Orbital Pseudotumor Can Be a Localized Form of Granulomatosis with Polyangiitis As Revealed by Gene Expression Profiling

Supplemental Table 1. Probe sets indicating increased expression of genes in anterior orbit tissues from subjects with GPA compared to uninflamed control tissues.

		Set 1		Set 2	
Probe Set	**Gene Symbol**	**Fold Difference**	**FDR P-value**	**Fold Difference**	**FDR P-value**
211430_s_at	IGHG1 /// IGHG2 /// IGHM /// IGHV4-31	34.60	2.24E-05	155.27	3.34E-04
224795_x_at	IGK /// IGKC	13.93	8.12E-04	81.13	2.89E-04
221671_x_at	IGK /// IGKC	12.66	4.51E-04	68.79	2.47E-04
221651_x_at	IGK /// IGKC	12.74	4.56E-04	60.21	4.35E-04
214677_x_at	IGLC1	9.35	9.63E-03	58.44	1.11E-03
209875_s_at	SPP1	56.68	7.04E-04	54.74	2.51E-03
209138_x_at	IGLC1	10.58	4.35E-03	53.30	9.09E-04
215176_x_at	IGK /// IGKC	13.68	7.08E-03	51.86	3.96E-03
214768_x_at	IGKV2-28 /// IGKV2-28 /// IGKV2D-28 /// IGKV2D-28	7.45	9.93E-03	50.04	8.01E-04
211637_x_at	IGH /// IGHA1 /// IGHA2 /// IGHD /// IGHG1 /// IGHG3 /// IGHG4 /// IGHM /// IGHV3-23 /// IGHV4-31	19.52	7.81E-04	45.18	2.43E-04
211644_x_at	IGK /// IGKC	15.46	2.22E-04	41.83	1.29E-03
216491_x_at	IGHM	15.85	1.30E-03	41.14	3.77E-04
214669_x_at	IGKC	13.28	3.77E-04	41.10	7.07E-04
211645_x_at	IGKV1-17 /// IGKV1-17	9.29	1.49E-02	38.12	4.71E-03
215121_x_at	CYAT1 /// IGLC1 /// IGLV1-44	8.73	4.10E-03	37.02	2.01E-03
215379_x_at	IGLV1-44	8.33	3.30E-03	36.77	1.38E-03
216576_x_at	IGK /// IGKC	13.44	3.05E-03	35.00	3.47E-03
216207_x_at	IGKC	8.30	5.82E-03	32.06	4.47E-03
211634_x_at	IGHM	10.20	6.24E-04	22.73	2.30E-03
211639_x_at	IGH /// IGHA1 /// IGHA2 /// IGHD /// IGHG1 /// IGHG3 /// IGHG4 /// IGHM /// IGHV4-31	8.10	9.08E-03	22.72	1.70E-04
217022_s_at	IGH /// IGHA1 /// IGHA2	7.13	2.76E-02	22.39	6.73E-03
214777_at	IGKV4-1 /// IGKV4-1	11.91	2.35E-03	21.00	1.81E-03
217378_x_at	AC016745.2 /// OTTHUMG00000153338	7.78	7.04E-03	20.71	3.92E-03
217480_x_at	AC127391.1 /// AC128677.4 /// IGKV1OR-2 /// IGKV1OR10-1 /// IGKV1OR2-118 /// OTTHUMG00000155081 /// OTTHUMG00000155090	6.06	7.40E-03	19.70	2.66E-03
214916_x_at	IGHA1 /// IGHA2 /// IGHG1 /// IGHG3 /// IGHM /// IGHV3-23 /// IGHV4-31	8.20	1.49E-03	19.59	2.63E-04
211633_x_at	---	11.54	1.06E-03	17.48	3.25E-03
214836_x_at	IGK /// IGKC	10.13	1.01E-03	17.33	2.51E-03
211643_x_at	IGK /// IGKC	8.78	1.27E-03	17.18	9.98E-03
