060	0.228	0.018	0.450	0.006	0.313	0.012
1380723_at	AI179188	---	---	0.736	0.061	0.810	0.004	0.598	0.035	0.805	0.000
1383625_a_at	BF288164	---	---	0.298	0.061	1.089	0.954	0.405	0.131	1.178	0.628
1380708_at	BF396522	---	---	1.396	0.062	0.964	0.867	0.996	0.331	1.103	0.410
1395858_at	AI548127	---	---	3.458	0.062	1.360	0.298	4.563	0.050	1.721	0.542
1388762_at	BF284125	---	---	1.995	0.062	2.759	0.002	1.426	0.158	2.352	0.036
1392145_at	BI281801	---	---	1.968	0.063	2.680	0.005	1.158	0.760	2.166	0.015
1371855_at	BM390254	---	---	0.705	0.064	0.802	0.029	0.742	0.057	0.923	0.043
1389443_at	AI236463	---	---	0.882	0.064	0.670	0.000	0.937	0.722	0.856	0.172
1398946_at	AI230278	---	---	0.430	0.065	1.379	0.016	0.469	0.011	1.313	0.014
1377707_at	BF417096	---	---	0.761	0.066	0.822	0.177	1.291	0.487	0.749	0.004
1377755_at	AI179403	---	---	1.445	0.066	1.896	0.018	1.346	0.390	2.222	0.005
1388998_at	AW522835	---	---	0.840	0.066	1.121	0.124	0.786	0.062	0.896	0.808
1373779_at	AI011878	---	---	0.610	0.066	0.399	0.005	0.713	0.020	0.496	0.003
1378472_at	BE108158	---	---	0.999	0.067	0.928	0.693	1.544	0.597	0.994	0.993
1393110_at	BI281552	---	---	0.842	0.067	1.081	0.289	0.987	0.903	1.144	0.091
1372919_at	AA851904	---	---	1.461	0.067	1.725	0.062	1.800	0.015	1.680	0.079
1379602_at	AI010055	---	---	1.047	0.068	0.997	0.990	1.309	0.064	1.000	0.942
1384494_at	BI303215	---	---	0.838	0.069	1.350	0.017	0.843	0.073	1.217	0.251
1391671_at	AA997871	---	---	2.505	0.070	1.372	0.078	1.862	0.163	1.166	0.082
1375048_at	AA799566	---	---	0.669	0.070	1.239	0.034	1.015	0.082	1.315	0.046
1376346_at	BM392156	---	---	0.817	0.072	0.956	0.398	1.003	0.071	0.962	0.438
1394020_at	AI412164	---	---	1.454	0.072	0.715	0.465	0.924	0.585	0.923	0.730
1375995_at	AI180370	---	---	0.718	0.072	0.695	0.019	0.601	0.045	0.803	0.068
1398931_at	BI282246	---	---	0.332	0.073	0.238	0.004	0.338	0.029	0.419	0.026
1376760_at	BF402128	---	---	1.848	0.073	3.677	0.000	1.882	0.094	4.052	0.001
1373533_at	AI412460	---	---	0.929	0.073	0.937	0.568	0.899	0.044	0.745	0.042
1386242_at	AI179722	---	---	1.395	0.073	1.645	0.073	1.368	0.224	1.451	0.236
1397326_at	BE119158	---	---	1.633	0.074	0.803	0.513	0.998	0.237	0.975	0.605
1367480_at	AI230248	---	---	0.689	0.074	0.963	0.288	0.693	0.022	0.936	0.420
1388754_at	AI176839	---	---	1.291	0.075	5.093	0.002	1.614	0.021	3.796	0.009
1397477_at	AA998512	---	---	0.755	0.075	0.943	0.351	0.599	0.078	0.846	0.331
1372627_at	BI299197	---	---	0.738	0.075	1.751	0.000	0.690	0.009	1.381	0.004
1390115_at	BM384667	---	---	0.491	0.076	0.531	0.000	0.703	0.039	0.581	0.003
1373659_at	AI639350	---	---	0.821	0.076	0.152	0.013	0.380	0.019	0.244	0.032
1392919_at	BI297513	---	---	0.825	0.076	0.998	0.327	0.783	0.125	0.856	0.318
1394065_at	AI179423	---	---	0.729	0.076	0.351	0.001	0.486	0.060	0.364	0.008

1390109_at	BI303073	---	---	1.531	0.076	4.470	0.006	1.152	0.173	3.423	0.016
1395896_at	AI233009	---	---	1.488	0.077	1.404	0.084	1.246	0.193	1.197	0.589
1382680_at	BG673602	---	---	1.640	0.077	0.823	0.016	1.555	0.774	0.767	0.206
1393152_at	AI007821	---	---	0.507	0.077	0.430	0.009	0.613	0.050	0.571	0.007
1395526_at	BE111618	---	---	0.699	0.078	0.543	0.956	0.551	0.058	0.719	0.437
1375535_at	AI103917	---	---	0.612	0.078	0.828	0.493	1.128	0.083	0.832	0.589
1373906_at	AI104594	---	---	0.490	0.078	0.432	0.007	0.832	0.283	0.623	0.070
1383388_at	BI303582	---	---	0.645	0.078	0.733	0.046	0.747	0.147	0.788	0.045
1392527_at	AI137840	---	---	0.536	0.078	0.572	0.003	0.717	0.015	0.553	0.002
1393097_at	AI709802	---	---	1.573	0.079	3.224	0.001	1.139	0.657	2.414	0.005
1384319_at	BE098518	---	---	1.958	0.079	3.022	0.013	1.287	0.334	1.591	0.029
1384022_at	BI288173	---	---	0.843	0.079	0.784	0.138	0.738	0.028	0.724	0.086
1390637_at	BF406280	---	---	0.994	0.079	1.113	0.907	0.898	0.994	0.750	0.960
1388653_at	AA849552	---	---	0.896	0.079	0.559	0.007	1.061	0.599	0.695	0.031
1382016_at	AI716661	---	---	0.738	0.080	1.917	0.189	0.692	0.122	1.704	0.241
1397600_at	AI717400	---	---	1.996	0.081	1.158	0.116	1.077	0.800	0.852	0.511
1375506_at	BG376675	---	---	0.519	0.082	0.554	0.018	0.648	0.378	0.756	0.071
1391168_at	BF407466	---	---	1.547	0.082	0.998	0.899	1.152	0.078	0.993	0.982
1395034_at	AI408816	---	---	2.389	0.082	1.279	0.351	4.015	0.026	2.782	0.410
1380268_at	AA956352	---	---	0.740	0.083	0.709	0.048	0.934	0.396	0.816	0.151
1392992_at	BF395999	---	---	0.528	0.083	0.935	0.990	0.256	0.053	1.319	0.226
1378061_at	AI043888	---	---	2.283	0.083	1.062	0.286	4.348	0.019	2.690	0.003
1394895_at	AI548194	---	---	0.610	0.084	1.631	0.013	0.662	0.014	1.322	0.109
1375998_at	BI279840	---	---	0.851	0.085	1.059	0.985	0.961	0.387	0.863	0.688
1394461_at	BF409715	---	---	2.375	0.085	3.277	0.004	2.224	0.020	1.233	0.016
1395636_at	AI576368	---	---	0.708	0.086	0.643	0.153	0.838	0.114	0.642	0.183
1390836_at	AI031048	---	---	1.373	0.086	0.998	0.368	1.850	0.012	1.840	0.256
1372411_at	BE110638	---	---	0.646	0.087	1.023	0.131	0.548	0.022	0.974	0.956
1379671_at	BE095923	---	---	2.296	0.088	1.956	0.037	2.175	0.056	2.519	0.030
1372944_at	BI275710	---	---	0.674	0.088	0.788	0.990	0.954	0.608	1.017	0.045
1394457_at	AW530304	---	---	1.341	0.089	0.877	0.232	1.668	0.241	1.302	0.197
1374789_at	BF550398	---	---	0.398	0.089	0.556	0.009	0.384	0.028	0.461	0.003
1378691_at	AA893871	---	---	0.629	0.089	0.697	0.144	0.824	0.431	1.186	0.883
1377069_at	BG379055	---	---	0.782	0.089	0.240	0.007	0.698	0.306	0.545	0.074
1388742_at	AA945877	---	---	1.290	0.090	1.616	0.016	1.602	0.075	2.122	0.035
1393142_at	BF562621	---	---	0.560	0.090	0.594	0.019	1.664	0.077	1.060	0.665
1383737_at	BM383406	---	---	0.927	0.090	1.943	0.009	0.657	0.131	1.996	0.014
1380474_at	AI013470	---	---	1.845	0.090	0.983	0.279	1.577	0.382	0.498	0.003
1389582_at	AI407405	---	---	0.582	0.090	3.403	0.012	0.233	0.043	3.102	0.034
1381256_at	BI276190	---	---	0.908	0.090	0.999	0.879	1.053	0.315	1.102	0.575
1389333_at	AI407074	---	---	1.445	0.091	0.838	0.050	1.219	0.127	0.845	0.860
1390831_at	BF407157	---	---	0.896	0.092	0.676	0.010	0.855	0.679	0.810	0.048
1382128_at	BI289196	---	---	1.554	0.092	0.794	0.056	1.224	0.534	0.835	0.101
1379673_at	AI230747	---	---	1.195	0.092	2.166	0.002	0.627	0.846	1.291	0.046
1381424_at	AI535231	---	---	0.627	0.093	0.639	0.158	0.803	0.533	1.174	0.934
1395128_at	AA899996	---	---	3.320	0.093	1.753	0.514	5.736	0.058	0.977	0.060
1373621_at	BI285949	---	---	0.406	0.095	1.188	0.495	0.339	0.001	1.374	0.110
1371190_at	BG153272	---	---	0.727	0.096	1.246	0.069	0.734	0.006	0.980	0.524
1397798_at	BE120611	---	---	1.189	0.096	1.516	0.259	1.055	0.008	1.301	0.682
1393151_at	BG668816	---	---	0.631	0.096	0.205	0.010	1.105	0.511	0.257	0.019
1384166_a_at	AW522260	---	---	1.691	0.097	0.996	0.897	1.232	0.072	0.867	0.393
1373758_at	AI171855	---	---	0.625	0.097	1.353	0.049	0.859	0.280	1.361	0.242
1393584_at	AI045201	---	---	0.285	0.097	0.756	0.030	0.174	0.045	0.671	0.036
1380780_at	BI300306	---	---	2.386	0.098	1.181	0.190	1.352	0.274	0.733	0.159
1381421_at	AA899688	---	---	0.803	0.098	0.917	0.024	0.743	0.112	0.875	0.357
1373895_at	BE118440	---	---	0.315	0.098	0.724	0.034	0.418	0.146	0.632	0.176
1376913_at	AA925375	---	---	0.396	0.098	0.809	0.078	0.668	0.065	0.818	0.122
1379853_at	AI058985	---	---	0.889	0.098	0.703	0.284	0.628	0.444	0.720	0.005
1381859_at	BE097018	---	---	2.182	0.101	2.096	0.189	1.633	0.100	1.659	0.033
1386660_at	BF565021	---	---	0.363	0.101	0.239	0.002	0.579	0.056	0.269	0.008
1388667_at	AI178793	---	---	0.457	0.101	0.421	0.003	0.458	0.008	0.358	0.003

1395714_at	AT005664	---	---	0.334	0.101	0.349	0.012	0.319	0.091	0.289	0.001
1393463_at	BM390801	---	---	1.496	0.101	0.776	0.093	1.158	0.191	0.762	0.093
1391374_at	BE106930	---	---	1.165	0.102	1.123	0.095	1.628	0.048	1.371	0.189
1379938_at	BE109444	---	---	0.551	0.104	0.544	0.035	0.476	0.113	0.476	0.038
1383052_a_at	BE112093	---	---	1.067	0.104	2.823	0.052	1.178	0.595	1.060	0.880
1393481_at	BM390812	---	---	0.721	0.104	0.567	0.018	0.540	0.067	0.485	0.015
1382951_at	AA957549	---	---	3.258	0.104	3.935	0.021	1.502	0.070	2.619	0.008
1395766_at	BM391518	---	---	1.804	0.104	1.195	0.310	1.597	0.139	1.140	0.262
1396941_at	AA997470	---	---	0.867	0.105	1.573	0.081	6.875	0.048	2.559	0.020
1392452_at	AI169548	---	---	0.608	0.105	0.704	0.039	0.586	0.079	0.752	0.232
1374194_at	AI170007	---	---	0.688	0.105	0.641	0.017	0.766	0.007	0.579	0.006
1377976_at	AI137539	---	---	1.065	0.106	0.745	0.084	1.472	0.126	0.806	0.783
1372463_at	AI010084	---	---	1.331	0.106	0.731	0.040	1.078	0.116	0.997	0.185
1375912_a_at	BI285430	---	---	0.834	0.106	0.246	0.002	1.454	0.381	0.587	0.099
1383665_at	BE096055	---	---	2.483	0.108	2.590	0.005	4.326	0.058	2.038	0.015
1397547_at	BF407913	---	---	1.621	0.108	0.933	0.750	1.507	0.974	1.831	0.186
1377955_at	AI137602	---	---	1.630	0.109	1.622	0.025	1.000	0.999	1.302	0.064
1399071_at	BI281808	---	---	3.047	0.109	2.607	0.092	5.595	0.021	2.337	0.045
1373470_at	BM388896	---	---	1.128	0.110	0.942	0.403	0.969	0.932	0.966	0.560
1371362_at	BI285402	---	---	0.728	0.111	0.515	0.001	0.794	0.007	0.549	0.015
1393318_at	BG379074	---	---	0.869	0.111	1.433	0.424	1.004	0.337	1.253	0.997
1381975_at	BG371767	---	---	0.633	0.111	0.349	0.001	0.427	0.006	0.452	0.012
1375362_at	BI304125	---	---	1.855	0.111	1.541	0.053	2.016	0.086	2.304	0.010
1394127_at	AA943800	---	---	0.825	0.111	0.812	0.377	0.959	0.104	0.651	0.377
1398981_at	AI171951	---	---	0.381	0.112	0.687	0.136	0.415	0.049	0.769	0.002
1397398_at	BG376725	---	---	0.723	0.112	0.906	0.153	0.785	0.315	0.627	0.041
1392062_a_at	BE097702	---	---	0.816	0.112	0.376	0.001	0.492	0.056	0.444	0.021
1399146_at	AI576776	---	---	0.335	0.113	0.388	0.000	0.141	0.001	0.263	0.035
1372098_at	AI172092	---	---	0.901	0.113	1.510	0.074	0.768	0.160	1.215	0.450
1372567_at	BI274544	---	---	0.384	0.113	0.730	0.913	0.276	0.025	0.432	0.048
1378916_at	AI029234	---	---	0.586	0.113	0.419	0.008	0.568	0.007	0.442	0.019
1396852_at	AW532366	---	---	2.402	0.114	0.733	0.157	1.163	0.331	0.946	0.752
1374501_at	BF550209	---	---	1.634	0.114	1.082	0.867	1.610	0.001	0.942	0.138
1376998_a_at	BI276006	---	---	1.983	0.114	0.869	0.962	2.446	0.011	0.564	0.113
1398669_at	AA893160	---	---	0.758	0.115	2.547	0.002	0.922	0.608	1.539	0.002
1371046_at	AW920849	---	---	1.158	0.115	1.315	0.121	0.945	0.975	1.207	0.970
1371648_at	BF284000	---	---	0.322	0.116	0.500	0.000	0.588	0.002	0.732	0.177
1383327_at	AI576297	---	---	0.497	0.116	0.293	0.005	0.619	0.032	0.263	0.009
1390163_at	BF282174	---	---	0.557	0.117	0.334	0.001	0.555	0.084	0.360	0.008
1376591_a_at	AA800172	---	---	0.773	0.117	0.780	0.007	0.700	0.054	0.867	0.092
1379438_at	AA944576	---	---	0.973	0.118	0.426	0.001	1.015	0.122	0.878	0.062
1397220_at	AW534601	---	---	0.632	0.119	0.945	0.663	0.633	0.085	0.858	0.043
1370217_at	L26525	---	---	0.473	0.119	0.872	0.039	0.466	0.003	0.706	0.116
1373384_at	BM391893	---	---	0.608	0.119	0.256	0.021	0.603	0.103	0.640	0.010
1382748_at	AI145481	---	---	0.612	0.121	0.678	0.015	0.468	0.072	0.655	0.021
1398403_at	BG381546	---	---	0.954	0.121	0.627	0.024	2.107	0.065	0.719	0.026
1390126_at	BE112913	---	---	0.838	0.121	0.820	0.159	0.901	0.170	0.815	0.236
1373566_at	AI103026	---	---	1.362	0.122	3.574	0.002	0.474	0.052	2.117	0.011
1373182_at	BF281899	---	---	0.584	0.122	1.347	0.001	0.711	0.056	1.181	0.002
1397867_at	BG379733	---	---	2.057	0.122	0.996	0.950	1.110	0.606	0.998	0.971
1393045_at	BF556405	---	---	1.236	0.123	1.377	0.134	0.641	0.261	1.163	0.247
1379094_at	BF386909	---	---	1.248	0.123	2.042	0.985	3.127	0.038	1.251	0.786
1378347_at	AW252020	---	---	1.661	0.124	1.887	0.115	0.981	0.663	1.583	0.510
1374407_at	AI227970	---	---	1.417	0.125	0.986	0.539	6.545	0.047	1.012	0.950
1396442_at	BE111933	---	---	1.457	0.126	0.833	0.055	2.108	0.074	0.810	0.080
1388774_at	BM389032	---	---	0.903	0.126	1.671	0.014	0.860	0.885	1.678	0.025
1390406_at	AI232065	---	---	0.552	0.126	0.908	0.706	0.352	0.073	0.784	0.021
1382487_at	AI500925	---	---	1.040	0.127	1.260	0.082	3.429	0.005	1.344	0.059
1377000_at	BI297041	---	---	1.844	0.127	3.259	0.006	2.357	0.010	2.462	0.021
1383619_at	BE105983	---	---	2.024	0.127	3.418	0.001	1.603	0.002	3.540	0.005
1381793_at	BE098864	---	---	1.268	0.129	0.852	0.321	0.862	0.098	0.844	0.960

