Geny se zvýšenou expresí v PR9692shHOPX a -E9

ID sondy	Symbol genu	Reprezentativní veřejné ID	míra velikosti účinku (PR9692-shHOPX vs. PR9692-shMOCK)	hodnota P (PR9692-shHOPX vs. PR9692-shMOCK)	míra velikosti učinku (PR9692-E9 vs. PR9692)	hodnota P (PR9692-E9 vs. PR9692)
GgaAffx.20516.1.S1_s_at	KLF15	CR524099.1	36.46	0.00409	5.329	0.04255
Gga.1169.1.S1_at		CR385239.1	24.58	0.00175	12.650	0.00203
Gga.9481.1.S1_s_at		NM_204932.1	21.68	0.00376	8.968	0.00711
GgaAffx.6456.4.S1_s_at		ENSGALT00000016	19.19	0.00081	18.418	0.00029
GgaAffx.12757.1.S1_s_at		AJ720654	17.51	0.00000	8.796	0.00000
Gga.17686.1.S1_at		AY574984.1	16.42	0.00077	32.653	0.00008
GgaAffx.6456.5.S1_s_at		ENSGALT00000016	11.79	0.02612	16.231	0.00665
Gga.3672.1.S1_at		NM_205217.1	11.05	0.00000	3.000	0.00003
GgaAffx.6456.8.S1_at		ENSGALT00000002	10.61	0.01147	14.201	0.00260
Gga.8200.1.S1_at		BU391632	9.47	0.01936	5.911	0.02202
Gga.16141.1.S1_at	ST3GAL1	BU236705	9.33	0.00001	3.878	0.00004
GgaAffx.24513.3.S1_s_at		ENSGALT00000023	6.81	0.00000	4.805	0.00000
Gga.8200.2.S1_a_at		BU123770	6.78	0.01973	3.939	0.03260
Gga.9002.1.S1_at	CISH	CD735855	6.66	0.00257	3.585	0.00646
Gga.8200.1.S1_s_at		BU391632	6.40	0.01568	5.196	0.01100
Gga.3393.1.S1_at		NM_204322.1	5.81	0.00119	9.993	0.00009
Gga.131.1.S1_at		NM_204609.1	4.97	0.00135	2.784	0.00458

Gga.2533.1.S1_s_at		L15386.1	4.77	0.00676	4.550	0.00299
Gga.12506.1.S1_at		CK612784	4.12	0.00651	2.579	0.01561
Gga.9903.1.S1_at	KIAA1210	BU207407	4.11	0.00022	12.099	0.00000
Gga.5954.1.S1_at	LOC100858647	BU125896	3.99	0.00824	2.237	0.03295
Gga.17118.1.S1_at	SALL3	BU208668	3.66	0.04326	6.707	0.00372
Gga.1615.1.S1_at		AL587697	3.65	0.00430	2.764	0.00519
GgaAffx.3789.1.S1_at		ENSGALT00000009	3.62	0.00073	5.702	0.00004
Gga.3115.1.S1_at	CXCL12	BU458248	3.46	0.00390	2.047	0.01827
Gga.5387.1.S1_at	DHX58	BX263553	3.23	0.02181	2.521	0.02494
Gga.7691.1.S1_at	EXOSC5	BX267130	3.13	0.01100	2.032	0.03296
Gga.15797.1.S1_at	FOXO3	BU426926	3.13	0.00191	2.786	0.00117
Gga.5735.1.S1_at		NM_204458.1	3.04	0.01514	12.918	0.00008
Gga.7415.1.S1_at		BU212378	3.02	0.01651	2.058	0.03880
Gga.7691.1.S1_x_at	EXOSC5	BX267130	2.84	0.00106	2.195	0.00162
Gga.12500.1.S1_at	ChEST548f14	BU378394	2.81	0.01699	2.105	0.02773
GgaAffx.12953.1.S1_at		AJ720850	2.72	0.00094	3.325	0.00011
Gga.16828.1.S1_at	FAM110B	BU354179	2.71	0.00450	4.130	0.00025
GgaAffx.21251.1.S1_at	LOC100858197	CR523364.1	2.50	0.01600	2.138	0.01515
Gga.2.1.S1_at	TGFB4/TGFB1?	M31160.1	2.39	0.04732	2.639	0.01455
Gga.13161.1.S1_at	FOXO3	BU306744	2.32	0.01892	3.386	0.00133
GgaAffx.7813.1.S1_at		ENSGALT00000020	2.30	0.00483	5.204	0.00004
Gga.15714.1.S1_at		BU474434	2.23	0.01396	3.635	0.00052
Gga.5239.1.S1_at	HAUS6	BU305999	2.20	0.01939	2.065	0.01195

GgaAffx.20439.1.S1_s_at		CR524176.1	2.14	0.04403	3.613	0.00193
Gga.1035.2.S1_a_at		BX929914.1	2.12	0.00036	2.970	0.00001
Gga.13323.2.S1_s_at		CR387432.1	2.10	0.00871	2.669	0.00081
Gga.13228.1.S1_at		BU253221	2.10	0.01433	2.238	0.00392
Gga.9930.1.S1_at	GBP4/LOC415922	CK610332	2.07	0.00738	2.074	0.00277
Gga.7691.1.S1_a_at	EXOSC5	BX267130	2.05	0.01108	2.060	0.00421

Geny se sníženou expresí v PR9692shHOPX a -E9

ID sondy	Symbol genu	Reprezentativní veřejné ID	míra velikosti účinku (PR9692-shHOPX vs. PR9692-shMOCK)	Hodnota P (PR9692-shHOPX vs. PR9692-shMOCK)	míra velikosti účinku (PR9692-E9 vs. PR9692)	Hodnota P (PR9692-E9 vs. PR9692)
Gga.19091.1.S1_at	HTR1D	BU261799	-192.015	3.58E-06	-9.54244	0.000146
GgaAffx.7341.1.S1_s_at		ENSGALT00000018	-92.3466	0.000234	-30.6564	0.000357
Gga.10266.1.S1_at	RAB15	BX934711.1	-70.3197	2.13E-05	-54.8991	9.28E-06
GgaAffx.12670.1.S1_s_at		AJ720567	-63.4914	2.77E-09	-18.5479	6.75E-09
Gga.2718.1.S1_at		BU274789	-56.1805	1.06E-06	-7.45204	1.92E-05
GgaAffx.8765.2.S1_at		ENSGALT00000022	-55.7211	6.67E-07	-251.417	2.99E-08
Gga.1081.1.S1_at		CD735411	-53.6621	1.24E-05	-7.23754	0.00021
Gga.7334.1.S1_at	RIAM	BX264894	-43.2126	2.93E-05	-13.3568	7.8E-05
Gga.8446.1.S1_at		BU476814	-42.5864	0.000405	-29.4414	0.000235
GgaAffx.7341.1.S1_at		ENSGALT00000018	-42.2613	1.03E-05	-22.4583	9.27E-06
GgaAffx.21467.1.S1_at	CLVS2	CR523148.1	-42.044	5.9E-05	-3.53942	0.006163

Gga.5198.1.S1_a_at		BX932365.1	-41.6739	8.32E-07	-13.1612	2.23E-06
Gga.8519.1.S1_a_at		BX931048.1	-33.4209	1.41E-08	-10.1611	4.99E-08
Gga.10138.1.S1_at	TXNL1	CR353500.1	-32.6963	1.76E-05	-3.53446	0.001582
Gga.12514.1.S1_a_at		AF133252.1	-30.7432	3.68E-05	-3.09381	0.004719
Gga.9699.4.S1_a_at		BX934714.2	-27.6292	5.39E-07	-2.08381	0.000942
Gga.9403.1.S1_a_at		BX932305.2	-26.9105	3.66E-05	-12.3212	5.41E-05
Gga.5787.1.S1_at	SMOC1	BU104016	-25.4023	0.000102	-3.18218	0.007417
Gga.9147.1.S1_at		BU297626	-25.0547	6.39E-05	-13.6348	6.63E-05
GgaAffx.26112.1.S1_at		ENSGALT00000006	-24.395	5.58E-06	-15.4041	4.23E-06
GgaAffx.20829.1.S1_at	ChEST559j8	CR523786.1	-24.362	0.000165	-3.59981	0.006486
Gga.9699.1.S1_a_at		BU243262	-21.8383	4.84E-06	-4.38253	0.000105
Gga.20029.1.S1_at	SLC38A7	BU433578	-20.133	3.85E-06	-6.37829	1.98E-05
GgaAffx.1993.5.S1_s_at		ENSGALT00000004	-19.5386	0.000347	-21.2163	9.65E-05
Gga.13978.1.S1_s_at		CR353711.1	-19.1961	0.000781	-70.5011	3.33E-05
Gga.352.1.S1_at		NM_204842.1	-18.6322	0.000182	-4.00354	0.003185
Gga.3518.1.S1_at	CLMP/ASAM	BU449434	-17.854	2.69E-05	-77.8123	7.29E-07
GgaAffx.4955.1.S1_at		ENSGALT00000012	-17.41	0.001032	-2.68091	0.046296
Gga.4113.1.S1_at		BU246909	-17.316	2.58E-06	-7.87317	5.25E-06
Gga.4491.1.S1_s_at		CR387714.1	-17.0726	0.000236	-37.0968	1.89E-05
Gga.12120.1.S1_at		BU337803	-16.8702	0.000647	-7.89669	0.001157
Gga.11925.1.S1_at		BU415914	-16.0421	0.000435	-126.263	5.81E-06
Gga.17586.1.S1_at	ADCY7	CR390795.1	-15.0127	7.48E-05	-29.9292	6.25E-06
GgaAffx.22647.2.S1_s_at		ENSGALT00000014	-14.0562	0.000209	-5.47502	0.000764

Gga.10703.1.S1_at		BU447950	-13.97	0.000476	-6.16088	0.001166
Gga.8515.1.S1_at		NM_204398.1	-13.957	0.002811	-29.8294	0.000256
GgaAffx.7184.2.S1_s_at		ENSGALT00000018	-13.3074	3.77E-06	-2.03529	0.001688
Gga.13553.1.S1_at		BU134676	-13.1392	0.001012	-6.84226	0.001607
Gga.9699.4.S1_x_at		BX934714.2	-13.0529	5.02E-05	-2.22566	0.007881
GgaAffx.11089.1.S1_at		ENSGALT00000027	-12.7274	0.000855	-3.7817	0.0077
Gga.1794.1.S1_at		BU323603	-12.5687	0.000969	-31.376	5.8E-05
Gga.2884.1.S1_at	ChEST583n1	CR388478.1	-12.5429	0.000102	-4.13289	0.000799
Gga.13519.1.S1_s_at		CR354055.1	-11.3019	0.027902	-11.0364	0.01286
Gga.13451.1.S1_at		BU112223	-10.5707	6.89E-07	-96.8374	3.95E-09
GgaAffx.539.1.S1_at		ENSGALT00000001	-10.2397	3.21E-05	-9.79692	1.11E-05
GgaAffx.21787.1.S1_s_at		NM_204503.1	-10.1886	0.001437	-2.78547	0.023901
Gga.15050.1.S1_at	ChEST217m12	CR386008.1	-10.1131	0.00054	-8.68962	0.000259
Gga.11730.1.S1_at		BU359446	-10.1089	0.000586	-4.30841	0.002228
GgaAffx.23947.1.S1_at		ENSGALT00000020	-9.90034	0.001065	-14.366	0.000157
GgaAffx.21851.1.S1_s_at		NM_001001603.1	-9.68684	9.17E-06	-5.04626	2.02E-05
Gga.8329.1.S1_at		BU397019	-9.49107	0.000512	-40.5288	9.75E-06
Gga.5198.3.S1_x_at	HSBP1L1	BX934295.2	-9.04814	0.000155	-7.82882	7.25E-05
Gga.3674.1.S1_at		BU118967	-8.98627	0.000312	-3.46634	0.002152
Gga.275.1.S1_at		NM_205029.1	-8.84235	0.000104	-11.8625	1.58E-05
Gga.13339.1.S1_at		BU136507	-8.83783	0.000267	-11.039	4.95E-05
Gga.3899.3.S1_a_at		AB031021.1	-8.72075	0.005413	-16.3955	0.000531
Gga.9491.1.S1_at		BU228626	-8.17204	0.000814	-5.83275	0.000703

Gga.18023.1.S1_at		CR389402.1	-8.10356	0.000444	-2.80006	0.005795
Gga.4491.1.S1_at		CR387714.1	-8.092	0.000798	-56.4956	6.23E-06
GgaAffx.2792.1.A1_at		ENSGALT00000007	-7.86923	5.15E-06	-3.97454	1.65E-05
Gga.16589.1.S1_at		NM_204342.1	-7.8382	0.001159	-57.2304	8.48E-06
Gga.643.1.S1_at		NM_205171.1	-7.66828	8.03E-05	-4.67888	0.000123
Gga.3899.1.S1_a_at		NM_204306.1	-7.57149	0.000764	-2.68939	0.009467
Gga.18649.1.S1_at	PDGFA	CR391158.1	-7.50414	0.004167	-5.77636	0.003061
Gga.16822.1.S1_at	MSRB3	CR391617.1	-7.46448	3.19E-06	-147.732	4.22E-09
Gga.1369.1.S1_at		AF020315.1	-7.4394	7.23E-05	-7.22211	2.46E-05
Gga.13251.1.S1_at	DGKI	BU362940	-7.33636	0.000164	-5.77718	0.000108
Gga.10956.1.S1_at		BX931554.1	-6.83532	0.016227	-14.5774	0.00132
GgaAffx.8298.1.S1_at		ENSGALT00000021	-6.83212	0.005046	-7.11996	0.00168
Gga.11065.1.S1_s_at	CHMP4C	BX931068.1	-6.79534	0.025814	-5.02413	0.022879
Gga.10214.1.S1_s_at		BX934975.1	-6.75582	0.00245	-9.09794	0.000398
Gga.6641.1.A1_at	ELMO3	CD737379	-6.74749	0.020408	-9.03433	0.004495
GgaAffx.12879.1.S1_s_at		AJ720776	-6.73453	5.39E-06	-5.2164	3.82E-06
Gga.6306.1.S1_at		BU339335	-6.62738	0.000105	-9.06617	1.36E-05
Gga.5111.1.S1_at		NM_204431.1	-6.60128	0.000689	-71.4848	2.08E-06
GgaAffx.8972.1.S1_s_at		ENSGALT00000022	-6.49708	0.003009	-23.2258	6.22E-05
GgaAffx.21035.1.S1_s_at		CR523580.1	-6.47798	9.39E-05	-10.0062	8.76E-06
Gga.9986.1.S1_at		CN218275	-6.39285	3.97E-05	-6.17759	1.37E-05
GgaAffx.21279.1.S1_at		CR523336.1	-6.37708	0.015523	-6.56185	0.005948
GgaAffx.12115.1.S1_at		AJ720012	-6.26358	9.87E-07	-7.62948	1.61E-07

Gga.7576.1.S1_at		BU243691	-6.18701	0.001083	-2.62365	0.008927
Gga.10596.1.S1_s_at		BX929327.2	-6.08327	0.000198	-3.05941	0.000886
Gga.10214.1.S1_at		BX934975.1	-6.04343	5.12E-05	-7.75983	7.45E-06
Gga.18272.1.S1_at	CCDC80	CR390110.1	-5.76358	0.002736	-57.2259	8.86E-06
GgaAffx.8765.1.S1_at		ENSGALT00000001	-5.7222	0.013296	-4.62593	0.009711
Gga.7499.1.S1_at	MITF	BX264698	-5.65412	0.000352	-8.85291	3.08E-05
Gga.7542.1.S1_at		CD739908	-5.5741	4.58E-05	-13.9194	1.16E-06
GgaAffx.10743.1.S1_at		ENSGALT00000027	-5.55133	0.000643	-19.6191	9.09E-06
Gga.666.1.S1_a_at		NM_205366.1	-5.43542	0.003257	-3.56415	0.004875
GgaAffx.12049.1.S1_at		AJ719946	-5.31529	0.00185	-5.9962	0.000442
Gga.12092.1.S1_at		BU369564	-5.19917	0.004396	-4.95955	0.00187
GgaAffx.7917.1.S1_at		ENSGALT00000020	-5.16138	0.008897	-11.3494	0.000458
Gga.2190.2.S1_a_at		AF540005.1	-4.84679	0.012015	-4.20013	0.007471
GgaAffx.12999.1.S1_s_at		AJ720896	-4.8408	0.008724	-2.36855	0.042885
GgaAffx.20697.1.S1_at	TBC1D30	CR523918.1	-4.8209	0.000587	-2.43231	0.00385
Gga.8231.1.S1_at	RPH3AL	CR353553.1	-4.79399	0.011476	-2.72734	0.030507
GgaAffx.6058.1.S1_at		ENSGALT00000015	-4.69446	0.011781	-2.58009	0.036532
Gga.10877.1.S1_at		BX950632.1	-4.54084	0.001085	-2.18816	0.00987
GgaAffx.25590.1.S1_s_at		ENSGALT00000004	-4.5292	0.004352	-2.02593	0.043806
Gga.19033.1.S1_at	CREG2	BU342250	-4.51511	0.001223	-7.98135	6.99E-05
GgaAffx.22647.3.S1_s_at		ENSGALT00000014	-4.48559	0.006976	-10.2386	0.000265
Gga.6402.1.S1_at		BU425537	-4.4289	0.00051	-2.79243	0.001242
Gga.10763.1.S1_at		NM_213572.1	-4.34828	0.005592	-15.156	7.54E-05

Gga.1440.1.S1_at		BU219408	-4.31008	0.012741	-3.95729	0.006784
Gga.12356.2.S1_a_at	VSIG10	BX279070	-4.29056	0.009945	-2.60879	0.024218
Gga.2330.1.S1_at		BU304608	-4.27987	0.026732	-21.5145	0.000282
Gga.17889.1.S1_at	ADAMTS3	BU221136	-4.27271	0.029962	-7.73746	0.002758
GgaAffx.6423.2.S1_at		ENSGALT00000016	-4.14676	0.008735	-3.64573	0.005335
Gga.1222.2.S1_s_at		BX267936	-4.13404	0.000151	-6.92327	7.97E-06
GgaAffx.12553.1.S1_at		AJ720450	-4.12201	0.004522	-3.25321	0.004113
Gga.10039.1.S1_at	FAP	CK609616	-4.10839	0.001818	-3.04353	0.002179
Gga.6796.1.S1_at		BU218668	-4.03972	0.001868	-3.42645	0.001258
Gga.19343.1.S1_at	RIMBP2	CR407131.1	-4.02079	0.005056	-5.13803	0.000809
Gga.2712.1.S1_at		NM_204565.1	-3.96573	0.007772	-5.30356	0.001132
Gga.20061.1.S1_at		BU396151	-3.85814	0.039673	-4.27268	0.013646
Gga.11643.2.S1_s_at		BU290715	-3.80736	0.012251	-3.93509	0.004376
Gga.1573.1.S1_at		BX934087.1	-3.73363	0.001168	-2.82321	0.001405
Gga.18933.1.S1_s_at		BU339641	-3.68944	0.013639	-4.0066	0.00414
Gga.4821.1.S1_at		NM_204164.1	-3.67682	0.003617	-4.55673	0.000586
GgaAffx.13096.1.S1_at		AJ720993	-3.66707	0.020706	-8.97967	0.00066
GgaAffx.25677.1.S1_s_at		ENSGALT00000004	-3.59362	0.021022	-26.1774	6.88E-05
Gga.12534.1.S1_at		BU418485	-3.58668	0.012512	-7.68568	0.000463
Gga.7424.1.S1_at		BU464769	-3.56695	1.24E-05	-2.86542	1.15E-05
GgaAffx.7332.1.S1_at		ENSGALT00000018	-3.51839	0.015212	-11.2948	0.000213
Gga.7057.1.S1_at		BX274047	-3.4957	0.031241	-9.58448	0.000819
GgaAffx.12589.1.S1_s_at		AJ720486	-3.49337	0.023147	-5.17423	0.002784

GgaAffx.1880.1.S1_at		ENSGALT00000004	-3.39214	1.65E-05	-3.01669	9.12E-06
Gga.16049.1.S1_at	ZBTB38	BU317850	-3.34416	0.000368	-3.92276	5.92E-05
Gga.10658.1.S1_at	AHNAK2	BU321027	-3.27505	0.000591	-2.65422	0.000567
GgaAffx.22781.1.S1_at		ENSGALT00000014	-3.19838	3.07E-05	-2.25275	7.49E-05
Gga.19588.1.S1_at		BU297453	-3.06888	0.029035	-3.14189	0.011805
GgaAffx.9436.1.S1_at		ENSGALT00000023	-3.06469	0.029601	-2.7785	0.01925
Gga.16782.1.S1_at		BU472294	-3.03049	0.021899	-3.68246	0.004457
GgaAffx.5549.1.S1_at		ENSGALT00000014	-3.03033	0.025152	-2.85101	0.013964
Gga.10365.1.S1_at	IL1RL2	BX934277.1	-2.96689	0.006446	-8.10121	7.18E-05
GgaAffx.7493.1.S1_s_at		ENSGALT00000019	-2.93578	0.043547	-8.28681	0.000862
GgaAffx.12006.1.S1_s_at		AJ719903	-2.922	0.003735	-2.79748	0.001676
GgaAffx.11575.1.S1_s_at		AJ719472	-2.91738	0.018332	-2.3479	0.020183
Gga.1582.1.A1_at	SETBP1	CF250932	-2.90719	0.035863	-3.43309	0.008828
GgaAffx.5401.1.S1_at		ENSGALT00000013	-2.85553	0.017934	-2.53494	0.012736
Gga.3131.1.S1_at		CR353563.1	-2.84509	0.010112	-4.23752	0.000775
GgaAffx.23623.2.S1_at		ENSGALT00000019	-2.83922	0.002982	-2.64617	0.00153
Gga.8858.1.S1_s_at		BU292551	-2.8087	0.00863	-4.56	0.000459
Gga.6099.1.S1_at		BU470318	-2.77458	0.000162	-2.59269	7.61E-05
Gga.16727.1.S1_at		BU418549	-2.77412	0.000531	-5.49062	9.31E-06
Gga.15768.1.S1_at		BU255099	-2.75894	0.010064	-6.57468	0.000154
Gga.9062.1.S1_at		BU397990	-2.70839	0.008671	-11.1917	2.78E-05
Gga.657.1.S1_at		NM_205193.1	-2.68694	0.021975	-2.1553	0.026626
GgaAffx.7641.1.S1_at		ENSGALT00000019	-2.67987	0.021319	-2.94457	0.006015

Gga.6300.1.S1_at	ATP9A	BU142539	-2.65563	0.011299	-2.62649	0.004743
Gga.4999.2.S1_at		AF074605.1	-2.60063	0.005688	-196.727	1.26E-07
Gga.8094.1.S1_a_at		BX929376.2	-2.59737	0.002692	-5.31952	4.33E-05
Gga.18411.1.A1_at	MAP1B	AL586630	-2.54495	0.033138	-2.68673	0.011812
Gga.17453.1.S1_at	TMEM47	CR390609.1	-2.52266	0.000546	-4.14524	1.55E-05
GgaAffx.8020.1.S1_at		ENSGALT00000020	-2.49388	0.022829	-3.65841	0.00186
Gga.8789.1.S1_at		BU285122	-2.48268	0.00813	-9.10618	2.52E-05
GgaAffx.20313.1.S1_at	ChEST814b18	CR524302.1	-2.47808	0.03724	-2.02241	0.044452
GgaAffx.20087.1.S1_s_at		AY342354.1	-2.47543	0.00248	-2.97416	0.000325
Gga.3264.1.S2_at		BU465235	-2.46446	0.012531	-2.19325	0.009477
Gga.3834.1.S2_at		AJ396719	-2.46155	0.000209	-2.00172	0.000289
Gga.10098.1.S1_s_at		BX935567.2	-2.41646	0.025233	-3.60367	0.001883
GgaAffx.4644.1.S1_at		ENSGALT00000007	-2.41391	0.009455	-2.06978	0.009008
Gga.20041.1.S1_at		BU244670	-2.39452	0.03049	-51.0854	4.49E-06
Gga.4056.1.S1_at		U14589.1	-2.3887	0.023839	-2.15828	0.01742
Gga.7652.1.S1_at	KIAA1244	BX263543	-2.37122	0.043803	-2.34601	0.021718
GgaAffx.23453.2.S1_s_at		ENSGALT00000018	-2.34295	0.016406	-2.97801	0.002054
Gga.8120.1.S1_at	INPP5J	BU427273	-2.33113	0.003918	-2.03256	0.003454
GgaAffx.23942.3.S1_s_at		ENSGALT00000020	-2.30456	0.017761	-2.97327	0.002067
Gga.3269.1.S1_at	FER	BU324194	-2.27858	0.037611	-2.11978	0.024953
Gga.7277.1.S1_at	unknown	BX267570	-2.25251	0.034544	-2.79115	0.005597
GgaAffx.4778.1.S1_s_at		ENSGALT00000012	-2.21867	0.003036	-12.1517	1.67E-06
Gga.12839.1.S1_at		BX950769.1	-2.13919	8.88E-06	-5.42042	2.34E-08

Gga.13197.1.S1_at		BU288636	-2.13533	0.012376	-4.61055	0.000127
Gga.8407.1.S1_s_at		BX270899	-2.13011	0.017823	-3.14659	0.000961
Gga.11749.1.S1_a_at		BU418268	-2.10493	0.040844	-2.5219	0.007516
GgaAffx.2790.1.S1_at		ENSGALT00000007	-2.08953	0.035135	-2.89336	0.003051
Gga.14009.1.S1_at	MAP1B	CN217117	-2.084	0.018985	-2.31357	0.004309
Gga.3572.1.S2_s_at		NM_204860.1	-2.07491	0.015081	-2.5605	0.001807
Gga.3639.1.S1_at	TMEM64	BU337994	-2.06482	0.000759	-2.46416	7.46E-05
GgaAffx.6895.1.S1_at		ENSGALT00000017	-2.06186	0.018105	-6.87474	4.36E-05
Gga.14549.1.S1_at		CR387604.1	-2.058	0.044465	-2.70181	0.005245
GgaAffx.23623.1.S1_at		ENSGALT00000019	-2.04078	0.030488	-3.45221	0.000971
Gga.13258.1.S1_at	EPB41L5	CR352764.1	-2.02175	0.036584	-2.01929	0.016919
GgaAffx.12977.1.S1_s_at		AJ720874	-2.01857	0.005213	-2.29996	0.000802
GgaAffx.12032.1.S1_s_at		AJ719929	-2.01517	0.008874	-2.42652	0.001052
GgaAffx.2958.1.S1_at		ENSGALT00000007	-2.004	0.022326	-2.41867	0.003139

Geny rozdílně exprimované v PR9692-E9 vs. PR9692

zvýšená exprese

ID sondy	Symbol genu	míra velikosti účinku (PR9692-E9 vs. PR9692)	Hodnota P (PR9692-E9 vs. PR9692)
Gga.1787.1.S1_at	---	63.1435	6.9941E-06
Gga.13235.1.S1_at	---	56.357	1.7707E-05
GgaAffx.9976.1.S1_s_at	LIPI	43.1229	3.1447E-08
Gga.3688.1.S1_at	FABP1	42.2552	0.00129529
GgaAffx.22602.1.S1_s_at	CACNA2D1	36.8293	4.4046E-05

Gga.1839.1.S1_at	EYA2	33.2985	4.9126E-06
Gga.17686.1.S1_at	KRT75	32.6529	7.5166E-05
Gga.12565.1.S1_s_at	CACNA2D1	32.2895	0.00016832
Gga.19368.1.S1_at	---	29.8741	3.1144E-06
Gga.6778.1.S1_x_at	LOC426912	27.3674	0.00025403
Gga.2554.1.A1_at	LOC429572 /// LOC430562	27.3241	6.9763E-07
Gga.7044.1.S1_s_at	SEPP1	27.0024	0.00013042
GgaAffx.3833.1.S1_at	SCN5A	26.0701	1.1467E-05
Gga.15598.1.S1_x_at	LOC770741	24.9749	5.6789E-06
Gga.18392.1.S1_at	NMU	24.0566	2.5681E-06
Gga.6778.2.S1_at	LOC426912	23.4528	0.00650494
Gga.5291.1.S1_at	CADM1	23.3436	2.6122E-05
Gga.7044.3.S1_s_at	SEPP1	23.1992	0.00015609
Gga.15598.3.S1_a_at	LOC777530	21.1735	7.9976E-07
Gga.13607.1.S1_at	---	19.2979	6.6436E-06
GgaAffx.25118.1.S1_at	SLITRK6	19.1855	0.00017844
GgaAffx.6456.4.S1_s_at	KRT75	18.418	0.00029131
Gga.14047.1.S1_at	---	17.5738	9.8201E-07
Gga.14454.1.S1_at	ZPD	16.3874	0.00014214
Gga.9386.1.S1_at	RBP7	16.3532	0.014584
GgaAffx.6456.5.S1_s_at	LOC431299 /// LOC768880 /// LOC768881	16.2306	0.00664609

Gga.14042.1.S1_at	CPEB1	15.8372	4.7212E-05
Gga.6778.2.S1_a_at	LOC431317	15.7672	0.00146927
Gga.8140.1.S1_at	FGFBP1	14.5841	0.00481829
GgaAffx.6456.8.S1_at	LOC431299	14.2013	0.00259533
Gga.1605.1.S1_s_at	RSPO3	13.1244	0.00040245
Gga.5735.1.S1_at	RFTN1	12.9178	7.8492E-05
Gga.16009.1.S1_at	---	12.866	5.444E-06
Gga.1169.1.S1_at	AADACL2	12.65	0.00203238
Gga.2699.1.S1_at	IRX1	12.45	1.5232E-05
Gga.9903.1.S1_at	---	12.0986	2.6237E-06
GgaAffx.11541.1.S1_at	SEPP1	11.8694	0.00051142
Gga.12485.2.S1_a_at	AQP9	11.4409	2.375E-05
Gga.1094.1.S1_at	CTSD	10.9314	8.1934E-05
Gga.16009.1.S1_s_at	---	10.3703	0.00041842
GgaAffx.9422.1.S1_at	PTGER4	10.0772	0.00217706
Gga.3393.1.S1_at	GLDC	9.99284	9.0922E-05
GgaAffx.4536.1.S1_s_at	ARHGAP12	9.91117	0.00090793
Gga.952.1.S1_at	NKX2-1	9.10033	0.00263145
Gga.9481.1.S1_s_at	LOC395772	8.96811	0.00710594
GgaAffx.12757.1.S1_s_at	RGL1	8.79557	4.5541E-06
GgaAffx.11849.1.S1_s_at	CD36	8.69453	0.0263086
Gga.7269.1.S1_s_at	NCOA4	8.48285	0.00051543
Gga.13583.1.S1_at	CD36	8.47044	0.0348875