216510_x_at	IGHA1 /// IGHG1 /// IGHM /// IGHV3-23 /// IGHV4-31	7.64	3.50E-03	16.84	4.41E-03
214973_x_at	IGHD	12.44	3.35E-04	15.87	6.54E-03
211650_x_at	IGH /// IGHA1 /// IGHD /// IGHG1 /// IGHG3 /// IGHM /// IGHV3-23 /// IGHV4-31	6.71	4.03E-04	15.15	8.77E-04
211635_x_at	IGHA1 /// IGHA2 /// IGHD /// IGHG1 /// IGHG3 /// IGHG4 /// IGHM /// IGHV4-31	4.36	2.30E-02	13.69	1.20E-03
211640_x_at	IGHG1 /// IGHM	8.43	3.04E-03	13.65	2.28E-03
209374_s_at	IGHM	6.82	9.16E-03	10.87	4.90E-03
209396_s_at	CHI3L1	20.75	2.12E-04	10.78	2.16E-02

1555745_a_at	LYZ	9.04	2.47E-03	10.53	1.83E-02
217235_x_at	IGLL5	6.24	7.73E-03	8.23	1.51E-02
1568574_x_at	SPP1	5.85	7.91E-03	8.21	7.26E-03
1555756_a_at	CLEC7A	10.12	1.38E-02	8.19	3.73E-02
202834_at	AGT	12.04	1.18E-03	8.18	4.06E-02
237625_s_at	---	7.11	2.96E-02	7.64	1.69E-02
209201_x_at	CXCR4	7.65	7.39E-03	7.58	1.10E-02
211919_s_at	CXCR4	8.67	1.13E-02	7.30	7.46E-03
209395_at	CHI3L1	23.21	1.27E-03	7.21	7.15E-03
216557_x_at	IGHA1 /// IGHD /// IGHG1 /// IGHG3 /// IGHM /// IGHV4-31	5.43	7.66E-03	7.07	1.50E-02
205267_at	POU2AF1	10.59	1.47E-03	7.01	1.47E-02
216542_x_at	IGHA1 /// IGHG1 /// IGHM	5.21	1.58E-02	6.66	9.82E-03
212827_at	IGHM	9.60	3.48E-02	6.49	2.56E-02
222838_at	SLAMF7	5.30	4.72E-03	6.46	3.09E-02
1554406_a_at	CLEC7A	4.06	1.37E-02	6.34	2.23E-04
211429_s_at	SERPINA1	11.48	1.75E-04	6.31	3.80E-02
1558199_at	FN1	4.89	2.41E-02	6.07	6.71E-03
220306_at	FAM46C	4.28	3.16E-02	6.01	2.99E-02
234792_x_at	IGHA1 /// IGHV4-31	6.28	1.79E-02	6.00	3.51E-02
204116_at	IL2RG	8.62	9.70E-04	5.94	1.70E-02
216560_x_at	IGLV3-10 /// IGLV3-10	3.81	1.80E-02	5.85	1.81E-02
219386_s_at	SLAMF8	11.25	8.00E-06	5.80	3.41E-02
217028_at	CXCR4	9.47	1.15E-02	5.70	4.22E-02
219890_at	CLEC5A	7.85	1.70E-06	5.68	6.26E-03
224342_x_at	LOC96610	6.29	2.66E-03	5.59	4.79E-02
211881_x_at	IGLJ3	3.10	4.14E-02	5.53	2.30E-02
213193_x_at	TRBC1	4.96	3.31E-03	5.37	1.81E-02
208506_at	HIST1H3A /// HIST1H3B /// HIST1H3C /// HIST1H3D /// HIST1H3E /// HIST1H3F /// HIST1H3G /// HIST1H3H /// HIST1H3I /// HIST1H3J	6.14	4.07E-03	5.16	1.16E-02
211908_x_at	IGK	3.52	1.58E-02	5.11	8.75E-04
1555349_a_at	ITGB2	6.57	2.61E-04	5.06	7.82E-03
215949_x_at	IGHM	3.95	1.52E-02	5.03	5.48E-03
217281_x_at	IGH /// IGHA1 /// IGHA2 /// IGHG1 /// IGHG2 /// IGHG3 /// IGHM /// IGHV4-31	6.77	6.04E-03	4.99	2.25E-02
203936_s_at	MMP9	10.40	2.16E-05	4.75	1.54E-02