1383040_a_at	AI044098	---	---	0.588	0.129	0.804	0.207	0.561	0.108	0.539	0.100
1373035_at	AI031032	---	---	0.551	0.129	1.017	0.907	0.381	0.009	0.892	0.294
1373341_at	AI231183	---	---	1.538	0.129	1.795	0.027	1.664	0.344	1.497	0.003
1393166_at	AA998749	---	---	0.737	0.129	2.801	0.004	0.654	0.019	2.150	0.001
1375863_a_at	AI411621	---	---	0.886	0.129	0.561	0.011	0.597	0.206	0.564	0.080
1384040_at	BE121108	---	---	1.199	0.130	0.975	0.861	1.042	0.920	0.738	0.215
1376077_at	BG374774	---	---	2.928	0.130	2.496	0.028	3.109	0.097	1.468	0.049
1392830_at	BF396625	---	---	2.027	0.131	2.008	0.053	1.701	0.070	1.691	0.136
1373695_at	AI176675	---	---	0.596	0.132	0.436	0.000	0.496	0.094	0.426	0.018
1391414_at	AI409142	---	---	0.759	0.133	0.901	0.091	0.893	0.367	1.061	0.696
1395856_at	BF289112	---	---	0.334	0.134	0.219	0.034	0.751	0.460	0.516	0.134
1372360_at	AA817862	---	---	1.609	0.135	1.043	0.176	1.390	0.060	1.146	0.400
1384649_at	AI170778	---	---	1.297	0.136	0.632	0.109	1.687	0.054	0.475	0.200
1394019_at	BI283971	---	---	1.513	0.137	1.230	0.108	1.778	0.063	1.325	0.013
1396403_at	BE107859	---	---	0.750	0.137	1.482	0.016	0.882	0.577	0.993	0.939
1376960_at	AA892240	---	---	0.892	0.138	1.034	0.785	1.031	0.928	1.047	0.695
1371345_at	AI008699	---	---	0.723	0.139	1.078	0.416	0.820	0.243	1.091	0.763
1373834_at	AI233983	---	---	0.679	0.141	0.998	0.517	0.614	0.117	1.000	0.997
1371438_at	BE113144	---	---	0.778	0.141	0.724	0.086	0.717	0.066	0.635	0.019
1374749_at	BM392169	---	---	1.659	0.142	0.630	0.038	0.833	0.256	0.674	0.046
1372450_at	AW916609	---	---	0.910	0.143	1.283	0.043	0.769	0.017	0.931	0.153
1383386_a_at	AI177465	---	---	0.677	0.143	0.788	0.223	1.119	0.159	0.890	0.080
1380203_at	BI285498	---	---	0.751	0.144	0.453	0.018	0.533	0.120	0.603	0.227
1392188_at	AI713162	---	---	1.877	0.144	1.340	0.076	1.678	0.999	1.632	0.071
1391578_at	BF397936	---	---	1.241	0.145	1.737	0.028	1.141	0.519	1.637	0.675
1372534_at	AW434092	---	---	0.720	0.145	1.359	0.123	0.598	0.032	1.268	0.024
1397918_at	BF411420	---	---	0.589	0.145	1.149	0.099	0.569	0.000	0.999	0.991
1386668_a_at	BF565188	---	---	0.693	0.145	1.725	0.132	0.736	0.043	1.328	0.025
1378221_at	BE117032	---	---	1.045	0.146	1.386	0.809	0.977	0.781	1.143	0.509
1397030_at	AI406451	---	---	1.519	0.146	1.786	0.002	1.677	0.031	1.346	0.194
1382515_at	AI059408	---	---	0.771	0.147	1.654	0.001	1.012	0.889	1.041	0.646
1381989_at	BI280114	---	---	0.703	0.148	0.854	0.500	0.604	0.343	0.586	0.053
1374905_at	AA925303	---	---	1.052	0.150	1.006	0.805	0.664	0.792	1.006	0.494
1386817_at	H32518	---	---	0.556	0.151	1.001	0.993	0.650	0.158	0.744	0.999
1390320_at	BF415486	---	---	1.672	0.151	1.006	0.933	1.381	0.533	0.870	0.175
1389084_at	AI177159	---	---	0.535	0.152	0.352	0.023	0.835	0.402	0.581	0.078
1383094_at	BI304048	---	---	1.407	0.153	0.808	0.118	2.092	0.012	1.515	0.020
1384215_at	AI144991	---	---	0.286	0.154	0.183	0.005	0.634	0.369	0.593	0.015
1390458_at	BG666849	---	---	0.840	0.154	0.793	0.737	0.855	0.549	0.788	0.442
1371398_at	BF281400	---	---	0.731	0.154	0.652	0.012	0.622	0.023	0.648	0.077
1373630_at	BG378832	---	---	0.784	0.154	0.299	0.047	0.759	0.428	0.519	0.017
1373027_at	AA944375	---	---	1.407	0.154	1.753	0.006	1.740	0.055	1.638	0.009
1391009_a_at	AA851338	---	---	1.516	0.154	2.025	0.080	1.530	0.011	1.036	0.741
1377105_at	BM385715	---	---	1.412	0.155	2.595	0.001	1.133	0.250	1.398	0.002
1378949_at	BF412698	---	---	0.464	0.155	0.433	0.042	0.600	0.160	0.497	0.002
1383074_at	H32368	---	---	0.507	0.157	1.296	0.990	0.426	0.112	1.168	0.816
1383599_at	BE101133	---	---	0.832	0.158	0.934	0.128	0.786	0.009	0.843	0.110
1378322_at	BM385592	---	---	0.757	0.158	0.680	0.020	0.669	0.060	0.635	0.074
1373536_at	AW525196	---	---	1.774	0.158	2.125	0.118	1.283	0.289	1.255	0.409
1374519_at	AI231782	---	---	0.815	0.159	0.263	0.011	5.835	0.013	0.902	0.419
1376582_at	BE108373	---	---	1.857	0.159	1.223	0.144	2.031	0.293	1.133	0.047
1399164_a_at	BE112193	---	---	0.439	0.160	0.634	0.052	0.312	0.003	0.504	0.155
1384475_at	AW918576	---	---	2.369	0.162	1.067	0.734	5.350	0.055	0.435	0.448
1370953_at	BE113639	---	---	0.628	0.163	1.848	0.007	0.479	0.026	1.664	0.024
1379975_at	AW529144	---	---	1.107	0.163	1.000	0.992	1.067	0.512	0.995	0.976
1389278_at	BI282934	---	---	0.603	0.165	0.913	0.144	0.603	0.168	0.792	0.401
1376630_at	AI599509	---	---	0.547	0.166	0.701	0.042	0.615	0.139	0.724	0.025
1372637_at	AI169241	---	---	0.795	0.167	0.880	0.953	0.817	0.168	1.041	0.491
1379325_at	BI274837	---	---	1.458	0.167	2.530	0.001	1.015	0.730	2.499	0.002
1384709_at	AA800711	---	---	0.762	0.167	0.829	0.355	0.554	0.128	0.798	0.047
1392161_at	AI030731	---	---	1.027	0.167	2.386	0.007	0.645	0.385	1.787	0.121

1383403_at	AW523626	---	---	0.597	0.168	0.379	0.005	0.781	0.466	0.419	0.036
1371484_at	BM390252	---	---	0.897	0.168	1.468	0.112	0.928	0.066	1.429	0.519
1375246_at	BG371965	---	---	1.080	0.169	1.217	0.191	0.871	0.194	1.246	0.014
1374611_at	AW535065	---	---	1.364	0.170	0.484	0.007	1.261	0.270	0.608	0.007
1383502_at	BE113753	---	---	0.743	0.170	1.148	0.232	1.292	0.339	1.761	0.559
1371792_at	AI102045	---	---	1.070	0.170	1.039	0.886	1.018	0.719	0.905	0.298
1398906_at	BM391354	---	---	0.372	0.170	0.401	0.015	0.390	0.075	0.558	0.000
1383093_at	AI029437	---	---	1.133	0.170	1.149	0.183	1.085	0.143	1.115	0.208
1390108_at	AI233162	---	---	0.490	0.170	0.460	0.048	0.395	0.003	0.357	0.035
1398603_at	AA957514	---	---	0.793	0.170	1.083	0.478	0.700	0.733	1.135	0.468
1373301_at	BE113133	---	---	0.927	0.171	1.073	0.068	0.629	0.021	0.807	0.581
1394563_at	AI230657	---	---	0.420	0.171	0.244	0.000	0.414	0.092	0.170	0.025
1372060_at	AI010668	---	---	1.408	0.172	0.413	0.007	2.100	0.128	0.841	0.161
1367521_at	BI281185	---	---	0.758	0.173	2.326	0.011	0.661	0.670	1.342	0.026
1382658_at	AI070638	---	---	0.710	0.173	1.288	0.727	1.268	0.438	0.826	0.505
1371523_at	AI104261	---	---	0.792	0.173	0.817	0.438	0.684	0.061	1.019	0.915
1389042_at	AI030916	---	---	1.119	0.174	0.901	0.975	0.844	0.475	0.790	0.520
1384188_at	AW142766	---	---	1.640	0.174	0.253	0.007	2.547	0.007	0.487	0.001
1371728_at	BF281133	---	---	0.864	0.177	0.746	0.905	0.820	0.110	0.853	0.623
1382707_at	BM386762	---	---	2.275	0.177	1.964	0.021	1.235	0.062	1.861	0.025
1379432_at	AW918404	---	---	0.891	0.177	1.185	0.336	1.120	0.325	1.126	0.303
1367479_at	AI599994	---	---	0.834	0.177	1.070	0.873	0.785	0.152	0.962	0.850
1387784_at	NM_053925	---	---	2.080	0.179	2.780	0.000	1.804	0.015	2.647	0.008
1383081_at	BM388245	---	---	0.582	0.181	0.445	0.000	0.675	0.009	0.538	0.001
1395211_s_at	BE118557	---	---	1.318	0.181	0.509	0.036	2.099	0.173	0.411	0.055
1381996_at	BG666712	---	---	1.135	0.181	0.470	0.001	1.188	0.248	0.641	0.027
1371651_at	BI295882	---	---	0.574	0.182	0.422	0.004	0.639	0.003	0.522	0.006
1390263_at	AI179936	---	---	0.643	0.182	0.234	0.002	0.303	0.019	0.154	0.006
1384043_at	BG667918	---	---	0.767	0.182	0.619	0.005	0.736	0.060	0.520	0.003
1393685_at	BF404962	---	---	1.091	0.183	0.809	0.075	1.183	0.873	0.727	0.113
1374909_at	BI296626	---	---	0.861	0.184	1.369	0.154	1.522	0.950	0.972	0.725
1385265_a_at	AW528215	---	---	0.919	0.184	0.991	0.510	1.131	0.971	1.325	0.011
1383728_at	BM387529	---	---	1.768	0.184	3.765	0.005	1.482	0.226	4.072	0.018
1385231_at	AI044528	---	---	1.461	0.185	1.411	0.174	2.186	0.026	1.691	0.133
1380294_at	AA859714	---	---	0.531	0.185	1.666	0.363	1.089	0.159	1.722	0.208
1373551_at	AA817753	---	---	1.572	0.185	0.725	0.112	1.818	0.004	0.637	0.048
1373250_at	AI229404	---	---	1.822	0.187	1.174	0.913	2.580	0.021	1.044	0.473
1392460_at	BF283685	---	---	0.826	0.187	0.866	0.263	0.758	0.158	0.869	0.970
1375223_at	BI294737	---	---	0.824	0.187	0.446	0.012	1.068	0.210	0.714	0.038
1372334_at	AW144821	---	---	0.868	0.189	0.524	0.009	0.719	0.005	0.678	0.038
1377157_at	BI273815	---	---	1.322	0.189	0.491	0.002	1.050	0.968	0.489	0.012
1395510_at	AW916573	---	---	0.826	0.190	0.998	0.710	1.188	0.890	1.002	0.882
1397492_at	BF410962	---	---	0.785	0.191	0.989	0.931	0.659	0.169	1.023	0.936
1371934_at	AI406487	---	---	0.787	0.192	0.994	0.962	1.192	0.927	0.999	0.991
1389902_at	BI285090	---	---	0.875	0.193	0.956	0.252	0.992	0.444	0.962	0.438
1379210_at	AI500867	---	---	0.999	0.193	0.543	0.030	0.522	0.057	0.565	0.036
1374924_at	BE098025	---	---	0.491	0.193	0.420	0.101	0.651	0.487	0.419	0.102
1382779_at	BF285833	---	---	0.680	0.195	0.828	0.200	0.557	0.047	1.015	0.345
1372721_at	AI175447	---	---	0.761	0.195	1.100	0.245	1.211	0.022	1.357	0.063
1388338_at	BI278637	---	---	0.722	0.195	0.799	0.181	0.725	0.002	0.764	0.726
1385076_at	BE120749	---	---	0.952	0.195	1.019	0.921	0.971	0.950	1.032	0.661
1377949_s_at	AA899043	---	---	1.334	0.199	1.596	0.214	1.447	0.114	1.397	0.147
1379601_at	AI030982	---	---	0.827	0.202	1.629	0.189	1.134	0.272	1.079	0.661
1373540_at	AA848306	---	---	1.263	0.202	0.990	0.720	1.346	0.108	1.031	0.431
1397267_at	BF410275	---	---	0.722	0.202	0.287	0.001	0.785	0.202	0.272	0.012
1393058_at	BE101947	---	---	0.548	0.203	0.667	0.200	0.353	0.019	0.655	0.112
1371653_at	BI281955	---	---	1.402	0.203	2.318	0.000	1.146	0.028	1.670	0.025
1382457_at	AI029816	---	---	0.923	0.206	0.846	0.332	1.500	0.036	0.915	0.573
1394857_at	AI535136	---	---	0.800	0.207	1.005	0.793	0.936	0.301	0.861	0.155
1398977_at	BF558116	---	---	0.707	0.207	1.195	0.156	0.589	0.201	1.506	0.039
1376363_at	AI233337	---	---	0.477	0.207	0.410	0.073	0.481	0.132	0.379	0.011