Gga.19305.1.S1_at	RSPO3	8.44047	0.00530749
Gga.3109.1.A1_s_at	SEPP1	8.43915	0.00129873
GgaAffx.23775.1.S1_at	SFRP4	8.41203	0.00022911
Gga.15505.1.S1_s_at	LOC425186 /// LOC425419 /// LOC770741 /// LOC777257 /// LOC777530	8.16132	4.2713E-06
Gga.16002.1.S1_at	ENOX1	8.06005	0.00786693
Gga.1742.1.S1_a_at	OSGIN1	8.05468	0.0479044
Gga.18199.1.S1_s_at	SLITRK6	8.03478	0.00011166
Gga.5465.1.S1_at	RCAN1	7.98966	1.0224E-05
GgaAffx.8369.1.S1_s_at	PCBP3	7.80513	0.0142635
Gga.9700.1.S1_at	TSPAN7	7.72079	0.00254777
Gga.9823.1.S1_s_at	NPTN	7.66065	1.2635E-05
GgaAffx.21116.1.S1_s_at	OSGIN1	7.43415	0.0346028
GgaAffx.24470.1.S1_at	FRMD4B	7.37304	0.00152653
Gga.17737.1.S1_at	---	7.29391	0.00048486
GgaAffx.3833.4.S1_s_at	SCN5A	7.25994	0.00020431
GgaAffx.23775.1.S1_s_at	SFRP4	7.22611	0.00027292
GgaAffx.9422.2.S1_s_at	PTGER4	7.11167	0.00294769
Gga.16268.1.S1_at	AADACL2	7.08376	4.0475E-05
Gga.11380.1.S1_at	FRMD3	7.0447	0.00103219
Gga.3714.1.S1_at	---	6.97783	0.00556529

Gga.6828.2.S1_a_at	LOC770481 /// LOC770742 /// LOC771926 /// LOC776957 /// LOC777154	6.97139	0.00211428
GgaAffx.21368.1.S1_at	NPTN	6.75855	0.00112986
Gga.17118.1.S1_at	---	6.70744	0.0037239
Gga.12406.1.S1_at	SLC16A10	6.69424	0.0351192
GgaAffx.6445.1.S1_at	TMEM90A	6.68611	0.00024819
Gga.7965.1.S1_at	RAMP3	6.48241	0.0003597
Gga.7720.3.S1_x_at	LOC776076	6.47416	0.00016797
Gga.4497.1.S1_at	---	6.36951	4.6962E-05
Gga.3337.1.S1_at	MUC5B	6.33929	0.00039881
Gga.18643.1.S1_s_at	CACNA2D1	6.26962	0.00900092
GgaAffx.4629.1.S1_at	MKX	6.25556	0.00087157
GgaAffx.8725.1.S1_s_at	CNDP2	6.24163	0.00011066
Gga.1812.1.S1_at	TNFRSF11B	6.11944	0.00041893
GgaAffx.22987.1.S1_at	THBS1	5.96765	0.00572102
Gga.8200.1.S1_at	SLC16A10	5.91098	0.0220195
Gga.167.1.S1_at	SALL3	5.82235	0.00290937
Gga.18885.1.S1_at	---	5.76414	5.111E-05
Gga.11987.1.S1_s_at	WASF3	5.71203	0.00290869
GgaAffx.3789.1.S1_at	GPC4	5.7024	4.3914E-05
GgaAffx.22126.1.S1_at	CADM1	5.68352	0.00207085

GgaAffx.24513.9.S1_s_at	EPB41L3	5.62809	0.00281566
Gga.17986.1.S1_at	FRMD4B	5.52622	5.7134E-06
GgaAffx.1849.1.S1_at	STC2	5.3692	0.00010287
GgaAffx.26742.1.S1_at	LOC769442	5.34846	0.0033457
GgaAffx.20516.1.S1_s_at	---	5.32885	0.0425471
GgaAffx.25200.1.S1_at	PANX1	5.29953	3.7439E-05
Gga.18977.1.S1_at	---	5.29636	1.5683E-05
Gga.11258.1.S1_at	EFHA1	5.21975	0.00066071
Gga.5576.2.S1_at	H4-VII /// LOC417946	5.21063	0.00653979
GgaAffx.7813.1.S1_at	UST	5.20408	4.2959E-05
Gga.8200.1.S1_s_at	SLC16A10	5.19591	0.010999
Gga.19070.1.S1_s_at	---	5.14493	0.00770248
Gga.19456.1.S1_at	---	5.13031	2.3054E-05
Gga.1727.1.S1_s_at	PPIF	5.11558	0.00109022
Gga.17737.1.A1_at	---	5.06273	0.00042181
GgaAffx.8712.1.S1_x_at	---	5.05461	0.00192895
GgaAffx.24802.1.S1_at	HTR1B	5.05299	0.00483082
Gga.14013.1.S1_at	---	5.04463	0.00020216
Gga.14195.1.S1_at	---	5.02719	0.00293047
Gga.19780.1.S1_at	---	5.02462	0.00766033
Gga.16100.1.S1_at	---	5.00325	0.00096169
GgaAffx.7814.1.S1_at	UST	4.92567	0.00255161
Gga.12475.1.S1_at	TTYH3	4.8479	0.00610932

Gga.7890.1.S1_at	SFRP4	4.83904	0.00137382
Gga.10300.1.S1_s_at	THBS1	4.83514	0.007819
GgaAffx.24513.3.S1_s_at	EPB41L3	4.80463	9.1694E-07
Gga.15771.1.S1_at	---	4.80118	2.5002E-05
Gga.1094.1.S2_at	CTSD	4.77096	0.00012639
GgaAffx.24929.1.S1_at	---	4.75862	0.0157426
GgaAffx.11732.1.S1_at	CNDP2	4.71598	0.00010338
Gga.3570.1.S1_at	---	4.69679	0.00020976
GgaAffx.7816.1.S1_at	UST	4.62819	0.00015974
GgaAffx.9347.1.S1_at	ELOVL7	4.60977	0.020763
Gga.14719.1.S1_at	LOC421768	4.59041	0.00070617
Gga.2533.1.S1_s_at	GSTA3	4.54959	0.00299391
GgaAffx.24751.1.S1_s_at	LOC418468	4.52104	1.2778E-05
GgaAffx.9627.1.S1_s_at	DSC2	4.49398	0.00011116
Gga.17170.1.S1_at	---	4.48401	0.0101772
GgaAffx.24678.1.S1_s_at	FAM110B	4.47738	0.00029282
Gga.17662.1.S1_s_at	RALGPS2	4.44826	0.00096783
Gga.17161.1.S1_at	---	4.4462	0.00059801
Gga.4939.1.S1_s_at	FABP4	4.43957	0.0354456
GgaAffx.22622.1.S1_s_at	FGD5	4.41804	0.00017461
GgaAffx.8812.1.A1_at	PCYOX1	4.41283	0.0005009
GgaAffx.3253.1.S1_s_at	ACSL3	4.39196	5.9886E-05
GgaAffx.8637.1.S1_at	LOC769442	4.38789	0.0148828

GgaAffx.1715.1.S1_s_at	FCHSD1	4.38176	0.00065733
GgaAffx.24858.1.S1_at	COLEC10	4.37301	0.00487178
Gga.5644.1.S1_s_at	DNAJA1	4.35927	6.7969E-06
GgaAffx.24300.1.S1_s_at	PCYOX1	4.31333	0.00578024
Gga.651.1.S1_at	EFNA5	4.29792	0.00170018
GgaAffx.23774.1.S1_at	EPDR1	4.29046	0.00214573
Gga.14013.1.S1_s_at	---	4.24914	0.00529951
GgaAffx.25801.1.S1_at	ADAMTS12	4.2324	0.00394446
GgaAffx.20316.1.S1_at	COL4A5	4.20665	0.0217317
GgaAffx.23001.1.S1_at	---	4.17065	0.00095232
GgaAffx.21260.1.S1_at	TRPM2	4.14375	0.00506168
Gga.12185.1.S1_at	MMP23B	4.1433	0.00315205
Gga.16828.1.S1_at	---	4.12968	0.00025075
GgaAffx.26166.2.S1_s_at	TTYH3	4.12779	0.0102438
Gga.19462.1.S1_at	SLC25A39	4.12065	0.0229642
Gga.2089.1.S1_at	EMG1	4.09813	0.0276338
Gga.17890.1.S1_at	PCDH7	4.09553	0.00530384
GgaAffx.24934.1.S1_s_at	GCLC	4.01744	0.00512474
GgaAffx.1849.2.S1_s_at	STC2	4.01637	0.00240375
GgaAffx.24513.7.S1_s_at	EPB41L3 /// LOC769874	4.01615	0.00938934
GgaAffx.6995.1.S1_s_at	LOC424180 /// SCN1A /// SCN2A	4.01573	0.00020783
Gga.10595.3.S1_s_at	REEP1	4.01527	0.00575529
Gga.19107.1.S1_at	---	4.00474	0.00122237

Gga.14536.1.S1_at	---	3.96068	0.00015871
GgaAffx.8655.1.S1_s_at	FAT	3.94698	0.00664833
GgaAffx.11497.1.S1_at	PPIF	3.94201	0.0227543
Gga.8200.2.S1_a_at	SLC16A10	3.93905	0.032604
GgaAffx.1633.1.S1_at	BDP1	3.91367	0.00065699
Gga.11477.1.S1_at	DRAM1	3.91214	0.0100134
GgaAffx.1661.1.S1_at	LOC427394 /// LOC769948	3.90057	0.00275622
Gga.16141.1.S1_at	---	3.8779	3.7367E-05
Gga.5187.1.S1_s_at	SQSTM1	3.86926	0.0242263
Gga.10012.1.S1_s_at	SLC30A1	3.84672	0.00722974
Gga.16001.1.S1_at	JAM3	3.84382	0.00057729
Gga.12471.1.S1_at	VASH2	3.8174	0.00038703
Gga.14517.1.S1_s_at	GSTK1	3.81063	3.4145E-05
Gga.16855.1.S1_at	FRMD4B	3.78791	0.0003156
Gga.14486.1.S1_at	CASP2	3.76196	5.7879E-05
Gga.2894.1.S1_at	JAG1	3.76189	0.00239702
Gga.18875.1.S1_s_at	---	3.72863	0.00035139
Gga.2971.2.S1_s_at	C3orf64	3.72109	0.00725708
Gga.7670.1.S1_at	---	3.708	0.0257354
GgaAffx.24634.1.S1_s_at	DCBLD2	3.70591	0.00114379
GgaAffx.8660.1.S1_at	FAT	3.663	0.0104683
Gga.3030.1.S1_at	RETSAT	3.65428	0.00551493
Gga.7349.1.S1_at	---	3.64538	7.8499E-05

GgaAffx.12697.1.S1_s_at	RCOR3	3.64471	0.00038019
Gga.15714.1.S1_at	SLC43A2	3.63534	0.00051758
GgaAffx.20439.1.S1_s_at	HS6ST2	3.61348	0.00192881
Gga.14861.1.S1_s_at	KIAA0355	3.60812	0.00100572
Gga.6877.1.S1_at	ROBO2	3.58896	3.914E-06
Gga.9002.1.S1_at	---	3.58513	0.0064566
GgaAffx.10840.1.S1_at	CLN5	3.58086	0.00614399
Gga.12409.1.S1_at	LOC429567	3.57383	0.00523857
Gga.3448.1.S1_at	THBS1	3.54324	0.0153817
GgaAffx.5798.1.S1_at	LOC422394	3.53897	0.00476859
Gga.9314.1.S1_at	SOX4	3.53476	0.00225606
Gga.6240.1.S1_at	DCBLD2	3.53381	0.00021056
Gga.7308.1.S1_at	---	3.53378	0.00894386
Gga.7615.1.S1_at	BRPF3	3.52963	0.00398197
Gga.16292.1.S1_at	TGOLN2	3.51866	0.00105582
Gga.6103.1.S1_at	H3-VIII /// LOC769809 /// LOC770022	3.50174	0.0104276
Gga.62.1.S1_at	LIFR	3.50155	0.00035198
GgaAffx.20459.1.S1_at	SLC30A1	3.46063	0.0194197
Gga.13065.1.S1_at	---	3.42531	0.00076348
Gga.1675.1.S1_at	MEGF9	3.42006	0.00181765
GgaAffx.21874.3.S1_s_at	LOC416033	3.41399	0.00379671
Gga.12469.1.S1_at	---	3.41003	0.00011367
Gga.7937.1.S1_at	CDS2	3.39562	3.9352E-06

GgaAffx.24513.10.S1_s_at	EPB41L3	3.39309	0.00892153
Gga.13161.1.S1_at	---	3.38607	0.00132538
Gga.2971.2.S1_at	C3orf64	3.38305	0.00998525
Gga.11539.1.S1_at	IFI30	3.37122	0.00573472
GgaAffx.21730.1.S1_s_at	---	3.36884	0.00334974
Gga.1205.1.S2_at	PLA2G7	3.34922	2.865E-05
Gga.9745.1.S1_at	LOC418817	3.34717	0.00376696
Gga.17160.1.S1_at	---	3.34646	0.00792537
Gga.5576.1.S1_a_at	H4-VII /// LOC417946 /// LOC427884 /// LOC770079 /// LOC770142	3.34191	0.0021346
Gga.6140.1.A1_s_at	PCYOX1	3.33748	0.00089842
GgaAffx.7449.1.S1_at	GRLF1	3.33445	8.3851E-06
Gga.7625.1.S1_at	---	3.33062	0.00010553
GgaAffx.12953.1.S1_at	SIRT2	3.32474	0.00011489
Gga.7769.1.S1_at	---	3.32114	2.6593E-05
Gga.13155.1.S1_at	---	3.31676	9.251E-05
Gga.17892.1.S1_at	---	3.31676	0.00618586
GgaAffx.20670.1.S1_at	---	3.31379	0.00023421
GgaAffx.23665.1.S1_x_at	H2B-V /// H2B-VII /// LOC769973 /// LOC770188	3.30413	0.00854292
Gga.3961.1.S1_at	SMN	3.29401	0.00019491

Gga.11134.1.S1_s_at	LOC422476	3.29319	0.0151553
Gga.11345.1.S1_at	---	3.28453	6.5789E-05
Gga.13923.1.S1_at	---	3.2826	3.1161E-05
Gga.7141.1.S1_at	---	3.26564	0.0360612
GgaAffx.22655.1.S1_at	---	3.25542	0.00127971
GgaAffx.23665.1.S1_at	H2B-V /// H2B-VII /// LOC769973 /// LOC770188	3.25362	0.0103086
Gga.5644.2.S1_s_at	DNAJA1	3.24182	0.00018386
GgaAffx.21204.1.S1_at	---	3.24169	0.00028549
GgaAffx.23294.1.S1_s_at	WWC2	3.23841	9.6473E-05
Gga.10006.1.S1_at	GCLC	3.23047	0.00194983
GgaAffx.3264.1.S1_at	MOGAT1	3.22375	0.00171279
Gga.9455.1.S1_at	---	3.21571	0.00080461
GgaAffx.6154.1.S1_at	FLVCR1	3.21221	0.00454834
Gga.4533.6.A1_at	DYNLT1	3.20512	0.00012718
GgaAffx.21373.1.S1_s_at	MBNL3	3.20408	0.0011712
GgaAffx.9161.1.S1_s_at	KPNA1	3.18983	0.00176877
Gga.19189.1.S1_a_at	---	3.18917	0.0105093
Gga.1216.1.S1_at	C12orf57	3.18522	0.00521005
Gga.16664.1.S1_at	---	3.16685	0.00045853
Gga.9476.1.S1_at	ROR1	3.15647	0.0197207
Gga.3125.1.S1_at	ID2	3.15537	0.0396615
Gga.1205.1.S1_at	PLA2G7	3.13822	3.2569E-05

Gga.14246.1.S1_at	---	3.13098	0.00111548
Gga.669.1.S1_at	MET	3.12801	0.00527492
Gga.1329.1.S1_at	ARNTL	3.12519	0.00044569
Gga.6249.1.S1_at	---	3.11807	0.0222722
GgaAffx.21228.1.S1_at	---	3.11358	0.00025894
Gga.7088.1.S1_at	---	3.11333	2.9876E-06
Gga.5513.1.S1_a_at	NOL1	3.09906	0.0413592
Gga.312.1.S1_at	FZD2	3.08597	0.00259396
GgaAffx.6738.1.S1_at	TTC8	3.06718	0.0207867
Gga.1106.1.S1_at	FAM129A	3.06321	0.045819
Gga.11456.1.S1_at	CSTA	3.06252	0.00278542
Gga.11811.1.S1_at	CXorf41	3.05953	0.0364789
Gga.3545.1.S2_at	HPRT1	3.05566	6.9652E-07
GgaAffx.22702.1.S1_at	TTLL7	3.03822	0.00232683
Gga.12481.1.S1_s_at	PTPLB	3.03396	0.0205631
Gga.5689.1.S1_at	GSTK1	3.02311	0.00024888
Gga.1503.1.S1_at	---	3.02169	2.148E-05
Gga.2547.1.S1_at	LOC771567	3.01929	0.00334558
GgaAffx.12873.1.S1_at	STRBP	3.01779	0.00031658
GgaAffx.1493.1.S1_at	DENND1B	3.01611	0.00344195
Gga.565.1.S1_at	GBX2	3.00348	0.0330289
Gga.3672.1.S1_at	ST3GAL1	2.99951	2.7856E-05
GgaAffx.8804.1.S1_at	SPIRE1	2.98589	0.00665937

Gga.9290.1.S1_at	HS2ST1	2.98551	0.00022404
Gga.1035.2.S1_a_at	LMAN1	2.96991	1.3822E-05
Gga.1252.1.S1_at	C6orf106	2.9585	0.00013367
GgaAffx.9882.2.S1_s_at	ROBO2	2.95686	4.9614E-05
GgaAffx.26459.1.S1_s_at	USP54	2.95454	0.00503787
Gga.3807.1.S2_s_at	ALDH1A3	2.92823	0.0287161
GgaAffx.3318.1.S1_s_at	APPBP2	2.928	6.2466E-05
GgaAffx.24773.1.S1_s_at	REEP1	2.91339	0.0233397
Gga.13496.1.S1_at	---	2.91034	0.00251384
GgaAffx.9557.1.S1_s_at	LAMA3	2.90744	0.00055433
GgaAffx.24399.1.S1_at	PCDH7	2.90377	0.00428338
Gga.504.1.S1_at	CASP2	2.89276	0.00551924
Gga.9937.1.S1_at	MAST2	2.88915	0.00031565
Gga.1647.1.S1_at	---	2.88838	4.8464E-05
Gga.2877.1.S1_at	DNAJC18	2.88511	0.0006051
Gga.15201.1.S1_at	ADAMTS12	2.87893	0.0408115
Gga.2212.1.S1_at	MOCS1	2.87776	0.00538457
Gga.15891.1.S1_at	NUP98	2.87283	0.00910651
GgaAffx.7448.2.S1_s_at	SEMA5B	2.86767	0.0288842

Gga.6847.1.S1_at	LOC425364 /// LOC425625 /// LOC427061 /// LOC770715 /// LOC776971 /// LOC777200	2.85526	0.00078
Gga.12469.1.S1_x_at	---	2.84542	8.6342E-05
Gga.16978.1.S1_at	KLHL29	2.83963	0.00029522
GgaAffx.11921.1.S1_at	SERPINB6	2.83061	0.00225051
Gga.5903.1.S1_at	PYCRL	2.82645	0.0032763
Gga.3125.1.S2_at	ID2	2.81743	0.0190047
Gga.15638.1.S1_x_at	LOC425186 /// LOC425419 /// LOC429618 /// LOC770741 /// LOC776076 /// LOC776348 /// LOC776601 /// LOC776673 /// LOC777257 /// LOC777346 /// LOC777530	2.80636	0.0068957
GgaAffx.12404.1.S1_s_at	GARNL3	2.80362	0.00232125
GgaAffx.24485.1.S1_s_at	ERAP1	2.79478	0.0152277

Gga.15797.1.S1_at	---	2.78615	0.00117271
Gga.131.1.S1_at	MX1	2.78387	0.00458255
Gga.324.1.S1_at	LOC395589	2.7824	0.0308319
GgaAffx.11370.1.S1_at	USE1	2.77875	0.034363
GgaAffx.7448.1.S1_at	SEMA5B	2.7691	0.0403958
Gga.15912.1.S1_at	CLUAP1	2.76762	0.0421192
GgaAffx.10705.1.S1_at	LOC422068	2.76592	0.00028113
Gga.1615.1.S1_at	TMTC1	2.76383	0.00519176
Gga.19506.1.S1_at	---	2.76225	0.00052963
Gga.17478.1.S1_at	---	2.76094	0.00877512
GgaAffx.6185.1.S1_at	LOC425522 /// LOC776113	2.75377	0.00951029
Gga.18905.2.S1_s_at	POLR2I	2.7501	0.00032615
Gga.12203.1.S1_at	SPC25	2.73989	0.00156072
Gga.14442.2.S1_a_at	FUNDC2	2.73528	0.00252959
GgaAffx.5515.1.S1_at	---	2.73452	3.3093E-05
GgaAffx.11785.1.S1_s_at	LIPA	2.7333	0.0129263
GgaAffx.11418.1.S1_at	XPO4	2.73326	0.0212996
GgaAffx.11284.1.S1_at	QPCTL	2.73091	0.0106015
Gga.11616.1.S1_at	MYCBP2	2.71999	0.00108074
GgaAffx.2999.1.S1_at	FAM129A	2.7191	0.0114841
GgaAffx.24870.1.S1_s_at	SLC23A2	2.71726	0.0003116
Gga.19123.1.S1_at	---	2.71649	0.00071843
Gga.9653.2.S1_a_at	CTNS	2.71603	0.00960061

Gga.8890.1.S1_at	---	2.71476	0.00871037
Gga.18896.1.S1_at	---	2.71159	1.4116E-05
Gga.17013.1.S1_at	FAM136A /// LOC426296	2.71158	0.00131021
Gga.13447.1.S1_at	---	2.71012	0.0175788
GgaAffx.26146.1.S1_at	NPAL3	2.70492	0.00442421
Gga.5736.1.S1_at	ANKRD57	2.7022	0.0142984
Gga.3961.1.S2_s_at	SMN	2.70219	0.00056477
GgaAffx.12226.1.S1_s_at	MRPL51	2.69692	0.0210234
GgaAffx.26656.1.S1_at	SQSTM1	2.69546	0.0147943
GgaAffx.11665.1.S1_at	ITGA9	2.69449	0.00070392
GgaAffx.21575.1.S1_at	---	2.69056	0.0422264
GgaAffx.25344.1.S1_s_at	ABCA3	2.6892	0.00013237
Gga.4512.3.S1_at	RPS14	2.684	0.00014249
GgaAffx.7514.1.S1_at	SPATA5	2.67143	0.00133241
Gga.13323.2.S1_s_at	IGF2BP3	2.66885	0.00080905
Gga.5548.1.S1_at	NPM3	2.65904	0.0476102
GgaAffx.7201.1.S1_s_at	LPHN3	2.65628	0.00256502
Gga.11356.1.S1_s_at	ATG12	2.65494	0.00062352
Gga.14733.1.S1_at	---	2.64787	0.00718098
Gga.17226.1.S1_at	---	2.64756	0.00023087
GgaAffx.20823.1.S1_s_at	DDX26B	2.64577	0.00030183
Gga.2532.1.S1_at	CEP110	2.64359	0.0255425
Gga.10794.1.S1_at	POR	2.64306	0.00050478

Gga.17217.1.S1_s_at	MTUS1	2.64135	0.0104037
GgaAffx.1665.1.S1_at	LOC769948	2.63911	0.00341864
Gga.2.1.S1_at	---	2.63853	0.0145512
GgaAffx.2005.1.S1_s_at	LOC768480 /// SLC16A9	2.63529	0.0117086
Gga.4306.1.S1_at	DMN	2.63383	0.0200442
GgaAffx.24025.1.S1_s_at	SERPINB6	2.63252	0.00327462
GgaAffx.9403.1.S1_s_at	NAT13	2.63036	0.00048982
GgaAffx.1292.1.S1_at	LOC768922	2.628	0.0319379
Gga.15201.1.S1_s_at	ADAMTS12	2.62733	0.0169233
Gga.17414.1.S1_s_at	---	2.62595	0.00993988
Gga.5540.1.S1_at	DAGLB	2.62348	0.00113528
Gga.9107.1.S1_at	UBE2E1	2.62044	0.0155131
Gga.749.1.S1_at	PLS1	2.61975	0.00187835
GgaAffx.12776.1.S1_at	PEO1	2.61972	0.014861
Gga.20062.1.S1_s_at	SIPA1L2	2.61329	0.0271593
GgaAffx.6545.4.S1_x_at	MBNL1	2.61049	0.00591224
Gga.4039.1.S1_s_at	IGF2BP3	2.6077	0.00108445
GgaAffx.12182.1.S1_at	ODF2	2.59855	0.00110163
GgaAffx.3804.1.S1_s_at	HPRT1	2.59821	1.0354E-05
Gga.4048.1.S1_at	ID3	2.59309	0.0145877
Gga.13846.1.S1_s_at	XPO4	2.59267	0.0115612
Gga.4533.6.S1_a_at	DYNLT1	2.59014	0.00035744
GgaAffx.11842.1.S1_s_at	RAP2C	2.58791	0.0060211
Gga.2858.1.S1_s_at	PTEN	2.58745	0.0205963

GgaAffx.3730.1.S1_at	BTBD8	2.58395	0.0197856
GgaAffx.2281.1.S1_at	UNC119	2.58316	0.00633662
Gga.12506.1.S1_at	EML4	2.57912	0.0156138
GgaAffx.20863.1.S1_at	---	2.57758	0.00447161
Gga.19681.1.S1_at	DUSP16	2.57547	0.00639369
Gga.3394.1.S1_at	OXSR1	2.56608	0.0107788
Gga.16077.1.S1_at	---	2.56593	0.00040056
Gga.7438.1.S1_at	TSHZ2	2.56462	0.00151778
GgaAffx.20494.1.S1_s_at	PTPLB	2.55572	0.0291993
Gga.11450.1.S1_at	ETNK1	2.55509	0.00244611
Gga.17193.1.S1_at	SLC9A6	2.54857	0.0060981
GgaAffx.4722.1.S1_s_at	PPP2R2B	2.54337	0.0117756
GgaAffx.11476.1.S1_at	KPNA1	2.5374	0.00345805
GgaAffx.5392.1.S1_s_at	ENTPD6	2.53669	0.00754246
GgaAffx.21896.1.S1_at	ACTR3B	2.53545	0.0126141
GgaAffx.10181.1.S1_at	FAM135A	2.53448	0.0381704
GgaAffx.10118.1.S1_s_at	PHIP	2.53253	0.0197004
Gga.9409.1.S1_at	---	2.53238	0.0125249
GgaAffx.6995.2.S1_at	SCN1A	2.53044	0.00986511
Gga.1967.1.S1_s_at	FAM107B	2.52894	0.011607
Gga.10595.1.S1_at	REEP1	2.52679	0.0198146
GgaAffx.12427.1.S1_s_at	CD2AP	2.52537	0.00015617
GgaAffx.5146.1.S1_s_at	NT5C2	2.52513	0.00050502

Gga.5387.1.S1_at	---	2.52144	0.0249389
GgaAffx.21868.1.S1_at	RAB7L1	2.52034	0.030658
Gga.10775.1.S1_s_at	NARG1L	2.51442	0.00844169
Gga.16103.1.S1_at	C3orf59	2.51054	0.00106594
GgaAffx.24644.1.S1_at	FOXO3	2.50126	0.00036372
Gga.16365.1.S1_at	SPIRE1	2.49871	0.00432205
GgaAffx.26511.1.S1_s_at	MPZL1	2.49601	0.0043003
Gga.710.6.S1_a_at	NFIA	2.49113	0.0106393
Gga.1535.1.S1_a_at	NCAPH2	2.48929	0.00398783
Gga.17216.1.S1_s_at	RRAGC	2.48719	0.0184104
GgaAffx.6182.1.S1_at	LOC421379	2.48661	0.016297
Gga.14419.1.S1_s_at	CHORDC1	2.48411	0.0224262
Gga.9349.1.S1_s_at	---	2.48339	0.00024948
GgaAffx.1121.1.S1_s_at	UBAC1	2.47973	0.0279711
Gga.14978.1.S1_at	---	2.47917	0.0126665
GgaAffx.3632.1.S1_at	Sep-02	2.47907	0.00140446
Gga.5695.1.A1_at	---	2.47684	0.0005046
GgaAffx.25410.1.S1_at	CPEB1	2.47146	0.00354272
Gga.7252.1.S1_at	MRPS12	2.47019	0.0346583
Gga.5118.1.S1_s_at	ALG6	2.46659	0.0104945
GgaAffx.24612.1.S1_at	LOC428238	2.46254	0.00138117
GgaAffx.12656.1.S1_s_at	SH3GLB2	2.46089	0.00102387
GgaAffx.20791.1.S1_at	---	2.45032	0.00050504

Gga.2057.1.S1_at	C1orf83	2.44546	0.0213794
Gga.11157.1.S1_at	B3GNT5	2.44238	0.00347277
Gga.983.1.S1_at	---	2.4407	0.00048096
Gga.4672.1.S1_at	ATP6V0A1	2.43663	0.00096507
Gga.9728.1.S1_at	CMAGE	2.43589	0.0368068
GgaAffx.25344.4.S1_s_at	ABCA3	2.42923	0.00026758
GgaAffx.9072.1.A1_at	---	2.42676	0.0043817
Gga.710.1.S1_a_at	NFIA	2.42537	0.00036064
Gga.12912.1.S1_at	---	2.41856	0.00695521
Gga.12038.1.S1_at	RRP15	2.41737	0.0250968
Gga.2037.1.S1_at	---	2.41574	6.8278E-05
Gga.2858.1.S1_at	PTEN	2.41567	0.00866097
GgaAffx.21470.1.S1_s_at	---	2.41369	0.00571381
GgaAffx.20225.1.S1_s_at	---	2.41285	0.00061797
Gga.4010.1.S1_s_at	CLSTN1	2.40378	0.00098188
Gga.13802.1.S1_at	KIDINS220	2.40251	0.00256533
Gga.15316.1.S1_s_at	STARD4	2.39454	0.0365082
GgaAffx.11785.1.S1_at	LIPA	2.39107	0.0177275
GgaAffx.4208.1.S1_s_at	EXOC6	2.38842	0.0247389
Gga.16053.1.S1_at	RCOR3	2.38044	0.00751315
GgaAffx.10417.3.S1_s_at	---	2.37793	0.0387685
Gga.5904.1.S1_s_at	COPS7A	2.37279	6.0075E-06
Gga.8004.3.S1_at	PEMT	2.37088	0.00449465