211641_x_at	IGHA1 /// IGHA2 /// IGHD /// IGHG1 /// IGHG3 /// IGHM /// IGHV4-31	3.55	2.25E-02	4.45	1.42E-03
205798_at	IL7R	6.15	1.21E-02	4.42	1.78E-02
226658_at	PDPN	3.28	1.54E-02	4.13	2.46E-02
211991_s_at	HLA-DPA1	3.21	2.22E-02	4.08	5.08E-03
210072_at	CCL19	8.99	1.37E-04	4.07	4.51E-02
208576_s_at	HIST1H3A /// HIST1H3B /// HIST1H3C /// HIST1H3D /// HIST1H3E /// HIST1H3F /// HIST1H3G /// HIST1H3H /// HIST1H3I /// HIST1H3J	9.15	3.00E-03	4.00	1.42E-02
216541_x_at	IGHG1 /// IGHM	5.72	3.58E-03	3.85	1.82E-02
216950_s_at	FCGR1A /// FCGR1B /// FCGR1C	4.12	1.35E-02	3.83	1.84E-02
205997_at	ADAM28	6.21	4.19E-03	3.80	4.67E-02
215946_x_at	IGLL3P	3.68	4.55E-02	3.78	2.39E-02
1552497_a_at	SLAMF6	3.30	4.60E-03	3.75	1.87E-03

212657_s_at	IL1RN	4.06	8.97E-03	3.69	4.68E-03
1553863_at	WDFY4	2.98	5.10E-03	3.68	3.86E-05
229041_s_at	ITGB2-AS1	4.05	1.73E-03	3.68	3.71E-02
219971_at	IL21R	2.88	4.59E-02	3.65	1.61E-03
1552960_at	LRRC15	3.66	2.53E-02	3.64	1.51E-02
209696_at	FBP1	3.32	2.01E-02	3.57	2.58E-02
211796_s_at	TRBC1	4.89	2.23E-02	3.50	1.24E-02
223562_at	PARVG	3.56	2.96E-03	3.49	2.40E-02
205213_at	ACAP1	4.85	6.72E-03	3.48	1.37E-03
202856_s_at	SLC16A3	2.76	8.22E-03	3.46	1.55E-03
204852_s_at	PTPN7	3.90	2.36E-04	3.44	3.27E-03
207794_at	CCR2	4.38	1.22E-02	3.40	1.82E-02
1552806_a_at	SIGLEC10	5.43	8.53E-05	3.35	4.11E-02
222858_s_at	DAPP1	4.07	1.40E-03	3.32	3.07E-02
210423_s_at	SLC11A1	3.48	3.64E-03	3.32	1.89E-02
216243_s_at	IL1RN	3.45	4.57E-02	3.29	5.42E-03
224310_s_at	BCL11B	3.65	4.56E-02	3.25	8.32E-04
228658_at	MIAT	3.25	2.39E-02	3.21	8.95E-03
229721_x_at	DERL3	3.87	8.11E-03	3.21	2.40E-02
233510_s_at	PARVG	5.44	5.90E-04	3.20	5.80E-03
201422_at	IFI30 /// PIK3R2	2.87	2.95E-02	3.13	4.20E-02
202857_at	CNPY2	2.96	7.32E-03	3.13	2.13E-03
221602_s_at	FAIM3	5.07	1.84E-02	3.10	1.69E-02
204430_s_at	SLC2A5	2.37	4.83E-02	3.00	1.81E-02
204429_s_at	SLC2A5	3.53	6.21E-03	2.98	7.75E-03
205713_s_at	COMP	4.31	2.49E-02	2.94	7.18E-03
214366_s_at	ALOX5	2.90	1.57E-02	2.91	3.03E-02
239740_at	ETV6	2.67	2.76E-02	2.89	4.35E-02
220918_at	RUNX1-IT1	3.57	5.54E-03	2.88	4.31E-04
203554_x_at	PTTG1	2.57	3.07E-02	2.87	8.93E-03
205237_at	FCN1	4.51	1.08E-03	2.86	3.76E-03
219559_at	SLC17A9	2.42	3.46E-02	2.78	7.13E-04
219385_at	SLAMF8	2.86	1.38E-02	2.77	3.45E-02
228674_s_at	EML4	2.76	2.09E-02	2.76	6.30E-04
204269_at	PIM2	3.13	2.11E-02	2.71	1.46E-02
204858_s_at	TYMP	2.45	3.30E-02	2.71	1.43E-04