1385346_at	BE103347	---	---	1.767	0.208	1.625	0.021	1.646	0.929	1.557	0.066
1390623_at	BI279799	---	---	0.870	0.209	3.115	0.014	0.871	0.173	2.189	0.003
1385639_at	AI058950	---	---	1.058	0.209	1.243	0.072	1.123	0.273	1.323	0.033
1375579_at	BG377374	---	---	0.786	0.210	1.412	0.012	0.783	0.196	1.251	0.165
1372319_at	BF282811	---	---	1.087	0.210	0.700	0.042	0.716	0.014	0.530	0.041
1380763_at	AI101194	---	---	1.504	0.211	0.571	0.137	1.633	0.075	0.903	0.256
1392530_at	AI409545	---	---	0.524	0.212	0.562	0.094	0.404	0.039	0.868	0.009
1398486_at	BF400868	---	---	0.572	0.213	0.495	0.007	0.501	0.137	0.404	0.018
1390266_at	BF397998	---	---	0.791	0.213	0.954	0.464	0.748	0.132	0.820	0.137
1399014_at	AA894099	---	---	1.529	0.213	1.235	0.077	1.142	0.322	1.150	0.122
1388421_at	BI295895	---	---	0.791	0.214	1.676	0.218	1.182	0.871	1.173	0.778
1380404_at	H31722	---	---	0.667	0.214	0.956	0.724	0.956	0.883	0.998	0.994
1375179_at	AI231282	---	---	0.787	0.214	2.548	0.010	0.965	0.532	1.858	0.040
1373241_at	AW252569	---	---	0.528	0.214	0.449	0.004	0.409	0.026	0.529	0.012
1391607_at	BE109653	---	---	1.281	0.215	1.658	0.005	1.174	0.392	1.566	0.011
1382840_at	AI232423	---	---	1.343	0.215	0.950	0.115	0.975	0.948	0.900	0.067
1374049_at	AI230220	---	---	0.580	0.216	0.852	0.139	0.508	0.201	0.937	0.508
1385487_at	AW530957	---	---	1.128	0.216	2.431	0.004	1.040	0.591	2.415	0.001
1391583_at	BI280377	---	---	0.811	0.218	0.991	0.997	0.820	0.168	1.160	0.223
1384394_at	BF548081	---	---	0.833	0.218	0.749	0.193	0.526	0.008	0.646	0.084
1394721_at	BF412697	---	---	1.095	0.218	1.400	0.162	1.108	0.124	1.415	0.051
1376868_at	BM389293	---	---	0.537	0.218	0.806	0.014	0.209	0.053	0.551	0.001
1375790_at	BI300458	---	---	0.756	0.219	0.560	0.049	2.127	0.019	0.501	0.195
1372472_at	AA859614	---	---	0.440	0.219	0.429	0.003	0.437	0.013	0.440	0.009
1390576_at	BE116370	---	---	1.261	0.219	1.527	0.004	0.737	0.221	1.316	0.064
1383041_x_at	AI044098	---	---	0.729	0.219	0.807	0.016	0.662	0.021	0.913	0.060
1382944_at	AA891161	---	---	1.088	0.220	0.424	0.000	1.530	0.021	0.844	0.098
1397622_at	AI578003	---	---	0.999	0.220	0.899	0.070	0.797	0.171	0.778	0.054
1395146_at	BI290608	---	---	0.853	0.220	1.737	0.007	0.313	0.043	0.931	0.794
1389198_at	AI179893	---	---	0.459	0.220	0.745	0.008	0.394	0.139	0.732	0.001
1383666_at	BG378435	---	---	1.219	0.222	2.967	0.002	0.995	0.987	2.130	0.018
1374315_at	AI228079	---	---	0.466	0.222	0.228	0.002	0.278	0.035	0.237	0.007
1367527_at	AI600258	---	---	0.761	0.224	0.607	0.005	0.908	0.637	0.779	0.166
1381786_at	BE114356	---	---	1.277	0.225	3.718	0.077	0.819	0.384	1.453	0.514
1376629_at	AA946327	---	---	0.884	0.225	1.007	0.350	0.899	0.478	1.164	0.133
1376158_at	BG373073	---	---	0.570	0.226	0.912	0.119	0.525	0.052	0.840	0.188
1389667_at	AA944552	---	---	0.777	0.226	1.565	0.033	1.050	0.842	1.276	0.032
1395319_at	BM383557	---	---	0.849	0.226	1.219	0.136	0.868	0.223	1.794	0.050
1397088_at	BE110222	---	---	1.168	0.227	1.185	0.767	1.104	0.481	0.998	0.506
1398905_at	BI285183	---	---	1.486	0.227	2.485	0.012	1.415	0.069	2.126	0.017
1379181_at	BF405290	---	---	1.064	0.230	1.197	0.854	0.992	0.660	1.168	0.948
1382189_at	AI574779	---	---	0.522	0.231	0.424	0.000	0.184	0.023	0.358	0.012
1389093_at	BI281735	---	---	1.543	0.232	0.674	0.071	1.439	0.081	0.678	0.072
1381522_at	BI280528	---	---	0.866	0.233	1.409	0.995	1.293	0.142	1.935	1.000
1389923_at	BE104474	---	---	1.587	0.233	1.420	0.063	1.048	0.508	1.434	0.034
1386483_at	AI639028	---	---	0.563	0.234	0.590	0.375	0.417	0.080	1.002	0.999
1384224_at	BE120549	---	---	1.098	0.234	0.806	0.028	1.009	0.899	0.879	0.257
1392897_at	AA924586	---	---	0.511	0.235	0.787	0.199	0.493	0.005	0.897	0.288
1389556_at	BI286000	---	---	0.743	0.236	0.534	0.008	0.582	0.004	0.539	0.017
1379918_at	BE115821	---	---	0.889	0.236	0.988	0.895	1.031	0.984	0.994	0.972
1392393_at	AI501356	---	---	1.124	0.239	1.018	0.580	1.203	0.755	0.974	0.755
1385919_at	AA957343	---	---	1.358	0.241	1.013	0.176	1.595	0.192	1.266	0.058
1383154_at	H34497	---	---	1.149	0.242	0.766	0.086	1.579	0.046	0.958	0.238
1382539_at	AI171022	---	---	0.799	0.243	0.478	0.187	0.756	0.410	0.415	0.078
1372862_at	BM390237	---	---	0.820	0.244	1.305	0.159	0.614	0.001	1.062	0.917
1386148_at	AI409284	---	---	0.753	0.245	0.684	0.192	1.455	0.021	0.789	0.759
1393333_at	BF561617	---	---	1.320	0.247	1.857	0.090	1.190	0.472	1.537	0.627
1394459_at	AI715738	---	---	0.834	0.247	0.529	0.061	1.294	0.433	0.472	0.042
1371870_at	AI169493	---	---	0.980	0.248	1.047	0.486	1.038	0.525	0.893	0.024
1367500_at	AI169461	---	---	1.169	0.248	1.236	0.313	0.671	0.054	1.136	0.112
1390367_at	BF406195	---	---	0.695	0.248	1.137	0.979	0.294	0.007	0.881	0.440

1384122_at	AA996697	---	---	0.590	0.248	0.768	0.812	0.381	0.034	0.899	0.491
1396401_at	AW433899	---	---	0.760	0.252	1.221	0.977	0.729	0.209	0.804	0.367
1378568_a_at	BM389379	---	---	1.580	0.253	2.364	0.002	0.774	0.009	1.500	0.012
1371795_at	AA848795	---	---	0.658	0.256	0.422	0.018	0.768	0.002	0.423	0.017
1374106_at	AI412389	---	---	0.979	0.257	1.033	0.408	2.131	0.036	3.414	0.025
1394943_at	AA893197	---	---	0.746	0.257	0.409	0.012	1.049	0.739	0.717	0.025
1397230_at	BE096562	---	---	0.777	0.258	1.506	0.284	1.564	0.501	1.326	0.412
1376608_at	AI236535	---	---	1.067	0.258	1.095	0.233	1.434	0.047	1.698	0.026
1382538_at	AI555902	---	---	0.832	0.258	0.710	0.191	1.110	0.441	0.771	0.118
1380530_at	BF568014	---	---	0.993	0.259	0.999	0.998	1.018	0.733	0.993	0.988
1379591_at	AI228518	---	---	0.618	0.259	0.307	0.000	0.660	0.318	0.474	0.105
1382010_at	AI711537	---	---	0.517	0.260	2.126	0.041	0.307	0.024	1.783	0.057
1377114_at	AI410861	---	---	0.710	0.260	0.602	0.048	0.897	0.515	0.750	0.222
1371727_at	AA893350	---	---	0.495	0.261	0.264	0.000	0.695	0.312	0.513	0.028
1383735_at	BI274202	---	---	0.998	0.261	1.001	0.642	1.080	0.760	1.341	0.025
1390770_at	BF396139	---	---	0.999	0.262	1.426	0.468	1.080	0.697	0.737	0.215
1383860_at	BI296947	---	---	1.096	0.263	3.247	0.019	1.068	0.161	1.912	0.045
1390020_at	BI277513	---	---	0.694	0.263	0.444	0.000	0.751	0.027	0.551	0.029
1372655_at	BG380323	---	---	0.437	0.263	0.580	0.004	0.379	0.014	0.517	0.027
1388854_at	AI233309	---	---	0.674	0.264	1.350	0.012	0.807	0.172	1.233	0.015
1374351_at	AI044117	---	---	0.859	0.264	0.737	0.003	0.846	0.167	0.812	0.158
1393500_at	AI029289	---	---	1.253	0.265	0.996	0.493	1.013	0.914	1.002	0.522
1375423_at	BE098181	---	---	0.410	0.266	0.518	0.102	0.164	0.002	0.432	0.125
1372730_at	BF282327	---	---	0.590	0.266	1.105	0.620	0.522	0.042	0.684	0.435
1372742_at	AI410058	---	---	0.595	0.267	1.210	0.214	0.552	0.260	1.157	0.438
1376180_at	AW915012	---	---	0.615	0.269	0.912	0.653	0.975	0.511	1.114	0.226
1377886_at	BI274321	---	---	2.738	0.270	0.835	0.732	2.310	0.174	0.637	0.197
1369631_at	AI012566	---	---	0.734	0.272	1.146	0.154	0.537	0.014	1.033	0.182
1375422_at	AI710284	---	---	1.127	0.272	0.818	0.670	0.915	0.335	1.167	0.990
1374316_at	AI229612	---	---	0.993	0.274	1.270	0.118	1.623	0.398	1.303	0.004
1397586_at	BI300588	---	---	0.757	0.274	0.781	0.049	0.837	0.444	0.938	0.045
1379247_at	BI275237	---	---	0.874	0.274	0.521	0.018	0.832	0.064	0.696	0.030
1389866_at	AI599296	---	---	0.733	0.274	0.856	0.249	0.638	0.055	0.771	0.077
1388386_at	AA799822	---	---	0.724	0.275	0.655	0.007	0.814	0.087	0.710	0.027
1371531_at	AI012962	---	---	0.702	0.276	0.427	0.000	0.768	0.572	0.495	0.023
1395413_at	BE116600	---	---	1.151	0.276	0.773	0.126	1.751	0.159	0.700	0.128
1367543_at	BG377443	---	---	1.147	0.276	2.505	0.048	0.999	0.576	1.477	0.319
1371938_at	BM390336	---	---	0.785	0.277	1.325	0.029	0.692	0.113	1.163	0.106
1372608_at	BM388814	---	---	0.765	0.277	1.018	0.493	0.988	0.952	1.198	0.540
1372032_at	AA851914	---	---	1.448	0.277	1.016	0.550	1.932	0.018	1.045	0.612
1394042_at	AI011673	---	---	1.187	0.277	0.970	0.028	1.023	0.733	0.999	0.978
1396291_at	BI290733	---	---	0.890	0.277	0.677	0.154	0.959	0.448	1.460	0.323
1385916_at	AI639015	---	---	1.311	0.278	0.946	0.649	1.386	0.012	0.896	0.415
1385133_at	BF388651	---	---	0.724	0.278	1.160	0.115	0.839	0.964	0.978	0.678
1374380_at	BF403474	---	---	0.414	0.278	0.417	0.004	0.649	0.259	0.386	0.001
1389546_at	BF418582	---	---	0.999	0.279	1.439	0.825	1.780	0.064	0.787	0.040
1371399_at	AA818196	---	---	0.655	0.279	1.531	0.043	0.655	0.001	1.330	0.038
1381773_at	BM383335	---	---	0.794	0.280	1.000	0.530	0.690	0.029	0.604	0.021
1386185_at	H31802	---	---	1.466	0.282	1.231	0.459	1.490	0.294	0.615	0.043
1389186_at	AA944175	---	---	1.375	0.282	0.333	0.069	1.092	0.966	0.922	0.622
1384887_at	AI070185	---	---	0.783	0.282	0.475	0.059	0.781	0.296	0.532	0.400
1382104_at	AI113277	---	---	0.810	0.283	1.738	0.068	0.591	0.054	1.689	0.006
1396244_at	AA964859	---	---	0.884	0.283	0.973	0.520	1.008	0.934	0.966	0.974
1372477_at	BG373744	---	---	1.315	0.285	0.920	0.042	1.255	0.691	0.855	0.014
1374185_at	AI232819	---	---	0.452	0.287	0.824	0.997	0.488	0.029	0.797	0.267
1379222_at	BE120167	---	---	1.897	0.287	1.736	0.137	2.792	0.024	2.495	0.103
1394524_at	AW921279	---	---	0.744	0.287	0.217	0.017	0.442	0.065	0.201	0.003
1372537_at	BI289642	---	---	1.192	0.288	0.751	0.124	4.545	0.028	0.846	0.949
1397155_at	BF393137	---	---	0.936	0.289	0.817	0.315	0.715	0.064	0.933	0.670
1381864_at	AI059122	---	---	0.618	0.290	4.028	0.040	0.608	0.345	2.022	0.049
1367504_at	AI411286	---	---	0.764	0.291	1.266	0.048	0.586	0.048	1.104	0.998