Gga.15847.1.S1_at	---	2.36967	0.00823192
GgaAffx.21119.1.S1_at	---	2.36906	0.00461149
GgaAffx.8693.1.S1_at	LOC771331 /// ZMIZ2	2.36502	0.0037448
Gga.8338.1.S1_at	NIP7	2.36486	0.00064434
Gga.11820.1.S1_at	HMBOX1	2.36426	0.0125836
Gga.3300.2.S1_a_at	C3orf28	2.36383	0.0014464
GgaAffx.11358.1.S1_s_at	ZC3HAV1	2.35974	0.00208771
GgaAffx.1883.3.S1_at	ADAMTSL2	2.35898	0.0133978
Gga.7977.1.S1_at	---	2.35897	0.00823092
GgaAffx.10384.1.S1_at	SRPX	2.35386	0.00481422
GgaAffx.20714.1.S1_s_at	ITPR2	2.35274	0.00605354
GgaAffx.24427.1.S1_at	MLF2	2.35174	3.3369E-05
Gga.7101.1.S1_at	NOLC1	2.3501	0.0402712
GgaAffx.8575.1.A1_s_at	STX17	2.34657	0.00193718
Gga.13072.1.S1_s_at	CCDC58	2.343	0.00053434
Gga.11908.3.S1_at	CMC1	2.34297	0.00113859
GgaAffx.5618.1.S1_at	CASP7	2.33453	0.0273685
Gga.13380.1.S1_at	ZBED1	2.33434	0.0486576
GgaAffx.26358.1.S1_at	ATPAF2	2.33398	0.00879724
GgaAffx.1597.1.S1_at	---	2.33369	0.00226546
GgaAffx.12914.1.S1_at	SLC30A6	2.33197	0.0052501
Gga.9200.1.S1_s_at	AP3S1	2.32815	1.6654E-06
GgaAffx.10598.1.S1_s_at	EPT1	2.32472	0.0306958

Gga.16792.1.S1_at	ATAD1	2.32342	0.00017031
GgaAffx.12969.1.S1_at	PIK3R5	2.32125	0.0169942
Gga.2537.1.S1_at	HMGCL	2.31957	0.00242288
GgaAffx.1492.1.S1_at	DENND1B	2.31932	1.953E-05
Gga.11353.1.S1_s_at	ASXL3	2.31715	0.0449857
GgaAffx.9196.1.S1_s_at	LOC429336	2.31644	0.00872005
Gga.11307.1.S1_at	SVIL	2.31472	0.00665837
Gga.4006.1.S1_at	PPARA	2.31413	0.00045515
Gga.2707.2.S1_a_at	CLOCK	2.3125	0.0103377
Gga.11486.1.S1_at	RPL9	2.31172	0.00187568
GgaAffx.25272.2.S1_s_at	WWC1	2.31164	0.00483586
GgaAffx.12737.1.S1_at	MPP1	2.30901	0.00023896
Gga.12786.1.S1_at	DCLRE1B	2.30873	0.0439894
Gga.13077.1.S1_s_at	PHLDB2	2.30824	0.0115776
Gga.1328.2.A1_at	B2M	2.30754	0.00617473
Gga.5104.1.S1_at	---	2.30708	0.00791947
GgaAffx.1143.1.S1_s_at	NPTN	2.30595	0.00024568
Gga.9426.1.S1_at	NUDCD3	2.3045	1.2142E-05
GgaAffx.20644.1.S1_s_at	FAM107B	2.3024	0.00424863
Gga.1948.1.S1_at	TMEM106C	2.30166	0.00227508
Gga.5630.1.S1_at	MBNL3	2.29575	0.0277817
GgaAffx.8767.1.S1_at	---	2.29504	0.02107
Gga.6002.1.S1_a_at	DNMT3A	2.29239	7.7406E-06

Gga.12135.1.S1_at	MLF1	2.29223	0.0131653
Gga.16222.1.S1_at	TBC1D14	2.29025	0.0399625
Gga.16892.1.S1_at	---	2.28937	0.00020655
GgaAffx.25209.3.S1_s_at	NOX4	2.28667	0.0178859
GgaAffx.12892.1.S1_at	CTSA	2.27997	0.00779446
Gga.18194.1.S1_at	RTEL1	2.27919	0.00172612
Gga.12095.1.S1_at	C6orf57	2.27803	0.0319624
Gga.1851.1.S1_at	---	2.27224	0.00289266
Gga.15325.1.S1_at	---	2.27147	0.036882
GgaAffx.1544.1.S1_s_at	COMMD10	2.27073	0.0142137
Gga.19162.1.S1_at	RET	2.26824	0.00079264
GgaAffx.21159.1.S1_at	---	2.26741	0.0182674
GgaAffx.24678.2.S1_at	FAM110B	2.26559	0.0251873
Gga.15938.1.S1_at	RABGAP1	2.26485	6.5932E-05
Gga.9608.1.S1_at	HSPA4	2.26435	0.00066928
Gga.12087.1.S1_s_at	NKTR	2.26352	0.0044626
GgaAffx.23312.1.S1_at	TMEM48	2.26289	0.0351768
Gga.16411.1.S1_at	---	2.2606	0.00053357
GgaAffx.11756.1.S1_at	GPR137B	2.253	0.00493497
Gga.1350.1.S1_at	ACTR3B	2.24735	0.00189274
Gga.812.1.S1_at	HSF1	2.24302	0.00131654
Gga.9769.2.S1_at	LOC416381	2.24077	0.0240532
GgaAffx.10181.2.S1_s_at	FAM135A	2.23874	0.0157401

Gga.13228.1.S1_at	PALLD	2.23811	0.00391739
GgaAffx.20246.1.S1_s_at	---	2.23761	0.0281293
Gga.14880.1.S1_at	PSMD5	2.23759	0.00106342
Gga.5954.1.S1_at	---	2.23693	0.0329493
GgaAffx.2640.1.S1_s_at	NPAL3	2.23463	0.0358856
GgaAffx.11323.1.S1_at	SMG1	2.23309	0.0250476
Gga.5241.1.S1_at	---	2.23263	0.0111875
Gga.5114.1.S1_at	FUT10	2.23163	0.0143428
GgaAffx.24608.1.S1_at	C9orf93	2.22759	0.00896962
Gga.5421.1.S1_at	ATPAF2	2.22557	0.00302025
Gga.7642.1.S1_at	TRIM69	2.22254	0.00235485
Gga.11655.2.S1_a_at	GPR56	2.22213	0.0178736
Gga.4457.1.S1_s_at	BCL6	2.22121	0.0402807
Gga.19723.1.S1_at	---	2.21834	0.00483999
Gga.17417.1.S1_at	ANKS3	2.2179	0.0015556
GgaAffx.3346.1.S1_at	MSLN	2.21668	0.0105602
Gga.15604.1.S1_at	---	2.21631	0.0101449
GgaAffx.12798.1.S1_at	MFSD1	2.21393	0.00053643
GgaAffx.2187.1.S1_at	ADAM8	2.20888	0.00700692
Gga.2750.1.S1_at	LOC769676 /// PLAGL1	2.20658	0.00672264
Gga.13047.1.S1_s_at	ZNF384	2.2037	0.00188859
Gga.12136.1.S1_at	CHCHD1	2.20143	0.00945076
Gga.5758.1.S1_s_at	LYN	2.20102	0.00519998

Gga.13897.1.S1_x_at	XPC	2.19965	0.00079402
GgaAffx.24266.1.S1_at	TXNDC10	2.19819	3.2715E-05
Gga.9578.1.S1_s_at	---	2.19771	0.00117635
Gga.9729.1.S1_s_at	DCUN1D2	2.19633	0.00415939
Gga.5922.2.S1_a_at	PNPLA7	2.19595	0.00708228
Gga.7691.1.S1_x_at	---	2.19473	0.00162199
Gga.4883.1.S1_at	---	2.19466	0.0228629
Gga.12068.1.S1_s_at	PTBP2	2.19402	0.00313455
Gga.13082.1.S1_at	---	2.19384	0.00537213
Gga.12530.1.S1_s_at	RTEL1	2.19227	0.00834209
Gga.6189.1.S1_at	PORCN	2.19122	0.00011899
GgaAffx.12174.1.S1_s_at	PEPD	2.19018	0.00127577
Gga.1864.1.S1_at	---	2.18795	0.00620194
GgaAffx.520.1.S1_at	VPS72	2.1862	0.00110058
Gga.12905.1.S1_at	MARK1	2.18611	0.011062
Gga.12499.1.S1_at	C7orf50	2.1846	0.00996687
GgaAffx.8630.2.S1_s_at	C1orf43	2.18322	0.00331287
Gga.11421.1.S1_at	---	2.18254	0.00343937
Gga.17229.1.S1_at	---	2.17876	0.0401644
Gga.18340.1.A1_at	---	2.17533	0.0219926
Gga.5546.1.S1_at	SCYL3	2.17449	0.0431672
Gga.11348.2.S1_a_at	---	2.1726	0.0120779
GgaAffx.2819.1.S1_at	TNRC18	2.16932	0.0033364

Gga.7525.1.S1_at	---	2.16865	7.3374E-09
Gga.13501.1.S1_at	LY75	2.16759	0.0373303
Gga.16044.1.S1_at	ABCB7	2.16717	0.00020202
Gga.5473.1.S1_at	LOC416933	2.16708	0.00759262
Gga.13387.1.S1_at	---	2.16642	0.00668137
Gga.10293.3.S1_a_at	LOC420991	2.16573	0.0108762
Gga.6347.2.A1_at	C7orf30	2.16439	0.00224903
Gga.13129.1.S1_s_at	LOC419204	2.16363	0.0386639
GgaAffx.21393.1.S1_s_at	SLC25A13	2.1625	0.00536136
Gga.5668.1.S1_s_at	IDH3B	2.15962	0.0305646
GgaAffx.12743.1.S1_at	NT5C2	2.1588	0.00010191
GgaAffx.13127.1.S1_s_at	FUBP1	2.15811	0.00099728
Gga.17595.1.S1_at	CDK5RAP2	2.15686	0.0200893
GgaAffx.20765.1.S1_at	SLC45A4	2.15662	0.00271243
Gga.3255.2.S1_a_at	---	2.15257	0.0143665
Gga.15064.1.S1_at	TNPO1	2.15119	0.00496671
Gga.19462.1.S1_s_at	SLC25A39	2.14976	0.00439014
GgaAffx.22250.1.S1_at	CTSZ	2.14855	0.00190749
GgaAffx.10612.1.S1_s_at	RAB9A	2.14662	0.0391634
GgaAffx.13152.1.S1_s_at	---	2.14616	0.010016
Gga.10461.2.S1_a_at	HMGCLL1	2.1384	0.00155813
Gga.9879.1.S1_at	LIPA	2.13803	0.019884
GgaAffx.21251.1.S1_at	---	2.1375	0.0151471

Gga.19422.1.S1_s_at	DHX33	2.1372	0.00767467
GgaAffx.21483.1.S1_at	FARP1	2.13629	0.0285961
Gga.14247.1.A1_at	---	2.13615	0.001032
Gga.6253.1.S1_at	PSMD5	2.13567	0.00023901
Gga.2795.1.S1_at	---	2.13539	0.0148717
Gga.13324.1.S1_at	BBS12	2.13293	0.0374486
GgaAffx.24895.1.S1_at	FUNDC1	2.13249	0.00010513
Gga.16627.1.S1_at	C1orf88	2.13186	0.00258468
Gga.1371.2.S1_a_at	MRPL45	2.1307	0.00286482
Gga.7808.1.S1_at	C7orf24	2.12934	0.00890757
GgaAffx.13053.1.S1_s_at	C10orf58	2.12919	0.00023496
Gga.14616.1.S1_at	---	2.12734	0.00087592
Gga.7197.1.S1_at	LOC771974	2.12324	0.0113585
Gga.10301.1.S1_at	GOLM1	2.12246	0.0131036
Gga.9847.1.S1_s_at	ITSN1	2.12145	0.0361373
GgaAffx.21209.1.S1_at	---	2.12039	0.0036526
GgaAffx.26766.1.S1_at	TMEM32	2.11775	0.00903076
Gga.16111.1.S1_at	VMA21	2.11736	0.0187382
Gga.8915.1.S1_s_at	C20orf108	2.11726	0.0192664
Gga.19112.1.S1_at	MBOAT5	2.11711	0.0142254
GgaAffx.9286.1.S1_at	KIAA0372	2.11707	0.00036383
GgaAffx.11962.1.S1_at	PSME4	2.11498	0.0123732
Gga.13348.1.S1_at	---	2.11491	0.0130538

Gga.1054.1.S1_at	SARNP	2.11375	0.0146131
Gga.3779.1.S1_at	---	2.11052	0.00672778
GgaAffx.3315.1.S1_at	CLSTN2	2.10826	0.0296781
GgaAffx.4782.1.S1_s_at	C10orf76	2.10746	0.0001772
Gga.4672.1.S2_at	ATP6V0A1	2.10701	0.00096671
GgaAffx.24946.1.S1_s_at	ZHX1	2.10584	0.0267311
Gga.12500.1.S1_at	---	2.10465	0.0277301
Gga.2155.1.S1_at	ATP1A1	2.10344	0.00354955
GgaAffx.7747.2.S1_s_at	TSPAN5	2.10282	0.00439439
Gga.6242.1.S1_at	CISD2	2.10259	0.00277192
GgaAffx.12072.1.S1_at	ARL2BP	2.1015	0.00040798
Gga.7847.1.S1_at	ACSL5	2.10018	0.00826086
Gga.8040.1.S1_at	---	2.09826	0.0216063
GgaAffx.8571.1.S1_at	PARD3B	2.09598	0.020884
GgaAffx.12946.1.S1_at	---	2.09009	0.0316374
GgaAffx.21061.1.S1_at	---	2.08906	0.00280807
Gga.895.2.S1_at	MLF2	2.08782	0.00010698
GgaAffx.20473.1.S1_at	---	2.08684	0.00855717
Gga.9832.1.S1_a_at	LOC418453	2.08074	0.0231208
Gga.17202.1.S1_s_at	WWC1	2.08065	0.00980082
Gga.3676.1.S1_at	CHST15	2.08036	0.0269576
Gga.15766.1.S1_at	EIF6	2.07942	0.0009385
Gga.12103.1.S1_at	TM4SF18	2.07862	0.0176955

GgaAffx.6294.1.S1_at	SOCS5	2.0786	0.0102565
GgaAffx.25374.2.S1_at	WDR33	2.07833	0.00011562
GgaAffx.8131.1.S1_s_at	LOC418108	2.07828	0.00656399
Gga.6272.1.S1_a_at	TLK2	2.07767	0.00506556
Gga.11134.1.S1_at	LOC422476	2.07662	0.0494041
Gga.12934.1.S1_at	---	2.07576	0.00610058
Gga.156.2.S1_a_at	NBL1	2.07469	0.0163796
Gga.16477.1.S1_at	---	2.07446	0.00727387
Gga.9930.1.S1_at	---	2.07395	0.00276513
Gga.12214.2.S1_a_at	MBNL3	2.07381	0.00807875
Gga.2648.1.S2_at	HOXB3	2.07381	0.0492546
GgaAffx.22951.1.S1_at	LOC424150	2.0735	0.0283445
GgaAffx.8109.1.S1_s_at	PARP12	2.07144	0.00405574
Gga.1477.1.S1_at	---	2.07051	0.0356933
Gga.5046.1.A1_s_at	SLC45A4	2.06951	0.00069455
GgaAffx.9087.2.S1_s_at	ARL2BP	2.0687	4.7118E-05
Gga.5239.1.S1_at	---	2.06483	0.0119484
GgaAffx.21893.1.S1_at	GALNS	2.06177	0.0209559
Gga.19242.1.S1_at	---	2.06085	0.0015438
GgaAffx.13113.1.S1_at	WDR36	2.06052	0.00726852
Gga.7691.1.S1_a_at	---	2.06049	0.00420865
Gga.9305.1.S1_at	LOC416033	2.05832	0.00204451
GgaAffx.3415.1.S1_at	ZDHHC21	2.05821	0.0168922

Gga.7415.1.S1_at	TPP1	2.05778	0.0387954
GgaAffx.13065.1.S1_s_at	NUPL2	2.0575	0.0100289
Gga.18866.1.S1_at	---	2.05745	0.00655959
Gga.2296.1.S1_at	---	2.05712	0.025177
Gga.17193.1.S1_s_at	SLC9A6	2.05698	0.00374678
Gga.14426.1.S1_at	LIPA	2.05684	0.0003683
Gga.11704.1.S1_at	UGCGL1	2.05617	0.00499154
Gga.12402.1.S1_at	R3HCC1	2.05489	0.0429606
Gga.18388.1.S1_at	---	2.05383	0.00626318
GgaAffx.24290.1.S1_at	DUSP16	2.05255	0.00118057
GgaAffx.8575.1.A1_at	STX17	2.05219	0.00095952
GgaAffx.23312.2.S1_s_at	TMEM48	2.04891	0.0477805
Gga.253.1.S1_at	FOXD1	2.04699	0.0051243
Gga.3115.1.S1_at	---	2.04686	0.0182721
Gga.12907.1.S1_at	C7orf42	2.04641	0.0024209
Gga.7271.1.S1_s_at	MPP1	2.04598	0.0004848
GgaAffx.11797.1.S1_at	SMARCE1	2.04537	0.0453451
Gga.8055.1.S1_a_at	RPUSD1	2.04323	0.00128643
GgaAffx.23003.1.S1_at	---	2.04301	0.00625257
Gga.5240.1.S1_s_at	SLC25A14	2.0417	0.0108875
Gga.4869.1.S1_at	AKR1B10	2.04055	0.00719114
Gga.11605.1.S1_at	---	2.03948	0.00206545
GgaAffx.4851.1.S1_at	EIF4E3	2.03866	0.00122584

Gga.12273.1.S1_at	PINX1	2.03822	0.00928394
GgaAffx.12241.1.S1_s_at	GMNN	2.03815	0.0195661
GgaAffx.25128.1.S1_at	MYCBP2	2.03767	0.00746249
Gga.4188.1.S1_s_at	SLC25A13	2.03321	0.00297166
Gga.17394.1.S1_at	---	2.03259	0.0001256
Gga.7691.1.S1_at	---	2.03231	0.0329582
GgaAffx.1064.1.S1_s_at	ATG16L1	2.03111	0.00242296
Gga.14155.1.S1_at	TSPAN2	2.02991	0.00287381
Gga.5401.1.S1_at	DHRS7	2.02959	0.0257305
GgaAffx.9750.2.S1_s_at	LNPEP	2.02955	0.0306383
Gga.14400.1.S1_at	IFT122	2.02766	0.0281505
GgaAffx.21656.1.S1_s_at	GIT1	2.02646	0.00161696
Gga.16458.1.S1_at	SPATA17	2.02634	0.0061608
GgaAffx.12815.1.S1_at	C20orf108	2.02452	0.0109822
GgaAffx.5895.2.S1_s_at	HN1L	2.02239	0.00883903
Gga.3423.1.S1_at	PEX1	2.02161	0.00873909
GgaAffx.1328.2.S1_s_at	STXBP3	2.01693	0.00907337
Gga.8273.1.A1_at	---	2.01679	0.0166174
Gga.13063.1.S1_at	---	2.01622	2.4139E-05
Gga.18340.1.S1_at	---	2.01443	0.0330982
Gga.8847.1.S1_at	C6orf106	2.01413	0.00676168
GgaAffx.12639.1.S1_s_at	WBSCR16	2.01413	0.0242798
GgaAffx.4710.1.S1_at	TPCN2	2.01143	0.00279308

GgaAffx.13042.1.S1_s_at	PWP1	2.01057	0.0372831
Gga.1337.1.S1_at	LOC395787	2.00907	0.0403404
GgaAffx.3390.2.S1_s_at	WDR32	2.00839	0.00559069
Gga.8000.1.S1_at	FARP1	2.0068	0.00425411
Gga.15109.1.S1_at	LOC417151	2.00644	0.0182597
GgaAffx.11454.1.S1_s_at	PHB2	2.00615	0.00109654
Gga.7358.3.S1_a_at	MRPL10	2.00604	0.01298
Gga.8053.1.S1_at	TIMM22	2.00603	0.00023549
GgaAffx.8903.3.S1_at	ARHGAP18	2.00499	0.00189528
GgaAffx.23570.1.S1_at	CCNI	2.00494	0.0350531
Gga.5435.1.S1_at	RRAGB	2.00433	0.0160424
Gga.19239.1.S1_at	ZNF407	2.00308	0.0124112
GgaAffx.7313.1.S1_at	LOC419095	2.00246	0.0444895
GgaAffx.8007.1.S1_at	FANCC	2.00237	0.00114075

snížená exprese

ID sondy	Symbol genu	míra velikosti účinku (PR9692-E9 vs. PR9692)	hodnota P (PR9692-E9 vs. PR9692)
Gga.888.1.S1_at	COL6A3	-1917.22	2.1097E-07
Gga.2592.1.S1_at	COL5A1	-394.432	1.1195E-06
Gga.4257.1.S1_at	COL6A2	-296.091	8.6137E-08
GgaAffx.8765.2.S1_at	GFPT2 /// LOC416372	-251.417	2.9914E-08
Gga.4305.1.S1_at	---	-222.629	7.6647E-07
Gga.4999.2.S1_at	ITGA4	-196.727	1.255E-07

Gga.16822.1.S1_at	---	-147.732	4.2201E-09
GgaAffx.21771.1.S1_at	COL6A1	-141.682	9.1279E-05
Gga.3110.1.S1_x_at	COL6A1	-127.746	3.0081E-07
Gga.11925.1.S1_at	ANXA7	-126.263	5.8111E-06
Gga.7352.1.S1_at	---	-101.431	1.1662E-07
Gga.5255.1.S1_at	EFEMP1	-100.932	0.00097445
GgaAffx.8765.3.S1_s_at	GFPT2	-100.796	8.3091E-11
Gga.13451.1.S1_at	CCDC104	-96.8374	3.9502E-09
GgaAffx.22999.1.S1_s_at	COL1A2	-88.7075	0.0024132
Gga.5500.2.S1_a_at	MRAS	-87.1834	4.2607E-07
Gga.6106.1.S1_a_at	RARRES2	-84.5793	5.4264E-06
Gga.11913.1.S1_at	GPX8	-82.5318	1.2036E-06
Gga.5496.1.S1_at	---	-82.0061	2.6949E-06
Gga.5928.1.S1_at	LOXL1	-79.8153	0.00100112
Gga.3518.1.S1_at	---	-77.8123	7.2941E-07
Gga.1768.1.S1_at	MGAT3	-76.7794	8.0362E-05
Gga.5111.1.S1_at	CCDC80	-71.4848	2.0773E-06
Gga.13978.1.S1_s_at	LHFPL5	-70.5011	3.3266E-05
Gga.14963.1.S1_at	---	-64.0562	6.9546E-08
Gga.15844.1.S1_s_at	---	-58.9899	3.2026E-06
Gga.10389.1.S1_at	ITGA11	-57.5039	6.7099E-05
Gga.9580.2.S1_a_at	AKR1B1 /// LOC425137 /// LOC772271	-57.3017	2.9883E-09

Gga.16589.1.S1_at	LSP1	-57.2304	8.4751E-06
Gga.18272.1.S1_at	---	-57.2259	8.8574E-06
Gga.13294.1.S1_at	---	-57.2182	0.00038053
Gga.4491.1.S1_at	LSP1	-56.4956	6.2343E-06
Gga.10266.1.S1_at	LOC429955	-54.8991	9.2819E-06
Gga.226.1.S1_at	F13A1	-52.975	0.00927674
Gga.20041.1.S1_at	PCSK6	-51.0854	4.494E-06
Gga.226.2.S1_a_at	F13A1	-46.9127	0.00361513
Gga.12598.1.S1_at	RHOJ	-46.5886	3.8244E-06
Gga.10748.1.S1_at	---	-46.3438	2.5017E-07
GgaAffx.4585.1.S1_at	LOC422293	-43.1922	2.5468E-05
GgaAffx.2113.1.S1_s_at	CDK2AP1	-41.5457	4.9068E-06
Gga.8329.1.S1_at	PRKCH	-40.5288	9.7455E-06
GgaAffx.1718.1.S1_at	CSPG4	-40.444	3.5324E-06
Gga.4491.1.S1_s_at	LSP1	-37.0968	1.8883E-05
Gga.1158.3.S1_s_at	HOPX	-36.6526	0.00845519
GgaAffx.11467.1.S1_s_at	CDK2AP1	-36.2874	8.8684E-08
Gga.13238.1.S1_at	---	-36.1943	1.0828E-06
Gga.2527.1.S1_at	---	-35.3812	8.3235E-09
Gga.1158.3.S1_a_at	HOPX	-34.8018	0.0065152
GgaAffx.6053.1.S1_at	COL1A2	-34.1497	0.0108377
GgaAffx.26136.1.S1_at	LOC422154	-33.3345	7.2898E-06
Gga.8030.1.S1_at	TFPI2	-32.277	2.5585E-06

Gga.1794.1.S1_at	NCAM1	-31.376	5.8034E-05
GgaAffx.7341.1.S1_s_at	SLC22A3	-30.6564	0.00035692
Gga.3099.1.S1_at	---	-29.9778	0.0104242
Gga.17586.1.S1_at	---	-29.9292	6.2508E-06
Gga.8515.1.S1_at	LHFPL5	-29.8294	0.00025609
Gga.8446.1.S1_at	GSR	-29.4414	0.00023548
Gga.19950.1.S1_s_at	F13A1	-29.112	0.0056485
GgaAffx.22242.2.S1_s_at	---	-28.7298	9.8381E-07
GgaAffx.25662.1.S1_at	ENPP3	-28.6091	8.4115E-06
Gga.2680.1.S1_at	AQP1	-28.4549	1.4885E-05
GgaAffx.7559.1.S1_s_at	PRKCH	-27.736	3.3794E-06
GgaAffx.21534.1.S1_s_at	LOC417962	-27.2425	3.725E-05
Gga.8359.1.S1_at	GSTA3	-27.0581	0.00235165
Gga.14273.1.S1_at	---	-26.8072	0.00061488
Gga.9764.1.S1_at	---	-26.3693	4.6805E-06
GgaAffx.11729.1.S1_at	GLT1D1	-26.344	0.00019344
GgaAffx.25677.1.S1_s_at	ENPP3	-26.1774	6.8824E-05
GgaAffx.23017.1.S1_at	PTX3	-24.8572	0.00068401
GgaAffx.11738.1.S1_s_at	EGR1	-24.0838	0.00093145
Gga.2974.1.S1_at	CACNG3	-23.8659	1.5956E-05
GgaAffx.8972.1.S1_s_at	MANSC1	-23.2258	6.2214E-05
Gga.8823.1.S1_s_at	CMTM7	-23.2008	1.8908E-06
Gga.5629.1.S1_at	LOC415671	-23.1648	3.8242E-05

Gga.2625.1.S1_at	RARRES1	-22.8732	0.00038177
Gga.5879.1.S1_at	---	-22.7838	0.00089431
GgaAffx.7341.1.S1_at	SLC22A3	-22.4583	9.2731E-06
GgaAffx.4824.1.S1_s_at	PHLDB1	-22.1417	8.2283E-07
Gga.4052.1.S1_at	MYL9	-22.0454	5.7423E-05
Gga.11634.1.S1_at	CTHRC1	-21.8467	2.1986E-07
Gga.2330.1.S1_at	LOC415822	-21.5145	0.00028204
Gga.8853.3.S1_s_at	SULT1B1	-21.3276	0.0018912
GgaAffx.7262.1.S1_at	TNFAIP2	-21.3186	0.00012076
GgaAffx.1993.5.S1_s_at	ITPR3	-21.2163	9.6505E-05
Gga.9813.1.S1_at	---	-20.7175	4.322E-05
Gga.4922.1.S2_at	EGR1	-20.5021	0.00129951
Gga.329.1.S1_at	HAS2	-19.8247	0.00123494
Gga.10286.1.S1_at	PBLD	-19.6457	0.00012073
GgaAffx.10743.1.S1_at	IL1RL2	-19.6191	9.0937E-06
GgaAffx.12670.1.S1_s_at	NUDT14	-18.5479	6.7533E-09
Gga.8051.1.S1_at	---	-18.0296	9.2008E-07
Gga.6121.1.S1_at	---	-18.0207	6.9473E-11
Gga.4292.1.S1_at	LAMB2	-17.5409	6.1949E-08
GgaAffx.11201.1.S1_s_at	TLR6	-17.5254	3.396E-06
Gga.17254.1.S1_at	---	-17.5055	2.9529E-05
GgaAffx.5015.1.S1_at	ITGA11	-17.301	0.00312698
Gga.2827.2.S1_a_at	TIMP3	-17.2046	0.0308853