220832_at	TLR8	3.38	2.25E-02	2.70	1.04E-02
208161_s_at	ABCC3	2.57	1.92E-02	2.67	2.88E-03
211795_s_at	FYB	3.55	2.30E-02	2.66	4.04E-02
224406_s_at	FCRL5	3.37	4.13E-02	2.56	2.75E-03
230682_x_at	ABCC3	2.07	4.70E-02	2.56	3.78E-04
204924_at	TLR2	3.14	3.34E-02	2.55	2.61E-02
221698_s_at	CLEC7A	4.22	1.02E-02	2.55	3.43E-02
229045_at	SNX20	2.34	2.24E-02	2.55	3.72E-03
205298_s_at	BTN2A2	2.16	4.26E-02	2.49	6.70E-04
1555626_a_at	SLAMF1	2.89	1.82E-02	2.45	2.13E-02
211884_s_at	CIITA	4.54	2.23E-03	2.43	7.01E-03
232922_s_at	SLC17A9	2.73	4.48E-03	2.41	1.43E-03
214398_s_at	IKBKE	2.71	2.16E-03	2.40	7.24E-04
209641_s_at	ABCC3	2.76	1.64E-02	2.40	1.04E-03
213475_s_at	ITGAL	3.23	2.04E-02	2.39	2.71E-02
208268_at	ADAM28	3.34	2.37E-02	2.38	4.08E-02
212020_s_at	MKI67	2.85	3.13E-02	2.37	6.26E-04

204057_at	IRF8	2.52	1.93E-02	2.36	6.05E-03
215923_s_at	PSD4	3.74	7.04E-03	2.35	2.88E-02
207187_at	JAK3	2.43	6.17E-03	2.35	3.05E-03
208496_x_at	HIST1H3A /// HIST1H3B /// HIST1H3C /// HIST1H3D /// HIST1H3E /// HIST1H3F /// HIST1H3G /// HIST1H3H /// HIST1H3I /// HIST1H3J	2.84	2.37E-02	2.34	2.07E-02
210663_s_at	KYNU	2.27	4.98E-02	2.33	4.55E-02
202954_at	UBE2C	2.50	3.93E-02	2.33	1.87E-03
239287_at	AC079767.4 /// OTTHUMG00000154786	2.10	1.00E-02	2.33	2.52E-02
1555213_a_at	CLEC7A	4.04	1.84E-05	2.31	2.12E-03
221581_s_at	LAT2	2.97	2.84E-03	2.30	4.79E-03
243158_at	---	2.96	1.82E-03	2.28	2.51E-03
222866_s_at	FLVCR2	2.67	4.49E-03	2.27	3.16E-02
205179_s_at	ADAM8	2.44	3.64E-02	2.25	1.04E-02
207521_s_at	ATP2A3	2.79	4.90E-02	2.25	4.26E-02
1570165_at	---	2.80	2.03E-03	2.22	1.69E-02
204401_at	KCNN4	2.54	1.46E-02	2.21	8.35E-03
210184_at	ITGAX	2.86	1.32E-03	2.21	3.00E-02
228094_at	AMICA1	2.30	2.08E-02	2.21	7.28E-04
219256_s_at	SH3TC1	2.86	5.57E-03	2.20	1.55E-03
206934_at	SIRPB1	3.31	1.34E-03	2.20	6.97E-03
1552772_at	CLEC4D	2.00	4.57E-02	2.19	3.48E-02
204254_s_at	VDR	2.18	1.42E-02	2.19	1.42E-02
1556797_at	RNF144A-AS1	2.54	8.29E-03	2.18	1.24E-02
236988_x_at	ITGB2	2.81	1.16E-03	2.18	1.72E-03
216166_at	---	2.88	2.81E-02	2.18	3.26E-02
226906_s_at	ARHGAP9	3.25	3.49E-03	2.18	4.23E-04
222782_s_at	GMIP	2.55	3.53E-03	2.17	2.22E-03
207339_s_at	LTB	2.45	3.98E-02	2.16	6.81E-03
1556959_at	ANHX	2.24	2.48E-02	2.16	1.83E-04
204445_s_at	ALOX5	3.02	9.34E-04	2.15	9.67E-03
204158_s_at	TCIRG1	2.68	5.88E-03	2.15	2.54E-02
244352_at	CD84	2.26	1.87E-02	2.15	1.87E-03
216240_at	MIR1204 /// PVT1	2.20	1.42E-02	2.15	6.23E-03