1385780_at	BF416348	---	---	1.780	0.291	0.984	0.723	1.180	0.135	0.999	0.952
1372465_at	AI409184	---	---	0.734	0.291	1.166	0.244	0.970	0.795	1.223	0.924
1398966_at	AI169154	---	---	0.526	0.292	1.021	0.867	0.419	0.001	0.908	0.840
1383004_at	BF397074	---	---	0.530	0.294	0.515	0.030	0.545	0.100	0.294	0.003
1390345_at	BG375523	---	---	0.579	0.294	0.501	0.007	0.885	0.847	0.367	0.058
1386439_at	H31323	---	---	1.098	0.294	0.436	0.142	0.463	0.135	0.528	0.676
1381682_at	BE106750	---	---	2.570	0.295	1.860	0.035	2.511	0.153	1.075	0.213
1382092_at	AA965250	---	---	1.151	0.301	0.392	0.070	1.548	0.046	0.760	0.333
1388954_at	BI295749	---	---	0.960	0.302	0.780	0.978	0.616	0.056	1.008	0.894
1383129_at	AI072254	---	---	0.584	0.302	0.511	0.033	0.692	0.014	0.583	0.111
1376634_a_at	BE109067	---	---	0.999	0.302	1.006	0.500	1.067	0.283	1.316	0.023
1386029_at	BF284035	---	---	1.463	0.303	0.479	0.005	1.067	0.435	0.817	0.062
1392837_at	AA859108	---	---	0.711	0.305	1.031	0.196	1.095	0.540	1.020	0.735
1373173_at	BM390182	---	---	1.580	0.305	0.981	0.843	1.438	0.032	1.175	0.946
1382318_at	AA964856	---	---	0.906	0.308	0.715	0.029	0.695	0.151	0.746	0.044
1371543_at	AI170047	---	---	0.768	0.309	1.324	0.002	0.822	0.024	1.297	0.013
1388647_at	AI233753	---	---	0.536	0.309	0.803	0.092	0.651	0.016	1.008	0.312
1373394_at	BM391986	---	---	0.533	0.309	0.757	0.956	0.757	0.104	0.969	0.674
1380890_at	BE118102	---	---	1.241	0.310	0.597	0.064	1.302	0.320	0.737	0.269
1374438_at	AI103962	---	---	1.117	0.310	1.885	0.003	1.063	0.767	1.847	0.035
1396671_at	BF400889	---	---	1.848	0.311	2.200	0.301	2.727	0.033	2.139	0.316
1377445_at	BF388223	---	---	0.975	0.312	0.176	0.022	2.915	0.070	0.186	0.015
1385211_at	BE116091	---	---	0.712	0.312	0.901	0.542	0.763	0.629	0.978	0.429
1375906_at	BM389920	---	---	0.782	0.313	0.942	0.553	0.786	0.230	0.964	0.620
1397644_at	BI278369	---	---	1.418	0.314	2.940	0.005	1.422	0.073	2.655	0.011
1392895_at	BE101114	---	---	0.669	0.315	0.679	0.003	0.557	0.020	0.638	0.005
1383520_at	AA859127	---	---	1.052	0.315	0.626	0.060	0.947	0.620	0.732	0.614
1376310_at	BI285686	---	---	0.410	0.316	0.442	0.003	0.560	0.018	0.443	0.072
1384963_at	BI277632	---	---	1.309	0.316	1.011	0.945	1.011	0.506	1.040	0.782
1399115_at	AI411999	---	---	1.096	0.317	1.082	0.286	1.086	0.563	1.359	0.085
1385220_at	BG377563	---	---	1.224	0.317	0.996	0.939	0.966	0.488	0.999	0.588
1374504_at	BF415402	---	---	0.847	0.317	0.840	0.193	1.189	0.416	1.002	0.984
1375629_at	AI230371	---	---	0.523	0.318	0.876	0.964	0.510	0.341	0.781	0.437
1372447_at	BI275155	---	---	1.095	0.319	0.989	0.955	1.007	0.774	0.995	0.704
1376621_at	BM390561	---	---	0.578	0.321	0.760	0.213	1.001	0.341	0.756	0.060
1384101_at	BM388523	---	---	1.567	0.323	3.117	0.000	1.509	0.739	1.244	0.319
1377885_at	BI281851	---	---	0.876	0.324	1.605	0.010	0.907	0.052	1.058	0.562
1372659_at	BE113269	---	---	1.446	0.327	1.919	0.002	1.432	0.142	1.793	0.004
1379576_at	AA848479	---	---	0.599	0.327	1.011	0.246	0.935	0.824	1.058	0.845
1376068_at	BF283674	---	---	0.922	0.327	0.801	0.979	0.752	0.608	0.999	0.996
1391161_at	BE107322	---	---	1.563	0.328	2.687	0.008	1.632	0.027	1.789	0.044
1381977_at	BI299008	---	---	0.827	0.328	0.573	0.009	0.810	0.612	0.941	0.199
1394476_at	AW535213	---	---	0.795	0.328	0.521	0.002	0.504	0.023	0.647	0.008
1382691_at	AI234943	---	---	0.843	0.332	1.487	0.140	1.198	0.392	1.313	0.416
1385964_at	AI237569	---	---	0.626	0.333	0.449	0.062	0.480	0.008	0.509	0.055
1385503_at	BM387442	---	---	0.592	0.333	0.305	0.014	0.401	0.376	0.328	0.007
1375186_at	AI169144	---	---	0.678	0.333	1.681	0.132	0.604	0.007	1.217	0.485
1393813_at	BF388771	---	---	1.168	0.335	1.187	0.403	1.093	0.142	0.880	0.230
1376875_at	AI454691	---	---	1.208	0.336	1.148	0.651	0.755	0.055	0.982	0.870
1373260_at	AI412606	---	---	1.487	0.336	0.772	0.006	1.994	0.352	0.910	0.598
1379242_at	BI275646	---	---	0.793	0.338	0.620	0.031	0.843	0.438	0.825	0.200
1388707_at	BF284919	---	---	1.010	0.339	1.138	0.085	0.594	0.747	1.032	0.291
1375029_at	AI235912	---	---	1.113	0.339	2.953	0.000	1.790	0.157	1.811	0.005
1397813_at	AW915896	---	---	1.020	0.340	0.962	0.313	1.007	0.973	0.954	0.498
1383305_at	AW530081	---	---	1.052	0.340	1.124	0.645	1.275	0.192	0.761	0.286
1389196_at	AI180051	---	---	0.527	0.341	0.780	0.290	0.413	0.022	0.843	0.489
1372996_at	AI411245	---	---	0.535	0.341	0.684	0.110	0.795	0.077	0.609	0.162
1388357_at	BI282972	---	---	1.103	0.343	0.566	0.064	1.141	0.495	0.463	0.025
1377149_at	BM386122	---	---	0.859	0.343	0.567	0.040	0.866	0.069	0.566	0.006
1388119_at	BM392140	---	---	0.970	0.346	1.194	0.140	0.873	0.707	0.986	0.429
1371694_at	AI317805	---	---	0.941	0.348	0.733	0.001	0.981	0.596	0.768	0.026

1383931_at	AA901043	---	---	0.803	0.350	0.178	0.003	1.279	0.347	0.176	0.006
1372385_at	AA957292	---	---	1.387	0.350	1.886	0.008	1.586	0.718	1.296	0.016
1383799_at	BF567886	---	---	1.308	0.350	1.142	0.293	1.081	0.385	1.482	0.956
1374687_at	BF283386	---	---	1.054	0.351	0.645	0.013	0.687	0.127	0.664	0.000
1378099_at	AI412479	---	---	0.769	0.353	0.528	0.023	0.775	0.107	0.597	0.129
1376517_at	AW530281	---	---	1.001	0.353	0.999	0.963	1.001	0.260	1.002	0.982
1389957_at	BG378149	---	---	0.782	0.353	1.293	0.634	1.355	0.867	0.705	0.209
1383092_a_at	BE115060	---	---	0.839	0.354	1.766	0.002	0.544	0.355	1.574	0.001
1375944_at	AA849497	---	---	0.618	0.356	1.433	0.209	0.781	0.351	1.107	0.234
1381111_at	BI275744	---	---	1.113	0.357	1.124	0.480	0.993	0.952	1.002	0.694
1389835_at	AI598405	---	---	0.574	0.359	1.010	0.557	0.350	0.020	0.763	0.905
1385538_at	AI059209	---	---	1.002	0.359	1.203	0.178	1.441	0.225	1.161	0.632
1375077_at	BE099881	---	---	1.014	0.361	0.759	0.401	1.195	0.579	1.288	0.093
1391302_at	BE098463	---	---	0.763	0.362	0.248	0.001	0.907	0.712	0.144	0.002
1383359_at	BI389176	---	---	0.427	0.363	1.346	0.135	0.433	0.009	0.955	0.199
1378263_at	BF403483	---	---	0.629	0.363	0.432	0.008	0.954	0.752	0.609	0.026
1375988_at	AW914928	---	---	0.949	0.364	0.773	0.018	1.180	0.969	0.645	0.380
1377042_at	BI288196	---	---	1.021	0.365	2.251	0.002	1.693	0.125	2.357	0.001
1389005_at	BI282843	---	---	0.736	0.365	0.631	0.093	0.864	0.074	0.578	0.099
1391867_at	BI293159	---	---	0.997	0.367	1.167	0.386	1.003	0.669	0.858	0.437
1380090_at	BF407443	---	---	0.787	0.368	0.994	0.359	0.777	0.136	1.005	0.492
1390023_at	AI171686	---	---	1.046	0.369	0.946	0.162	1.749	0.019	0.849	0.088
1399116_at	AI171781	---	---	1.046	0.372	1.182	0.036	0.823	0.083	1.148	0.080
1373974_at	BE110545	---	---	0.764	0.377	1.209	0.075	0.772	0.129	0.802	0.145
1396479_at	BF420007	---	---	1.072	0.378	1.063	0.282	1.068	0.738	1.007	0.946
1375062_at	BM392237	---	---	0.711	0.380	0.338	0.010	0.720	0.429	0.487	0.015
1385836_at	AI454586	---	---	0.891	0.381	0.597	0.001	0.827	0.667	0.716	0.003
1374201_at	AI712727	---	---	0.813	0.381	0.649	0.014	0.986	0.603	0.713	0.021
1394946_at	BI289481	---	---	1.524	0.383	0.430	0.781	1.126	0.048	0.568	0.189
1382126_at	AW528959	---	---	0.536	0.383	0.489	0.013	0.936	0.762	0.679	0.016
1375289_at	BM387047	---	---	0.573	0.384	1.522	0.164	0.955	0.780	1.165	0.977
1371844_at	AW144530	---	---	0.623	0.384	0.550	0.000	0.746	0.053	0.554	0.001
1371393_at	AA851222	---	---	0.371	0.384	0.265	0.023	0.565	0.079	0.236	0.004
1388571_at	BF285314	---	---	0.662	0.384	1.389	0.018	1.215	0.856	1.906	0.002
1399113_at	AI111683	---	---	0.897	0.384	0.808	0.013	1.127	0.591	0.680	0.001
1383633_at	BI289884	---	---	0.599	0.385	0.496	0.001	1.063	0.586	0.651	0.061
1376089_at	BI294974	---	---	0.847	0.386	0.970	0.646	0.885	0.859	0.739	0.019
1383941_at	BF411395	---	---	0.798	0.386	3.160	0.008	0.834	0.281	1.878	0.033
1382014_at	AW521951	---	---	0.893	0.388	0.629	0.006	0.769	0.038	0.768	0.003
1393470_at	BE097303	---	---	0.959	0.388	0.941	0.087	1.214	0.530	1.022	0.089
1384046_at	BF543195	---	---	1.516	0.389	0.960	0.219	1.022	0.819	0.843	0.242
1381906_at	AA944304	---	---	0.931	0.390	1.059	0.468	1.339	0.478	0.934	0.889
1396489_at	BF404442	---	---	0.954	0.391	0.119	0.001	0.936	0.508	0.154	0.000
1374662_at	AA891848	---	---	1.030	0.392	0.274	0.004	1.056	0.257	0.709	0.084
1372948_at	BG376761	---	---	0.476	0.394	0.669	0.133	0.466	0.020	0.888	0.678
1377595_at	AI044347	---	---	1.387	0.395	2.146	0.066	1.466	0.809	1.664	0.053
1384810_at	BF393740	---	---	0.832	0.395	1.169	0.094	0.835	0.727	1.253	0.081
1389661_at	AI599413	---	---	0.850	0.398	0.935	0.045	0.933	0.750	0.982	0.051
1394834_at	BF393831	---	---	1.126	0.400	1.721	0.100	1.000	0.917	0.999	0.990
1390178_at	BM387756	---	---	0.568	0.400	1.130	0.111	0.645	0.035	1.014	0.822
1376737_at	BE110674	---	---	1.005	0.404	3.269	0.005	0.854	0.402	2.432	0.004
1384171_x_at	AA900477	---	---	1.064	0.405	0.733	0.015	0.998	0.948	0.666	0.018
1386006_at	AA866456	---	---	0.804	0.406	0.893	0.500	1.059	0.809	0.880	0.285
1397962_at	BF405788	---	---	0.879	0.407	0.557	0.094	0.943	0.377	0.532	0.151
1379256_at	BF397911	---	---	1.139	0.410	0.854	0.217	1.395	0.045	0.960	0.345
1389544_at	BG669998	---	---	0.814	0.412	1.038	0.382	0.743	0.002	1.046	0.339
1380392_at	BF406259	---	---	1.734	0.413	1.058	0.943	1.367	0.405	1.471	0.231
1390447_at	BI295918	---	---	1.265	0.415	1.798	0.006	1.006	0.273	1.291	0.122
1397604_at	BE128641	---	---	1.368	0.415	1.943	0.100	1.056	0.471	1.186	0.197
1372678_at	AA800044	---	---	1.111	0.417	1.244	0.071	0.605	0.038	1.297	0.037
1392162_at	BF391447	---	---	0.561	0.417	3.145	0.050	0.779	0.115	1.489	0.037

1372336_at	BE115454	---	---	1.016	0.418	0.806	0.034	0.849	0.137	0.873	0.020
1371323_at	BG666002	---	---	0.756	0.419	0.332	0.007	0.755	0.279	0.482	0.015
1385401_at	BI290381	---	---	0.716	0.420	0.744	0.011	0.730	0.092	1.066	0.536
1382172_at	AI228660	---	---	1.013	0.420	0.958	0.713	0.998	0.910	0.968	0.727
1393951_at	BI302706	---	---	0.913	0.420	1.845	0.030	0.795	0.801	1.847	0.001
1380080_at	AW535933	---	---	0.807	0.423	0.999	0.995	0.819	0.415	1.000	0.986
1373043_at	BI275923	---	---	0.590	0.425	1.494	0.008	0.741	0.106	1.083	0.470
1377176_at	BG381076	---	---	0.826	0.425	1.027	0.072	0.759	0.139	1.096	0.512
1389406_at	BI296349	---	---	0.748	0.425	0.647	0.203	0.797	0.026	0.704	0.331
1389110_at	AI639387	---	---	1.283	0.427	1.846	0.041	1.481	0.042	1.952	0.037
1397575_at	BF415880	---	---	0.857	0.427	0.119	0.004	0.969	0.925	0.257	0.007
1397913_at	AW526277	---	---	1.165	0.428	0.678	0.144	0.729	0.667	1.204	0.291
1371848_at	AA799526	---	---	0.622	0.429	1.734	0.014	0.612	0.014	1.653	0.010
1396477_at	AI010663	---	---	1.245	0.429	1.034	0.837	1.207	0.192	1.074	0.843
1378308_at	AI231054	---	---	0.904	0.430	1.660	0.094	0.990	0.153	1.082	0.678
1392707_at	AA946455	---	---	1.792	0.430	1.045	0.170	1.195	0.834	1.228	0.409
1389220_at	BE112918	---	---	0.634	0.432	0.851	0.187	0.355	0.001	0.934	0.029
1388663_at	AI100783	---	---	1.350	0.432	12.406	0.000	1.161	0.171	7.655	0.002
1375049_at	AI711132	---	---	0.865	0.432	0.999	0.995	0.849	0.161	0.999	0.979
1377719_a_at	AA892765	---	---	0.789	0.433	0.910	0.227	0.943	0.575	0.912	0.750
1383669_at	AI556424	---	---	0.822	0.435	0.684	0.245	0.822	0.999	0.602	0.163
1384290_at	BG373809	---	---	0.664	0.436	0.431	0.031	0.629	0.004	0.626	0.378
1384357_at	BG665592	---	---	1.188	0.436	0.500	0.073	1.382	0.422	0.506	0.020
1395857_at	AI717309	---	---	0.857	0.436	1.002	0.991	0.678	0.023	1.121	0.917
1392156_at	BF388086	---	---	1.411	0.437	1.172	0.375	0.858	0.357	0.993	0.978
1367513_at	BI284935	---	---	0.804	0.437	0.581	0.005	0.832	0.282	0.452	0.002
1392883_at	AI013730	---	---	1.309	0.437	2.429	0.014	0.698	0.346	1.140	0.412
1382222_at	BI293607	---	---	0.814	0.438	1.425	0.053	0.926	0.582	0.925	0.407
1380445_at	BI294409	---	---	2.074	0.440	1.680	0.052	1.400	0.785	1.474	0.133
1368852_at	BG668811	---	---	0.669	0.442	0.652	0.009	0.973	0.897	0.793	0.002
1380504_at	BI282488	---	---	0.963	0.444	0.386	0.087	1.161	0.456	0.698	0.199
1396223_at	AW252930	---	---	0.684	0.444	0.944	0.809	0.569	0.055	0.835	0.745
1376851_at	AW520324	---	---	0.996	0.448	0.998	0.963	0.891	0.972	0.998	0.960
1388546_at	AI013328	---	---	0.850	0.453	0.694	0.056	0.654	0.044	0.509	0.042
1388489_at	AA875107	---	---	0.843	0.453	1.070	0.913	0.879	0.895	1.013	0.567
1383586_at	BI295793	---	---	1.117	0.455	2.851	0.067	1.040	0.853	1.795	0.361
1398706_at	BI294633	---	---	1.107	0.456	3.655	0.026	1.131	0.653	1.914	0.054
1382233_a_at	AI030449	---	---	0.827	0.456	0.632	0.045	0.812	0.449	1.082	0.425
1391349_at	BG375114	---	---	0.892	0.457	1.050	0.963	1.005	0.627	0.996	0.969
1395432_at	AI716103	---	---	1.443	0.458	0.999	0.892	1.142	0.978	0.938	0.418
1385351_at	AW528754	---	---	0.767	0.459	1.034	0.762	1.296	0.404	1.000	0.313
1374513_at	BM389104	---	---	0.894	0.459	0.820	0.028	0.934	0.759	0.822	0.062
1378493_at	BE117901	---	---	0.860	0.460	1.404	0.278	0.661	0.245	1.020	0.510
1377891_at	AI407265	---	---	0.498	0.461	1.342	0.221	0.913	0.790	0.789	0.337
1388404_at	AA799724	---	---	0.806	0.461	1.522	0.029	0.433	0.004	1.125	0.288
1376076_at	BI282296	---	---	1.153	0.462	7.785	0.000	1.393	0.078	6.822	0.000
1374297_at	BE100843	---	---	0.623	0.464	0.882	0.044	0.453	0.008	0.728	0.004
1381826_at	AI070839	---	---	0.593	0.468	0.392	0.011	0.794	0.494	0.872	0.450
1390419_a_at	AI454905	---	---	0.771	0.468	0.560	0.002	0.843	0.439	0.584	0.032
1399080_at	BI292036	---	---	0.591	0.468	0.511	0.005	0.460	0.081	0.410	0.011
1395632_at	AI715532	---	---	0.895	0.469	0.661	0.892	1.008	0.213	0.800	0.185
1377243_at	AI172211	---	---	1.073	0.470	0.660	0.135	0.884	0.562	1.071	0.318
1384213_at	AA955944	---	---	1.058	0.471	0.889	0.322	1.106	0.191	0.777	0.089
1376787_at	BE097267	---	---	0.609	0.471	0.224	0.043	0.742	0.046	0.559	0.378
1369410_at	NM_053584	---	---	0.974	0.471	0.856	0.073	0.957	0.262	0.934	0.056
1393125_a_at	AA955445	---	---	1.266	0.472	1.338	0.103	0.700	0.796	0.992	0.550
1392872_at	BF397413	---	---	0.960	0.473	1.545	0.012	0.969	0.556	1.369	0.014
1381844_at	BM389974	---	---	0.705	0.474	0.347	0.018	1.001	0.540	0.484	0.017
1389428_at	AI104431	---	---	0.716	0.474	0.776	0.012	0.700	0.029	0.820	0.054
1385326_at	BI275550	---	---	1.192	0.475	1.328	0.287	0.921	0.368	0.914	0.049
1376272_s_at	AI178914	---	---	0.959	0.475	0.924	0.079	1.375	0.127	1.088	0.355