GgaAffx.7003.1.S1_at	CLMN	-17.1499	7.5175E-06
Gga.2876.1.S1_a_at	VAV3	-16.6179	6.6012E-05
Gga.3899.3.S1_a_at	PDGFA	-16.3955	0.00053066
GgaAffx.24196.1.S1_at	EDG4	-15.4624	0.0001881
GgaAffx.26112.1.S1_at	FUCA1	-15.4041	4.2255E-06
Gga.10763.1.S1_at	SLC6A4	-15.156	7.5368E-05
Gga.5353.1.S1_at	---	-15.1414	8.2984E-07
Gga.16244.1.S1_a_at	---	-15.0394	0.00078001
Gga.10956.1.S1_at	AP1S3	-14.5774	0.00131969
Gga.10617.1.S1_a_at	MSRB3	-14.3664	0.00011522
GgaAffx.23947.1.S1_at	PRDM4	-14.366	0.00015697
GgaAffx.8811.1.S1_at	FAM83H	-14.3439	0.00122033
Gga.1759.1.S1_at	PIK3IP1	-14.3298	7.3224E-06
Gga.1378.1.S1_s_at	HDAC9	-14.238	0.00156595
Gga.5385.1.S1_s_at	ASS1	-13.9522	0.00028741
Gga.15867.1.S1_at	---	-13.923	2.0483E-05
Gga.7542.1.S1_at	EHHADH	-13.9194	1.1588E-06
Gga.12194.1.S1_at	CBY1	-13.8775	1.4298E-05
Gga.2876.2.S1_x_at	VAV3	-13.7981	0.00073984
Gga.6223.1.S1_at	ADAM33	-13.6677	8.6104E-06
Gga.9147.1.S1_at	LOC424588	-13.6348	6.6311E-05
GgaAffx.3568.1.S1_at	CRISPLD2	-13.6137	0.00014078
Gga.133.1.S1_at	SULT1B1	-13.5327	0.00013289

Gga.11190.1.S1_a_at	---	-13.4807	0.0010638
Gga.7334.1.S1_at	APBB1IP	-13.3568	7.796E-05
Gga.20.1.S1_at	FTD	-13.1783	0.00022354
Gga.5198.1.S1_a_at	LOC420812	-13.1612	2.2313E-06
Gga.3402.1.S2_at	OLFM1	-13.0626	2.7099E-05
Gga.13891.1.S1_s_at	GLT1D1	-12.8418	5.7534E-05
Gga.18993.1.S1_at	DGKI	-12.7929	0.00183283
GgaAffx.12413.1.S1_at	RBM38	-12.6509	0.00037109
GgaAffx.10437.1.S1_at	FAM83B	-12.3983	1.0098E-05
Gga.9403.1.S1_a_at	CCDC109B	-12.3212	5.4094E-05
GgaAffx.4778.1.S1_s_at	SLC9A3R1	-12.1517	1.6718E-06
Gga.9473.1.S1_at	ITGB5	-12.1375	0.00050183
Gga.20.1.S2_at	FTD	-12.0027	5.9949E-05
Gga.9012.1.S1_at	STK17B	-11.993	0.00073386
Gga.5591.1.S1_at	---	-11.9842	0.00039308
Gga.4424.1.S1_at	SH3GL3	-11.8663	0.0020478
Gga.275.1.S1_at	MITF	-11.8625	1.5758E-05
Gga.17905.1.S1_at	---	-11.6728	3.9608E-06
GgaAffx.7917.1.S1_at	TNFAIP6	-11.3494	0.00045755
GgaAffx.7332.1.S1_at	LOC772201	-11.2948	0.00021323
Gga.9062.1.S1_at	ENPP3	-11.1917	2.7773E-05
Gga.13339.1.S1_at	ST8SIA6	-11.039	4.9455E-05
Gga.13519.1.S1_s_at	SLC7A5	-11.0364	0.0128597
Gga.14884.1.S1_s_at	CCDC88A	-11.0174	0.00020071

GgaAffx.11653.1.S1_s_at	STK17B	-10.7539	0.00065626
GgaAffx.7930.2.S1_at	CD1C	-10.6882	0.00235016
Gga.1150.2.S1_a_at	OLFML3	-10.6266	1.9531E-05
Gga.7140.2.S1_s_at	FXYD6	-10.4561	2.7737E-05
Gga.4901.1.S1_at	CA9	-10.3685	0.0104402
GgaAffx.5267.1.S1_at	LMCD1	-10.3642	0.0029198
Gga.10038.1.A1_at	GRAMD1C	-10.2945	3.7361E-06
GgaAffx.22647.3.S1_s_at	MAPK12	-10.2386	0.000265
Gga.8519.1.S1_a_at	TTC32	-10.1611	4.9917E-08
Gga.1846.1.S1_at	SEMA3C	-10.0234	0.00032401
GgaAffx.21035.1.S1_s_at	EHHADH	-10.0062	8.7622E-06
GgaAffx.4531.1.S1_at	LOC769198	-9.90198	0.00254761
Gga.15955.1.S1_s_at	SLC16A2	-9.8865	0.00163527
GgaAffx.539.1.S1_at	HTR1D	-9.79692	1.1076E-05
GgaAffx.23696.1.S1_s_at	PRKCH	-9.76917	2.0589E-05
GgaAffx.6203.1.S1_at	CSPG4	-9.72791	5.7866E-06
Gga.18773.1.S1_at	ADAMTS15	-9.68134	6.9909E-05
Gga.19300.1.S1_at	SLC16A2	-9.66654	0.00234154
Gga.2876.1.S2_a_at	VAV3	-9.64691	0.00065146
Gga.1750.1.S1_at	SLC16A2	-9.59541	0.00060681
Gga.7057.1.S1_at	CARD11	-9.58448	0.00081931
Gga.9675.1.S1_at	PDGFD	-9.58436	0.0159697
Gga.19091.1.S1_at	---	-9.54244	0.00014611

GgaAffx.24033.2.S1_s_at	DGKI	-9.3981	0.00119073
Gga.8160.1.S1_at	C16orf45	-9.27659	3.7677E-07
GgaAffx.24196.1.S1_s_at	EDG4	-9.2251	0.00091079
GgaAffx.24033.1.S1_s_at	DGKI	-9.17771	0.00137368
Gga.18968.1.S1_at	---	-9.11873	0.00011906
Gga.10321.1.S1_a_at	PTX3	-9.11085	0.00775963
Gga.8789.1.S1_at	PIK3CD	-9.10618	2.5248E-05
Gga.10214.1.S1_s_at	MAPK12	-9.09794	0.00039833
Gga.6306.1.S1_at	BAMBI	-9.06617	1.3646E-05
Gga.6641.1.A1_at	---	-9.03433	0.0044954
GgaAffx.13096.1.S1_at	RASSF5	-8.97967	0.00066034
Gga.9580.1.S1_at	AKR1B1 /// LOC425137 /// LOC772271	-8.92742	5.7549E-05
GgaAffx.3792.1.S1_at	LOC415464	-8.88172	3.5639E-05
Gga.7499.1.S1_at	---	-8.85291	3.0802E-05
Gga.18801.1.S1_at	---	-8.80923	2.6775E-06
Gga.15312.1.S1_a_at	UBAP2	-8.77536	0.00025665
Gga.15050.1.S1_at	---	-8.68962	0.00025889
Gga.4328.1.S1_at	IGFBP7	-8.60794	6.19E-05
Gga.3259.1.S1_at	ANGPT2	-8.56538	8.4544E-06
Gga.14212.1.S1_at	---	-8.44583	0.00090126
Gga.7318.1.S1_at	---	-8.44372	0.00054079
GgaAffx.20592.1.S1_at	GALNT5	-8.43423	3.945E-05

GgaAffx.5084.3.S1_s_at	CCDC88A	-8.33552	0.00242658
GgaAffx.7493.1.S1_s_at	UGT2A3	-8.28681	0.00086169
Gga.1846.1.S2_at	SEMA3C	-8.25266	0.00080112
GgaAffx.10088.2.A1_s_at	PRSS35	-8.19568	0.00551109
Gga.12884.1.S1_at	PLA2R1	-8.10122	2.5372E-05
Gga.10365.1.S1_at	---	-8.10121	7.1757E-05
Gga.4900.1.S1_a_at	17.5 /// LOC776463	-8.05769	0.0001153
GgaAffx.10088.1.S1_at	PRSS35	-8.01928	0.00583025
Gga.19033.1.S1_at	---	-7.98135	6.9928E-05
Gga.12120.1.S1_at	PACSIN3	-7.89669	0.0011572
GgaAffx.4559.2.S1_s_at	LEPREL1	-7.87911	0.00038128
Gga.4113.1.S1_at	RHOF	-7.87317	5.2539E-06
Gga.4668.2.S1_a_at	DNER	-7.84006	0.00279331
Gga.5198.3.S1_x_at	---	-7.82882	7.253E-05
Gga.10214.1.S1_at	MAPK12	-7.75983	7.4532E-06
GgaAffx.8420.1.S1_at	VAT1L	-7.73752	8.1467E-06
Gga.17889.1.S1_at	---	-7.73746	0.00275754
Gga.16422.1.S1_at	C10orf72	-7.72085	0.00223235
Gga.4051.1.S1_at	CTGF	-7.70786	0.0272263
Gga.12534.1.S1_at	LXN	-7.68568	0.00046345
GgaAffx.12115.1.S1_at	RHOF	-7.62948	1.6128E-07
Gga.18814.1.S1_at	LOC418298	-7.61883	2.1155E-05
GgaAffx.1404.1.S1_at	LOC415671	-7.61416	4.7382E-06

GgaAffx.6203.2.S1_s_at	CSPG4	-7.48363	0.00035705
Gga.2718.1.S1_at	NUDT14	-7.45204	0.00001919
Gga.3402.1.S1_a_at	OLFM1	-7.42126	0.00042132
GgaAffx.23235.1.S1_at	EBF3	-7.2865	0.00013042
Gga.1081.1.S1_at	ATAD1	-7.23754	0.00021046
Gga.1369.1.S1_at	P2RX4	-7.22211	2.4635E-05
Gga.11468.1.S1_a_at	PPIC	-7.1383	5.2732E-05
GgaAffx.8298.1.S1_at	UPP1	-7.11996	0.0016797
Gga.17604.1.S1_s_at	PRDM4	-7.02332	0.00013662
GgaAffx.25541.1.S1_s_at	PIK3CD	-7.0117	0.0003509
Gga.1222.2.S1_s_at	SLC9A3R1	-6.92327	7.9666E-06
GgaAffx.6895.1.S1_at	LASS6	-6.87474	4.3553E-05
Gga.13553.1.S1_at	FSCN1	-6.84226	0.00160664
GgaAffx.6430.1.S1_at	LOC424588	-6.84075	1.0181E-06
GgaAffx.22014.2.S1_s_at	EHHADH	-6.66706	2.7678E-05
GgaAffx.21176.1.S1_at	---	-6.65849	0.00018438
Gga.9234.1.S1_at	---	-6.64863	0.0003499
Gga.15768.1.S1_at	TNFAIP6	-6.57468	0.00015364
GgaAffx.21279.1.S1_at	UPP1	-6.56185	0.00594811
GgaAffx.23709.2.S1_s_at	PRDM5	-6.52004	0.00085073
Gga.9077.1.S1_at	HVCN1	-6.48997	0.0010199
GgaAffx.21354.1.S1_at	YPEL1	-6.38537	0.00591638
Gga.20029.1.S1_at	---	-6.37829	1.9759E-05

GgaAffx.21386.1.S1_s_at	CALD1	-6.37071	7.6294E-05
GgaAffx.4531.1.S1_s_at	LOC769198	-6.3305	0.00112413
Gga.14579.1.S1_at	CUBN	-6.31866	2.8772E-05
GgaAffx.3903.1.S1_s_at	---	-6.26495	1.7109E-06
Gga.8853.2.S1_a_at	SULT1B1	-6.234	0.00188649
GgaAffx.25083.1.S1_at	CENTB5	-6.22219	0.00016708
GgaAffx.22462.1.S1_at	---	-6.21568	0.00092298
Gga.17933.1.S1_at	---	-6.21306	0.00163792
Gga.3972.1.S1_at	SEMA3D	-6.19751	0.00159472
Gga.19400.1.A1_s_at	ODZ3	-6.18713	0.00032678
Gga.9986.1.S1_at	FSCN1	-6.17759	1.3698E-05
GgaAffx.941.1.S1_s_at	ADAMTS15	-6.17119	0.00203542
Gga.10703.1.S1_at	CHID1	-6.16088	0.00116628
Gga.11352.1.S1_at	SCN4B	-6.15521	9.518E-06
Gga.714.1.S2_at	FMN1	-6.13697	0.00249023
GgaAffx.22381.3.S1_s_at	ANKK1	-6.10627	0.00220881
GgaAffx.5084.2.S1_s_at	CCDC88A	-6.05963	0.00483066
Gga.3973.1.S1_at	TWIST1	-5.99718	0.00558924
GgaAffx.12049.1.S1_at	MANSC1	-5.9962	0.00044218
Gga.12591.1.S1_at	NEK3	-5.98844	9.8885E-05
GgaAffx.21017.1.S1_s_at	CALD1	-5.96298	0.00038753
Gga.4491.1.A1_at	LSP1	-5.93058	0.00160425
Gga.12157.1.S1_at	LOC421390	-5.92345	5.5093E-05

Gga.19588.1.A1_at	---	-5.90857	0.00315181
GgaAffx.8780.1.S1_at	UBAP2	-5.84896	0.00017499
GgaAffx.24116.1.S1_at	ADAMTS15	-5.84338	0.00049613
Gga.9491.1.S1_at	DNM1	-5.83275	0.00070301
Gga.13251.1.S1_at	---	-5.77718	0.0001078
Gga.18649.1.S1_at	---	-5.77636	0.00306093
Gga.19434.1.S1_at	---	-5.71768	0.00106308
GgaAffx.23304.1.S1_s_at	ODZ3	-5.7147	0.00828914
Gga.1939.1.S1_at	EMP1	-5.68339	9.7658E-05
Gga.257.1.S1_s_at	ITGB8	-5.67099	1.9337E-05
GgaAffx.25168.2.S1_s_at	LOC415664 /// LOC427532	-5.64484	0.00512754
Gga.9338.1.S1_at	HINTW	-5.59009	1.7316E-05
Gga.2663.1.S1_at	FKBP9	-5.5847	0.00111614
Gga.5350.1.S1_at	OSGEPL1	-5.5783	0.00039827
Gga.4083.1.S1_at	NKX-6.1	-5.51885	0.00257859
Gga.714.1.S1_at	FMN1	-5.50863	0.0005904
Gga.16727.1.S1_at	LOC429030	-5.49062	9.3105E-06
GgaAffx.22647.2.S1_s_at	MAPK11	-5.47502	0.00076438
GgaAffx.7512.1.S1_at	---	-5.46014	0.0160573
GgaAffx.10745.1.S1_at	IL18R1	-5.45516	0.00158402
GgaAffx.1151.1.S1_at	---	-5.45201	0.00211671
Gga.20014.1.S1_s_at	DNER	-5.43457	0.00040799
Gga.12839.1.S1_at	C14orf79	-5.42042	2.3391E-08

Gga.2128.1.S1_at	LOC768920	-5.40367	0.00335803
GgaAffx.26737.1.S1_at	PLEKHA7	-5.40118	2.8238E-05
Gga.19012.1.S1_at	C10orf72	-5.40002	0.0179574
Gga.13368.1.S1_at	---	-5.39102	0.00894557
GgaAffx.8428.1.S1_at	BCAN	-5.36575	0.0005531
GgaAffx.11201.3.S1_at	LOC768669 /// TLR6	-5.3597	0.00143569
Gga.19077.1.S1_at	---	-5.35657	0.00074881
Gga.4668.1.S1_at	DNER	-5.35046	0.00092716
GgaAffx.24553.1.S1_at	DSE	-5.34876	0.00168312
Gga.8094.1.S1_a_at	ARHGDIB	-5.31952	4.3276E-05
Gga.13416.1.S1_at	---	-5.30461	0.00064789
Gga.2712.1.S1_at	NSG1	-5.30356	0.00113207
GgaAffx.4004.2.S1_at	C16orf45	-5.29279	0.00037322
Gga.4988.1.S1_at	CALD1	-5.283	0.00028399
GgaAffx.21527.1.S1_at	---	-5.24457	0.00128083
Gga.3578.1.S1_at	---	-5.23549	0.00039075
Gga.1837.1.S1_s_at	---	-5.23291	2.3828E-06
GgaAffx.12879.1.S1_s_at	MAPK11	-5.2164	3.8154E-06
GgaAffx.12589.1.S1_s_at	CCDC88A	-5.17423	0.00278387
Gga.2705.1.S1_at	---	-5.17246	0.0142904
Gga.16199.1.S1_at	---	-5.16344	0.00024278
Gga.19343.1.S1_at	---	-5.13803	0.00080879
GgaAffx.12062.1.S1_s_at	FLI1	-5.12534	0.00471801

GgaAffx.7456.1.S1_at	---	-5.109	7.4284E-05
Gga.19221.1.S1_at	---	-5.10586	0.00436289
GgaAffx.7454.1.S1_at	NPHP3	-5.10427	0.00118996
GgaAffx.2287.1.S1_at	FANCF	-5.09244	0.00089827
GgaAffx.23361.1.S1_at	ITGB8	-5.08534	0.00038964
Gga.15019.1.S1_s_at	TUFT1	-5.07011	0.00055049
GgaAffx.23970.1.S1_s_at	NUAK1	-5.06112	3.8172E-05
GgaAffx.21851.1.S1_s_at	ST8SIA6	-5.04626	2.0205E-05
GgaAffx.2686.1.S1_at	---	-5.02979	2.9535E-05
Gga.11065.1.S1_s_at	---	-5.02413	0.0228788
Gga.19818.1.S1_s_at	LOC769198 /// PLEKHQ1	-5.00268	0.00255839
Gga.4988.2.S1_a_at	CALD1	-4.98502	0.00030879
Gga.5690.1.S1_s_at	RBM38	-4.97215	0.00019431
Gga.12092.1.S1_at	FAM20C	-4.95955	0.00187034
Gga.100.1.S1_a_at	FAS	-4.94564	0.00177476
Gga.1906.1.S2_at	CRISPLD1	-4.91104	0.00449449
Gga.16765.1.S1_at	---	-4.89603	0.0009057
Gga.12209.2.A1_at	C4orf31	-4.85992	0.00047431
GgaAffx.3796.1.S1_s_at	PLEKHA7	-4.83897	3.044E-06
Gga.8904.1.S1_at	---	-4.83622	0.0492437
Gga.8510.1.S1_at	---	-4.83418	3.2703E-05
GgaAffx.12398.1.S1_s_at	TMEM194B	-4.81872	1.7431E-05
GgaAffx.20832.1.S1_s_at	PCSK6	-4.81635	8.232E-05

Gga.3348.2.S1_s_at	PCDH9	-4.81484	0.0015573
Gga.4401.1.S1_a_at	PTGS2	-4.81479	0.0118231
Gga.12998.1.S1_at	CA3	-4.76392	0.00035108
Gga.14931.1.S1_at	---	-4.73673	0.00077597
Gga.643.1.S1_at	SYT1	-4.67888	0.00012263
GgaAffx.25991.1.S1_at	KLF13	-4.67883	0.00190266
Gga.15866.2.S1_a_at	SLC25A12	-4.6607	0.0097205
GgaAffx.8765.1.S1_at	GFPT2 /// LOC416372	-4.62593	0.00971075
GgaAffx.10841.1.S1_s_at	LMO7	-4.62421	0.00618665
GgaAffx.11918.1.S1_s_at	MXD4	-4.62401	0.047115
Gga.13197.1.S1_at	MAST3	-4.61055	0.00012668
GgaAffx.26432.1.S1_s_at	COL11A1	-4.57169	0.00060816
Gga.8858.1.S1_s_at	FKBP7	-4.56	0.00045886
Gga.4821.1.S1_at	COL18A1	-4.55673	0.00058638
GgaAffx.23472.1.S1_at	CHN2	-4.5543	0.00093077
GgaAffx.8901.1.S1_at	LRMP	-4.54556	0.0002552
Gga.12209.2.S1_a_at	C4orf31	-4.5281	3.2227E-05
Gga.12233.1.S1_at	ASAHL	-4.52498	0.0203636
GgaAffx.12014.1.S1_s_at	APBB1IP	-4.5204	9.2535E-07
Gga.4357.1.A1_at	---	-4.51507	0.00337171
Gga.10951.1.S1_s_at	PRDM5	-4.51453	0.00566748
GgaAffx.20295.1.S1_at	NUAK1	-4.46651	0.00374595
Gga.12561.1.A1_at	DSE	-4.46245	0.00021409

Gga.7228.1.S1_at	CMBL	-4.45513	0.0170048
Gga.957.1.S1_at	HOXA11	-4.45278	0.0026559
GgaAffx.20936.1.S1_at	---	-4.4013	0.0069855
Gga.12209.1.S1_at	C4orf31	-4.4001	1.0278E-05
Gga.9699.1.S1_a_at	JMJD7-PLA2G4B	-4.38253	0.00010482
GgaAffx.7916.1.S1_at	RBM43	-4.3806	1.6102E-05
GgaAffx.23988.2.S1_s_at	NEDD9	-4.35789	0.0125759
GgaAffx.21484.1.S1_s_at	---	-4.349	0.00024202
Gga.11730.1.S1_at	SLC2A10	-4.30841	0.00222779
Gga.12745.1.S1_at	UGT2A3	-4.28084	0.00266163
Gga.12387.1.S1_at	PGCP	-4.28014	0.00033282
Gga.20061.1.S1_at	NINJ2	-4.27268	0.0136458
Gga.8736.1.S1_at	MICAL1	-4.27268	0.030102
Gga.5350.1.S1_a_at	OSGEPL1	-4.27105	0.00019202
Gga.7781.1.S1_at	C17orf28	-4.26243	0.0009682
GgaAffx.26202.1.S1_at	CARD11	-4.24729	1.2782E-05
GgaAffx.1139.1.S1_at	MGAT5B	-4.2376	6.2934E-06
Gga.3131.1.S1_at	FKBP7	-4.23752	0.00077461
Gga.2073.1.S1_at	LOC395532	-4.23671	0.00329182
Gga.6298.2.S1_a_at	---	-4.23245	0.00509579
GgaAffx.11252.1.S1_at	LOC428499	-4.23241	3.3709E-05
Gga.13003.1.S1_at	---	-4.21218	0.00020496
GgaAffx.3482.1.S1_at	---	-4.20026	0.00041815

Gga.2190.2.S1_a_at	SOCS2	-4.20013	0.0074713
Gga.4992.1.S1_at	LOC396511	-4.1963	0.00145213
Gga.6690.2.S1_a_at	---	-4.16648	0.00098541
Gga.17352.1.S1_at	---	-4.15317	0.0017614
Gga.18648.1.S1_at	---	-4.14972	0.0279877
Gga.17453.1.S1_at	---	-4.14524	1.553E-05
Gga.9093.1.S1_a_at	DBN1	-4.13472	0.00726508
Gga.2884.1.S1_at	---	-4.13289	0.00079935
GgaAffx.12364.1.S1_at	GLRX5	-4.12994	6.5557E-07
Gga.6161.1.S1_a_at	LOC768436	-4.11562	0.00795638
GgaAffx.25542.1.S1_at	GULP1	-4.10935	0.0020833
GgaAffx.21411.1.S1_s_at	---	-4.10109	0.0134107
GgaAffx.5172.1.S1_at	LOC425409	-4.08063	0.00107115
GgaAffx.26339.1.S1_s_at	DNM1	-4.07851	0.00057831
Gga.18980.1.S1_at	NUAK1	-4.0734	0.00265523
Gga.3019.1.S1_at	MAGI1	-4.04708	0.00115328
GgaAffx.1156.1.S1_s_at	CENTB5	-4.02291	6.054E-05
Gga.2405.1.S1_at	PCDH19	-4.01778	0.00100061
Gga.14171.1.S1_at	---	-4.01589	0.0107648
GgaAffx.25521.1.S1_s_at	COL5A2	-4.00844	0.0155772
Gga.18933.1.S1_s_at	RASSF5	-4.0066	0.00414002
Gga.14417.2.S1_a_at	SLC41A1	-4.00543	0.0245688
Gga.7617.1.S1_at	---	-4.00382	0.00010028

Gga.352.1.S1_at	RGS20	-4.00354	0.00318523
GgaAffx.2792.1.A1_at	LOC770379	-3.97454	1.6486E-05
GgaAffx.20260.1.S1_s_at	---	-3.96403	0.00325738
Gga.3397.1.S1_at	NAT2	-3.96044	0.00071032
Gga.1440.1.S1_at	TECR	-3.95729	0.00678423
GgaAffx.3482.1.S1_s_at	---	-3.93769	0.00107125
Gga.4900.6.S1_x_at	CD69 /// LOC768754	-3.93745	0.00073892
Gga.12262.1.S1_at	---	-3.93671	0.00003091
Gga.11643.2.S1_s_at	C20orf42	-3.93509	0.00437628
Gga.16208.1.S1_at	---	-3.92705	0.0053435
Gga.16049.1.S1_at	---	-3.92276	5.9185E-05
GgaAffx.7012.1.S1_at	CLMN	-3.8927	0.00688571
GgaAffx.9363.1.S1_at	RGS7BP	-3.88891	0.00075368
Gga.8408.2.S1_s_at	TNFSF10	-3.8873	0.022366
Gga.10304.1.S1_s_at	INF2	-3.88152	0.0198122
Gga.17542.1.S1_at	---	-3.88146	0.0258025
Gga.11081.1.S1_s_at	KLF13	-3.84407	0.00055913
GgaAffx.7250.1.S1_at	AMDHD1	-3.84073	0.0179478
GgaAffx.4004.2.S1_s_at	C16orf45	-3.80415	1.9276E-07
GgaAffx.22824.1.S1_s_at	OSBPL6	-3.79326	0.00564619
GgaAffx.6391.2.S1_s_at	ANKRD15	-3.78742	0.00964756
Gga.14876.1.S1_s_at	SMURF2	-3.78609	0.00165974
GgaAffx.11089.1.S1_at	KLHDC5	-3.7817	0.0076999

Gga.6730.1.S1_at	---	-3.77982	0.00029225
GgaAffx.22287.1.S1_s_at	APBB1IP	-3.7705	0.00086414
GgaAffx.549.1.S1_at	MAPK13	-3.76332	0.00083309
Gga.7582.1.S1_at	---	-3.75951	0.00119814
GgaAffx.21522.1.S1_at	---	-3.75539	0.00105995
Gga.15781.1.S1_a_at	---	-3.75254	0.00031077
GgaAffx.7377.1.S1_at	---	-3.74217	0.0106341
Gga.10185.1.S1_at	SF3B1	-3.74195	0.0017922
Gga.11671.2.S1_at	LOC415664	-3.74084	0.00256209
Gga.998.2.S1_a_at	CD3D	-3.73936	0.00693309
Gga.5710.1.S1_a_at	HTRA3	-3.73799	0.00657675
Gga.19161.1.S1_at	---	-3.71805	0.00112921
Gga.5953.1.S1_s_at	SLC43A3	-3.71337	0.00139861
Gga.11925.2.S1_a_at	ANXA7	-3.71148	2.1412E-05
Gga.2734.1.S2_at	ALCAM	-3.70597	0.00040817
Gga.7303.2.S1_a_at	---	-3.69846	0.0003593
Gga.7843.1.S1_at	SYPL1	-3.69393	0.0060559
GgaAffx.4314.1.S1_at	LOC422075	-3.6911	0.00928102
Gga.16719.1.S1_at	---	-3.69102	0.00726394
Gga.17021.1.S1_at	MXRA7	-3.68479	1.48E-05
Gga.16782.1.S1_at	PIK3CD	-3.68246	0.0044566
Gga.13740.1.S1_at	GULP1	-3.67313	0.00028155
Gga.16783.1.S1_at	---	-3.67149	0.00149311

Gga.9765.1.S1_at	ANKRD9	-3.65954	0.00295186
GgaAffx.8020.1.S1_at	CKAP4	-3.65841	0.00186001
GgaAffx.6423.2.S1_at	KCNC2	-3.64573	0.0053347
GgaAffx.21766.1.S1_s_at	TCP11L2	-3.64548	0.0204644
Gga.12631.1.S1_at	---	-3.63771	0.00086171
GgaAffx.26011.1.S1_s_at	ADCY7	-3.63514	0.00106542
GgaAffx.21036.1.S1_at	---	-3.63332	0.0055863
Gga.9162.1.S1_at	SLC9A3R2	-3.62748	0.00081541
Gga.14884.1.S1_at	CCDC88A	-3.60509	3.541E-06
Gga.10098.1.S1_s_at	FAP	-3.60367	0.00188311
GgaAffx.20829.1.S1_at	---	-3.59981	0.00648613
Gga.19482.1.S1_at	---	-3.59614	0.00342487
GgaAffx.20694.1.S1_s_at	ORMDL1	-3.59208	0.00019596
Gga.12190.1.S1_at	---	-3.5915	0.00298979
Gga.11182.1.S1_at	---	-3.58858	0.0146931
Gga.11627.1.S1_at	TROJAN	-3.58335	0.00988966
GgaAffx.4987.1.S1_at	GATSL3	-3.5813	0.00113056
Gga.8086.1.S1_a_at	---	-3.58032	0.00881263
Gga.15859.1.S1_a_at	---	-3.56874	0.00087756
Gga.11081.1.S1_at	KLF13	-3.56539	0.00054227
Gga.666.1.S1_a_at	VIP	-3.56415	0.00487508
Gga.16921.1.S1_at	TCP11L2	-3.55228	0.00516153
Gga.4955.1.S1_at	FRZB	-3.54997	0.00077939

GgaAffx.12557.1.S1_s_at	TPST2	-3.54912	0.0048631
GgaAffx.711.1.A1_at	ST3GAL4	-3.54257	0.00227817
GgaAffx.21467.1.S1_at	---	-3.53942	0.00616339
GgaAffx.23361.2.S1_s_at	ITGB8	-3.53821	0.00014581
Gga.11856.1.S1_at	NRSN1	-3.53564	0.00872566
Gga.10138.1.S1_at	---	-3.53446	0.00158222
GgaAffx.4483.1.S1_at	LOC427844 /// LRRK2	-3.52689	0.0154875
GgaAffx.22246.1.S1_at	MPG	-3.52578	0.00067241
Gga.7323.1.S1_at	NEDD9	-3.52143	0.0165628
GgaAffx.673.1.S1_s_at	MAN1C1	-3.51658	0.0038572
GgaAffx.11639.1.S1_at	---	-3.49801	0.00010568
Gga.19862.1.S1_at	---	-3.48018	0.00069643
Gga.254.1.S1_at	KCNJ2	-3.47222	0.00105461
Gga.3674.1.S1_at	STK39	-3.46634	0.00215216
GgaAffx.22557.1.S1_s_at	HIP1	-3.4523	0.00029387
GgaAffx.23623.1.S1_at	AHNAK2	-3.45221	0.00097139
Gga.275.2.S1_a_at	MITF	-3.43409	5.7383E-08
Gga.1582.1.A1_at	---	-3.43309	0.00882776
Gga.19132.1.S1_at	---	-3.43196	0.00315552
Gga.6796.1.S1_at	ENG	-3.42645	0.00125758
Gga.1309.1.S1_at	---	-3.42581	0.00022096
Gga.5011.1.S1_at	---	-3.41892	0.00313275
Gga.1746.1.S1_s_at	LOC420108	-3.41768	0.0482201