210804_x_at	SLC8A1	2.57	1.22E-02	2.14	6.27E-03
201291_s_at	TOP2A	4.58	3.49E-03	2.13	4.76E-02
214860_at	SLC9A7	2.67	4.97E-02	2.13	4.89E-02
209670_at	TRAC	2.85	3.82E-02	2.09	4.30E-02
210133_at	CCL11	2.59	6.76E-03	2.09	2.41E-02
238976_at	---	2.19	1.47E-02	2.09	7.46E-03
1563590_at	---	2.20	2.15E-02	2.08	8.69E-03
219316_s_at	FLVCR2	2.07	3.60E-02	2.06	2.48E-02
211210_x_at	SH2D1A	2.06	3.78E-02	2.06	1.90E-03
233855_at	SCIMP	2.07	1.30E-02	2.06	1.14E-03
224249_at	---	2.33	4.18E-02	2.06	2.90E-02
220365_at	ALLC	2.05	3.17E-02	2.05	2.65E-02
234973_at	SLC38A5	2.21	4.77E-02	2.05	9.34E-03
219282_s_at	TRPV2	2.37	2.79E-03	2.05	9.30E-04
235629_at	---	2.13	4.82E-02	2.03	9.29E-03
208364_at	INPP4A	2.30	3.40E-02	2.01	1.20E-03
204265_s_at	GPSM3	2.55	1.10E-02	2.00	1.02E-03
1552671_a_at	SLC9A7	2.46	4.48E-03	1.99	1.64E-03

218600_at	LIMD2	2.66	5.21E-03	1.99	1.56E-02
211188_at	CD84	2.83	1.32E-02	1.98	2.70E-02
236673_at	TIFAB	2.32	2.88E-02	1.97	4.12E-02
229635_at	LOC100505702	2.90	3.18E-02	1.96	2.92E-02
1567687_at	CECR9	1.95	4.78E-02	1.95	3.55E-02
202580_x_at	FOXM1	2.03	8.97E-03	1.94	9.31E-04
213888_s_at	TRAF3IP3	2.30	4.75E-02	1.93	4.22E-02
239769_at	---	2.70	1.61E-02	1.93	4.91E-02
241234_at	LOC100506797	1.86	2.67E-02	1.93	4.27E-02
201631_s_at	IER3	2.56	2.55E-02	1.90	1.48E-02
203379_at	RPS6KA1	2.69	2.08E-02	1.89	3.58E-02
210052_s_at	TPX2	2.32	2.87E-02	1.89	1.71E-02
1566043_at	---	2.24	1.77E-02	1.89	2.97E-02
223987_at	CHRDL2	1.97	2.11E-02	1.88	9.79E-03
218811_at	ORAI2	2.19	2.34E-02	1.88	5.67E-03
227487_s_at	SERPINE2	2.25	4.71E-02	1.88	2.58E-02
227828_s_at	EVA1A	2.43	3.17E-03	1.87	2.30E-02
217424_at	---	2.20	2.81E-02	1.87	2.31E-02
229479_at	---	1.97	4.57E-02	1.87	3.33E-02
206485_at	CD5	2.39	2.39E-02	1.86	1.83E-02
1568846_at	---	1.89	4.83E-02	1.85	4.86E-03
218913_s_at	GMIP	2.54	3.15E-02	1.85	4.54E-02
1555447_at	GPR114	2.23	2.50E-02	1.85	1.09E-02
204561_x_at	APOC2 /// APOC4 /// APOC4-APOC2	2.77	7.85E-03	1.85	4.24E-02
1555282_a_at	PPARGC1B	1.86	4.94E-02	1.84	8.58E-03
1565660_at	FUT6	2.11	1.57E-02	1.82	1.92E-02
203805_s_at	FANCA	2.39	1.25E-02	1.82	2.99E-03
236943_at	---	1.84	4.12E-02	1.82	6.82E-04
1565754_x_at	FGD2	2.23	1.85E-02	1.82	1.65E-02
216316_x_at	OTTHUMG00000161327 /// RP11-548H18.2	1.89	1.25E-02	1.81	3.49E-02
210784_x_at	LILRA6 /// LILRB3	2.25	1.26E-02	1.81	2.90E-02
218376_s_at	MICAL1	2.08	4.87E-02	1.81	1.17E-02