1373883_at	BE102485	---	---	1.141	0.475	0.810	0.219	2.420	0.085	0.958	0.866
1381661_at	BF394303	---	---	1.284	0.476	0.937	0.505	1.036	0.837	0.894	0.271
1378936_at	AW533986	---	---	0.693	0.476	1.535	0.003	1.309	0.599	1.767	0.156
1379855_at	BF413298	---	---	0.856	0.476	1.274	0.568	1.045	0.936	0.992	0.958
1383626_at	BI274049	---	---	0.537	0.476	1.278	0.250	0.702	0.163	1.376	0.241
1376057_at	BG377379	---	---	0.610	0.480	0.344	0.000	0.628	0.027	0.557	0.034
1391195_at	BF401728	---	---	1.114	0.480	2.912	0.011	1.139	0.618	1.840	0.032
1394866_at	AI511410	---	---	0.764	0.482	0.512	0.080	0.787	0.539	0.635	0.195
1378938_at	AI175561	---	---	1.126	0.482	1.307	0.584	0.908	0.688	1.608	0.620
1382971_at	BF389407	---	---	1.086	0.483	0.741	0.151	1.055	0.108	0.638	0.016
1394759_at	BF289157	---	---	0.920	0.484	0.934	0.057	0.738	0.291	0.881	0.043
1377262_at	BI291600	---	---	1.274	0.484	0.597	0.409	0.842	0.442	0.790	0.199
1370988_at	BE349751	---	---	1.360	0.485	1.474	0.226	1.369	0.093	1.138	0.222
1389564_at	AA892159	---	---	1.227	0.485	1.447	0.004	1.360	0.395	1.208	0.012
1397466_at	BI292573	---	---	1.020	0.485	1.145	0.727	0.409	0.343	0.984	0.922
1395630_at	BF413510	---	---	1.193	0.486	0.970	0.824	1.082	0.697	1.061	0.897
1390258_at	AA893505	---	---	1.019	0.487	0.763	0.653	1.223	0.048	0.632	0.449
1384237_at	BF420822	---	---	0.871	0.488	1.265	0.149	0.573	0.617	1.565	0.010
1389082_at	BF398612	---	---	1.001	0.491	0.447	0.017	0.703	0.285	0.588	0.083
1376748_at	AI406684	---	---	0.755	0.492	0.453	0.043	0.892	0.486	0.731	0.027
1374272_at	BI280268	---	---	0.775	0.493	0.662	0.178	0.822	0.901	0.808	0.213
1374657_at	AA848437	---	---	0.765	0.493	1.659	0.110	1.139	0.220	1.586	0.059
1393238_at	AA900649	---	---	0.924	0.498	0.605	0.485	0.637	0.007	0.718	0.241
1398979_at	BF405079	---	---	1.121	0.499	1.728	0.079	0.737	0.038	1.349	0.967
1392505_at	AI232232	---	---	1.293	0.500	2.457	0.075	0.921	0.256	1.901	0.040
1393037_at	BG373089	---	---	1.234	0.502	0.601	0.036	1.033	0.864	0.449	0.060
1383592_at	AA925988	---	---	1.142	0.504	3.861	0.001	0.983	0.669	2.847	0.000
1373738_at	BG379494	---	---	0.509	0.504	1.541	0.050	0.550	0.048	0.962	0.220
1384176_at	BF419876	---	---	1.080	0.506	0.892	0.450	1.111	0.038	0.865	0.951
1374040_at	BI286772	---	---	0.899	0.506	0.999	0.431	0.966	0.854	1.122	0.855
1383942_at	BI275795	---	---	0.599	0.506	1.868	0.011	0.986	0.219	1.728	0.005
1377720_x_at	AA892765	---	---	0.824	0.508	0.663	0.019	0.953	0.806	0.788	0.323
1376339_at	BM385270	---	---	0.822	0.509	0.800	0.841	0.583	0.018	0.735	0.113
1385556_at	AW521143	---	---	0.874	0.511	0.799	0.060	0.910	0.581	0.677	0.085
1392736_at	AW532939	---	---	1.313	0.512	1.503	0.901	1.227	0.276	1.143	0.179
1372925_at	AI233135	---	---	0.756	0.513	1.034	0.806	1.204	0.466	1.187	0.340
1378905_at	BF557456	---	---	0.939	0.514	0.857	0.294	1.070	0.529	0.743	0.208
1384200_at	BE107328	---	---	0.950	0.515	2.897	0.000	0.675	0.009	2.434	0.004
1383161_a_at	AI008646	---	---	0.856	0.515	0.889	0.220	0.989	0.950	0.990	0.331
1372508_at	BE113266	---	---	1.179	0.521	0.487	0.006	1.284	0.980	0.655	0.009
1389695_at	AI410976	---	---	1.176	0.524	0.919	0.547	0.748	0.043	0.599	0.039
1392905_at	BF552733	---	---	0.662	0.529	0.718	0.050	0.561	0.028	0.405	0.017
1376649_at	AI111965	---	---	0.787	0.529	0.968	0.942	0.762	0.035	0.944	0.984
1376563_at	BG375165	---	---	0.629	0.529	1.939	0.347	0.908	0.201	1.587	0.578
1375360_at	BE099437	---	---	0.751	0.530	1.379	0.207	0.600	0.199	1.022	0.634
1374293_at	AI137495	---	---	0.802	0.532	1.745	0.192	0.896	0.101	1.891	0.081
1392865_at	BG371594	---	---	0.797	0.532	0.998	0.800	1.306	0.190	0.799	0.991
1388441_at	BG379987	---	---	0.697	0.533	0.783	0.081	0.636	0.022	0.790	0.599
1379745_at	AI102041	---	---	0.857	0.533	1.496	0.169	1.023	0.729	1.540	0.108
1375045_at	BM387520	---	---	1.607	0.534	1.839	0.005	1.561	0.016	1.333	0.024
1392753_at	AA875468	---	---	0.921	0.534	0.669	0.019	0.873	0.272	1.253	0.348
1394304_at	BF556357	---	---	1.136	0.535	0.476	0.002	1.139	0.731	0.559	0.012
1380486_at	BM383047	---	---	0.875	0.536	0.460	0.031	1.070	0.930	0.622	0.032
1383994_at	BI289342	---	---	0.922	0.537	0.752	0.372	1.118	0.861	0.985	0.696
1373876_at	BI295945	---	---	0.440	0.538	1.293	0.099	0.791	0.331	1.318	0.085
1393307_at	AI136599	---	---	1.013	0.539	1.155	0.734	1.014	0.767	1.112	0.416
1394268_at	BF564783	---	---	1.079	0.543	0.999	0.080	1.055	0.523	1.219	0.006
1378033_at	AI029178	---	---	1.853	0.547	1.380	0.138	2.650	0.049	0.570	0.009
1375339_at	BI296679	---	---	1.249	0.548	1.068	0.098	0.973	0.488	0.713	0.070
1380219_at	BE117902	---	---	1.049	0.548	1.700	0.014	1.061	0.116	1.840	0.045
1396436_at	BF406417	---	---	1.120	0.549	0.809	0.308	2.870	0.060	0.970	0.312

1376723_a_at	AW142765	---	---	0.886	0.550	2.683	0.009	0.918	0.503	1.549	0.070
1397788_at	AW521711	---	---	0.819	0.550	0.389	0.001	0.693	0.233	0.559	0.064
1392767_at	AI502349	---	---	1.517	0.551	1.144	0.206	1.119	0.412	0.934	0.187
1372474_at	AI172184	---	---	0.943	0.552	1.048	0.959	0.740	0.011	1.035	0.461
1385595_at	BE114414	---	---	0.762	0.553	1.029	0.521	0.371	0.008	1.064	0.738
1393283_at	AA924915	---	---	1.215	0.553	1.044	0.999	1.180	0.095	1.020	0.600
1382547_at	AA859744	---	---	1.089	0.553	1.244	1.000	1.684	0.129	1.241	0.983
1375345_at	AW919569	---	---	0.528	0.555	0.604	0.076	0.500	0.005	0.736	0.061
1372623_at	BE101435	---	---	0.655	0.562	1.391	0.230	0.679	0.038	1.066	0.285
1381448_at	AW535305	---	---	0.930	0.565	1.470	0.818	1.570	0.292	1.559	0.840
1372718_at	AA799572	---	---	0.753	0.566	0.992	0.950	0.611	0.033	0.848	0.092
1372445_at	AI171783	---	---	0.714	0.568	1.000	0.600	0.759	0.631	0.797	0.313
1380202_at	AI070003	---	---	0.634	0.569	0.485	0.042	1.000	0.317	1.072	0.156
1384724_at	AA850766	---	---	1.195	0.569	0.981	0.794	1.005	0.374	0.983	0.857
1382500_at	BF408533	---	---	0.980	0.570	1.430	0.066	0.855	0.182	1.289	0.021
1397917_at	BF412498	---	---	0.879	0.571	0.773	0.359	0.885	0.598	1.787	0.017
1373402_at	AA848980	---	---	1.105	0.573	1.114	0.577	0.987	0.056	0.953	0.640
1395962_at	BI278960	---	---	0.908	0.574	0.576	0.288	0.624	0.060	0.547	0.108
1378249_x_at	BE110241	---	---	0.961	0.575	1.021	0.275	1.243	0.060	1.198	0.292
1386662_at	BF553981	---	---	1.233	0.575	2.175	0.081	1.013	0.411	1.193	0.272
1397097_x_at	BI285806	---	---	0.918	0.578	0.761	0.048	1.036	0.834	0.749	0.132
1395721_at	AW917486	---	---	0.435	0.579	0.161	0.004	0.421	0.404	0.192	0.000
1367538_at	BF284303	---	---	0.955	0.579	0.655	0.003	1.257	0.169	0.642	0.000
1389242_at	BG377726	---	---	1.051	0.580	0.386	0.003	0.813	0.095	0.510	0.007
1381175_at	BE114469	---	---	1.130	0.582	1.577	0.024	1.115	0.300	0.920	0.403
1391625_at	AI706673	---	---	0.878	0.582	0.989	0.980	0.659	0.233	0.572	0.051
1397845_at	BE106909	---	---	1.230	0.584	0.976	0.465	0.933	0.317	1.472	0.070
1375651_at	AI230164	---	---	1.011	0.586	0.836	0.090	1.077	0.205	0.874	0.149
1388361_at	BI303856	---	---	0.499	0.588	0.892	0.449	0.338	0.104	0.656	0.342
1374014_at	AI410079	---	---	1.099	0.589	0.750	0.636	1.159	0.343	1.685	0.016
1378849_at	BF414619	---	---	0.803	0.590	0.605	0.034	0.722	0.241	0.524	0.128
1375940_a_at	BF396656	---	---	1.226	0.590	0.432	0.001	1.286	0.245	0.582	0.003
1375238_at	BM385814	---	---	1.069	0.594	1.022	0.885	0.796	0.024	0.932	0.718
1391709_at	BE108699	---	---	1.009	0.595	0.337	0.075	0.981	0.759	0.334	0.060
1396136_at	BF386241	---	---	1.118	0.597	1.149	0.996	0.843	0.963	1.001	0.033
1391376_at	BF405737	---	---	1.024	0.598	0.914	0.581	1.014	0.976	0.836	0.414
1371933_at	AI228039	---	---	1.071	0.598	0.494	0.026	1.248	0.116	0.371	0.015
1378846_at	BF387240	---	---	1.178	0.602	0.994	0.282	1.001	0.998	1.000	0.923
1377833_at	BF396950	---	---	0.804	0.603	1.076	0.228	0.832	0.980	1.556	0.015
1367489_at	BE114147	---	---	0.912	0.603	0.857	0.350	0.745	0.511	1.026	0.755
1389101_at	BE120340	---	---	0.899	0.604	1.331	0.007	0.806	0.337	1.617	0.008
1374447_at	BG672082	---	---	1.034	0.604	1.235	0.030	0.936	0.355	1.133	0.424
1395456_at	AW919228	---	---	0.882	0.607	0.363	0.002	1.278	0.146	0.561	0.207
1399004_at	BM986309	---	---	0.887	0.607	1.027	0.464	0.911	0.601	0.952	0.667
1379338_at	AI044115	---	---	0.959	0.608	2.362	0.001	1.574	0.206	1.508	0.123
1376935_at	BE113667	---	---	1.023	0.610	4.712	0.003	0.942	0.227	3.346	0.001
1389238_at	BG376577	---	---	1.128	0.610	3.269	0.011	1.392	0.311	1.922	0.030
1394837_at	BF405797	---	---	1.680	0.611	0.663	0.211	2.021	0.143	0.663	0.117
1373692_at	BM391907	---	---	1.064	0.611	1.218	0.034	0.972	0.817	1.077	0.306
1383401_at	BI288769	---	---	0.827	0.613	1.016	0.931	0.933	0.701	0.943	0.851
1372545_at	AI411021	---	---	0.955	0.618	0.679	0.038	0.842	0.197	0.776	0.075
1385343_at	AW523620	---	---	1.944	0.618	2.084	0.600	1.042	0.746	1.091	0.894
1375821_at	BF390754	---	---	1.007	0.618	2.431	0.064	1.765	0.793	1.162	0.675
1395914_at	AA684862	---	---	1.207	0.622	0.473	0.175	0.925	0.367	0.352	0.008
1372173_at	AI407945	---	---	0.870	0.623	0.996	0.843	0.916	0.863	1.060	0.484
1377861_at	AI011151	---	---	0.704	0.623	0.386	0.002	1.181	0.036	0.473	0.009
1396301_x_at	BI277442	---	---	0.994	0.626	0.740	0.352	2.095	0.191	0.678	0.482
1371512_at	AA818692	---	---	0.806	0.627	0.907	0.098	0.700	0.041	0.837	0.502
1379141_at	BF402028	---	---	1.455	0.627	1.453	0.032	1.298	0.380	1.158	0.932
1373355_at	BI299014	---	---	1.058	0.628	1.708	0.072	1.079	0.410	1.403	0.064
1376240_at	BG378240	---	---	1.235	0.628	2.024	0.014	1.121	0.555	1.846	0.006