Gga.8506.1.S2_s_at	TRIB2	-3.41296	0.00131937
GgaAffx.21092.1.S1_s_at	NUP35	-3.40055	0.0129773
Gga.14954.1.S1_at	NAALADL2	-3.39341	0.0017288
Gga.14417.1.S1_a_at	SLC41A1	-3.38367	0.0153537
Gga.4498.1.S1_s_at	ELK3	-3.3768	0.00177224
Gga.1005.1.S1_s_at	---	-3.36362	0.00813156
Gga.7038.1.S1_at	---	-3.36243	0.0001117
Gga.14818.1.S1_s_at	NEDD4	-3.34953	0.00182848
GgaAffx.23449.1.S1_at	IFIH1 /// LOC776699	-3.33614	0.0167175
Gga.16124.1.S1_at	STAG1	-3.33448	0.0006208
Gga.554.1.S1_at	HGF	-3.33309	0.0114341
Gga.7705.1.S1_at	---	-3.3204	0.0388857
Gga.8366.1.S1_at	ALDH2	-3.3193	0.00331314
Gga.8083.2.S1_a_at	ORMDL1	-3.31925	0.00067976
Gga.8860.1.S1_at	BRD1	-3.31701	0.00020508
Gga.8445.1.S1_at	DUSP6	-3.31094	0.0007841
Gga.12323.1.S1_at	KDELR3	-3.30567	0.0186885
GgaAffx.21348.1.A1_s_at	LOC417031	-3.29778	0.0106355
Gga.16261.1.S1_a_at	---	-3.2964	0.00613039
Gga.16447.1.S1_at	TMEM55A	-3.28914	0.00114854
Gga.4669.1.S1_at	CDKL2	-3.28716	0.00031752
Gga.15399.1.S1_s_at	EVL	-3.28317	0.00068273
Gga.3113.1.S1_at	NCALD	-3.27804	0.00437244

Gga.11275.1.S1_at	PAQR5	-3.27592	0.0233243
GgaAffx.12553.1.S1_at	SAMD11	-3.25321	0.00411294
Gga.8417.1.S1_s_at	DERL3	-3.25292	0.0017101
Gga.19039.1.S1_at	LOC768754	-3.25067	9.7371E-06
Gga.1740.1.S1_at	EAF1 /// LOC420679	-3.25023	0.0071643
Gga.19423.1.S1_at	LOC417031	-3.24487	0.0393902
Gga.7256.1.S1_at	SEC14L2	-3.24238	0.00059474
Gga.12349.1.S1_at	ASAM	-3.24236	0.00029315
GgaAffx.20406.1.S1_at	C4orf31	-3.24143	0.00227257
GgaAffx.23612.1.S1_at	ADSSL1	-3.23974	0.022482
Gga.17918.1.S1_at	---	-3.23857	0.0015756
Gga.5710.2.S1_a_at	HTRA3	-3.23824	0.00195416
Gga.8227.1.S1_s_at	IFI27L2	-3.22953	0.0301238
Gga.17222.1.S1_at	---	-3.22927	0.00138189
Gga.3651.1.S1_at	MAPK9	-3.22789	0.00020329
GgaAffx.1141.1.S1_at	MGAT5B	-3.22074	0.00047295
Gga.6448.1.S1_s_at	PHLDA2	-3.21532	0.00528037
Gga.15104.1.S1_at	---	-3.21292	0.00029679
GgaAffx.25879.3.S1_s_at	MAST3	-3.20708	0.00164481
GgaAffx.20260.1.S1_at	---	-3.20644	0.00585511
Gga.5787.1.S1_at	---	-3.18218	0.00741699
GgaAffx.3975.1.S1_at	CRKL	-3.18092	0.00018119
Gga.19487.1.S1_s_at	---	-3.17953	0.0009407

GgaAffx.2225.1.S1_s_at	AYTL1	-3.16879	0.00119239
GgaAffx.6136.1.S1_at	GOLGB1	-3.16832	0.00029547
Gga.2613.1.S1_s_at	SPARC	-3.16626	0.017519
Gga.12373.1.S1_at	---	-3.16602	0.00253182
Gga.4900.3.S1_s_at	LOC425783	-3.16552	8.4082E-06
GgaAffx.6592.1.S1_at	---	-3.1628	0.00877897
Gga.20074.1.S1_at	---	-3.15221	0.0045358
Gga.3040.1.S1_at	COL5A2	-3.15016	0.00267166
Gga.8407.1.S1_s_at	C20orf42	-3.14659	0.00096103
Gga.19588.1.S1_at	KCNMA1	-3.14189	0.0118054
Gga.2497.1.S1_at	---	-3.13164	0.00010551
Gga.854.1.S1_a_at	LGALS1	-3.13132	9.6276E-05
Gga.15700.1.S1_at	BHLHB2	-3.1313	0.00046924
Gga.1292.1.S1_s_at	NEDD4	-3.12818	0.00309872
Gga.8365.1.A1_at	GUSB	-3.11301	0.00687109
Gga.13023.1.S1_at	---	-3.1058	0.0470435
Gga.4345.1.S1_at	SFRP2	-3.10102	0.010294
GgaAffx.4610.1.S1_s_at	MAGI1	-3.09451	0.00414784
Gga.12514.1.S1_a_at	LOC395611	-3.09381	0.00471924
GgaAffx.395.1.S1_at	ANGPTL4	-3.08633	0.00169022
Gga.3754.2.S1_at	HES1	-3.08579	0.0448275
GgaAffx.23623.1.S1_s_at	AHNAK2	-3.08332	0.00110051
GgaAffx.21556.1.S1_s_at	CHD2	-3.083	0.0170316

GgaAffx.3690.1.S1_at	PPYR1	-3.08171	0.0042779
Gga.9394.1.S1_at	---	-3.07902	0.00028416
GgaAffx.22454.4.S1_s_at	LLGL2	-3.07793	0.00418363
Gga.4900.4.S1_at	LOC776458	-3.06841	0.0135849
Gga.2240.2.S1_a_at	FREQ	-3.06537	0.00028621
Gga.10596.1.S1_s_at	AMPD3	-3.05941	0.00088593
Gga.894.1.S1_at	LOC769132 /// ST8SIA4	-3.05931	0.00200984
GgaAffx.12451.1.S1_s_at	RIPK2	-3.04932	0.00026939
Gga.10039.1.S1_at	---	-3.04353	0.00217902
GgaAffx.20588.1.S1_at	---	-3.03354	0.0013395
Gga.746.1.S1_at	PNAT10	-3.02674	0.00125972
GgaAffx.22664.1.S1_s_at	SLC25A43	-3.02166	0.00738924
Gga.5211.1.S1_a_at	---	-3.01766	0.00073602
GgaAffx.1880.1.S1_at	MST1R	-3.01669	9.1169E-06
Gga.7434.1.S1_at	GORASP2	-3.01381	0.0419616
Gga.7527.1.S1_at	NUP35	-3.00644	0.0118286
GgaAffx.12102.1.S1_s_at	PMS1	-3.00279	0.00576965
Gga.5594.1.S1_at	TRPV2	-3.00039	1.2878E-05
Gga.17014.1.S1_at	---	-2.98903	0.0265993
GgaAffx.5073.2.S1_s_at	PIK3CG	-2.9867	0.00305124
GgaAffx.3792.2.S1_s_at	LOC415464	-2.98395	2.8259E-05
GgaAffx.23453.2.S1_s_at	FAP	-2.97801	0.00205357
Gga.2965.1.S1_at	TIMP2	-2.97696	5.3199E-05

GgaAffx.20087.1.S1_s_at	SALL4	-2.97416	0.00032525
Gga.6736.1.S1_at	---	-2.97356	0.00606556
GgaAffx.23942.3.S1_s_at	LOC425812 /// TRIOBP	-2.97327	0.00206683
GgaAffx.8005.1.S1_s_at	C9orf3	-2.9731	0.00061033
Gga.6309.1.S1_at	---	-2.97308	0.00058873
Gga.19463.1.S1_at	---	-2.97304	0.00190124
GgaAffx.20589.1.S1_at	LOC768699	-2.97194	1.9658E-05
GgaAffx.9337.1.S1_at	---	-2.96517	0.00247895
Gga.18969.1.S1_s_at	TMBIM1	-2.95452	0.0175638
Gga.4811.3.S1_s_at	HNRPK	-2.95025	6.8896E-05
GgaAffx.9336.1.S1_at	IL31RA	-2.94892	0.00223735
Gga.14289.1.S1_at	---	-2.94565	0.0182149
Gga.19578.1.S1_s_at	PLEKHA7	-2.9454	8.9734E-07
GgaAffx.7641.1.S1_at	FAM83F	-2.94457	0.00601451
Gga.3111.1.S2_at	CLDN5	-2.94278	0.0164232
Gga.18195.1.S1_at	TPRN	-2.94127	0.00109723
Gga.12155.1.S1_at	CSGALNACT1	-2.94122	0.00465708
GgaAffx.25289.2.S1_s_at	RASA1	-2.94065	0.00137987
Gga.2556.1.S1_at	---	-2.94004	0.00609754
Gga.7289.1.S1_at	---	-2.93923	0.00273458
GgaAffx.13035.1.S1_s_at	DAP	-2.93458	0.0177511
Gga.18959.1.S1_at	LOC423323	-2.92528	0.0112321
GgaAffx.23937.1.S1_s_at	MYH9	-2.91681	0.00093335

Gga.5622.1.S1_at	PIK3R1	-2.91468	0.00212505
GgaAffx.10280.1.S1_s_at	TRPS1	-2.90982	0.0197969
Gga.8168.1.S1_a_at	GALK1	-2.89906	0.00186559
Gga.6199.1.S1_s_at	SPG3A	-2.89742	0.00138618
GgaAffx.2790.1.S1_at	TRPV2	-2.89336	0.00305072
Gga.1587.1.A1_at	---	-2.88843	0.00089824
Gga.15105.1.S1_at	---	-2.88636	0.00113341
Gga.3374.1.S1_at	SPRY2	-2.88574	0.00060308
GgaAffx.12040.1.S1_at	TBL1XR1	-2.88534	0.0149612
Gga.4556.1.S1_at	ATIC	-2.88455	3.4855E-05
Gga.177.1.S1_at	GLIS2	-2.8832	0.00067276
GgaAffx.23748.1.S1_at	LOC418009	-2.88052	0.00022943
GgaAffx.2114.1.S1_at	UNC93B1	-2.87874	0.0396896
GgaAffx.25872.1.S1_at	LOC417414	-2.87784	0.00404866
GgaAffx.2182.3.S1_at	ALDH3B1 /// LOC428812	-2.87591	9.3155E-05
Gga.20056.1.S1_at	PALM2	-2.86998	0.00158409
Gga.7183.1.S1_at	NDUFA12	-2.86773	0.00236949
Gga.5969.2.S1_a_at	PAQR7	-2.86761	0.00145149
Gga.7424.1.S1_at	SYNJ2	-2.86542	1.1486E-05
Gga.16155.1.S1_at	---	-2.86483	0.0118117
Gga.9165.1.S1_s_at	DNAL4	-2.85928	0.00363575
GgaAffx.21372.1.S1_s_at	---	-2.85798	0.0024292
Gga.12422.1.S1_at	RUSC2	-2.85471	0.00580099

GgaAffx.21489.1.S1_s_at	TBL1XR1	-2.85445	0.0012677
Gga.3175.1.S1_at	PIK3R1	-2.85348	0.00839791
GgaAffx.5549.1.S1_at	ATP6AP1	-2.85101	0.0139637
Gga.15913.1.S1_at	---	-2.84335	0.00503152
GgaAffx.4209.1.S1_s_at	MCAM	-2.84322	0.00614122
Gga.7896.1.S1_at	---	-2.84187	0.0339895
GgaAffx.23830.1.S1_at	KLHDC1	-2.8398	0.0057495
GgaAffx.9424.1.S1_at	LOC421714	-2.8397	0.00461395
Gga.18089.1.S1_s_at	---	-2.83658	0.00802105
GgaAffx.7069.1.S1_s_at	CREB5	-2.82973	0.037356
Gga.12737.1.S1_at	LOC426031	-2.82745	0.00035592
GgaAffx.3975.2.S1_s_at	CRKL	-2.82437	0.00170609
Gga.1573.1.S1_at	HPD	-2.82321	0.00140502
Gga.1019.1.S1_at	---	-2.82243	5.5278E-05
Gga.3867.1.S1_at	PRNP	-2.81512	0.0104668
Gga.19099.2.S1_a_at	SPARC	-2.81351	0.0101647
Gga.3633.1.S1_at	---	-2.81064	0.00396415
Gga.6199.1.S1_at	SPG3A	-2.80708	0.00317965
Gga.19825.1.S1_at	SLC25A43	-2.80665	0.00235596
Gga.17625.1.S1_at	---	-2.8046	0.00046488
Gga.18023.1.S1_at	LOC419171	-2.80006	0.00579507
Gga.18411.1.S1_at	---	-2.79751	0.012341
GgaAffx.12006.1.S1_s_at	PLEKHA3	-2.79748	0.00167624

GgaAffx.5821.1.S1_at	TTC30A	-2.79456	0.0206047
Gga.5817.1.S1_at	---	-2.79326	0.00763709
Gga.6402.1.S1_at	C1orf190	-2.79243	0.00124154
Gga.7277.1.S1_at	---	-2.79115	0.00559686
Gga.1709.2.S1_s_at	---	-2.78817	4.7573E-06
GgaAffx.21787.1.S1_s_at	BETA3	-2.78547	0.0239009
GgaAffx.2985.1.S1_s_at	TRAFD1	-2.7845	0.033989
GgaAffx.9436.1.S1_at	RLBP1L2	-2.7785	0.0192497
Gga.7225.1.S1_at	LOC418040	-2.77306	0.00180562
Gga.5148.1.S1_at	TNFRSF1B	-2.7725	0.0411225
GgaAffx.2221.1.S1_s_at	SMURF2	-2.77155	0.0169283
Gga.3078.1.S1_at	LOC430910	-2.77051	0.00082267
GgaAffx.3409.1.S1_at	ALS2CL	-2.76381	0.0016668
Gga.18278.1.S1_s_at	PLEKHA7	-2.75821	3.7061E-05
GgaAffx.331.1.S1_at	SPIRE2	-2.75128	5.7447E-05
GgaAffx.21023.1.S1_s_at	MBNL2	-2.75113	0.00376622
Gga.8506.1.S1_s_at	TRIB2	-2.74543	0.00012665
Gga.14979.1.S1_at	---	-2.74079	0.00096416
Gga.16717.1.S1_at	---	-2.73673	0.0117338
GgaAffx.7508.1.S1_at	SGPP1	-2.73581	0.00037278
Gga.17317.1.S1_s_at	TRPV6	-2.73199	4.8427E-05
GgaAffx.20772.1.S1_at	---	-2.73043	0.0162029
Gga.8231.1.S1_at	---	-2.72734	0.0305068

GgaAffx.21619.1.S1_at	LOC771190	-2.72168	0.00071127
GgaAffx.11362.1.S1_at	TNK2	-2.72152	0.0124861
GgaAffx.21404.1.S1_at	MAGI1	-2.72072	0.00169787
Gga.13187.1.S1_s_at	LOC768699	-2.71809	0.00070194
GgaAffx.22084.1.S1_at	LYPLA3	-2.71675	0.00935993
GgaAffx.25485.1.S1_at	ORMDL1 /// SLC40A1	-2.71628	0.00984945
Gga.15828.1.S1_at	---	-2.71261	0.00491841
GgaAffx.26688.2.S1_s_at	PDE8A	-2.70805	0.00574733
Gga.9671.1.S1_at	GPX7	-2.70717	0.00581041
Gga.8316.1.S1_at	ATHL1	-2.703	0.00224053
Gga.14549.1.S1_at	PRKCA	-2.70181	0.00524464
GgaAffx.20725.1.S1_at	CKAP4	-2.7014	0.00833502
Gga.1840.1.S2_at	---	-2.69944	0.0461809
GgaAffx.22428.2.S1_s_at	FDXACB1	-2.69892	0.0169335
Gga.639.1.S1_at	S100A11	-2.69215	0.00235141
Gga.3899.1.S1_a_at	PDGFA	-2.68939	0.00946722
GgaAffx.23423.2.S1_s_at	KCNJ5	-2.68745	0.00982946
Gga.16825.1.S1_at	---	-2.68709	0.003017
Gga.18411.1.A1_at	---	-2.68673	0.0118117
GgaAffx.2811.1.S1_at	TRPV2	-2.6864	0.00039985
GgaAffx.1097.1.S1_at	SETBP1	-2.68366	0.00023862
Gga.17513.1.S1_at	PLEKHC1	-2.68325	0.00060621
GgaAffx.12834.1.S1_at	HNRPK	-2.68178	0.00458988

GgaAffx.4955.1.S1_at	LAMB1	-2.68091	0.0462964
GgaAffx.6891.1.S1_at	---	-2.67771	0.00463036
Gga.17626.1.S1_at	---	-2.67372	0.00375918
GgaAffx.3119.1.S1_at	SHC4	-2.67221	0.0460848
Gga.17141.1.S1_at	---	-2.67153	0.0088384
Gga.12497.1.S1_at	AS3MT	-2.66874	0.0027327
Gga.17239.1.S1_at	---	-2.66503	0.0413673
Gga.5985.2.S1_a_at	LOC426514	-2.66455	0.00059284
GgaAffx.1213.1.S1_s_at	PHTF1	-2.65764	0.00124586
Gga.19031.1.S1_at	---	-2.6568	0.00955922
Gga.10658.1.S1_at	---	-2.65422	0.00056654
GgaAffx.26094.1.S1_at	LARP6	-2.64918	0.00925867
Gga.4128.3.S1_a_at	TNS1	-2.64825	0.00433406
GgaAffx.23623.2.S1_at	AHNAK2	-2.64617	0.00153038
Gga.5626.1.S1_s_at	EVL	-2.63932	0.00464903
GgaAffx.25120.1.A1_at	PCDH9	-2.63843	0.0047685
GgaAffx.25280.1.S1_at	COTL1	-2.63656	0.0110593
Gga.11729.1.S1_s_at	XRCC5	-2.63652	0.00145508
GgaAffx.9034.1.S1_at	LRDD	-2.63583	0.00300152
Gga.3075.1.S1_at	ADAMTSL3	-2.63569	0.00016718
Gga.14492.1.S1_at	NT5C1B	-2.63019	0.00339077
GgaAffx.26108.1.S1_at	FAM81A	-2.62921	0.00219129
Gga.6300.1.S1_at	---	-2.62649	0.00474297

GgaAffx.23423.1.S1_at	KCNJ5	-2.62635	0.0339229
Gga.7576.1.S1_at	ACAA1	-2.62365	0.00892743
Gga.17101.1.S1_at	---	-2.6223	0.0109412
GgaAffx.1841.1.S1_at	ZBTB38	-2.61884	0.00037603
GgaAffx.9423.1.S1_at	C6orf174	-2.61819	0.00133797
Gga.17616.1.S1_at	---	-2.61686	0.00279867
Gga.11995.1.S1_s_at	---	-2.61626	0.00503888
GgaAffx.396.1.S1_at	ANKRD47	-2.6107	0.00184531
Gga.12356.2.S1_a_at	---	-2.60879	0.0242179
GgaAffx.12762.1.S1_s_at	AYTL1	-2.60818	0.00140168
GgaAffx.2087.1.S1_at	RAI14	-2.6057	0.00157838
Gga.15713.1.S1_at	---	-2.60292	0.00603095
Gga.8438.1.S1_a_at	LOC422079	-2.60187	0.00031993
Gga.5717.1.S1_at	---	-2.59944	0.00109387
Gga.6099.1.S1_at	LOC771753	-2.59269	7.6068E-05
Gga.10918.1.S1_at	C22orf13	-2.59049	0.0366025
GgaAffx.25567.1.S1_at	NEFL	-2.59039	0.0257451
Gga.16130.1.S1_at	---	-2.58962	0.00449991
Gga.12393.1.S1_at	CHST6	-2.58539	0.00997417
Gga.4962.4.S1_at	SEC61B	-2.58443	0.00146085
GgaAffx.6058.1.S1_at	AADAT	-2.58009	0.0365319
GgaAffx.5154.1.S1_s_at	CHAC2	-2.57477	0.0453459
Gga.17132.1.S1_at	---	-2.57337	0.00077458

GgaAffx.9420.2.S1_s_at	C17orf68	-2.56906	0.00263112
GgaAffx.5291.1.S1_at	CREB3L1	-2.56361	0.0166698
Gga.13428.1.S1_at	---	-2.56291	0.00793946
Gga.3572.1.S2_s_at	CD44	-2.5605	0.00180694
Gga.3677.1.S1_at	CAPN2	-2.55932	0.00022391
GgaAffx.5355.1.S1_at	KLF7	-2.55747	0.0115331
GgaAffx.6709.1.S1_at	SPATA7	-2.556	0.00033115
Gga.10673.1.S1_at	LRRC20	-2.54824	0.00840801
GgaAffx.23420.2.S1_s_at	DICER1	-2.54677	0.00011333
GgaAffx.5266.1.S1_s_at	KIAA0652	-2.54434	0.0176287
GgaAffx.454.1.S1_s_at	SLC41A1	-2.54377	0.0238988
Gga.19452.1.S1_at	CD44	-2.53806	0.00486786
Gga.11872.1.S1_s_at	VPS54	-2.53777	0.0424412
Gga.13144.1.S1_at	C14orf32	-2.53612	0.00751322
GgaAffx.5401.1.S1_at	DUSP5	-2.53494	0.0127361
GgaAffx.26494.1.S1_at	FRRS1	-2.53216	0.0083939
Gga.11708.1.S1_at	CARKL	-2.5288	0.00840406
Gga.18960.1.S1_at	---	-2.52763	0.0083809
GgaAffx.25114.3.S1_s_at	MBNL2	-2.52553	0.00310608
Gga.11749.1.S1_a_at	CDC42EP3	-2.5219	0.00751597
GgaAffx.22926.1.S1_at	EVI1	-2.52088	0.00035814
Gga.17820.1.S1_at	---	-2.51863	0.00034536
Gga.4128.1.S2_at	TNS1	-2.51831	0.00524413

Gga.9267.1.S1_at	PLA2G6	-2.51495	6.6738E-05
Gga.14924.1.S1_s_at	---	-2.5118	0.0353562
GgaAffx.8793.1.S1_s_at	TBL1XR1	-2.51145	0.00254025
Gga.15788.1.S1_at	---	-2.50568	0.00012425
Gga.19606.1.S1_at	---	-2.5022	0.00896506
Gga.11749.2.A1_at	CDC42EP3	-2.50204	0.0319436
Gga.15979.1.S1_s_at	AKAP13	-2.502	0.00313376
Gga.7860.1.S1_at	XPO6	-2.49815	0.00016881
GgaAffx.4209.2.S1_at	MCAM	-2.49797	0.00325956
GgaAffx.22420.1.S1_s_at	HECW2	-2.49164	0.00187026
GgaAffx.6378.1.S1_at	SGK196	-2.49084	0.0199209
GgaAffx.7882.1.S1_at	LOC771207	-2.49035	0.0385458
Gga.19419.1.S1_at	---	-2.48833	0.00531699
Gga.17322.1.S1_at	---	-2.48816	0.0394302
Gga.9618.1.S1_at	UCHL1	-2.48615	0.0160214
Gga.10737.1.S1_s_at	NCKAP1	-2.48319	4.303E-05
Gga.3250.1.S1_at	VSNL1	-2.48086	8.0984E-06
GgaAffx.23988.1.S1_at	NEDD9	-2.47804	0.00508336
GgaAffx.22720.1.S1_at	---	-2.47796	0.00020967
GgaAffx.6131.1.S1_at	---	-2.47113	0.0102813
Gga.18080.1.S1_at	---	-2.46799	0.00083947
Gga.7899.1.S1_at	GPHN	-2.46556	0.0126108
Gga.1842.1.S1_at	C12orf31	-2.46451	0.00949012

Gga.3639.1.S1_at	---	-2.46416	7.459E-05
Gga.1906.1.S1_at	CRISPLD1	-2.46385	0.00000154
Gga.13995.1.S1_s_at	HDAC10 /// LOC769732	-2.46221	0.00961501
Gga.7764.1.S1_at	---	-2.45861	0.015911
Gga.4416.1.S1_at	SERPINI1	-2.45838	0.00333323
GgaAffx.6748.1.S1_at	C14orf102	-2.45819	0.0296098
Gga.10555.1.S1_at	---	-2.45571	0.00022654
Gga.15893.1.S1_at	---	-2.45481	0.00403732
Gga.11844.1.S1_s_at	KLF10	-2.45365	0.0109598
Gga.6066.1.S1_at	TCF7	-2.4533	0.0253051
GgaAffx.23440.4.S1_s_at	HOXA11	-2.45244	8.4284E-05
GgaAffx.22454.1.S1_s_at	LLGL2	-2.44785	0.00037278
Gga.819.1.S1_at	TUBB1	-2.44663	0.0257636
Gga.1687.1.S1_at	ALS2CR4	-2.4444	0.00227884
Gga.19816.1.S1_at	---	-2.44333	0.00148082
Gga.4516.2.S1_at	Sep-11	-2.44267	9.2659E-05
Gga.19575.1.A1_at	HNRPK	-2.43852	0.00029557
GgaAffx.20697.1.S1_at	---	-2.43231	0.00385043
GgaAffx.7359.1.S1_at	TMEM177	-2.43198	0.00025684
GgaAffx.5095.1.S1_at	SATB2	-2.43079	8.6684E-06
GgaAffx.1285.1.S1_s_at	RHBDF2	-2.43059	0.00077667
GgaAffx.12032.1.S1_s_at	ORAI1	-2.42652	0.00105166
GgaAffx.1650.1.S1_s_at	WDR75	-2.42587	0.0185228

Gga.14469.1.S1_at	---	-2.4207	8.8271E-05
GgaAffx.2958.1.S1_at	SCG3	-2.41867	0.0031387
GgaAffx.21452.2.S1_s_at	MESDC1	-2.4177	0.0144293
GgaAffx.23575.1.S1_at	XRCC5	-2.41705	0.00012861
GgaAffx.26599.1.S1_s_at	LOC416916	-2.41122	0.00692414
Gga.19385.1.S1_at	---	-2.41034	0.00017315
Gga.3713.1.S1_at	MBNL2	-2.40977	0.00593879
GgaAffx.25485.2.S1_s_at	ORMDL1 /// SLC40A1	-2.40728	0.00991268
Gga.7990.1.S1_at	IQCB1	-2.40551	0.00270296
Gga.558.1.S1_at	---	-2.40537	0.00154707
GgaAffx.25281.1.S1_at	TTC9	-2.40278	0.0357866
Gga.17004.1.S1_at	ST3GAL5	-2.40101	0.00115429
Gga.1827.1.S1_s_at	---	-2.40052	0.0127822
GgaAffx.5451.1.S1_at	HDAC10	-2.39947	0.00673385
Gga.17249.1.S1_at	ZNF827	-2.39778	0.0177385
Gga.15257.1.S1_at	---	-2.39729	0.00102148
Gga.8870.1.S1_at	---	-2.39643	0.0132093
Gga.3852.1.S1_at	RHOB	-2.38743	0.0419466
GgaAffx.21112.1.S1_at	C14orf32	-2.38711	0.00228279
GgaAffx.4434.1.S1_s_at	CYTH1	-2.38381	0.00304962
GgaAffx.7901.1.S1_at	C14orf106	-2.38321	0.00249933
Gga.10425.1.S1_s_at	VSNL1	-2.38225	0.00112301
GgaAffx.3119.2.S1_s_at	SHC4	-2.38222	0.0286692

Gga.13373.1.S1_at	CSGALNACT1	-2.38132	9.619E-05
GgaAffx.2691.1.S1_at	SETD1B	-2.38114	0.00971312
GgaAffx.22069.1.S1_s_at	AKAP13	-2.38032	1.5963E-05
GgaAffx.23234.2.S1_s_at	LTBP1	-2.37984	0.00468448
Gga.15853.1.S1_at	---	-2.37953	0.00218332
Gga.7045.1.S1_a_at	---	-2.37877	0.0021074
Gga.427.1.S1_at	PCBD1	-2.37793	0.0275148
Gga.5544.1.S1_at	LOC395100	-2.37514	0.0004112
Gga.8348.1.S1_s_at	---	-2.37327	0.00800085
GgaAffx.25117.1.S1_s_at	DZIP1	-2.3729	0.0339355
GgaAffx.21593.1.S1_s_at	---	-2.37267	0.00339423
Gga.13040.1.S1_at	---	-2.37162	0.00062759
GgaAffx.6265.1.S1_at	HEATR5A	-2.37148	0.0002701
GgaAffx.12999.1.S1_s_at	TEC	-2.36855	0.0428854
Gga.3180.1.S1_at	LFNG	-2.36847	0.0266424
GgaAffx.8456.1.S1_at	CEP152	-2.36821	0.00139225
GgaAffx.8396.1.S1_s_at	PITPNM1	-2.3663	0.0391446
Gga.11671.1.S1_a_at	LOC415664 /// LOC427532	-2.366	0.00393275
GgaAffx.12190.2.A1_at	COG1	-2.36583	0.00037402
GgaAffx.10167.1.A1_at	---	-2.36387	0.00042326
Gga.19064.1.S1_at	---	-2.36313	0.00031842
Gga.16655.1.S1_at	HMHA1	-2.36288	0.0339727
Gga.14691.1.S1_at	TUFT1	-2.36184	0.00167506