1398950_at	BI275914	---	---	0.888	0.631	0.607	0.029	0.697	0.119	0.770	0.143
1376489_at	BF397919	---	---	1.078	0.631	1.332	0.033	0.911	0.442	1.044	0.611
1392702_at	BM387858	---	---	1.038	0.631	1.059	0.585	1.020	0.038	1.081	0.369
1372550_at	AI169278	---	---	1.086	0.633	2.227	0.000	0.840	0.073	1.724	0.019
1395869_at	BI296231	---	---	1.019	0.633	1.006	0.176	1.283	0.151	1.100	0.688
1399010_at	BG381740	---	---	0.926	0.633	1.488	0.016	0.806	0.019	1.659	0.005
1394815_at	BE107436	---	---	1.058	0.634	0.866	0.141	1.462	0.087	0.958	0.301
1387345_at	NM_023986	---	---	0.569	0.634	0.526	0.016	0.592	0.045	0.549	0.002
1379705_at	AI511060	---	---	1.173	0.635	0.806	0.247	1.464	0.273	0.723	0.238
1381905_at	AI230826	---	---	0.521	0.638	0.285	0.024	0.494	0.047	0.217	0.014
1391286_at	AA818116	---	---	0.934	0.638	1.938	0.011	1.065	0.979	1.484	0.073
1399106_at	AI176121	---	---	0.804	0.642	0.950	0.281	0.749	0.018	0.785	0.388
1398690_at	BF284365	---	---	1.772	0.646	0.420	0.022	0.853	0.624	0.514	0.012
1374456_at	AI179562	---	---	0.893	0.646	1.032	0.544	1.142	0.298	0.940	0.644
1378930_a_at	BG371548	---	---	1.180	0.647	0.831	0.744	1.247	0.678	0.508	0.202
1373930_at	BM388963	---	---	1.222	0.652	0.986	0.492	1.247	0.602	1.105	0.273
1371680_at	BI303631	---	---	0.829	0.653	1.187	0.092	0.606	0.004	1.031	0.620
1396213_at	BF547413	---	---	0.637	0.656	0.900	0.289	0.625	0.558	0.370	0.023
1382220_at	AI180454	---	---	1.400	0.657	1.184	0.989	1.815	0.025	0.922	0.249
1389978_at	BF396079	---	---	1.011	0.657	0.466	0.044	1.715	0.164	0.438	0.059
1383162_at	AI008646	---	---	0.932	0.658	1.178	0.677	1.078	0.506	1.212	0.293
1391663_at	AI511259	---	---	0.682	0.660	1.098	0.293	0.523	0.407	0.946	0.608
1384222_at	BG669046	---	---	0.924	0.661	0.694	0.003	1.106	0.786	0.647	0.021
1371428_at	AI170002	---	---	0.916	0.661	0.992	0.914	0.938	0.179	0.985	0.732
1372397_at	BE349744	---	---	1.160	0.664	1.438	0.011	0.978	0.452	1.265	0.025
1395208_at	AW526049	---	---	0.999	0.664	1.130	0.489	0.968	0.749	1.058	0.729
1382853_at	AW915066	---	---	1.131	0.665	1.247	0.079	0.613	0.047	1.020	0.931
1396300_at	BI277442	---	---	0.818	0.666	1.613	0.572	1.384	0.329	0.998	0.750
1379335_at	AI639045	---	---	0.780	0.666	0.533	0.007	1.184	0.419	0.810	0.120
1392877_at	AA859524	---	---	1.158	0.668	0.154	0.010	1.482	0.244	0.549	0.001
1384585_at	BI279337	---	---	1.009	0.668	0.614	0.020	1.291	0.133	0.640	0.035
1395132_at	BE115432	---	---	1.240	0.668	0.820	0.215	1.016	0.283	0.321	0.007
1367475_at	AI227695	---	---	0.955	0.669	1.108	0.422	0.968	0.527	1.095	0.138
1378573_at	BE109768	---	---	1.406	0.669	1.039	0.965	1.536	0.307	0.800	0.729
1376488_at	AI101689	---	---	0.881	0.670	0.611	0.025	0.849	0.451	0.666	0.019
1389184_at	AA818914	---	---	1.006	0.670	1.351	0.271	0.945	0.600	1.284	0.991
1397534_at	AW918914	---	---	1.308	0.671	1.155	0.333	0.949	0.540	1.867	0.826
1375595_at	AI231433	---	---	1.300	0.675	4.556	0.004	1.188	0.763	3.550	0.013
1377910_at	BF407333	---	---	0.905	0.676	1.474	0.018	0.872	0.470	1.010	0.097
1377013_at	AI639108	---	---	0.772	0.678	0.070	0.007	1.078	0.026	0.125	0.044
1394477_at	BG380672	---	---	1.044	0.679	0.945	0.060	0.969	0.693	0.968	0.756
1382429_at	AI059574	---	---	1.088	0.679	0.850	0.191	1.011	0.699	0.717	0.043
1393715_s_at	BG376382	---	---	0.479	0.679	1.157	0.133	0.554	0.275	1.242	0.578
1372291_at	BI274517	---	---	0.668	0.685	0.944	0.993	0.419	0.008	0.946	0.611
1378954_at	AI711116	---	---	0.892	0.686	0.974	0.973	0.838	0.428	0.885	0.553
1389046_at	AA860015	---	---	1.021	0.686	1.035	0.482	1.022	0.911	1.015	0.030
1375952_at	AI178495	---	---	0.987	0.686	0.993	0.974	1.056	0.579	0.690	0.124
1375107_at	AI170758	---	---	0.959	0.688	0.814	0.049	1.002	0.704	0.856	0.035
1395945_at	AW535178	---	---	1.123	0.688	1.012	0.784	1.187	0.494	0.943	0.328
1394623_at	AA851041	---	---	1.043	0.690	1.123	0.718	0.973	0.935	0.937	0.931
1379574_at	AI575248	---	---	1.330	0.690	0.930	0.856	0.681	0.544	0.892	0.440
1380301_at	BM385833	---	---	0.935	0.692	0.852	0.632	0.981	0.950	1.115	0.778
1385634_at	AA817959	---	---	0.968	0.692	1.823	0.080	0.831	0.297	1.972	0.018
1371693_at	AA849757	---	---	0.918	0.694	1.642	0.051	1.025	0.909	1.793	0.053
1396123_at	BG377335	---	---	1.057	0.695	0.675	0.015	1.039	0.768	1.000	0.301
1395303_at	BF397734	---	---	1.254	0.696	1.128	0.352	1.397	0.064	0.903	0.205
1383195_at	AW521311	---	---	1.135	0.698	1.286	0.483	0.713	0.960	1.617	0.831
1397337_at	BE119980	---	---	0.904	0.698	0.991	0.859	0.907	0.676	1.000	0.888
1389173_at	AI411575	---	---	0.668	0.698	0.496	0.062	1.465	0.082	1.122	0.570
1376983_at	BF417687	---	---	2.663	0.699	1.687	0.088	2.391	0.179	3.304	0.010
1390563_at	BE096678	---	---	1.156	0.703	0.868	0.026	1.052	0.536	0.762	0.031

1372998_at	BG381555	---	---	0.960	0.705	0.889	0.970	1.096	0.527	0.851	0.596
1397870_at	BF390925	---	---	0.992	0.706	0.577	0.039	0.988	0.886	1.365	0.714
1392546_at	AI145332	---	---	0.834	0.706	0.724	0.059	0.953	0.745	0.852	0.102
1382624_at	AA858768	---	---	1.152	0.711	1.103	0.274	1.135	0.475	0.744	0.297
1392283_at	BI288834	---	---	0.887	0.712	1.939	0.669	1.054	0.876	1.926	0.792
1374608_at	BF415553	---	---	1.342	0.712	2.101	0.009	0.846	0.156	1.534	0.064
1391751_at	BE107919	---	---	1.142	0.713	1.186	0.456	1.366	0.140	1.053	0.461
1391466_at	AI170347	---	---	0.654	0.714	1.714	0.091	0.662	0.427	1.254	0.127
1389611_at	AA849857	---	---	0.754	0.715	2.393	0.001	0.339	0.053	2.283	0.001
1379749_at	AI230509	---	---	1.191	0.717	1.103	0.957	0.995	0.964	1.093	0.452
1372311_at	BG380795	---	---	0.578	0.719	1.305	0.673	0.452	0.273	1.115	0.550
1388308_at	AA800576	---	---	0.758	0.720	1.091	0.978	0.651	0.041	0.900	0.282
1389956_a_at	AI180257	---	---	1.120	0.720	0.922	0.221	1.054	0.375	0.906	0.389
1398527_at	BE108292	---	---	1.084	0.720	0.933	0.312	1.295	0.076	1.079	0.402
1395662_at	AW531934	---	---	1.025	0.720	1.135	0.047	1.019	0.877	1.136	0.353
1381341_at	BE111796	---	---	1.482	0.720	2.215	0.081	1.143	0.408	1.406	0.357
1395772_at	BF290181	---	---	0.871	0.720	1.217	0.287	0.856	0.622	1.269	0.639
1397343_at	BE113258	---	---	1.411	0.721	1.160	0.031	1.125	0.594	1.257	0.041
1384100_at	AI043947	---	---	0.980	0.722	1.081	0.887	1.020	0.981	0.928	0.547
1373667_at	BF400674	---	---	0.938	0.722	0.563	0.001	0.709	0.160	0.672	0.215
1379405_at	AI235642	---	---	0.892	0.723	0.514	0.065	0.797	0.728	0.647	0.034
1381898_at	AI576907	---	---	1.001	0.724	1.197	0.334	0.999	0.989	1.241	0.360
1396192_at	H31517	---	---	1.044	0.725	2.081	0.116	0.979	0.928	1.773	0.457
1395044_at	AI179766	---	---	0.853	0.727	0.981	0.618	0.933	0.676	0.760	0.158
1377716_at	BE116101	---	---	1.259	0.728	1.130	0.728	1.454	0.028	1.132	0.761
1396228_at	BG380184	---	---	1.034	0.733	3.078	0.001	0.884	0.036	2.327	0.004
1398997_at	AI102252	---	---	0.932	0.734	1.383	0.352	0.651	0.140	1.553	0.039
1372078_at	AA891681	---	---	0.832	0.735	1.076	0.387	1.060	0.158	1.005	0.548
1391315_at	BM386843	---	---	0.917	0.735	4.468	0.025	0.805	0.449	2.977	0.050
1395446_at	AW916813	---	---	2.527	0.735	2.404	0.261	2.101	0.059	1.970	0.976
1383589_at	BE103947	---	---	1.302	0.735	1.452	0.158	2.222	0.005	1.759	0.002
1372046_at	BG378725	---	---	0.848	0.735	0.610	0.045	0.692	0.038	0.727	0.085
1372181_at	BM392229	---	---	0.869	0.736	0.837	0.332	0.649	0.984	0.941	0.757
1388345_at	AI599882	---	---	1.116	0.736	1.459	0.006	1.045	0.803	1.334	0.010
1384087_at	AA925049	---	---	0.701	0.737	3.696	0.000	1.224	0.738	3.638	0.001
1381969_at	AA998296	---	---	1.308	0.737	1.605	0.004	0.931	0.117	1.265	0.194
1389031_at	AI179537	---	---	0.904	0.737	1.298	0.370	0.944	0.870	1.226	0.356
1378019_at	AI104278	---	---	0.662	0.738	0.648	0.094	1.045	0.903	1.003	0.999
1398730_at	BF401468	---	---	1.004	0.739	1.046	0.988	1.003	0.897	1.086	0.722
1393587_a_at	AI578061	---	---	0.953	0.740	1.071	0.149	1.064	0.482	0.819	0.296
1380689_at	BM389555	---	---	1.200	0.742	1.544	0.803	1.412	0.259	1.077	0.455
1392134_x_at	BE099652	---	---	1.062	0.744	1.609	0.136	1.003	0.999	1.628	0.212
1395728_at	BF290109	---	---	1.096	0.744	1.554	0.139	2.039	0.292	1.378	0.564
1393796_at	BG375986	---	---	1.020	0.745	3.509	0.042	0.865	0.653	1.452	0.884
1392519_at	AA998248	---	---	1.015	0.745	1.631	0.039	1.449	0.108	1.153	0.418
1395542_at	BF549929	---	---	0.899	0.746	2.821	0.005	1.021	0.908	2.025	0.005
1389375_at	AI232407	---	---	1.016	0.748	1.540	0.004	1.145	0.327	1.393	0.035
1374347_at	BF412225	---	---	0.745	0.753	1.123	0.666	0.976	0.830	1.133	0.227
1395280_at	AA899303	---	---	1.210	0.754	1.050	0.844	1.137	0.681	0.964	0.713
1386794_at	BF544968	---	---	1.393	0.755	1.080	0.611	1.006	0.802	0.911	0.751
1392735_at	AI229265	---	---	1.390	0.755	1.079	0.712	1.283	0.508	1.402	0.117
1395802_at	BF419095	---	---	0.862	0.757	0.933	0.792	0.508	0.206	0.942	0.643
1391926_at	BM385008	---	---	1.146	0.757	1.263	0.499	2.721	0.054	1.326	0.175
1397634_at	BE098186	---	---	0.961	0.757	0.982	0.866	1.421	0.873	0.944	0.177
1370524_at	AW142720	---	---	1.031	0.757	1.031	0.534	0.906	0.496	0.956	0.498
1378990_at	BI274964	---	---	0.947	0.757	0.877	0.052	0.573	0.220	1.011	0.482
1384151_at	AI578392	---	---	1.204	0.759	0.997	0.602	1.111	0.942	1.433	0.090
1384802_at	AI715326	---	---	0.921	0.759	0.749	0.353	1.409	0.064	0.844	0.052
1378283_at	AI411185	---	---	1.244	0.759	1.116	0.956	1.119	0.171	1.053	0.836
1377343_at	BF405097	---	---	0.970	0.759	0.766	0.246	1.010	0.896	0.987	0.926
1384938_at	AI535143	---	---	0.999	0.759	0.924	0.551	0.986	0.721	0.700	0.166