Gga.8021.5.A1_at	IMMP1L	-2.36117	0.00675946
Gga.6873.1.S1_at	---	-2.36085	0.0005006
GgaAffx.1421.4.S1_s_at	DGKQ	-2.35667	0.00635399
Gga.13214.1.S1_at	PJA2	-2.35624	0.0111809
Gga.6175.1.S1_s_at	C12orf31	-2.3562	0.011079
GgaAffx.7204.1.S1_at	GLB1L	-2.35353	3.3328E-09
GgaAffx.23964.2.S1_s_at	POLR3B	-2.35235	0.00037666
Gga.1139.1.A1_at	MESDC1	-2.3506	0.0263853
GgaAffx.11575.1.S1_s_at	HEBP1	-2.3479	0.0201826
Gga.2535.2.S1_a_at	LTBP1	-2.34709	0.00326617
Gga.15323.1.S1_at	---	-2.34685	0.00031821
Gga.7652.1.S1_at	---	-2.34601	0.0217184
GgaAffx.5951.1.S1_s_at	EVI1	-2.34277	0.006843
GgaAffx.22654.1.S1_at	HDAC10	-2.34035	0.00300291
Gga.3572.1.S2_at	CD44	-2.33899	0.00459315
Gga.19802.1.S1_at	---	-2.33842	0.00401284
Gga.6315.1.S1_s_at	KCTD2	-2.33756	0.00706122
GgaAffx.12187.1.S1_s_at	LYSMD3	-2.33736	0.0221224
GgaAffx.26607.5.S1_s_at	ZNF143	-2.337	0.0012671
Gga.4900.2.S1_at	LOC776463	-2.33686	0.0123563
Gga.17855.1.S1_at	---	-2.33682	0.0158018
Gga.693.1.S1_at	CSRP1	-2.33493	0.0102854
Gga.3599.3.S1_a_at	SEC23A	-2.33315	0.00044713

GgaAffx.20232.1.S1_at	BCL7A	-2.33117	0.00189664
Gga.13147.1.S1_at	KLC1	-2.32987	0.00094928
Gga.17691.1.S1_at	---	-2.32868	3.4808E-05
Gga.19575.1.S1_at	HNRPK	-2.32802	5.7706E-06
Gga.18711.1.S1_s_at	ASPSCR1	-2.32571	0.00618478
Gga.7979.1.S1_at	VAT1	-2.32158	0.038085
Gga.2734.1.S1_at	ALCAM	-2.32143	0.00604006
GgaAffx.5578.1.S1_s_at	RGS3	-2.31796	0.0201557
GgaAffx.20683.1.S1_at	SSFA2	-2.31754	0.00043643
Gga.8999.1.S1_at	AKAP13	-2.3172	8.7392E-05
Gga.19127.1.S1_at	TCTE3	-2.31594	8.9385E-05
Gga.11488.1.S1_s_at	SERHL2	-2.31457	0.020211
Gga.6797.1.S1_at	---	-2.314	0.00198139
Gga.14009.1.S1_at	---	-2.31357	0.00430939
Gga.9791.1.S1_at	LOC427134	-2.31283	0.00883415
Gga.14878.1.S1_at	---	-2.31185	0.00801447
Gga.17117.1.S1_at	TXNRD2	-2.31027	0.00052682
GgaAffx.12958.1.S1_at	EVL	-2.3053	0.00069613
Gga.4211.1.S1_at	CRTAP	-2.30382	0.00333432
GgaAffx.6898.2.S1_s_at	SP4	-2.3014	0.00015772
Gga.10888.2.S1_a_at	LOC425610	-2.30134	0.0111289
GgaAffx.12977.1.S1_s_at	SDF2L1	-2.29996	0.00080189
Gga.1748.1.S1_at	PNPLA2	-2.29734	0.00571788

Gga.16457.1.S1_s_at	LOC776699	-2.29591	0.0139552
Gga.12173.1.S1_s_at	ZDHHC8	-2.29236	0.00045226
GgaAffx.20762.1.S1_at	LOC396152	-2.2916	0.00405248
Gga.19554.1.S1_at	---	-2.28914	0.017249
GgaAffx.24837.1.S1_at	KLF10	-2.28726	0.00207323
GgaAffx.3811.1.S1_at	PLXNA1	-2.28723	0.0310506
Gga.8010.1.S1_at	---	-2.28706	0.00457638
Gga.1149.1.S1_at	---	-2.2852	0.021256
Gga.3214.1.S1_at	XRCC5	-2.28465	6.5522E-05
Gga.16133.1.S1_at	---	-2.28439	0.0133996
Gga.4516.2.S1_s_at	Sep-11	-2.28376	0.00116191
Gga.18953.1.S1_at	MLL5	-2.2834	0.00033011
Gga.11548.1.S1_at	---	-2.28179	0.00288061
GgaAffx.6269.1.S1_at	C14orf126	-2.27981	0.00249426
GgaAffx.22522.1.S1_at	BHLHB2	-2.27844	0.0131902
Gga.16204.1.S1_at	---	-2.2738	0.00654453
Gga.1814.1.S1_at	PUNC	-2.2728	2.2428E-05
GgaAffx.3778.1.S1_at	PLXNA1	-2.26881	0.00134499
GgaAffx.25782.2.S1_at	LOC427010	-2.26844	0.00019037
Gga.17931.1.S1_at	---	-2.26687	0.0162951
GgaAffx.4644.2.S1_s_at	SSH1	-2.2665	0.0360387
Gga.10923.1.S1_s_at	NAV3	-2.26242	0.00152856
Gga.15502.1.A1_at	CBX8	-2.26122	0.00180315

GgaAffx.9942.1.S1_at	ACOX3	-2.26074	0.00043189
Gga.8807.1.S1_at	---	-2.25901	0.00188612
Gga.16264.1.S1_at	MFSD6	-2.25852	0.00237953
Gga.2292.2.S1_at	CDC37	-2.25787	0.00761637
Gga.11757.1.S1_at	UBTD1	-2.25786	0.0357988
GgaAffx.21089.1.S1_s_at	LMO7	-2.25775	0.0281267
Gga.6836.1.S1_at	---	-2.25582	0.00805691
Gga.13103.1.S1_s_at	---	-2.25527	0.00378192
Gga.13413.1.S1_at	APBB3	-2.25312	0.00924944
GgaAffx.22781.1.S1_at	SESTD1	-2.25275	7.4863E-05
Gga.3852.1.S2_s_at	RHOB	-2.25018	0.00417228
Gga.707.1.S1_at	NFIX	-2.2494	0.00085109
Gga.11040.2.S1_a_at	CCDC45	-2.24845	0.00248412
Gga.7845.1.S1_at	---	-2.24814	0.00016665
Gga.9816.1.S1_s_at	CLIC2	-2.24462	0.0178074
Gga.3291.1.S1_at	POLK	-2.23709	0.00236177
GgaAffx.6057.1.S1_at	CASD1	-2.23669	0.00406227
Gga.11068.1.S1_s_at	POLR3B	-2.23626	0.00144556
GgaAffx.12825.1.S1_s_at	LPIN2	-2.23497	0.00980791
Gga.6203.2.S1_a_at	BTBD11	-2.2337	0.00278948
Gga.13215.1.S1_at	NUDT4	-2.22989	0.0384882
Gga.7588.1.S1_at	GGTL3	-2.22988	0.0228444
Gga.14428.1.S1_at	---	-2.22838	6.4001E-05

Gga.12573.1.S1_at	---	-2.22769	7.5067E-05
GgaAffx.11371.1.S1_s_at	MDM1	-2.22754	0.0157823
Gga.4360.1.S1_at	TAOK3	-2.2265	0.00014055
Gga.9699.4.S1_x_at	JMJD7-PLA2G4B	-2.22566	0.00788074
GgaAffx.22549.1.S1_at	AMBRA1	-2.22546	0.00919542
Gga.12631.2.S1_a_at	MLL5	-2.22496	0.00289092
GgaAffx.3488.1.S1_s_at	NLGN3	-2.22336	0.00955441
Gga.19330.1.S1_at	LOC417231	-2.22171	0.00143778
Gga.8512.1.S1_at	GPR155	-2.21635	0.00425449
GgaAffx.20536.1.S1_at	---	-2.21582	2.5475E-05
Gga.3260.2.S1_a_at	KCNMA1	-2.21432	0.0192579
Gga.2840.1.S1_at	B4GALT1	-2.2139	0.0253986
Gga.2770.2.S1_s_at	LOC421044	-2.21342	0.0178972
Gga.10088.1.S1_at	---	-2.21063	0.00322503
Gga.3274.2.S1_a_at	LLGL2	-2.20663	0.00152154
GgaAffx.20757.1.S1_s_at	TNS1	-2.2059	0.00633466
Gga.16544.1.S1_s_at	CLIC2	-2.20482	0.0456755
Gga.2384.1.S1_at	ZFYVE1	-2.20424	0.00345171
Gga.9389.1.S1_at	SELO	-2.20313	0.0244882
GgaAffx.23573.1.S1_at	Sep-11	-2.20305	0.00056413
Gga.2251.1.S1_at	IQGAP1	-2.2022	0.00300836
Gga.3682.1.S1_at	RIMBP2	-2.20195	0.00265437
Gga.13723.1.S1_at	---	-2.19941	0.0232906

GgaAffx.7782.1.S1_at	SHPRH	-2.19851	0.00955351
GgaAffx.24966.2.S1_s_at	---	-2.19796	0.0202502
Gga.14939.1.S1_at	---	-2.19545	0.0155161
GgaAffx.25609.2.S1_s_at	NCKAP1	-2.19479	0.00035558
Gga.12453.1.S1_a_at	DUS4L	-2.19384	0.00148311
GgaAffx.2611.2.S1_s_at	FBXL10	-2.19326	0.00752686
Gga.3264.1.S2_at	AHR	-2.19325	0.00947687
Gga.17549.1.S1_at	PNPLA3	-2.19091	0.00140821
Gga.12606.1.S1_s_at	RAI14	-2.19018	0.0149425
GgaAffx.22761.1.S1_at	TMEM220	-2.18966	0.00184024
GgaAffx.7477.1.S1_at	APOLD1	-2.18817	0.023106
Gga.10877.1.S1_at	TBC1D8	-2.18816	0.00987014
Gga.7913.2.S1_s_at	SHROOM3	-2.18814	0.00756425
Gga.10683.1.S1_at	FAS	-2.18804	0.0399384
Gga.10347.1.S1_at	SLC25A10	-2.18455	0.0156941
Gga.17590.1.S1_s_at	CLIC2	-2.184	0.0379326
GgaAffx.6401.1.S1_at	LOC431643	-2.1834	0.0054617
Gga.9028.1.S1_s_at	STX2	-2.18183	9.1148E-05
Gga.8935.2.S1_s_at	RAPGEF1	-2.18172	0.00529756
GgaAffx.855.2.S1_s_at	STAG1	-2.18125	0.00215309
Gga.8083.1.S1_at	ORMDL1	-2.18122	0.0326825
Gga.7538.1.S1_at	TMBIM4	-2.17658	0.00502983
Gga.17978.1.S1_at	---	-2.17517	0.00252485

Gga.4108.4.S1_a_at	TPM1	-2.17297	0.00038602
Gga.12462.1.S1_at	CD274	-2.17064	0.00292394
Gga.1845.1.S1_at	SPINW	-2.17045	0.00053583
GgaAffx.12190.2.A1_s_at	COG1	-2.1689	0.0042757
GgaAffx.12811.1.S1_at	ARID4A	-2.16831	0.00611802
Gga.18602.1.S1_s_at	LCORL	-2.1676	0.0004634
Gga.7553.1.S1_at	---	-2.16692	0.0195706
Gga.8938.1.S1_at	---	-2.16591	0.0127407
Gga.7420.1.S1_at	CDC34	-2.16404	0.0376064
Gga.1139.1.S1_at	MESDC1	-2.16241	0.00048234
GgaAffx.4209.3.S1_s_at	MCAM	-2.16196	0.0136299
Gga.447.1.S1_at	ETV5	-2.16172	0.00393793
Gga.13488.1.S1_at	---	-2.16146	0.00110583
Gga.9713.2.S1_a_at	HINTW	-2.16048	0.00470807
Gga.15327.1.S1_at	SPG3A	-2.16017	0.00860876
GgaAffx.11401.1.S1_at	STX2	-2.1596	0.00274901
Gga.8115.1.S1_at	---	-2.15886	0.0119996
Gga.4056.1.S1_at	PXN	-2.15828	0.0174199
Gga.14418.1.S1_s_at	SETD5	-2.15655	0.0300579
Gga.657.1.S1_at	FOXG1	-2.1553	0.0266257
Gga.16745.2.S1_at	---	-2.15521	0.00201572
GgaAffx.21183.1.S1_s_at	---	-2.15317	0.0144993
Gga.14947.1.S1_at	---	-2.1508	2.9454E-05

Gga.7098.1.S1_at	PPP1R13B	-2.14902	0.00915808
GgaAffx.10522.1.S1_at	LOC421935	-2.14446	0.00082075
Gga.18981.1.S1_at	---	-2.14444	0.0185228
Gga.10370.1.S1_at	CDC14B	-2.14175	0.00199767
Gga.12071.1.S1_at	---	-2.1375	0.0414477
Gga.19962.1.S1_at	---	-2.13742	0.0181361
GgaAffx.23028.1.S1_s_at	SPRED1	-2.13704	0.00530985
Gga.1443.2.S1_s_at	MAP2K1	-2.13658	8.0421E-05
Gga.16696.1.S1_at	PPP2R5E	-2.13615	0.00232772
Gga.4296.3.S1_a_at	CLK3	-2.13268	0.00214516
GgaAffx.21949.1.S1_at	PHLDA2	-2.13216	0.0110274
Gga.3303.1.S1_s_at	LOC425172 /// TRMU	-2.13215	0.0159075
Gga.9944.1.S1_at	BOC	-2.13105	1.8591E-06
Gga.14146.1.S1_at	LOC426031	-2.12923	2.9691E-05
Gga.12596.1.S1_at	STK11	-2.1277	0.022728
Gga.11630.2.S1_at	LOC426615	-2.12737	7.7845E-05
GgaAffx.24771.1.S1_at	RRAGD	-2.12392	0.00246345
Gga.13291.1.S1_at	OIT3	-2.12349	0.0286066
Gga.14820.1.S1_at	---	-2.12319	0.0193869
GgaAffx.26182.1.S1_s_at	NEDD4	-2.12304	0.00267093
Gga.13543.1.S1_at	LOC423323	-2.12252	0.00076648
Gga.6168.2.S1_a_at	---	-2.12215	0.00373312
Gga.5950.1.S1_s_at	---	-2.12188	0.00712904

GgaAffx.26677.1.S1_at	LOC423775	-2.1209	0.0308475
Gga.3269.1.S1_at	---	-2.11978	0.0249532
GgaAffx.7635.1.S1_s_at	ARID4A	-2.11945	0.00164246
Gga.13322.1.S1_at	LOC423097	-2.11847	0.018253
GgaAffx.12517.1.S1_at	NET1	-2.11336	0.00105777
GgaAffx.23900.2.S1_s_at	PLEKHC1	-2.1128	0.00503415
Gga.9734.1.S1_at	---	-2.1128	0.0480909
Gga.15723.1.S1_at	LUC7L	-2.1116	0.0348545
Gga.17875.1.S1_at	---	-2.10667	0.00089154
GgaAffx.26186.1.S1_s_at	---	-2.10582	0.0175406
Gga.12494.1.S1_at	SETBP1	-2.10353	0.0128678
GgaAffx.20869.1.S1_s_at	TMEM196	-2.10307	0.0110621
GgaAffx.4555.1.S1_s_at	PCYT2	-2.1019	0.00042185
GgaAffx.25114.2.S1_s_at	MBNL2	-2.10154	0.0384365
GgaAffx.20304.1.S1_s_at	---	-2.10023	0.00018266
GgaAffx.25289.1.S1_at	RASA1	-2.09978	2.2714E-05
Gga.235.1.S1_at	NPAS2	-2.09956	0.0256122
Gga.7006.2.S1_a_at	---	-2.09944	0.025466
GgaAffx.25609.1.S1_at	NCKAP1	-2.09903	4.7457E-05
GgaAffx.7286.1.S1_s_at	PECR	-2.09775	0.00279643
GgaAffx.2053.1.S1_at	---	-2.0977	0.0127483
GgaAffx.1550.1.A1_at	---	-2.09703	0.0118478
Gga.9774.1.S1_at	RBM9	-2.09395	0.00308753

Gga.17470.1.S1_at	---	-2.09073	0.0240017
GgaAffx.13167.1.S1_at	CCDC98	-2.09022	0.00247673
Gga.902.1.A1_x_at	---	-2.08944	2.8066E-05
Gga.16148.1.S1_at	---	-2.0878	0.00025177
Gga.18785.1.S1_at	---	-2.0878	0.00449826
Gga.17411.1.S1_at	---	-2.08764	0.00128061
GgaAffx.25575.1.S1_at	SBNO2	-2.08614	0.00491751
Gga.9699.4.S1_a_at	JMJD7-PLA2G4B	-2.08381	0.00094156
Gga.4296.2.S1_a_at	CLK3	-2.0835	0.04521
GgaAffx.331.2.S1_s_at	SPIRE2	-2.08124	0.00217759
Gga.14265.1.S1_at	RASA1	-2.08055	0.00594468
Gga.10303.1.S1_at	CAV2	-2.07899	0.00340387
GgaAffx.855.1.S1_at	STAG1	-2.07778	0.00639138
Gga.15091.1.S1_at	---	-2.07644	0.0325665
Gga.11814.1.S1_at	RSU1	-2.07484	0.00554409
GgaAffx.24283.1.S1_at	UBAP2	-2.07411	0.00028127
Gga.7243.1.S1_at	AFMID	-2.07319	0.0242631
GgaAffx.23018.1.S1_at	---	-2.07119	0.028868
Gga.8155.1.S1_at	AR	-2.07002	0.0332445
GgaAffx.4644.1.S1_at	SSH1	-2.06978	0.00900785
Gga.3729.1.S1_at	CAMKK2	-2.06805	0.00546997
GgaAffx.7832.1.S1_at	FRMD6	-2.06681	0.00078596
Gga.9075.1.S1_at	TCN2	-2.06436	0.0235805

Gga.7144.1.S1_at	C19orf28	-2.06398	0.00457703
GgaAffx.22069.2.S1_s_at	AKAP13	-2.06398	0.00534983
Gga.17024.1.S1_at	CCDC131	-2.06308	0.0354661
Gga.5878.1.S1_at	MICALL2	-2.05949	0.00251873
Gga.15792.1.S1_at	---	-2.05948	0.00033145
Gga.17242.1.S1_at	---	-2.05846	0.00851185
Gga.10923.2.S1_s_at	NAV3	-2.0578	5.6698E-05
Gga.16585.1.S1_at	C15orf41	-2.05765	0.0313415
GgaAffx.21497.1.S1_at	---	-2.05483	0.0451612
GgaAffx.1601.2.S1_s_at	ASNSD1	-2.05411	0.00077811
Gga.2856.1.S1_a_at	APITD1	-2.05377	0.00538375
Gga.13404.1.S1_s_at	SP3	-2.05376	0.00101618
Gga.3848.1.S1_s_at	DTYMK	-2.05242	0.0010371
Gga.11703.1.S1_s_at	AARSD1	-2.05148	0.0353008
Gga.14425.1.S1_at	TMEM16E	-2.04587	0.00169012
Gga.19145.1.S1_at	---	-2.04186	0.0318547
GgaAffx.6136.4.A1_at	GOLGB1	-2.04164	6.6227E-05
Gga.2552.1.S1_at	ZNF280D	-2.0416	0.00526371
Gga.4108.4.S1_s_at	TPM1	-2.03941	0.00030283
Gga.7309.1.S1_at	LOC431003	-2.03886	0.00053608
GgaAffx.4549.1.S1_at	ZNF438	-2.03868	0.0108687
Gga.4900.5.S1_at	---	-2.0386	0.00817053
GgaAffx.20689.1.S1_at	SPI1	-2.03858	0.0116206

GgaAffx.22641.1.S1_s_at	IQGAP1	-2.03842	0.0006043
GgaAffx.6607.2.S1_s_at	LTBP1	-2.03758	0.0209436
Gga.9536.1.S1_s_at	CCDC131	-2.0362	0.0499135
GgaAffx.7184.2.S1_s_at	LRRC40	-2.03529	0.00168769
Gga.14122.1.S1_s_at	AHNAK2	-2.03345	0.0392259
Gga.7566.1.S1_at	LOC424918	-2.03266	0.0170603
Gga.8120.1.S1_at	---	-2.03256	0.00345425
GgaAffx.23039.3.S1_s_at	MON2	-2.03211	0.00598907
Gga.8839.1.S1_at	TUBD1	-2.03192	0.0317434
GgaAffx.5477.1.S1_at	TRABD	-2.03059	0.027119
Gga.7855.1.S1_at	BMPER	-2.03037	0.010469
GgaAffx.21780.2.S1_s_at	GCG	-2.02962	0.0119161
Gga.7440.1.S1_at	DZIP1	-2.02785	0.0003761
GgaAffx.25590.1.S1_s_at	LINGO1	-2.02593	0.0438063
Gga.1443.1.S1_s_at	MAP2K1	-2.02578	0.00020031
Gga.18697.1.S1_s_at	FBXL10	-2.02267	0.0330483
GgaAffx.20313.1.S1_at	---	-2.02241	0.0444516
Gga.5275.1.S1_at	CABIN1	-2.02164	9.5651E-05
Gga.13258.1.S1_at	---	-2.01929	0.0169191
GgaAffx.22689.1.S1_s_at	LRSAM1	-2.0191	0.0020744
Gga.7108.2.S1_a_at	TMEM14A	-2.01714	0.0125654
Gga.15385.1.S1_at	---	-2.01638	0.0429036
Gga.17257.1.S1_at	LOC424111	-2.01538	0.0133746

Gga.11349.1.S1_s_at	GOLGA5	-2.01205	0.0316175
Gga.3174.1.S1_at	---	-2.01128	0.0170325
GgaAffx.12786.1.S1_s_at	MTMR2	-2.00919	0.00468467
Gga.7268.2.S1_s_at	LOC431056	-2.0063	0.03375
Gga.11203.1.S1_s_at	LRRFIP1	-2.00605	0.0310616
Gga.17490.1.S1_at	---	-2.00602	0.0266324
Gga.7425.1.S1_at	ANXA8	-2.00575	0.0101716
Gga.3834.1.S2_at	PLEKHA2	-2.00172	0.00028865
GgaAffx.11787.1.S1_s_at	LOC431059	-2.00151	0.0101015
GgaAffx.7634.2.S1_s_at	SGSM3	-2.00071	0.00919078

Geny rozdílně exprimované v PR9692-shHOPX vs. PR9692-shMOCK

zvýšená exprese

ID sondy	Symbol genu	míra velikosti účinku (PR9692-shHOPX vs. PR9692-shMOCK)	Hodnota P (PR9692-shHOPX vs. PR9692-shMOCK)
Gga.3099.1.S1_at	---	113.245	0.00587519
Gga.6399.1.S1_at	MALL	90.475	1.4499E-07
Gga.2827.2.S1_a_at	TIMP3	89.7191	0.0110702
Gga.2184.1.S1_at	C5orf13	65.7949	0.00160973
Gga.16710.2.S1_a_at	FAM132A	64.4831	4.5421E-09

Gga.8510.1.S1_at	---	58.2103	4.1316E-07
Gga.14455.1.S2_at	GEM	56.1255	0.0317669
Gga.9133.1.S1_at	LOC417536	52.026	7.0749E-05
Gga.5505.1.S1_a_at	---	44.8174	7.2981E-06
GgaAffx.20516.1.S1_s_at	---	36.4567	0.00408809
Gga.5396.1.S1_at	C1QB	33.2005	5.1456E-11
Gga.5154.1.S1_at	POSTN	31.3151	0.00019382
Gga.1169.1.S1_at	AADACL2	24.5812	0.00174784
Gga.6561.1.S1_at	KRT5	24.0972	0.00010307
Gga.9481.1.S1_s_at	LOC395772	21.6808	0.00376223
Gga.7813.1.S1_at	CFI	19.3687	0.00308088
GgaAffx.6456.4.S1_s_at	KRT75	19.1884	0.00080672
Gga.15899.1.S1_at	TSHZ3	18.8227	5.5763E-06
GgaAffx.12757.1.S1_s_at	RGL1	17.5085	2.976E-06
Gga.12110.2.S1_a_at	OLFM3	16.8046	0.00085307
Gga.17686.1.S1_at	KRT75	16.4193	0.0007704
Gga.1287.1.S1_at	RASGRP3	13.712	0.00218964
Gga.6201.1.S1_at	ISG12-2	13.3558	0.00056445
Gga.1746.1.S1_s_at	LOC420108	13.1337	0.00548731
Gga.8023.1.S1_at	---	12.1745	0.00210776
GgaAffx.6456.5.S1_s_at	LOC431299 /// LOC768880 /// LOC768881	11.7867	0.0261219
Gga.16709.1.S1_at	---	11.6283	7.7649E-07

Gga.3672.1.S1_at	ST3GAL1	11.0453	9.327E-07
GgaAffx.6456.8.S1_at	LOC431299	10.6057	0.0114749
GgaAffx.12948.1.S1_s_at	RASGRP3	9.95274	0.00576234
Gga.8200.1.S1_at	SLC16A10	9.46791	0.0193578
Gga.16141.1.S1_at	---	9.33189	6.6744E-06
Gga.1941.1.S1_at	FZD4	9.24938	0.0122877
GgaAffx.10841.1.S1_s_at	LMO7	9.23874	0.00274002
Gga.4220.1.S2_at	SMYD1	8.99634	0.0002438
Gga.552.1.S1_at	DIO3	8.83598	5.3012E-05
GgaAffx.13057.1.S1_s_at	CR2	8.3258	1.3552E-05
Gga.8359.1.S1_at	GSTA3	8.22821	0.0390109
Gga.59.1.S1_at	LOC395260	8.09229	6.3551E-09
Gga.9103.1.S1_at	LYG2	7.4826	0.00774779
Gga.15354.1.S1_at	UGCG	7.37543	0.00527939
Gga.17342.1.S1_at	---	7.22046	0.0213087
Gga.11368.1.S1_at	F2RL2	6.83429	0.00177441
GgaAffx.25059.1.S1_at	LYG2	6.83062	0.0104095
GgaAffx.24513.3.S1_s_at	EPB41L3	6.81443	9.2631E-07
Gga.1442.1.S1_at	---	6.79471	0.00373383
Gga.8200.2.S1_a_at	SLC16A10	6.78255	0.0197301
Gga.3263.1.S1_at	---	6.72619	0.00036632
Gga.9002.1.S1_at	---	6.66012	0.00256558
Gga.8244.1.S1_at	CMPK2	6.5961	0.00045386
Gga.8200.1.S1_s_at	SLC16A10	6.40048	0.0156792

GgaAffx.21685.1.S1_at	---	6.01121	0.00094703
Gga.7323.1.S1_at	NEDD9	5.85292	0.00925315
Gga.3393.1.S1_at	GLDC	5.81234	0.00118686
GgaAffx.644.2.S1_s_at	MAP2K4	5.75787	0.00648824
Gga.536.1.S1_a_at	OASL	5.69456	0.0139873
Gga.2328.1.S1_at	ZNF521	5.35636	0.00268402
GgaAffx.5039.1.S1_at	CORO2B	5.30198	0.00041815
GgaAffx.8053.1.S1_at	JARID2	5.13246	0.0301229
Gga.9372.1.S1_at	---	5.13004	0.0085217
GgaAffx.8324.1.S1_s_at	GRB10	5.04839	0.00021722
Gga.1171.1.S1_at	LY6E	4.96973	0.00448341
Gga.131.1.S1_at	MX1	4.96968	0.00135276
GgaAffx.25830.1.S1_at	KAT2A	4.90284	0.0001088
GgaAffx.8324.2.S1_at	GRB10	4.85915	0.00058241
Gga.2533.1.S1_s_at	GSTA3	4.77279	0.00676466
Gga.19386.1.S1_at	---	4.76283	0.00106693
GgaAffx.10082.3.S1_at	GRIK1	4.71976	2.2043E-08
Gga.12073.1.S1_a_at	KRT23	4.60118	4.1107E-05
Gga.17352.1.S1_at	---	4.58928	0.0034465
Gga.16196.1.S1_at	KRT14	4.52368	0.0003414
Gga.6885.1.S1_at	---	4.51599	0.00298284
Gga.7573.1.S1_at	---	4.48118	0.00266228
Gga.1710.1.S1_at	---	4.42675	0.00282288

Gga.7638.2.S1_at	---	4.3666	0.0217192
Gga.19646.1.S1_at	PCDH1	4.34084	0.0208279
Gga.9513.1.S1_a_at	CXCL12	4.26273	0.00063224
GgaAffx.12579.1.S1_at	DUSP10	4.19916	0.0013605
Gga.12536.1.A1_at	---	4.14243	3.3658E-05
Gga.12506.1.S1_at	EML4	4.12492	0.00651208
Gga.9903.1.S1_at	---	4.11142	0.00022057
GgaAffx.20342.1.S1_at	---	4.09784	0.00011341
Gga.5954.1.S1_at	---	3.9938	0.00823815
Gga.19259.1.S1_at	---	3.89912	0.034759
Gga.701.1.S1_at	RSFR	3.86198	0.0404807
GgaAffx.21327.1.S1_at	CORO2A	3.84693	0.00179199
Gga.15176.1.S1_at	---	3.83331	6.7295E-05
GgaAffx.24587.2.S1_s_at	UHRF2	3.81607	0.00260003
Gga.14771.1.S1_at	---	3.80968	0.00027655
GgaAffx.25937.1.S1_s_at	KDM5B	3.76107	0.00038805
Gga.17118.1.S1_at	---	3.65644	0.0432572
Gga.1615.1.S1_at	TMTC1	3.65343	0.00429974
Gga.7673.2.S1_at	---	3.63739	0.0436178
Gga.9935.1.S1_at	DMBT1	3.63158	1.3935E-06
Gga.8958.1.S1_at	---	3.63038	0.00169842
Gga.16284.1.S1_at	---	3.62663	0.011762
GgaAffx.3789.1.S1_at	GPC4	3.61528	0.000729

Gga.15840.1.S1_at	---	3.5946	0.0190773
Gga.16074.1.S1_at	---	3.57146	1.4555E-08
GgaAffx.26344.1.S1_at	ZNFX1	3.52645	0.0395923
GgaAffx.12399.1.S1_s_at	COX10	3.47224	0.00031702
Gga.3115.1.S1_at	---	3.45978	0.00390272
Gga.1087.1.S1_at	IRF7	3.42278	0.0040109
RPTR-Gga-NC_002086-1_at	---	3.41724	0.00669925
Gga.13473.1.S1_x_at	ZNF250	3.35158	0.00377965
Gga.2888.2.S1_at	FBN1	3.32931	0.00244808
Gga.2073.1.S1_at	LOC395532	3.32475	0.0185984
Gga.7800.1.S1_at	LOC428660	3.28703	0.00386826
Gga.7777.1.S1_at	---	3.26767	0.00657173
Gga.16449.1.S1_at	---	3.25734	0.0008475
Gga.5387.1.S1_at	---	3.22986	0.0218061
GgaAffx.25695.6.S1_s_at	ZNF250	3.22902	0.00104239
GgaAffx.8923.1.S1_at	---	3.22792	0.00149415
GgaAffx.12117.1.S1_s_at	MARCKSL1	3.22773	0.0471012
Gga.15879.1.S1_s_at	---	3.2254	0.0195491
Gga.4038.1.S1_at	---	3.22454	0.023363
GgaAffx.10213.1.S1_at	VPS13B	3.21063	0.0053748
GgaAffx.12228.1.S1_at	LRP5	3.19136	0.011726
Gga.7255.1.S1_at	---	3.16488	0.00691744
Gga.2167.1.S1_at	GNAI1	3.16248	8.4936E-06

Gga.469.2.S1_at	---	3.14207	0.0209622
Gga.1909.1.S1_at	---	3.13798	0.00319812
Gga.7691.1.S1_at	---	3.13493	0.0109953
Gga.15797.1.S1_at	---	3.13187	0.00190555
Gga.9457.1.S1_at	LOC416888	3.12551	0.00345191
Gga.2728.1.S1_at	---	3.11858	0.00298637
GgaAffx.644.1.S1_at	MAP2K4	3.11263	0.00603025
Gga.140.1.S1_at	TCF7L1	3.10956	0.0087497
GgaAffx.24782.1.S1_at	BACH1	3.10669	0.0010363
GgaAffx.22418.1.S1_at	PHLPPL	3.04378	0.00254034
Gga.5735.1.S1_at	RFTN1	3.04151	0.015136
GgaAffx.21184.1.S1_at	---	3.02509	1.899E-05
Gga.7415.1.S1_at	TPP1	3.0199	0.0165062
Gga.9630.1.A1_at	---	3.00189	6.8378E-05
GgaAffx.231.1.S1_at	GAS7	3.00006	0.00011346
Gga.469.2.A1_at	---	2.96602	0.0307012
Gga.7659.1.S1_at	---	2.96389	0.0149638
Gga.2657.1.S1_s_at	---	2.9519	0.00067655
Gga.894.1.S1_at	LOC769132 /// ST8SIA4	2.9411	0.00637045
Gga.11876.3.S1_a_at	C9orf19	2.92522	0.011097
GgaAffx.9565.2.S1_s_at	PTPRD	2.90865	0.0145863
Gga.16155.1.S1_at	---	2.86049	0.0270115
Gga.3007.1.S1_at	---	2.85319	0.00026346

Gga.7691.1.S1_x_at	---	2.842	0.00106445
Gga.16098.1.S1_at	SOX5	2.84134	1.4034E-06
Gga.4168.1.S1_at	SERPINH1	2.83798	0.00230754
Gga.11703.1.S1_at	AARSD1	2.8244	0.022339
Gga.17419.1.S1_at	---	2.82317	0.00277756
GgaAffx.12178.1.S1_at	STX8	2.80842	5.6469E-05
Gga.12500.1.S1_at	---	2.80737	0.0169898
Gga.1137.1.S2_at	MYBPC3	2.8007	0.00405616
GgaAffx.24569.1.S1_s_at	TNPO1	2.79848	0.0152381
GgaAffx.4422.1.A1_at	---	2.79362	2.5686E-06
Gga.18951.1.S1_at	---	2.79349	0.00438016
Gga.19741.1.S1_at	---	2.78778	0.0171182
Gga.1745.3.S1_at	C16orf24	2.78612	3.0708E-05
Gga.9338.1.S1_at	HINTW	2.77035	0.00099638
Gga.19154.1.S1_at	---	2.76455	0.00678255
GgaAffx.12953.1.S1_at	SIRT2	2.72364	0.00093612
Gga.4409.1.S1_a_at	CCL4	2.71059	0.00693264
GgaAffx.23195.3.S1_s_at	---	2.70856	0.0278331
Gga.16828.1.S1_at	---	2.70593	0.00449555
Gga.679.1.S1_at	VLDLR	2.69918	0.0196371
GgaAffx.23235.1.S1_at	EBF3	2.69509	0.0123481
Gga.17820.1.S1_at	---	2.6585	0.00075773
GgaAffx.21089.1.S1_s_at	LMO7	2.63751	0.0312215

GgaAffx.23154.1.S1_at	LOC427351	2.62566	0.00166363
Gga.16370.1.S1_s_at	TMEM220	2.6046	0.0115133
Gga.14728.1.S1_at	LOC424623	2.59032	7.2622E-07
Gga.17085.2.A1_at	---	2.58791	0.00361118
GgaAffx.25936.1.S1_at	PRKAR1B	2.58579	0.0212367
GgaAffx.12178.1.S1_s_at	STX8	2.56567	0.00031022
Gga.16555.1.S1_at	---	2.56101	7.406E-05
GgaAffx.11521.1.S1_at	JMJD2B	2.55802	0.0486893
Gga.1972.1.S1_at	ACTN4	2.5548	8.8632E-07
Gga.11876.1.S1_a_at	C9orf19	2.53532	0.0225502
GgaAffx.10082.3.S1_s_at	GRIK1	2.53155	0.00269258
Gga.10985.1.S1_at	TMEM45A	2.53122	0.0158023
Gga.18910.1.S1_s_at	GNAI1	2.52728	0.00301031
Gga.9283.1.S1_at	POLR2L	2.51535	0.00315775
GgaAffx.21251.1.S1_at	---	2.50469	0.0159989
Gga.2289.2.S1_a_at	---	2.50387	0.0138457
GgaAffx.12543.1.S1_s_at	LOC417324	2.49394	0.0168329
Gga.16030.1.S1_at	TMEM220	2.49096	0.0228651
Gga.14158.1.S1_at	DET1	2.48785	0.00176593
Gga.11876.2.S1_at	C9orf19	2.48456	0.0314658
Gga.14036.1.S1_at	---	2.46799	0.00059647
GgaAffx.4610.1.S1_s_at	MAGI1	2.46791	0.0262261
Gga.17566.1.A1_at	---	2.46611	0.00176059

Gga.16827.1.S1_at	PARP3	2.45813	0.00046019
Gga.15312.1.S1_a_at	UBAP2	2.44079	0.0421496
Gga.8479.1.S1_at	FUBP1	2.43766	0.00994304
Gga.4087.1.S2_at	FZD1	2.43258	0.00013559
Gga.7024.1.S1_s_at	SIRT2	2.4167	0.00011269
Gga.8268.1.S1_at	NDST2	2.41444	0.01386
Gga.9791.1.S1_at	LOC427134	2.41277	0.0170291
Gga.4675.1.S1_at	SDC2	2.40396	0.00928325
Gga.11938.3.S1_s_at	ASTE1	2.4024	0.0045964
Gga.4776.1.S2_at	RPL9	2.39529	0.00031555
GgaAffx.7003.1.S1_at	CLMN	2.39287	0.0118134
Gga.2.1.S1_at	---	2.38728	0.0473219
Gga.10216.1.S1_at	PARS2	2.38158	0.0001773
Gga.2680.1.S1_at	AQP1	2.38104	0.0366197
Gga.4220.1.S1_a_at	SMYD1	2.37446	0.00413359
Gga.3019.1.S1_at	MAGI1	2.37045	0.0265358
Gga.14963.1.S1_at	---	2.37016	0.00180254
Gga.4719.1.S1_a_at	APOA1	2.36584	0.00624969
Gga.7402.1.S1_at	---	2.36473	0.00016351
Gga.3696.1.S1_at	SOX11	2.36317	0.0482033
Gga.15932.1.S1_at	LOC415374	2.33842	0.00023403
Gga.16674.1.S1_at	LOC427419	2.32511	0.0449322
GgaAffx.26404.1.S1_at	NDST2	2.32399	0.0368275
Gga.13161.1.S1_at	---	2.32383	0.0189237

Gga.12179.1.S1_at	---	2.32263	0.011604
Gga.19606.1.S1_at	---	2.32236	0.0291599
Gga.17789.1.S1_at	---	2.31434	0.00138116
Gga.9134.1.S1_at	---	2.31148	0.0187266
GgaAffx.7813.1.S1_at	UST	2.30215	0.00482714
GgaAffx.23633.1.S1_at	HIPK3	2.29294	0.00569379
Gga.4544.1.S1_at	BRG1	2.29278	0.00586997
Gga.18356.1.S1_at	---	2.28768	0.0113099
Gga.2603.1.S1_at	MAFB	2.27528	0.0374192
GgaAffx.23242.1.S1_at	C1orf165	2.2717	0.00243784
Gga.11703.1.S1_s_at	AARSD1	2.27122	0.0451547
Gga.17611.1.S1_at	---	2.26502	0.0138807
Gga.12422.1.S1_at	RUSC2	2.25636	0.0380858
Gga.1321.1.S1_s_at	IREB2	2.24928	0.00015953
Gga.15714.1.S1_at	SLC43A2	2.23466	0.0139555
GgaAffx.9861.1.S1_s_at	BCL9	2.23148	0.0126227
Gga.17711.1.S1_at	LOC428553	2.23117	7.4366E-05
Gga.17483.1.S1_at	CABLES1	2.22493	0.00619526
GgaAffx.687.2.S1_s_at	SLC4A9	2.20739	0.0158714
GgaAffx.25763.1.S1_s_at	TRIM25	2.20515	0.033935
Gga.7855.1.S1_at	BMPER	2.20509	0.0155203
Gga.5239.1.S1_at	---	2.20404	0.0193928
Gga.4979.2.S1_at	TCF3	2.20202	0.00975312

Gga.276.2.S1_a_at	EBF1	2.19966	0.0327679
Gga.4725.1.S1_at	---	2.19404	0.00128558
Gga.7460.1.S1_a_at	C9orf151	2.1901	0.00663459
Gga.7673.1.S1_at	C9orf18	2.17658	0.0146822
GgaAffx.21404.1.S1_at	MAGI1	2.1705	0.0144909
Gga.16152.1.S1_at	---	2.16542	0.00923172
Gga.8818.1.S1_at	---	2.16166	0.00730541
Gga.1789.1.S1_at	---	2.14844	0.00808243
GgaAffx.25555.1.S1_at	LOC772107	2.1465	0.0174055
GgaAffx.20439.1.S1_s_at	HS6ST2	2.143	0.0440257
Gga.10351.1.S1_s_at	C19orf12 /// LOC415755	2.13997	0.00676213
Gga.18910.1.S1_at	GNAI1	2.13785	0.00630397
Gga.4418.1.S1_at	IRF8	2.13119	0.013962
Gga.3754.1.S1_a_at	HES1	2.1299	0.03325
Gga.12271.1.S1_a_at	AP3S2	2.12959	0.035175
GgaAffx.10979.1.S1_s_at	LATS2	2.12494	0.0219559
Gga.5980.1.A1_at	JMJD2A	2.12431	0.00170399
GgaAffx.11584.1.S1_s_at	RBM24	2.1223	0.00248021
Gga.3987.1.S1_s_at	TOP1	2.11931	0.00872127
Gga.1035.2.S1_a_at	LMAN1	2.11563	0.00036131
Gga.2242.1.S1_at	---	2.11477	0.0222161
Gga.17967.1.S1_at	---	2.11366	9.251E-05
Gga.9873.1.S1_at	C1QC	2.11265	1.6982E-05

GgaAffx.8520.1.S1_at	SCO1	2.10743	0.00032317
Gga.13323.2.S1_s_at	IGF2BP3	2.09866	0.0087096
Gga.13228.1.S1_at	PALLD	2.09659	0.0143327
GgaAffx.13181.1.S1_s_at	ACBD5	2.09603	0.0128183
GgaAffx.20776.1.S1_at	---	2.09529	0.0367669
Gga.7802.2.S1_at	CCDC28A	2.09483	0.0437427
Gga.17180.1.S1_at	---	2.09174	0.0172043
Gga.2433.1.S1_at	---	2.09093	0.0123095
Gga.11406.1.S1_a_at	LOC426545	2.07856	0.00028547
Gga.9101.1.S1_at	---	2.07673	0.0258127
Gga.19934.1.S1_at	SNAI2	2.0742	0.0141867
Gga.9310.1.S1_at	HMOX2	2.07392	0.00097931
Gga.5058.1.S1_s_at	CST3	2.07051	0.0390049
GgaAffx.11958.1.S1_s_at	NOL11	2.07034	0.00010945
GgaAffx.25912.1.S1_s_at	---	2.06913	5.9187E-05
Gga.15803.1.S1_at	TXNDC16	2.06777	0.00918171
Gga.9930.1.S1_at	---	2.06768	0.00738152
Gga.17022.1.S1_at	WWOX	2.06427	0.00541375
Gga.9193.1.S1_s_at	ITPA	2.06162	0.0103039
Gga.791.1.S1_at	IRF1	2.05732	0.00112379
GgaAffx.8851.1.S1_at	---	2.05489	0.0475186
Gga.6994.1.S1_at	---	2.0547	0.00514688
Gga.7691.1.S1_a_at	---	2.04684	0.0110793

Gga.15783.1.S1_at	---	2.04667	0.0145258
Gga.8032.1.S1_at	---	2.04051	0.0173503
GgaAffx.8702.1.S1_at	ZNF516	2.04014	0.0487025
GgaAffx.20500.1.S1_s_at	GARS	2.03839	0.00155199
Gga.6104.1.S1_at	C6orf86	2.03642	0.0098183
Gga.10078.2.S1_a_at	ARHGAP32	2.02944	0.0269458
GgaAffx.20373.1.S1_at	---	2.02887	0.00582603
Gga.17398.1.S1_at	---	2.02661	0.00806483
Gga.4266.1.S1_at	TYRO3	2.02184	0.00221339
Gga.7709.1.S1_at	DAPK1	2.0209	0.00476236
GgaAffx.8427.1.A1_x_at	---	2.02046	0.00182092
Gga.2735.1.S1_at	---	2.01863	0.0228205
GgaAffx.25329.1.S1_at	TBC1D2	2.0172	0.00177241
Gga.12818.1.S1_at	PTPN13	2.01219	0.00438727
Gga.16711.1.S1_at	LOC418671	2.00973	0.00030373
Gga.12001.1.S1_at	---	2.00732	0.00664551
Gga.9906.1.S1_at	METRNL	2.00707	0.0149457
Gga.10077.2.S1_s_at	WDR35	2.00688	0.017368
Gga.4832.1.S1_at	LOC770612	2.00433	0.0174541
GgaAffx.20534.1.S1_s_at	ATPBD4	2.00423	0.00749594

snížená exprese

ID sondy	Symbol genu	míra velikosti účinku (PR9692-shHOPX vs. PR9692-shMOCK)	hodnota P (PR9692-shHOPX vs. PR9692-shMOCK)
GgaAffx.12290.1.S1_s_at	MVP	-281.792	7.8465E-08
Gga.19091.1.S1_at	---	-192.015	3.5753E-06
Gga.5401.1.S1_at	DHRS7	-163.422	2.3726E-06
Gga.17862.1.S1_at	---	-126.189	2.4171E-05
Gga.10035.1.S1_at	TMEM26	-121.369	7.8971E-07
GgaAffx.7341.1.S1_s_at	SLC22A3	-92.3466	0.00023442
Gga.6072.2.S1_at	SRGN	-81.6261	2.5015E-07
Gga.9109.1.S1_at	---	-71.9125	9.4978E-07
Gga.10266.1.S1_at	LOC429955	-70.3197	2.1285E-05
GgaAffx.12670.1.S1_s_at	NUDT14	-63.4914	2.7693E-09
Gga.2718.1.S1_at	NUDT14	-56.1805	1.0619E-06
GgaAffx.8765.2.S1_at	GFPT2 /// LOC416372	-55.7211	6.6683E-07
Gga.1081.1.S1_at	ATAD1	-53.6621	1.2402E-05
Gga.10093.1.S1_at	PDGFRL	-53.4933	1.2975E-05
Gga.7334.1.S1_at	APBB1IP	-43.2126	2.9338E-05
Gga.8446.1.S1_at	GSR	-42.5864	0.0004055
GgaAffx.7341.1.S1_at	SLC22A3	-42.2613	1.0286E-05
GgaAffx.21467.1.S1_at	---	-42.044	5.8961E-05
Gga.5198.1.S1_a_at	LOC420812	-41.6739	8.3152E-07
Gga.13148.1.S1_at	LOC416052	-38.2615	0.00014792
Gga.19305.1.S1_at	RSPO3	-37.18	0.00105385

Gga.16573.1.S1_at	---	-35.1934	0.00028136
Gga.8519.1.S1_a_at	TTC32	-33.4209	1.4085E-08
Gga.10138.1.S1_at	---	-32.6963	1.7611E-05
Gga.12514.1.S1_a_at	LOC395611	-30.7432	3.6842E-05
Gga.2679.2.S1_a_at	FBLN1	-30.4692	3.6562E-05
Gga.2679.1.S1_at	FBLN1	-29.88	1.0141E-05
Gga.1605.1.S1_s_at	RSPO3	-28.3048	0.00029235
Gga.9699.4.S1_a_at	JMJD7-PLA2G4B	-27.6292	5.3939E-07
Gga.9403.1.S1_a_at	CCDC109B	-26.9105	3.6622E-05
GgaAffx.11396.1.S1_s_at	SLC17A9	-25.4581	1.6205E-06
Gga.5787.1.S1_at	---	-25.4023	0.00010236
Gga.9147.1.S1_at	LOC424588	-25.0547	6.3858E-05
GgaAffx.26112.1.S1_at	FUCA1	-24.395	5.5788E-06
GgaAffx.20829.1.S1_at	---	-24.362	0.0001648
Gga.9699.1.S1_a_at	JMJD7-PLA2G4B	-21.8383	4.8354E-06
GgaAffx.13053.1.S1_s_at	C10orf58	-20.8362	2.3561E-07
Gga.20029.1.S1_at	---	-20.133	3.8541E-06
Gga.5758.1.S1_s_at	LYN	-19.955	1.1355E-05
GgaAffx.1993.5.S1_s_at	ITPR3	-19.5386	0.00034688
Gga.9304.1.S1_s_at	CRYL1	-19.482	1.2752E-06
Gga.13978.1.S1_s_at	LHFPL5	-19.1961	0.00078089
GgaAffx.7184.1.S1_s_at	LRRC40	-19.1912	6.5118E-06
GgaAffx.3953.1.S1_s_at	---	-18.7275	2.3542E-05

Gga.352.1.S1_at	RGS20	-18.6322	0.00018181
Gga.1231.1.S1_at	MCTP1	-17.9966	4.5324E-05
GgaAffx.21513.1.S1_at	---	-17.9219	0.00030505
Gga.3518.1.S1_at	---	-17.854	2.6937E-05
GgaAffx.4955.1.S1_at	LAMB1	-17.41	0.00103248
Gga.2668.2.S1_at	RARB	-17.3215	0.00013213
Gga.4113.1.S1_at	RHOF	-17.316	2.5825E-06
Gga.10138.2.S1_a_at	---	-17.0786	0.0004147
Gga.4491.1.S1_s_at	LSP1	-17.0726	0.0002356
Gga.12120.1.S1_at	PACSIN3	-16.8702	0.00064749
Gga.11925.1.S1_at	ANXA7	-16.0421	0.00043486
Gga.17586.1.S1_at	---	-15.0127	7.4844E-05
GgaAffx.3623.1.S1_at	ALOX5	-14.6633	9.8212E-06
Gga.3676.1.S1_at	CHST15	-14.0577	0.00013816
GgaAffx.22647.2.S1_s_at	MAPK11	-14.0562	0.00020934
Gga.10703.1.S1_at	CHID1	-13.97	0.00047576
Gga.8515.1.S1_at	LHFPL5	-13.957	0.00281055
GgaAffx.7184.2.S1_s_at	LRRC40	-13.3074	3.7661E-06
Gga.13553.1.S1_at	FSCN1	-13.1392	0.00101165
Gga.9699.4.S1_x_at	JMJD7-PLA2G4B	-13.0529	5.0173E-05
GgaAffx.10287.1.S1_at	BACE2	-13.0376	0.00059693
GgaAffx.11089.1.S1_at	KLHDC5	-12.7274	0.00085527
Gga.1794.1.S1_at	NCAM1	-12.5687	0.00096851

Gga.2884.1.S1_at	---	-12.5429	0.00010212
Gga.10138.3.S1_at	---	-11.7945	0.00217606
Gga.16770.1.S1_at	---	-11.6428	0.00514224
Gga.18300.1.S1_at	SLITRK2	-11.3943	3.7362E-05
Gga.13519.1.S1_s_at	SLC7A5	-11.3019	0.0279016
GgaAffx.9437.1.S1_at	---	-11.297	0.00023609
Gga.13451.1.S1_at	CCDC104	-10.5707	6.8946E-07
GgaAffx.539.1.S1_at	HTR1D	-10.2397	3.2081E-05
GgaAffx.21787.1.S1_s_at	BETA3	-10.1886	0.00143697
Gga.15050.1.S1_at	---	-10.1131	0.00053988
Gga.11730.1.S1_at	SLC2A10	-10.1089	0.00058555
Gga.18649.1.A1_at	---	-10.0523	0.0114465
GgaAffx.23947.1.S1_at	PRDM4	-9.90034	0.00106506
GgaAffx.10287.2.S1_s_at	BACE2	-9.80416	8.1532E-05
Gga.577.1.S1_at	ADORA2B	-9.76136	0.0215264
GgaAffx.21851.1.S1_s_at	ST8SIA6	-9.68684	9.1727E-06
Gga.16193.1.S1_at	GRAMD1B	-9.57838	0.0113727
Gga.16446.1.S1_s_at	NHEDC2	-9.56074	0.00164905
Gga.1930.1.S1_at	---	-9.49508	0.00051594
Gga.8329.1.S1_at	PRKCH	-9.49107	0.00051237
Gga.1114.1.S1_at	CIP1	-9.40488	0.0105519
Gga.4981.1.S1_s_at	HBG1 /// HBG2	-9.37374	3.7016E-05
Gga.5198.3.S1_x_at	---	-9.04814	0.000155

Gga.3674.1.S1_at	STK39	-8.98627	0.00031237
Gga.275.1.S1_at	MITF	-8.84235	0.00010396
Gga.13339.1.S1_at	ST8SIA6	-8.83783	0.00026691
Gga.3899.3.S1_a_at	PDGFA	-8.72075	0.00541287
Gga.11477.1.S1_at	DRAM1	-8.56677	0.00311024
GgaAffx.5831.1.S1_at	HSPA12A	-8.49023	0.00514108
Gga.195.1.S1_at	GPR149	-8.48053	1.2394E-05
Gga.9491.1.S1_at	DNM1	-8.17204	0.00081448
Gga.18023.1.S1_at	LOC419171	-8.10356	0.00044368
Gga.18155.1.S1_at	---	-8.09959	0.00047933
Gga.744.1.S1_at	GATA3	-8.0991	1.9458E-05
Gga.4491.1.S1_at	LSP1	-8.092	0.0007983
GgaAffx.2792.1.A1_at	LOC770379	-7.86923	5.1479E-06
Gga.16589.1.S1_at	LSP1	-7.8382	0.00115892
GgaAffx.11329.1.S1_at	LOC777504	-7.83692	0.0254801
Gga.9482.1.S1_at	UTS2D	-7.83355	0.00172733
Gga.643.1.S1_at	SYT1	-7.66828	8.0295E-05
Gga.13113.1.S1_at	LINGO1	-7.64618	0.00074395
Gga.3899.1.S1_a_at	PDGFA	-7.57149	0.00076358
Gga.18649.1.S1_at	---	-7.50414	0.00416666
Gga.16822.1.S1_at	---	-7.46448	3.1873E-06
Gga.1369.1.S1_at	P2RX4	-7.4394	7.2288E-05
Gga.13251.1.S1_at	---	-7.33636	0.00016418

Gga.12309.1.S1_at	AIFM2	-7.3361	0.0001155
Gga.927.1.S1_at	ANPEP	-7.29632	9.8349E-09
Gga.17781.1.S1_at	---	-7.08893	0.00862369
GgaAffx.13140.1.S1_at	CYP2J2	-7.07148	0.0003268
Gga.10956.1.S1_at	AP1S3	-6.83532	0.0162267
GgaAffx.8298.1.S1_at	UPP1	-6.83212	0.00504631
GgaAffx.20316.1.S1_at	COL4A5	-6.79929	0.0153699
Gga.11065.1.S1_s_at	---	-6.79534	0.0258137
Gga.10214.1.S1_s_at	MAPK12	-6.75582	0.00244963
Gga.6641.1.A1_at	---	-6.74749	0.0204081
GgaAffx.12879.1.S1_s_at	MAPK11	-6.73453	5.3933E-06
Gga.2361.2.S1_a_at	RIC3	-6.67131	1.2368E-05
Gga.6306.1.S1_at	BAMBI	-6.62738	0.00010519
Gga.13383.1.S1_at	---	-6.6184	0.00315861
Gga.5111.1.S1_at	CCDC80	-6.60128	0.00068904
GgaAffx.8972.1.S1_s_at	MANSC1	-6.49708	0.00300884
GgaAffx.21035.1.S1_s_at	EHHADH	-6.47798	9.3906E-05
Gga.9986.1.S1_at	FSCN1	-6.39285	3.969E-05
GgaAffx.21279.1.S1_at	UPP1	-6.37708	0.0155228
Gga.3264.1.S1_at	AHR	-6.30752	0.00363785
GgaAffx.12115.1.S1_at	RHOF	-6.26358	9.8697E-07
Gga.19097.1.S1_at	CMAS	-6.20957	0.00080822
Gga.7576.1.S1_at	ACAA1	-6.18701	0.00108343

GgaAffx.4478.1.S1_at	FAM3D	-6.11667	0.00013515
Gga.10596.1.S1_s_at	AMPD3	-6.08327	0.00019803
Gga.10214.1.S1_at	MAPK12	-6.04343	5.1183E-05
Gga.2714.1.S1_s_at	---	-5.97145	0.00149751
Gga.2149.1.S1_s_at	B3GNT2	-5.87528	0.00109279
GgaAffx.1717.2.S1_s_at	PCOLCE2	-5.8178	5.0154E-06
Gga.1906.2.S1_at	CRISPLD1	-5.81163	0.0103206
Gga.18072.1.S1_at	---	-5.79442	1.1579E-05
Gga.18272.1.S1_at	---	-5.76358	0.00273611
GgaAffx.8765.1.S1_at	GFPT2 /// LOC416372	-5.7222	0.0132955
GgaAffx.20545.1.S1_at	---	-5.6655	0.00076459
Gga.7499.1.S1_at	---	-5.65412	0.00035203
GgaAffx.25209.3.S1_s_at	NOX4	-5.63246	0.00149594
Gga.14398.1.S1_at	---	-5.60705	2.2055E-05
Gga.7542.1.S1_at	EHHADH	-5.5741	4.5847E-05
GgaAffx.10743.1.S1_at	IL1RL2	-5.55133	0.00064272
GgaAffx.4342.1.S1_at	FAM19A5	-5.52284	0.00210253
Gga.666.1.S1_a_at	VIP	-5.43542	0.00325702
Gga.7859.1.S1_at	---	-5.42557	0.0193091
GgaAffx.12049.1.S1_at	MANSC1	-5.31529	0.00185003
Gga.14401.1.S1_at	---	-5.30939	0.0186192
Gga.12092.1.S1_at	FAM20C	-5.19917	0.00439595
GgaAffx.7917.1.S1_at	TNFAIP6	-5.16138	0.00889721

GgaAffx.24216.1.S1_at	LOC415891	-5.11813	0.0425521
GgaAffx.20545.1.S1_s_at	---	-5.05655	0.00126487
Gga.643.1.S1_s_at	SYT1	-4.95071	0.00856794
Gga.3360.1.S1_at	NAT8B	-4.87576	0.00307143
Gga.6241.1.S1_at	---	-4.85439	0.00247142
Gga.9299.1.S1_at	CPT1A	-4.85328	0.0266306
Gga.2190.2.S1_a_at	SOCS2	-4.84679	0.0120152
GgaAffx.12999.1.S1_s_at	TEC	-4.8408	0.00872432
GgaAffx.20697.1.S1_at	---	-4.8209	0.00058687
Gga.8231.1.S1_at	---	-4.79399	0.0114755
Gga.19582.1.S1_at	---	-4.75138	0.00124082
Gga.13129.1.S1_s_at	LOC419204	-4.74168	0.00485963
GgaAffx.21730.1.S1_s_at	---	-4.70194	0.0027554
GgaAffx.6058.1.S1_at	AADAT	-4.69446	0.0117814
Gga.2668.1.S1_a_at	RARB	-4.65787	0.00010321
Gga.17391.1.S1_at	PTCHD1	-4.63847	0.00034506
Gga.8419.1.S1_at	---	-4.58012	4.3343E-05
Gga.10877.1.S1_at	TBC1D8	-4.54084	0.00108483
GgaAffx.25590.1.S1_s_at	LINGO1	-4.5292	0.0043515
Gga.19033.1.S1_at	---	-4.51511	0.00122339
GgaAffx.22647.3.S1_s_at	MAPK12	-4.48559	0.00697618
Gga.6402.1.S1_at	C1orf190	-4.4289	0.00050983
Gga.7235.1.S1_at	DHRS3	-4.42639	0.00470504