1378583_at	BI278145	---	---	0.862	0.759	1.035	0.809	0.732	0.733	1.095	0.146
1377007_at	AI409696	---	---	1.016	0.760	0.841	0.022	1.106	0.702	0.813	0.007
1382214_at	AI029201	---	---	0.838	0.760	1.190	0.187	0.829	0.096	1.097	0.511
1385834_at	AW532906	---	---	1.018	0.760	0.953	0.470	1.023	0.520	0.948	0.509
1372249_at	BE108148	---	---	0.644	0.763	0.638	0.075	0.615	0.229	0.580	0.006
1376059_at	AI716607	---	---	1.003	0.764	1.625	0.059	1.004	0.642	1.131	0.557
1395256_at	BI301996	---	---	1.211	0.766	1.065	0.773	1.826	0.049	1.084	0.737
1383228_at	AA875288	---	---	0.949	0.766	1.035	0.826	1.054	0.943	1.125	0.655
1383076_at	AA901203	---	---	1.075	0.766	0.935	0.740	1.077	0.072	1.061	0.413
1379136_at	BF410566	---	---	1.001	0.767	0.956	0.488	0.893	0.530	0.965	0.541
1374808_at	BG375471	---	---	1.106	0.767	0.640	0.026	0.825	0.028	0.651	0.062
1378747_x_at	AI013683	---	---	1.144	0.768	0.818	0.113	1.624	0.067	1.003	0.156
1381640_at	BM389537	---	---	0.881	0.769	0.536	0.025	0.924	0.607	0.589	0.001
1390157_at	BI295124	---	---	1.095	0.769	1.446	0.018	1.301	0.846	1.189	0.159
1382763_at	AW921300	---	---	0.906	0.770	0.898	0.067	0.578	0.207	0.884	0.168
1384230_at	AI576177	---	---	0.705	0.770	0.966	0.424	0.914	0.690	0.971	0.355
1388498_at	BF284014	---	---	0.889	0.771	1.319	0.060	0.823	0.109	1.148	0.002
1379815_at	AI713959	---	---	1.219	0.772	1.677	0.972	2.040	0.101	1.735	0.322
1386511_x_at	AI231356	---	---	0.989	0.773	0.927	0.563	1.296	0.429	1.274	0.227
1389910_at	BM390101	---	---	0.718	0.773	1.514	0.057	0.623	0.141	1.357	0.073
1388348_at	BI278590	---	---	0.829	0.775	0.846	0.038	0.805	0.172	0.848	0.016
1383325_at	AI712781	---	---	0.666	0.775	2.575	0.100	0.598	0.162	1.156	0.167
1392418_at	BE105603	---	---	1.399	0.776	1.488	0.035	2.192	0.286	0.838	0.622
1376836_at	BF419655	---	---	0.993	0.776	0.857	0.566	1.058	0.696	1.018	0.466
1374024_at	AA893640	---	---	0.976	0.778	1.338	0.159	0.948	0.385	1.460	0.003
1390484_at	AI176750	---	---	1.171	0.780	1.064	0.470	1.324	0.031	1.005	0.101
1378842_at	AI102520	---	---	0.903	0.780	2.951	0.009	0.674	0.055	2.178	0.006
1386766_at	BF522861	---	---	0.738	0.782	0.712	0.163	0.676	0.286	0.613	0.021
1391719_at	BE098936	---	---	1.072	0.782	0.661	0.035	1.555	0.285	1.229	0.205
1396612_at	BF413266	---	---	1.036	0.783	0.965	0.691	1.224	0.238	1.003	0.922
1396750_at	AW528700	---	---	1.279	0.784	0.914	0.773	1.818	0.153	0.891	0.970
1393380_at	AW917818	---	---	1.089	0.784	0.914	0.647	0.873	0.369	0.991	0.851
1397722_at	BF419387	---	---	0.923	0.785	0.867	0.158	0.998	0.988	0.966	0.340
1377470_at	AI007863	---	---	0.712	0.785	0.425	0.022	1.738	0.053	0.990	0.883
1377877_at	BF397870	---	---	1.008	0.786	1.000	0.616	2.105	0.051	1.000	0.821
1393635_x_at	AI230430	---	---	0.765	0.788	0.983	0.982	0.999	0.968	1.437	0.160
1372171_at	BE111559	---	---	0.947	0.790	1.270	0.467	0.994	0.982	1.074	0.634
1377342_s_at	BE105446	---	---	1.550	0.791	1.127	0.480	1.471	0.632	3.944	0.087
1380854_at	BF396482	---	---	1.054	0.791	1.176	0.087	0.957	0.818	1.088	0.074
1396490_at	BI296616	---	---	0.989	0.792	1.019	0.951	0.852	0.561	1.000	0.997
1390992_at	BI297479	---	---	0.881	0.796	1.083	0.135	1.009	0.965	0.665	0.046
1398535_at	AA998579	---	---	1.022	0.797	3.666	0.002	0.995	0.974	1.690	0.053
1379573_at	AA818730	---	---	1.055	0.799	0.607	0.931	1.377	0.304	0.992	0.714
1388746_at	BI297836	---	---	1.039	0.799	1.004	0.981	0.964	0.741	0.998	0.123
1389223_at	AI177186	---	---	0.811	0.802	1.269	0.313	0.777	0.043	0.877	0.612
1383124_at	BG672201	---	---	1.031	0.803	0.751	0.603	1.375	0.262	0.692	0.505
1386186_s_at	H31802	---	---	0.845	0.803	1.301	0.246	1.156	0.472	1.576	0.044
1373118_at	BM387460	---	---	0.812	0.804	0.462	0.065	1.001	0.928	0.462	0.065
1374771_at	BM388859	---	---	0.887	0.805	0.682	0.039	0.965	0.815	0.513	0.004
1380490_at	AW434884	---	---	0.950	0.805	1.045	0.033	1.119	0.593	1.309	0.049
1377126_at	BM386954	---	---	0.945	0.806	1.777	0.003	0.772	0.442	1.327	0.035
1377809_at	BE111879	---	---	0.974	0.807	0.956	0.869	1.455	0.047	1.094	0.611
1398082_at	BF404767	---	---	1.331	0.807	1.353	0.398	1.652	0.967	1.005	0.986
1398015_at	BF404613	---	---	1.070	0.808	0.988	0.605	1.003	1.000	0.986	0.629
1395164_at	AI549495	---	---	1.034	0.810	0.931	0.339	1.076	0.211	1.016	0.281
1389875_at	AI227951	---	---	0.959	0.810	0.995	0.873	1.297	0.424	1.058	0.999
1396267_at	N55607	---	---	1.036	0.810	1.505	0.247	0.755	0.992	1.004	0.037
1376606_a_at	BM387118	---	---	1.034	0.812	1.202	0.037	1.315	0.059	1.238	0.017
1394767_at	BF396817	---	---	1.154	0.812	1.365	0.304	1.150	0.179	0.943	0.109
1370195_at	AI408945	---	---	1.029	0.812	1.387	0.075	1.059	0.551	1.288	0.006
1394109_at	BF558056	---	---	0.830	0.813	0.433	0.002	0.472	0.150	0.453	0.173

1398549_at	AI412463	---	---	1.121	0.813	1.176	0.324	1.257	0.829	0.798	0.775
1378697_at	BI300550	---	---	0.914	0.817	0.999	0.992	1.398	0.531	1.037	0.588
1380598_at	AI101569	---	---	1.163	0.818	2.043	0.019	0.605	0.046	1.556	0.061
1371396_at	AI600035	---	---	0.700	0.818	0.776	0.172	0.626	0.363	1.029	0.821
1394965_at	BE099701	---	---	1.003	0.819	3.161	0.060	1.005	0.884	0.999	1.000
1389340_at	BI294227	---	---	1.096	0.820	0.929	0.464	1.486	0.026	0.687	0.001
1372772_at	BM385098	---	---	0.938	0.822	1.170	0.458	1.092	0.444	0.815	0.098
1390587_x_at	AW525862	---	---	0.923	0.825	1.408	0.444	0.661	0.026	1.167	0.225
1371971_at	AI599676	---	---	0.771	0.826	1.485	0.211	0.975	0.744	1.376	0.039
1377951_at	AA964993	---	---	1.008	0.827	1.136	0.174	1.002	0.988	1.026	0.076
1391369_at	BE095798	---	---	0.938	0.829	0.998	0.237	0.935	0.686	0.999	0.523
1375197_at	BG665384	---	---	0.893	0.830	0.819	0.231	0.797	0.018	0.568	0.146
1398128_at	AI548626	---	---	1.084	0.831	0.869	0.953	1.005	0.794	0.813	0.939
1389096_at	BI274243	---	---	1.098	0.833	0.617	0.179	0.720	0.984	0.816	0.113
1389995_at	BF546042	---	---	0.973	0.835	1.465	0.048	0.987	0.880	1.051	0.750
1393237_at	AI577833	---	---	0.927	0.835	1.004	0.188	0.948	0.328	1.118	0.170
1388879_at	BG669292	---	---	0.731	0.836	0.846	0.527	0.705	0.163	0.608	0.304
1394656_at	AW528815	---	---	0.926	0.836	0.851	0.312	1.374	0.018	0.685	0.298
1388678_at	AI176695	---	---	1.008	0.838	0.641	0.063	1.400	0.112	0.790	0.065
1383580_at	AA859643	---	---	1.713	0.838	1.746	0.687	1.068	0.791	0.611	0.035
1379702_at	AI410993	---	---	1.005	0.839	0.996	0.845	1.010	0.746	0.999	0.979
1388481_at	AI407731	---	---	0.960	0.839	1.710	0.000	0.708	0.041	1.472	0.001
1390141_at	BF281848	---	---	1.533	0.842	1.057	0.774	0.916	0.801	1.182	0.434
1385306_at	BI288042	---	---	0.780	0.842	1.234	0.106	1.173	0.514	1.001	0.409
1384643_at	AI071465	---	---	0.829	0.844	0.954	0.836	1.511	0.011	0.942	0.830
1372224_at	BE119694	---	---	1.044	0.849	1.035	0.693	1.077	0.802	1.081	0.977
1373444_at	BF285926	---	---	0.851	0.850	0.907	0.758	1.061	0.722	0.882	0.228
1394500_at	BI288738	---	---	0.998	0.851	0.934	0.972	1.000	0.963	0.998	0.980
1383975_at	AW435364	---	---	1.297	0.854	0.943	0.064	0.971	0.172	0.891	0.044
1374402_at	BM391160	---	---	1.043	0.855	0.852	0.723	1.018	0.766	1.156	0.460
1371884_at	AI009909	---	---	0.924	0.855	0.959	0.309	1.065	0.810	1.049	0.405
1394540_at	BF387197	---	---	1.763	0.856	1.046	0.603	1.311	0.259	0.881	0.611
1379135_at	BE112728	---	---	0.932	0.857	1.402	0.565	0.682	0.567	0.576	0.148
1379786_at	AI029721	---	---	0.956	0.858	1.169	0.698	1.329	0.088	1.349	0.579
1373579_at	AA945758	---	---	1.010	0.860	1.059	0.273	0.962	0.966	1.030	0.875
1394434_at	BF414439	---	---	0.575	0.861	2.377	0.005	0.588	0.245	2.062	0.072
1374179_at	BF285334	---	---	0.698	0.862	2.615	0.020	0.798	0.303	1.569	0.056
1373901_at	BI278570	---	---	0.907	0.862	2.480	0.013	1.005	0.978	2.252	0.024
1380733_at	BI286088	---	---	1.011	0.864	1.478	0.025	0.896	0.040	1.176	0.252
1397268_at	BI295515	---	---	1.859	0.864	0.875	0.431	1.104	0.652	0.909	0.495
1396773_at	BF391930	---	---	1.062	0.865	1.001	0.380	1.413	0.011	1.125	0.801
1379314_at	BF283985	---	---	0.884	0.865	0.824	0.049	0.745	0.462	0.910	0.203
1381003_at	BE096129	---	---	1.178	0.866	0.798	0.209	1.296	0.943	0.671	0.398
1397012_at	AI411908	---	---	0.972	0.866	0.956	0.460	1.612	0.117	1.001	0.954
1381129_at	BF392367	---	---	1.022	0.867	1.392	0.708	1.341	0.208	1.357	0.120
1388374_at	AI412011	---	---	0.929	0.867	0.713	0.094	0.738	0.983	1.000	0.335
1380027_at	AW523502	---	---	0.987	0.868	0.997	0.979	0.992	0.999	0.992	0.977
1395935_at	BF282716	---	---	1.098	0.869	0.969	0.277	1.144	0.950	0.901	0.674
1388159_at	AA849795	---	---	1.157	0.870	0.759	0.041	0.987	0.232	0.780	0.065
1379862_at	BF400663	---	---	1.056	0.870	1.092	0.312	0.984	0.870	1.095	0.205
1389683_at	AI170768	---	---	1.207	0.871	1.182	0.193	1.504	0.009	1.142	0.336
1382574_at	AI176776	---	---	0.995	0.871	1.636	0.064	1.219	0.074	1.566	0.146
1372058_at	AI177914	---	---	0.963	0.872	1.213	0.009	0.953	0.540	1.470	0.005
1373517_at	BG671501	---	---	1.185	0.873	1.497	0.001	1.007	0.805	1.482	0.010
1377328_at	BI290012	---	---	1.459	0.873	1.299	0.361	1.789	0.633	1.084	0.961
1386039_x_at	BF288392	---	---	0.929	0.874	1.440	0.389	1.243	0.110	1.624	0.688
1375266_at	BG380633	---	---	0.805	0.874	0.416	0.040	0.742	0.225	0.354	0.007
1392713_a_at	AA892541	---	---	0.741	0.875	0.999	0.684	0.641	0.515	0.802	0.171
1376822_at	BI297481	---	---	1.000	0.877	1.002	0.975	1.006	0.985	0.995	0.932
1375602_at	BG378103	---	---	1.070	0.879	0.796	0.544	1.696	0.037	0.786	0.455
1372743_at	AI409727	---	---	1.058	0.879	1.065	0.495	0.939	0.680	1.398	0.025

1392709_at	BF286936	---	---	1.089	0.881	1.467	0.347	1.284	0.171	1.322	0.572
1397949_at	BE117532	---	---	1.024	0.881	1.087	0.963	1.148	0.043	1.099	0.166
1396493_at	BF403409	---	---	1.099	0.882	0.650	0.370	1.396	0.559	1.145	0.674
1395314_at	AA924452	---	---	1.062	0.883	1.072	0.747	1.220	0.199	0.975	0.805
1394000_at	BM391003	---	---	1.001	0.883	1.123	0.674	0.796	0.733	0.999	0.996
1397355_at	AW916626	---	---	1.061	0.885	0.824	0.907	1.187	0.405	0.995	0.981
1394886_at	AI235545	---	---	0.883	0.886	1.218	0.422	1.046	0.078	1.023	0.816
1392356_at	AW528693	---	---	1.005	0.886	1.310	0.994	1.330	0.245	0.999	0.993
1394471_at	BF291036	---	---	0.934	0.886	1.026	0.558	1.046	0.745	0.452	0.089
1395566_at	AW524204	---	---	1.002	0.887	0.990	0.990	1.348	0.097	1.068	0.837
1378123_x_at	BI285319	---	---	1.064	0.888	0.825	0.370	1.124	0.291	1.169	0.903
1373426_at	BI282894	---	---	0.942	0.889	1.117	0.438	0.774	0.006	1.223	0.982
1389904_at	AI171529	---	---	0.963	0.889	0.789	0.001	1.019	0.445	0.800	0.021
1372337_at	AA800242	---	---	0.845	0.889	1.234	0.599	0.618	0.140	1.290	0.094
1396571_at	BF418055	---	---	0.968	0.890	0.914	0.169	0.966	0.861	0.897	0.553
1392828_at	BI283139	---	---	0.683	0.890	0.626	0.023	1.359	0.352	0.930	0.652
1383054_at	BE111631	---	---	1.174	0.890	3.084	0.004	1.443	0.553	2.002	0.007
1384260_at	BE095699	---	---	1.057	0.891	1.107	0.487	1.176	0.349	1.315	0.911
1389424_at	BI289475	---	---	0.921	0.891	0.510	0.014	1.566	0.316	1.027	0.234
1376882_at	BF398580	---	---	1.018	0.892	0.560	0.083	0.841	0.666	0.936	0.259
1371508_at	AI412098	---	---	0.922	0.893	0.859	0.287	1.011	0.415	0.690	0.064
1386102_at	AA851046	---	---	1.004	0.894	0.956	0.929	1.035	0.767	1.010	0.946
1392953_at	BI296250	---	---	0.951	0.897	1.340	0.020	0.807	0.211	1.307	0.088
1376342_at	BI295185	---	---	1.004	0.899	1.000	0.998	1.382	0.108	0.950	0.962
1393053_at	AI179443	---	---	0.725	0.900	0.789	0.031	0.737	0.816	0.787	0.014
1397834_at	BI294052	---	---	1.035	0.901	0.875	0.964	1.245	0.070	0.932	0.946
1390808_at	AW534721	---	---	1.550	0.903	1.000	0.671	1.047	0.205	1.154	0.438
1374926_at	AI102985	---	---	1.026	0.904	2.391	0.039	0.938	0.812	1.895	0.035
1383168_at	BE102209	---	---	0.751	0.904	1.268	0.090	0.770	0.371	1.427	0.040
1376472_at	AI714119	---	---	1.019	0.906	1.092	0.947	1.118	0.498	1.147	0.993
1389820_at	BF289041	---	---	0.994	0.906	0.857	0.252	0.755	0.168	0.932	0.974
1377652_at	BE103109	---	---	0.951	0.906	1.065	0.740	1.518	0.095	0.716	0.740
1394701_at	BF290084	---	---	1.001	0.907	1.001	0.923	1.002	0.930	1.001	0.961
1379366_a_at	AW529938	---	---	0.945	0.907	4.113	0.030	0.964	0.739	1.867	0.301
1378122_a_at	BI285319	---	---	0.789	0.916	0.773	0.756	1.170	0.695	0.833	0.850
1396160_at	BF419307	---	---	0.702	0.916	0.658	0.102	0.958	0.859	0.755	0.200
1379008_at	BE104149	---	---	0.539	0.916	1.299	0.632	0.649	0.727	1.030	0.635
1394629_at	AA944369	---	---	0.958	0.916	1.001	0.958	0.960	0.151	1.138	0.843
1390430_at	BF284190	---	---	0.955	0.916	1.474	0.242	0.954	0.634	1.548	0.183
1398376_at	AI104587	---	---	0.904	0.918	2.518	0.001	0.757	0.122	1.668	0.009
1385056_at	BG372572	---	---	1.169	0.918	1.645	0.083	0.965	0.261	0.933	0.978
1394694_at	AI454646	---	---	0.967	0.919	1.000	0.979	0.988	0.435	1.001	0.989
1383947_at	AI556074	---	---	0.987	0.919	0.999	0.992	0.974	0.872	1.102	0.585
1372367_at	BF414035	---	---	1.040	0.919	1.019	0.051	0.933	0.765	1.078	0.325
1390722_at	AW531272	---	---	1.021	0.921	0.582	0.104	0.450	0.237	0.620	0.162
1375127_at	BI395849	---	---	0.864	0.922	1.431	0.144	0.734	0.495	1.425	0.013
1373776_at	AI406341	---	---	1.017	0.924	0.595	0.273	1.085	0.538	0.854	0.015
1373897_at	AI103106	---	---	0.969	0.925	0.603	0.030	0.993	0.968	0.475	0.024
1372405_at	BE107128	---	---	0.981	0.928	0.764	0.050	0.844	0.435	0.498	0.018
1386071_at	AI070564	---	---	0.966	0.929	0.924	0.155	1.028	0.784	0.853	0.023
1389359_at	BE120823	---	---	1.007	0.929	1.725	0.004	1.039	0.483	1.598	0.018
1383017_at	AI639001	---	---	1.038	0.930	0.592	0.096	0.785	0.340	0.615	0.119
1394413_at	AA819514	---	---	0.983	0.932	0.696	0.068	1.034	0.748	0.957	0.876
1382650_at	AA850953	---	---	1.154	0.932	1.191	0.987	1.519	0.326	1.131	0.676
1390728_at	AI501517	---	---	0.950	0.932	0.740	0.498	0.567	0.029	0.688	0.147
1386467_at	H33140	---	---	0.970	0.933	0.998	0.432	1.001	0.116	0.974	0.310
1375340_at	AI104151	---	---	1.038	0.933	0.829	0.054	0.999	0.064	0.842	0.087
1388726_a_at	AA800242	---	---	1.015	0.934	1.229	0.540	0.840	0.159	1.118	0.070
1390378_at	BE107173	---	---	0.979	0.934	0.791	0.652	1.023	0.246	0.669	0.033
1375108_at	AI008105	---	---	1.010	0.934	0.629	0.033	0.962	0.274	0.777	0.165
1398410_at	AW535349	---	---	1.761	0.935	1.184	0.670	1.810	0.944	1.080	0.808