Gga.16915.1.S1_at	TMEM150	-4.41542	5.2426E-05
Gga.10763.1.S1_at	SLC6A4	-4.34828	0.00559243
Gga.1440.1.S1_at	TECR	-4.31008	0.0127407
Gga.12932.1.S1_at	LOC776655	-4.29986	4.5988E-06
Gga.12356.2.S1_a_at	---	-4.29056	0.00994498
Gga.2330.1.S1_at	LOC415822	-4.27987	0.0267316
Gga.18813.1.S1_at	---	-4.27475	0.00027659
Gga.17889.1.S1_at	---	-4.27271	0.029962
GgaAffx.7674.1.S1_at	AOAH	-4.25635	0.00485393
Gga.2729.1.S1_at	---	-4.21544	0.00192588
Gga.12505.1.S1_at	ZDHHC4	-4.20151	0.00070753
Gga.18770.1.S1_at	NEIL3	-4.18351	0.00184626
Gga.11048.1.S1_at	SLMAP	-4.17635	0.00962472
GgaAffx.6423.2.S1_at	KCNC2	-4.14676	0.00873547
Gga.1222.2.S1_s_at	SLC9A3R1	-4.13404	0.00015093
GgaAffx.12553.1.S1_at	SAMD11	-4.12201	0.00452202
GgaAffx.23993.3.S1_s_at	GNPTAB	-4.11726	0.00068577
Gga.10039.1.S1_at	---	-4.10839	0.00181776
Gga.1307.1.S1_s_at	IL16	-4.08221	0.0366216
Gga.6796.1.S1_at	ENG	-4.03972	0.00186811
Gga.19343.1.S1_at	---	-4.02079	0.00505595
Gga.16006.1.S1_at	---	-3.98746	6.0239E-05
Gga.2712.1.S1_at	NSG1	-3.96573	0.0077721

Gga.16014.1.S1_at	LOC425209	-3.92212	0.00278883
Gga.20061.1.S1_at	NINJ2	-3.85814	0.0396727
Gga.18934.1.S1_at	---	-3.84549	0.00040495
GgaAffx.3519.1.S1_at	SLC44A3	-3.82185	0.0245742
Gga.4170.1.S1_at	AKR1B10	-3.81855	0.00183543
Gga.11643.2.S1_s_at	C20orf42	-3.80736	0.0122508
GgaAffx.12520.1.S1_s_at	DDB2	-3.79742	0.00011894
Gga.13644.1.S1_at	---	-3.78597	0.00101003
Gga.15139.1.S1_at	---	-3.7708	0.00146369
GgaAffx.20557.1.S1_at	---	-3.76984	0.00025205
Gga.1573.1.S1_at	HPD	-3.73363	0.00116783
GgaAffx.25985.1.S1_at	OTUD7A	-3.69498	1.0011E-05
Gga.18933.1.S1_s_at	RASSF5	-3.68944	0.0136394
Gga.4821.1.S1_at	COL18A1	-3.67682	0.00361699
GgaAffx.13096.1.S1_at	RASSF5	-3.66707	0.0207058
Gga.7960.1.S1_at	WNT5B	-3.64889	0.00277611
Gga.12042.1.S1_at	IL1RAP	-3.64007	0.00306062
Gga.2478.1.S1_at	---	-3.63589	0.0012323
Gga.10973.1.S1_at	ICA1	-3.62685	0.00242125
GgaAffx.10679.1.S1_at	CSF2RA	-3.62295	0.0112038
GgaAffx.5797.1.S1_at	AADACL1	-3.59895	0.00027451
Gga.156.2.S1_a_at	NBL1	-3.59777	0.00322828
GgaAffx.25677.1.S1_s_at	ENPP3	-3.59362	0.0210222

Gga.12534.1.S1_at	LXN	-3.58668	0.0125121
Gga.1530.1.S1_at	---	-3.57818	0.00680236
Gga.18266.1.S1_at	ANKRD26	-3.56944	0.00056612
Gga.7424.1.S1_at	SYNJ2	-3.56695	1.2443E-05
GgaAffx.7332.1.S1_at	LOC772201	-3.51839	0.0152117
GgaAffx.8903.1.S1_s_at	ARHGAP18	-3.51024	0.0129952
Gga.7057.1.S1_at	CARD11	-3.4957	0.031241
GgaAffx.12589.1.S1_s_at	CCDC88A	-3.49337	0.0231469
GgaAffx.12253.1.S1_at	NPL	-3.47084	0.0028581
Gga.19034.1.S1_at	---	-3.46784	0.0241179
Gga.12448.2.S1_a_at	AGPHD1	-3.43501	0.00316124
Gga.15046.1.S1_at	---	-3.4026	0.00337737
Gga.1579.1.S1_at	DBNDD2	-3.40145	0.00149513
Gga.13627.1.S1_s_at	ACBD7	-3.39662	0.0128627
GgaAffx.1880.1.S1_at	MST1R	-3.39214	1.6488E-05
Gga.1661.3.S1_s_at	ELMO1	-3.34881	0.00532615
Gga.16049.1.S1_at	---	-3.34416	0.00036764
Gga.10931.1.S1_at	---	-3.3029	0.00286996
GgaAffx.6403.1.S1_at	SLC29A1	-3.29957	0.00949009
Gga.8588.1.S1_s_at	NAPEPLD	-3.27587	0.00782244
Gga.10658.1.S1_at	---	-3.27505	0.00059051
Gga.3807.1.S2_s_at	ALDH1A3	-3.26926	0.0419573
Gga.7159.1.S1_at	LAPTM5	-3.26218	0.00330637

Gga.5367.1.S1_at	---	-3.25675	0.00088468
Gga.17171.1.S1_at	---	-3.25595	0.00879731
GgaAffx.6117.2.S1_s_at	RPAP3	-3.2536	0.00955739
Gga.10595.1.S1_at	REEP1	-3.24033	0.0172038
Gga.7212.1.S1_at	LOC421447	-3.23141	0.0231754
Gga.11692.1.S1_at	LOC418120	-3.22807	0.0057118
GgaAffx.6042.1.S1_at	GPR176	-3.2201	0.00345492
GgaAffx.6955.1.S1_s_at	MPP6	-3.20813	0.0196824
GgaAffx.22781.1.S1_at	SESTD1	-3.19838	3.0668E-05
Gga.15960.1.S1_at	---	-3.19432	0.0245566
Gga.1132.1.S1_at	ME1	-3.16298	0.02641
GgaAffx.20670.1.S1_at	---	-3.15562	0.00087804
GgaAffx.8046.4.S1_s_at	SLC41A2	-3.15244	0.0292552
Gga.18863.1.S1_at	---	-3.1499	0.0260388
Gga.9321.1.S1_at	RPS6KA1	-3.14943	0.0239913
GgaAffx.26385.1.S1_s_at	DOCK10	-3.1388	0.00962469
Gga.15235.1.S1_at	---	-3.11911	0.0118968
Gga.1361.1.S1_at	PARP11	-3.10504	0.00351556
GgaAffx.20535.1.S1_at	---	-3.0936	1.4658E-05
GgaAffx.21582.1.S1_at	LOC416951	-3.09142	0.0379092
Gga.7364.1.S1_a_at	TESC	-3.0909	0.00389646
Gga.19588.1.S1_at	KCNMA1	-3.06888	0.0290352
GgaAffx.9436.1.S1_at	RLBP1L2	-3.06469	0.029601

Gga.8095.1.S1_at	MPP6	-3.05202	0.00190922
Gga.5253.1.S1_at	---	-3.05202	0.00756704
Gga.15708.2.S1_a_at	TMEM184B	-3.05057	0.0397443
GgaAffx.8095.1.S1_at	GNPTAB	-3.04926	0.0006707
Gga.16782.1.S1_at	PIK3CD	-3.03049	0.0218991
GgaAffx.5549.1.S1_at	ATP6AP1	-3.03033	0.0251517
Gga.10291.1.S1_at	LOC424274	-3.02542	0.00385612
GgaAffx.12253.1.S1_s_at	NPL	-3.01435	0.00010696
Gga.14867.1.S1_at	C12orf26	-3.01145	0.0087007
GgaAffx.6071.1.S1_at	MFAP3L	-2.99727	0.00590475
Gga.8213.1.S1_at	CCDC81	-2.97626	0.00121874
Gga.10365.1.S1_at	---	-2.96689	0.00644595
Gga.10092.1.S1_at	PTCHD1	-2.96525	0.034572
Gga.5217.1.S1_at	---	-2.96271	0.0013005
GgaAffx.7493.1.S1_s_at	UGT2A3	-2.93578	0.043547
Gga.10877.1.S1_s_at	TBC1D8	-2.93068	0.0118887
GgaAffx.3255.1.S1_s_at	WNK2	-2.92865	0.0174171
GgaAffx.12006.1.S1_s_at	PLEKHA3	-2.922	0.00373469
GgaAffx.11575.1.S1_s_at	HEBP1	-2.91738	0.0183317
GgaAffx.9557.1.S1_s_at	LAMA3	-2.90861	0.0016031
Gga.1582.1.A1_at	---	-2.90719	0.0358633
Gga.18424.1.S1_at	---	-2.90051	0.00141234
Gga.3090.1.S1_at	---	-2.89066	0.039057

Gga.12557.1.S1_at	TMEFF2	-2.8786	0.00218681
GgaAffx.12848.1.S1_at	LRPPRC	-2.87795	0.0010066
Gga.13575.1.S1_at	RPL21	-2.86315	0.0223527
Gga.8323.1.S1_at	TMEM51	-2.85899	0.00201988
GgaAffx.5401.1.S1_at	DUSP5	-2.85553	0.017934
GgaAffx.2599.1.S1_at	---	-2.85467	0.00069156
Gga.16349.1.S1_s_at	LOC415511	-2.85385	0.00040562
Gga.3131.1.S1_at	FKBP7	-2.84509	0.0101123
GgaAffx.23623.2.S1_at	AHNAK2	-2.83922	0.00298201
Gga.5778.1.S1_a_at	LOC769246	-2.83899	0.00016927
Gga.17696.1.S1_at	---	-2.83432	0.0147925
Gga.13372.1.S1_s_at	LIMS2	-2.81176	0.0207195
Gga.18732.1.S1_at	---	-2.80918	0.0246692
Gga.8858.1.S1_s_at	FKBP7	-2.8087	0.00863007
GgaAffx.1924.3.A1_at	---	-2.80855	0.00114251
GgaAffx.24056.1.S1_s_at	CAPRIN2	-2.79328	0.028896
Gga.14072.1.S1_s_at	AEBP2	-2.78312	0.00408718
Gga.6099.1.S1_at	LOC771753	-2.77458	0.00016173
Gga.16727.1.S1_at	LOC429030	-2.77412	0.00053111
GgaAffx.24532.1.S1_at	LOC421712 /// LOC769246	-2.76323	0.00375762
Gga.15768.1.S1_at	TNFAIP6	-2.75894	0.0100637
GgaAffx.24104.1.S1_at	MGST1	-2.7517	0.00029364
Gga.3831.1.S1_at	PACSIN2	-2.75033	0.00026642

Gga.11452.2.S1_a_at	OFD1	-2.72628	0.00032099
Gga.6745.1.S1_s_at	SLC35F2	-2.72044	0.00698037
Gga.13545.1.S1_at	ALS2	-2.71349	5.7577E-05
Gga.14630.1.S1_s_at	LOC422479	-2.70857	0.0130833
Gga.9062.1.S1_at	ENPP3	-2.70839	0.00867053
Gga.18320.1.S1_at	---	-2.70684	2.3908E-05
GgaAffx.11543.1.S1_s_at	PYGB	-2.70441	0.0207144
Gga.18051.1.S1_s_at	E4F1	-2.69443	0.00059044
Gga.7757.1.S1_at	UNC50	-2.68978	0.00281225
Gga.12960.1.S1_at	---	-2.68892	0.00590771
Gga.4306.1.S1_at	DMN	-2.68732	0.0397031
Gga.657.1.S1_at	FOXG1	-2.68694	0.0219749
Gga.16811.1.S1_at	---	-2.68642	0.0110085
GgaAffx.12498.1.S1_s_at	TMEM120B	-2.68095	0.0155985
GgaAffx.7641.1.S1_at	FAM83F	-2.67987	0.0213186
Gga.19147.1.S1_at	---	-2.6764	0.00615842
GgaAffx.25186.1.S1_at	SLC35F2	-2.67353	5.4984E-05
Gga.11667.1.S1_at	LOC427005	-2.66924	0.0088073
Gga.16169.1.S1_at	---	-2.66456	0.00308173
GgaAffx.25163.1.S1_at	FRY	-2.66058	0.00065512
GgaAffx.21694.1.S1_at	---	-2.65689	0.00860659
Gga.5408.1.S1_at	---	-2.65645	0.00093725
Gga.6300.1.S1_at	---	-2.65563	0.0112985

GgaAffx.6177.1.S1_at	GNS	-2.65561	0.0219353
Gga.12566.1.S1_at	LRRC42	-2.65278	0.014394
Gga.11487.1.S1_s_at	KCTD3	-2.64727	0.0111078
Gga.2300.1.S1_at	FAM116A	-2.64391	0.00474394
Gga.18638.1.S1_at	---	-2.64013	0.0332509
GgaAffx.21085.1.S1_at	---	-2.61857	0.00534485
Gga.12885.1.S1_a_at	---	-2.60286	0.0083589
Gga.4999.2.S1_at	ITGA4	-2.60063	0.00568753
Gga.13564.1.S1_at	KIAA1946	-2.60047	0.00146474
Gga.8094.1.S1_a_at	ARHGDIB	-2.59737	0.00269234
Gga.8984.1.S1_at	ACTR3	-2.59431	0.00183919
Gga.870.2.S1_a_at	FGFR1	-2.58933	0.00315655
GgaAffx.5460.1.S1_at	---	-2.58414	0.00193156
GgaAffx.25354.1.S1_at	---	-2.57576	0.0325175
Gga.12410.1.S1_at	---	-2.5732	0.00068458
Gga.6884.1.S1_at	---	-2.57218	0.0217892
Gga.17702.1.S1_at	---	-2.56861	0.0166833
Gga.16033.1.S1_at	CHAD	-2.56843	0.0135357
GgaAffx.21150.1.S1_at	---	-2.55171	0.00803976
Gga.16720.1.S1_at	LOC424878	-2.54573	0.00856228
Gga.8809.2.S1_at	CUL4B	-2.54516	0.00024159
GgaAffx.4102.1.S1_at	SORL1	-2.54515	0.00145041
Gga.18347.1.S1_at	---	-2.5451	1.3078E-05

Gga.18411.1.A1_at	---	-2.54495	0.0331375
GgaAffx.9284.1.S1_at	MCTP1	-2.5429	0.0346377
Gga.12764.1.S1_s_at	SRGAP1	-2.54253	0.0259848
Gga.2954.1.S1_at	LOC420562	-2.5368	0.0307858
Gga.17453.1.S1_at	---	-2.52266	0.00054628
GgaAffx.21161.1.S1_at	FICD	-2.522	0.0228293
Gga.16371.1.S1_s_at	STT3A	-2.51934	0.0464425
Gga.7331.1.S1_at	RAI2	-2.51397	3.8848E-06
Gga.17065.1.S1_at	CCDC66	-2.5104	0.0485004
Gga.8371.1.S1_s_at	ADIPOR2	-2.50481	0.0212025
Gga.10812.1.S1_at	ZBTB38	-2.5041	0.00254073
Gga.14229.1.S1_at	---	-2.50205	1.8534E-05
Gga.15958.1.S1_at	---	-2.50027	0.0341072
Gga.12914.1.S1_at	C12orf11	-2.495	0.0106911
GgaAffx.8020.1.S1_at	CKAP4	-2.49388	0.0228285
GgaAffx.12469.1.S1_s_at	ELOVL6	-2.49363	0.010875
Gga.6261.1.S1_at	MGST1	-2.48501	0.00125077
Gga.2923.1.S1_at	FRY	-2.48352	0.0165004
Gga.8789.1.S1_at	PIK3CD	-2.48268	0.00812969
GgaAffx.20313.1.S1_at	---	-2.47808	0.0372398
Gga.12025.1.S1_at	TMTC3	-2.47698	0.0269596
GgaAffx.20087.1.S1_s_at	SALL4	-2.47543	0.00247978
GgaAffx.23163.3.S1_s_at	MFSD8	-2.47474	0.0160824

Gga.13489.1.S1_at	C2CD2	-2.47216	0.00700622
Gga.4107.1.S1_at	CRY1	-2.47131	0.00045788
Gga.6597.1.S1_at	SDC1	-2.47109	0.00881876
Gga.3264.1.S2_at	AHR	-2.46446	0.0125314
Gga.12862.1.S1_s_at	GNPTAB	-2.46368	0.00142075
Gga.16236.1.S1_s_at	---	-2.46324	8.6257E-05
Gga.3834.1.S2_at	PLEKHA2	-2.46155	0.0002095
Gga.4681.2.S1_s_at	DOCK10	-2.44231	0.0339939
Gga.12347.1.S1_at	VEGFC	-2.43333	0.00188019
GgaAffx.25272.2.S1_s_at	WWC1	-2.43121	0.00936165
Gga.18429.1.S1_at	UBASH3B	-2.42622	0.0112215
GgaAffx.6434.1.S1_s_at	CCDC107	-2.42326	0.0149247
GgaAffx.4562.1.S1_at	CARHSP1	-2.42107	0.00021405
Gga.988.1.S1_at	VDAC1	-2.42071	0.0159065
GgaAffx.6948.2.S1_s_at	TMTC2	-2.42066	0.00078933
GgaAffx.11713.1.S1_s_at	ARHGEF3	-2.4197	0.00251793
Gga.10098.1.S1_s_at	FAP	-2.41646	0.0252329
GgaAffx.4644.1.S1_at	SSH1	-2.41391	0.0094547
GgaAffx.24377.2.S1_s_at	PARVB	-2.41166	0.0183644
Gga.6122.1.S1_a_at	TSPO	-2.41145	0.00559912
GgaAffx.8557.1.S1_s_at	TULP3	-2.40645	0.0158679
Gga.16807.1.S1_s_at	CREB3L2	-2.4052	0.001644
Gga.11728.1.S1_at	TUBD1	-2.39958	0.00138478

Gga.20041.1.S1_at	PCSK6	-2.39452	0.0304895
Gga.9934.1.S1_s_at	ANKRD13A	-2.39337	0.0102379
GgaAffx.23993.1.S1_at	GNPTAB	-2.3923	0.00016757
GgaAffx.13116.1.S1_at	RAP1B	-2.39117	0.00333389
GgaAffx.6963.1.S1_at	KCNK1	-2.38887	0.00052825
Gga.4056.1.S1_at	PXN	-2.3887	0.0238391
Gga.18042.1.S1_at	---	-2.38177	0.00991593
GgaAffx.964.1.S1_at	LOC419409	-2.38046	0.00803109
GgaAffx.21433.1.S1_s_at	STK25	-2.37858	0.00246736
Gga.8069.2.S1_s_at	MGAT4B	-2.37155	0.0284061
Gga.7652.1.S1_at	---	-2.37122	0.0438034
Gga.5631.1.S1_at	IKBIP	-2.37076	0.0111123
GgaAffx.23867.1.S1_at	NHEDC2	-2.36917	0.00027551
GgaAffx.5274.1.S1_at	THBD	-2.36303	0.00046151
GgaAffx.12628.1.S1_at	LOH12CR1	-2.36038	0.00395042
Gga.12872.1.S1_at	---	-2.35854	3.5192E-05
GgaAffx.24844.1.S1_at	LRP12	-2.35789	0.00110734
Gga.19272.1.S1_at	---	-2.34591	0.0111949
Gga.16070.1.S1_s_at	ANTXR2	-2.34579	0.0132408
GgaAffx.23453.2.S1_s_at	FAP	-2.34295	0.0164055
Gga.15862.1.S1_at	C22orf9	-2.34115	0.00275868
Gga.12436.1.S1_at	RAD51AP1	-2.33942	0.0091535
GgaAffx.21088.1.S1_at	ADCK2	-2.33353	0.0324864

Gga.8120.1.S1_at	---	-2.33113	0.00391814
GgaAffx.12750.1.S1_s_at	RASSF3	-2.32986	0.00278802
GgaAffx.23990.1.S1_at	CCDC53	-2.32195	0.00529434
Gga.2152.1.S1_at	LOC395762	-2.32112	0.00256897
GgaAffx.24090.1.S1_s_at	FBXL14	-2.31436	0.0326029
Gga.5542.1.S1_at	TBC1D8	-2.31325	0.00746165
GgaAffx.21698.1.S1_at	SYT1	-2.31018	0.0100173
Gga.15148.1.S1_at	---	-2.30798	0.00105836
GgaAffx.23942.3.S1_s_at	LOC425812 /// TRIOBP	-2.30456	0.017761
GgaAffx.21140.1.S1_s_at	TTLL12	-2.30403	0.00101027
GgaAffx.25839.2.S1_s_at	SBNO1	-2.30255	0.0117132
GgaAffx.8852.1.S1_at	LOC426320	-2.29943	3.161E-05
Gga.1452.1.S1_at	UNC5B	-2.2914	0.00857085
Gga.15231.1.S1_at	C21orf70	-2.28778	0.00697869
GgaAffx.12771.1.S1_at	SLC25A15	-2.28077	0.00177079
Gga.3269.1.S1_at	---	-2.27858	0.0376105
GgaAffx.3442.2.S1_s_at	ARHGEF3	-2.27739	0.0165848
Gga.14848.1.S1_at	---	-2.27418	0.00333393
GgaAffx.5692.3.S1_s_at	CWC22	-2.27151	0.0424264
Gga.13805.1.S1_at	---	-2.26481	3.6756E-05
Gga.1444.1.S1_at	---	-2.26301	0.00164248
Gga.4727.1.S1_at	PPFIBP1	-2.25783	0.00359134
Gga.10138.3.A1_at	---	-2.25602	1.351E-08

Gga.7277.1.S1_at	---	-2.25251	0.0345438
Gga.1792.1.S1_at	C9orf58	-2.25185	0.00178346
Gga.3974.1.S1_at	CCND2	-2.25173	0.00354459
GgaAffx.2187.1.S1_at	ADAM8	-2.25173	0.0152896
Gga.3220.1.S1_at	HEMK1	-2.251	0.00955268
GgaAffx.23130.1.S1_at	---	-2.24721	0.0077687
GgaAffx.12269.1.S1_at	LOC418246	-2.24626	0.00770019
Gga.5578.1.S1_at	---	-2.24131	0.0290606
GgaAffx.20471.2.A1_at	LOC423879	-2.23956	0.0202087
GgaAffx.7613.1.S1_s_at	TRIM7.2	-2.23532	0.00624751
GgaAffx.889.1.S1_at	ZBTB44	-2.23521	0.00390756
Gga.14598.1.S1_at	---	-2.23257	0.00406688
Gga.10188.1.S1_s_at	CASP8AP2	-2.22867	0.0421666
Gga.8123.1.S1_at	FICD	-2.22805	0.0147753
Gga.4775.1.S1_at	---	-2.22718	0.0231658
Gga.13125.1.S1_at	---	-2.22594	0.00171945
Gga.1979.1.S1_at	---	-2.22564	0.0375903
GgaAffx.20839.1.S1_s_at	---	-2.22476	0.00029983
GgaAffx.12193.1.S1_s_at	FGFR1OP2	-2.22467	0.0228862
Gga.2125.1.S1_at	---	-2.21961	0.00031234
Gga.11387.1.S1_s_at	FILIP1L	-2.21939	0.0164845
Gga.8005.1.S1_at	---	-2.2192	0.0193066
GgaAffx.4778.1.S1_s_at	SLC9A3R1	-2.21867	0.00303608

GgaAffx.22623.1.S1_at	ZBED4	-2.21765	0.0016111
Gga.5522.1.S1_at	SLC25A1	-2.21224	0.0150834
Gga.18364.1.S1_at	---	-2.21217	0.00318691
Gga.5365.1.S1_at	GPR157	-2.20978	0.00222369
GgaAffx.11923.1.S1_at	NAPEPLD	-2.20179	0.00270948
Gga.11198.1.S1_at	ZDHHC2	-2.19924	0.0137718
GgaAffx.21381.2.S1_s_at	COX10	-2.19845	0.00535519
Gga.1486.1.S1_at	GNS	-2.19563	0.00882033
Gga.16807.1.S1_at	CREB3L2	-2.19366	0.00056404
GgaAffx.22583.1.S1_s_at	MAPK8IP1	-2.19324	0.0163884
Gga.1851.1.S1_at	---	-2.18773	0.00933015
Gga.8597.1.S1_s_at	LOC429143	-2.18696	0.0143098
Gga.16752.1.S1_at	TUSC2	-2.18387	0.00758651
Gga.19999.1.S1_at	---	-2.18303	0.00872988
Gga.9931.2.S1_at	FAM38A	-2.17601	0.0242465
GgaAffx.8046.1.S1_s_at	SLC41A2	-2.16347	0.00080321
Gga.11456.1.S1_at	CSTA	-2.16122	0.033746
GgaAffx.23800.1.S1_at	SLC35F5	-2.16079	0.00084611
Gga.12429.1.S1_at	LOC419842	-2.16022	0.00045937
Gga.6175.2.A1_at	C12orf31	-2.15574	0.00595166
GgaAffx.9441.2.S1_s_at	LOC776223	-2.14386	0.00755731
Gga.11690.1.S1_at	PHOSPHO2	-2.14293	0.00022825
Gga.4823.1.S1_s_at	---	-2.14262	0.00045715

Gga.2905.1.S1_s_at	LOC424204	-2.13957	0.00036807
Gga.12839.1.S1_at	C14orf79	-2.13919	8.8754E-06
Gga.5207.1.S1_at	---	-2.13891	0.0257949
GgaAffx.10732.1.S1_at	MGAT4A	-2.13658	0.0328886
Gga.13197.1.S1_at	MAST3	-2.13533	0.0123756
GgaAffx.6948.1.S1_at	TMTC2	-2.13377	0.00993044
Gga.8407.1.S1_s_at	C20orf42	-2.13011	0.0178234
Gga.11346.1.S1_at	CRLS1	-2.12958	0.00393077
Gga.2152.1.S2_at	LOC395762	-2.11306	0.0111452
Gga.18520.1.S1_at	---	-2.10934	0.00103076
Gga.11749.1.S1_a_at	CDC42EP3	-2.10493	0.0408438
Gga.5941.1.S1_at	---	-2.10328	0.0232342
GgaAffx.23008.1.S1_s_at	KCTD3	-2.10285	0.0331326
GgaAffx.22565.2.S1_s_at	ALS2	-2.0981	0.0292604
Gga.17032.1.S1_a_at	---	-2.09447	0.0256123
GgaAffx.9262.1.S1_at	MT3	-2.08985	0.00013014
GgaAffx.2790.1.S1_at	TRPV2	-2.08953	0.0351347
GgaAffx.8903.3.S1_at	ARHGAP18	-2.08405	0.00394814
Gga.14009.1.S1_at	---	-2.084	0.0189846
Gga.5362.1.S1_a_at	PDLIM1	-2.0809	0.0317967
Gga.3705.1.S1_at	CENPF	-2.08049	0.0440081
Gga.9318.1.S1_at	---	-2.07893	0.01276
GgaAffx.6597.1.S1_at	TM4SF1	-2.07658	0.0326196

Gga.3572.1.S2_s_at	CD44	-2.07491	0.0150812
Gga.4105.2.S1_a_at	SERPINE2	-2.07137	0.0452109
Gga.3639.1.S1_at	---	-2.06482	0.00075902
GgaAffx.6895.1.S1_at	LASS6	-2.06186	0.0181052
GgaAffx.21206.1.S1_s_at	---	-2.06123	0.0288035
GgaAffx.21427.1.S1_at	CARHSP1	-2.05823	0.0110723
Gga.14549.1.S1_at	PRKCA	-2.058	0.044465
Gga.12019.1.S1_at	KIAA1715	-2.0559	0.00195173
Gga.17623.1.S1_at	CCDC53	-2.05041	0.00018047
GgaAffx.6859.1.S1_at	MTHFD2L	-2.04936	0.0053316
Gga.5286.1.S1_at	---	-2.04722	0.0154961
GgaAffx.6341.2.S1_s_at	---	-2.0458	0.00018756
GgaAffx.12220.1.S1_s_at	TMPO	-2.04452	0.00331754
Gga.3489.1.S1_at	PPIG	-2.04431	0.0296407
Gga.12339.1.S1_at	HNMT	-2.04157	0.0355419
GgaAffx.23623.1.S1_at	AHNAK2	-2.04078	0.0304875
GgaAffx.24028.1.S1_s_at	CREB3L2	-2.03619	0.00105449
Gga.2024.1.S1_at	MSI1	-2.03356	0.00717047
Gga.2519.1.S1_at	---	-2.03349	4.2136E-05
Gga.5219.2.S1_a_at	LOC424109	-2.03316	0.00252216
GgaAffx.20957.1.S1_at	---	-2.02985	0.0144719
GgaAffx.23685.1.S1_at	LIMD1	-2.02774	0.00935617
GgaAffx.3419.1.S1_at	CCDC66	-2.02572	0.0312082

Gga.9760.1.S1_at	C12orf5	-2.02509	0.027347
Gga.1456.1.S1_at	---	-2.02454	0.00055798
Gga.14111.1.S1_at	---	-2.02413	0.0467148
GgaAffx.2474.3.S1_s_at	BCORL1	-2.02408	0.00373776
Gga.13258.1.S1_at	---	-2.02175	0.0365843
Gga.17510.1.S1_at	---	-2.0211	0.0166614
GgaAffx.20518.1.S1_at	---	-2.02056	0.0213131
GgaAffx.12977.1.S1_s_at	SDF2L1	-2.01857	0.0052129
Gga.5850.1.S1_at	MED21	-2.01812	0.0006692
Gga.12848.1.S1_at	CCDC77	-2.01801	0.0382066
GgaAffx.12032.1.S1_s_at	ORAI1	-2.01517	0.00887404
Gga.3330.1.S1_at	SPON1	-2.01262	0.00984754
Gga.1661.2.S1_s_at	ELMO1	-2.01135	0.00200444
Gga.9140.1.S1_at	---	-2.01133	0.0262245
Gga.15357.1.S1_at	---	-2.01085	0.00014549
Gga.10001.1.S1_at	---	-2.01061	0.00258256
Gga.1799.1.S2_at	RPL29	-2.01044	0.0116891
Gga.4107.1.S2_at	CRY1	-2.01	0.00209723
GgaAffx.24406.1.S1_at	SEL1L3	-2.00881	0.0131664
GgaAffx.24354.5.S1_s_at	ITPR2	-2.00582	0.0017277
GgaAffx.8014.1.S1_at	RIC8B	-2.00546	0.0083147
Gga.13607.1.S1_at	---	-2.00476	0.0316127
Gga.9776.1.S1_at	---	-2.00451	0.00595113

GgaAffx.7173.1.S1_at	EEA1	-2.00403	0.00062668
GgaAffx.2958.1.S1_at	SCG3	-2.004	0.0223259
Gga.3130.1.S1_a_at	CLIP1	-2.00242	0.0044655