1394447_at	BF419701	---	---	1.014	0.936	1.040	0.920	1.149	0.165	1.013	0.758
1398726_at	AI502051	---	---	1.034	0.936	1.330	0.303	1.643	0.089	0.435	0.515
1397323_x_at	AW141996	---	---	1.150	0.937	0.566	0.063	1.107	0.802	0.609	0.142
1391551_at	BM391857	---	---	1.300	0.938	0.994	0.206	1.309	0.209	1.257	0.304
1372600_at	BI289613	---	---	1.007	0.938	1.048	0.977	1.271	0.072	1.046	0.986
1383712_at	BF524281	---	---	0.826	0.939	1.528	0.039	0.860	0.086	1.234	0.023
1385959_at	AI176851	---	---	0.884	0.940	1.577	0.079	0.954	0.401	1.031	0.963
1393285_at	BF561264	---	---	1.191	0.940	1.195	0.524	1.349	0.990	1.003	0.824
1372997_at	AI105243	---	---	1.090	0.943	0.968	0.595	1.250	0.667	1.313	0.191
1395848_at	AA998703	---	---	0.974	0.943	0.988	0.105	1.292	0.933	1.036	0.914
1394318_at	AW918228	---	---	0.997	0.943	1.480	0.059	1.000	0.988	1.312	0.063
1394798_at	AA859580	---	---	1.390	0.943	0.963	0.095	1.275	0.192	1.112	0.630
1386037_at	BF288392	---	---	0.969	0.944	1.185	0.469	1.377	0.054	1.301	0.484
1371854_at	BG374451	---	---	0.980	0.944	5.675	0.014	0.856	0.020	1.820	0.074
1378746_at	AI013683	---	---	0.970	0.946	1.001	0.180	1.420	0.102	1.287	0.436
1392884_at	AI172267	---	---	0.993	0.946	0.742	0.016	0.965	0.614	0.852	0.109
1379391_at	AI103389	---	---	1.128	0.947	1.337	0.990	1.486	0.059	0.998	0.994
1396769_at	AW527250	---	---	1.002	0.947	2.678	0.040	1.332	0.500	1.277	0.986
1397869_at	AI453907	---	---	1.001	0.949	0.913	0.160	1.000	0.290	0.911	0.165
1375418_at	BI275823	---	---	0.992	0.950	0.944	0.671	0.993	0.968	0.697	0.752
1373387_at	BF558946	---	---	0.973	0.951	1.035	0.871	0.724	0.351	1.106	0.835
1376085_at	AA849731	---	---	1.013	0.952	1.123	0.854	0.980	0.873	1.036	0.777
1373291_at	AI176713	---	---	0.961	0.953	0.311	0.002	0.998	0.969	0.387	0.002
1391525_at	AW141615	---	---	1.472	0.954	2.262	0.345	1.289	0.691	1.098	0.762
1375708_at	BF392901	---	---	1.047	0.954	0.539	0.002	1.870	0.157	0.747	0.189
1378360_at	BF397301	---	---	1.172	0.956	1.068	0.098	0.901	0.055	1.297	0.440
1382838_at	AA799942	---	---	1.067	0.956	0.813	0.119	1.021	0.640	0.967	0.091
1373088_at	BI295811	---	---	0.992	0.957	1.519	0.001	0.810	0.368	1.350	0.000
1384390_at	BI278808	---	---	1.002	0.957	1.297	0.039	0.998	0.713	1.119	0.209
1374705_at	AA891834	---	---	1.025	0.958	0.369	0.014	1.664	0.808	0.509	0.079
1386038_x_at	BF288392	---	---	1.063	0.958	1.341	0.230	1.295	0.119	1.056	0.140
1397577_at	BF397749	---	---	1.395	0.959	0.815	0.759	1.248	0.425	1.119	0.794
1391710_at	AW251144	---	---	1.001	0.959	1.221	0.079	1.012	0.857	1.010	0.176
1385264_at	AA892746	---	---	1.002	0.959	1.006	0.959	1.003	0.999	1.008	0.998
1374897_at	AI406842	---	---	0.838	0.960	1.290	0.086	0.904	0.200	1.054	0.465
1393517_at	BE097991	---	---	0.988	0.960	0.891	0.660	1.000	0.967	0.953	0.394
1371521_at	BI284797	---	---	0.874	0.961	1.717	0.013	0.784	0.101	1.775	0.025
1382897_at	BF393872	---	---	1.005	0.962	0.610	0.001	0.949	0.994	0.532	0.026
1397408_at	AI407913	---	---	1.001	0.963	1.040	0.949	1.010	0.765	0.997	0.613
1397606_at	D85807	---	---	0.960	0.963	1.464	0.381	1.538	0.075	1.730	0.210
1372686_at	BE113476	---	---	0.978	0.964	1.575	0.175	1.388	0.716	1.610	0.238
1373353_at	BE097309	---	---	0.911	0.966	1.156	0.324	1.002	0.980	0.875	0.828
1392227_at	BI288917	---	---	0.554	0.967	1.109	0.997	0.998	0.995	1.035	0.649
1376352_at	BF394095	---	---	1.010	0.967	0.998	0.462	1.048	0.745	0.997	0.015
1383517_at	AA998001	---	---	1.010	0.969	0.884	0.123	1.216	0.173	0.966	0.080
1384692_at	AI172110	---	---	1.013	0.969	0.953	0.666	1.469	0.147	1.716	0.142
1378595_at	BE113427	---	---	1.154	0.970	1.166	0.842	1.111	0.639	1.154	0.467
1378031_at	AI230161	---	---	1.093	0.971	1.553	0.069	0.738	0.060	1.066	0.122
1395259_at	BI295572	---	---	1.001	0.971	0.995	0.958	1.016	0.926	0.998	0.576
1374482_at	AW142993	---	---	0.937	0.972	0.533	0.036	1.076	0.603	0.629	0.103
1374932_at	BI282731	---	---	0.843	0.972	2.097	0.095	0.533	0.003	1.613	0.661
1399103_at	BF414041	---	---	0.824	0.973	0.488	0.062	1.025	0.855	0.815	0.155
1375860_at	AI011063	---	---	0.947	0.973	1.251	0.131	0.679	0.072	0.899	0.109
1374529_at	AI406660	---	---	1.220	0.973	0.149	0.000	1.032	0.758	0.154	0.001
1390128_at	BF557618	---	---	1.003	0.973	1.090	0.936	1.003	0.905	0.988	0.929
1383361_at	BM383741	---	---	1.151	0.973	1.054	0.259	0.826	0.255	1.122	0.039
1389434_at	BE110675	---	---	1.011	0.974	0.995	0.153	1.064	0.947	1.378	0.047
1383053_x_at	BE112093	---	---	1.000	0.974	2.939	0.066	1.027	0.923	0.967	0.817
1393305_at	BF399398	---	---	0.914	0.975	0.334	0.005	0.945	0.994	0.477	0.113
1394491_at	BI301512	---	---	1.016	0.975	0.958	0.579	1.227	0.004	0.971	0.718
1395069_at	BF400622	---	---	0.567	0.975	2.831	0.015	1.268	0.882	2.352	0.525

1373010_at	BG372059	---	---	1.049	0.976	0.995	0.960	1.003	0.808	0.974	0.573
1396079_at	BF558358	---	---	1.003	0.977	1.002	0.253	0.727	0.016	0.828	0.627
1379098_at	AI071602	---	---	0.999	0.977	1.150	0.511	1.580	0.616	1.232	0.384
1383433_at	BI281874	---	---	0.997	0.979	0.246	0.018	1.004	0.984	0.254	0.020
1372943_at	AI072985	---	---	0.885	0.979	1.398	0.187	0.737	0.043	1.283	0.013
1378928_at	BF387639	---	---	0.998	0.979	0.999	0.992	1.003	0.998	1.000	0.995
1397538_at	BF407593	---	---	0.995	0.980	1.442	0.018	0.820	0.375	1.935	0.027
1395047_at	BF397243	---	---	1.375	0.980	0.837	0.083	0.997	0.988	0.793	0.053
1393662_at	BF396974	---	---	0.750	0.980	0.883	0.950	1.486	0.112	0.713	0.552
1380138_at	AI385182	---	---	1.006	0.980	1.089	0.412	1.184	0.208	1.454	0.212
1386302_at	AI179140	---	---	0.999	0.980	2.376	0.103	1.246	0.742	1.660	0.259
1384010_at	AW920178	---	---	1.045	0.980	0.541	0.175	1.280	0.229	0.612	0.194
1390603_at	AA956317	---	---	0.996	0.980	1.444	0.053	0.918	0.629	1.220	0.238
1395501_at	BE120578	---	---	1.006	0.981	0.457	0.059	1.002	0.989	0.444	0.045
1391518_at	AI579823	---	---	0.775	0.982	0.885	0.135	1.002	0.993	0.596	0.147
1397338_at	AI137999	---	---	1.027	0.982	0.853	0.067	0.758	0.433	1.054	0.297
1394633_at	BF288321	---	---	1.655	0.983	1.387	0.133	1.012	0.864	1.537	0.196
1378743_at	BE106252	---	---	1.006	0.983	0.735	0.019	1.010	0.784	0.984	0.914
1378121_at	AI600165	---	---	0.954	0.983	0.692	0.151	0.929	0.725	0.617	0.817
1381734_at	BF400855	---	---	0.979	0.983	0.671	0.064	1.739	0.056	1.117	0.479
1397895_at	BI290793	---	---	0.825	0.985	0.558	0.000	0.818	0.993	0.878	0.559
1396371_at	BF412674	---	---	0.990	0.986	1.005	0.917	1.158	0.369	1.611	0.069
1371994_at	AI412316	---	---	1.143	0.986	0.780	0.046	1.084	0.737	0.767	0.026
1396498_at	BF393477	---	---	0.998	0.987	0.987	0.806	1.001	0.711	0.998	0.072
1392239_at	BF386993	---	---	1.000	0.987	1.269	0.050	1.001	0.989	1.032	0.609
1390975_at	BE111775	---	---	1.000	0.988	0.987	0.966	1.250	0.063	1.001	0.996
1389603_at	AA964544	---	---	0.903	0.989	0.984	0.869	1.031	0.574	0.995	0.829
1383329_at	BI303892	---	---	0.999	0.990	0.915	0.439	1.004	0.996	0.771	0.751
1372589_at	AI177689	---	---	0.417	0.990	1.469	0.249	0.894	0.665	1.388	0.874
1396973_at	BF404479	---	---	0.995	0.990	0.997	0.550	1.000	0.981	1.002	0.903
1395048_at	BM384985	---	---	0.996	0.991	1.026	0.897	1.302	0.022	0.871	0.681
1395660_at	BE114185	---	---	1.004	0.991	0.139	0.000	0.869	0.996	0.201	0.024
1377839_at	BG378776	---	---	0.889	0.991	1.044	0.509	0.998	0.425	1.029	0.838
1382597_at	BF288069	---	---	1.004	0.991	1.073	0.296	1.013	0.957	0.993	0.202
1389000_at	AA964998	---	---	1.001	0.992	0.646	0.013	1.406	0.149	0.813	0.495
1384936_at	AI136316	---	---	1.089	0.992	0.256	0.008	1.146	0.923	0.278	0.019
1396179_at	BF406314	---	---	1.003	0.992	0.998	0.978	1.341	0.317	0.999	0.998
1386850_x_at	AW921365	---	---	1.002	0.993	1.001	0.554	0.999	0.825	0.924	0.933
1375913_at	BI285430	---	---	0.999	0.993	0.260	0.022	1.265	0.328	0.274	0.024
1397974_at	BE110207	---	---	1.001	0.993	1.095	0.843	0.933	0.077	0.878	0.300
1393551_at	AI044529	---	---	0.907	0.993	1.395	0.038	2.457	0.257	2.432	0.053
1377199_at	BI274530	---	---	0.998	0.994	0.325	0.005	0.556	0.146	0.468	0.239
1373154_at	BI278842	---	---	0.998	0.994	0.786	0.240	0.819	0.991	0.740	0.994
1394444_at	BF286450	---	---	0.998	0.994	0.999	0.983	0.966	0.990	0.999	0.888
1384538_at	BE115544	---	---	0.998	0.994	0.937	0.992	0.985	0.955	0.940	0.335
1393455_at	AA998007	---	---	1.002	0.994	0.549	0.002	0.752	0.980	0.676	0.005
1383379_at	AI059153	---	---	0.999	0.994	1.446	0.007	1.001	0.997	1.096	0.821
1376948_at	BI281216	---	---	0.984	0.994	0.593	0.691	1.009	0.183	0.793	0.576
1374986_x_at	BI281143	---	---	1.069	0.995	0.980	0.462	1.240	0.485	1.307	0.299
1388419_at	AW915005	---	---	1.002	0.995	0.843	0.033	0.998	0.980	0.942	0.436
1392377_at	BF409415	---	---	1.007	0.995	0.782	0.371	1.125	0.067	0.897	0.859
1381284_at	BF386160	---	---	1.002	0.996	1.727	0.004	0.742	0.506	1.579	0.045
1391097_at	BF418831	---	---	0.999	0.996	0.645	0.065	0.717	0.080	0.464	0.036
1383845_at	AI059929	---	---	1.027	0.996	0.987	0.178	0.999	0.993	1.034	0.232
1395645_at	BF408105	---	---	1.002	0.996	1.941	0.024	1.404	0.537	1.505	0.052
1384449_at	AA964588	---	---	1.000	0.996	1.709	0.016	0.574	0.112	1.814	0.011
1396440_at	BF419659	---	---	1.044	0.996	0.986	0.767	1.049	0.826	1.077	0.333
1375971_at	BM386028	---	---	0.798	0.997	1.072	0.386	0.744	0.213	0.999	0.982
1396598_at	BF405060	---	---	0.999	0.997	1.093	0.371	1.005	0.971	1.097	0.400
1384195_at	BM388427	---	---	1.853	0.997	1.142	0.212	1.612	0.890	1.219	0.642
1381103_a_at	AA996485	---	---	0.954	0.997	3.358	0.000	0.978	0.693	2.724	0.003

1396792_at	BF392277	---	---	1.023	0.997	0.994	0.963	0.860	0.456	1.061	0.471
1377802_at	BE098769	---	---	0.911	0.998	1.716	0.153	0.755	0.999	1.599	0.180
1383233_at	BI289032	---	---	0.999	0.998	1.355	0.145	0.574	0.997	1.075	0.217
1384533_at	AW527248	---	---	1.000	0.998	0.955	0.976	1.046	0.821	0.959	0.144
1380622_at	BI289578	---	---	1.001	0.998	0.999	0.997	1.003	0.963	1.189	0.445
1397910_at	BF411180	---	---	1.005	0.999	1.001	0.609	1.015	0.686	0.998	0.393
1398076_at	BF399749	---	---	1.012	1.000	1.006	0.978	1.234	0.473	0.993	0.699
1385560_at	AI716213	---	---	0.773	1.000	0.510	0.002	1.310	0.119	0.619	0.041

Primary rat β-cells were left untreated or exposed to IL1β+IFN-γ (IL+IFN) or TNF-α+IFN-γ (TNF+IFN) for 6 and 24h. Data are means of three independente experiments and are expressed as fold change versus control cells, studied at the same time points. Pval = p value of Student t-test agains control condition at the same time point. Some genes are represented by more than one probe.