1552787_at	HELB	2.28	2.03E-02	1.81	2.23E-02
202997_s_at	LOXL2	1.96	3.67E-02	1.80	1.64E-03
211178_s_at	PSTPIP1	2.17	1.27E-02	1.80	4.00E-02
206890_at	IL12RB1	1.99	4.32E-02	1.80	3.03E-02
232607_at	---	1.90	8.79E-03	1.79	4.61E-03
1561194_at	---	2.39	1.04E-02	1.79	1.68E-02
1554258_a_at	DNAJC5B	2.08	1.05E-02	1.79	4.94E-02
241780_at	---	2.61	1.48E-02	1.78	2.49E-02
1569003_at	VMP1	1.88	4.90E-02	1.78	2.39E-02
223876_at	SPATA16	2.11	9.95E-03	1.78	9.03E-03
216015_s_at	NLRP3	2.39	1.44E-02	1.78	7.65E-03
217689_at	PTPN1	2.14	2.02E-02	1.77	2.54E-02
1555678_at	ST3GAL3	2.16	1.74E-02	1.77	3.65E-02
223583_at	TNFAIP8L2	2.70	1.38E-04	1.77	3.08E-02
1556471_at	SCML4	2.26	2.03E-02	1.77	2.52E-02
211791_s_at	KCNAB2	2.25	3.21E-02	1.76	5.54E-03
1555096_at	STPG2	2.10	3.48E-02	1.76	2.18E-02
206881_s_at	LILRA3	2.26	1.58E-02	1.75	1.92E-03
230850_at	---	2.38	6.57E-03	1.74	7.48E-03
221414_s_at	DEFB126	2.23	6.61E-03	1.74	2.19E-02
232498_at	LOC377711 /// MROH1	2.33	7.66E-03	1.73	1.89E-02

205643_s_at	PPP2R2B	1.82	2.50E-02	1.73	2.10E-02
211133_x_at	LILRA6 /// LILRB3	2.44	1.58E-03	1.73	2.37E-02
210457_x_at	HMGA1	2.00	4.83E-02	1.72	5.76E-03
217056_at	TRAJ20 /// TRAJ20 /// TRAV36DV7 /// TRAV36DV7	1.72	3.50E-02	1.72	3.08E-03
210225_x_at	LILRA6 /// LILRB3	2.15	1.45E-02	1.72	4.51E-02
207111_at	EMR1	2.12	2.73E-02	1.72	2.72E-02
209367_at	STXBP2	2.19	4.20E-02	1.72	3.78E-02
228685_at	IL17RA	1.99	3.33E-02	1.71	7.53E-03
215937_at	PTGDR	1.88	4.75E-02	1.71	1.48E-02
41660_at	CELSR1	2.07	2.63E-02	1.71	2.15E-02
234412_at	---	2.40	2.07E-02	1.70	2.37E-02
233358_at	---	2.00	2.76E-02	1.70	1.98E-03
235437_at	---	2.42	1.41E-02	1.70	1.65E-02
216337_at	---	2.20	4.10E-02	1.69	1.60E-02
1562562_at	ANKUB1	2.76	2.50E-02	1.69	2.52E-02
221807_s_at	TRABD	2.06	2.19E-02	1.68	4.08E-03
215926_x_at	SNAPC4	1.91	2.46E-02	1.68	5.75E-03
212443_at	NBEAL2	1.93	2.78E-02	1.67	1.06E-02
221334_s_at	FOXP3	2.15	1.13E-02	1.66	1.69E-02
1553647_at	CDYL2	1.76	3.17E-02	1.66	1.39E-02
223545_at	FANCD2	2.04	2.26E-02	1.66	2.98E-02
232830_at	RNF32	1.92	1.86E-02	1.65	2.40E-02
1561718_at	---	1.81	4.69E-02	1.65	8.25E-03
219332_at	MICALL2	1.89	4.55E-02	1.64	3.50E-03
208175_s_at	DMP1	1.98	8.51E-03	1.64	2.56E-02
211543_s_at	GRK6	1.81	4.93E-02	1.64	3.66E-03
237030_at	ACPP	1.71	4.85E-02	1.64	4.94E-02
236322_at	---	2.00	4.44E-02	1.64	3.19E-02
229971_at	GPR114	2.19	8.47E-03	1.62	4.50E-02
202850_at	ABCD3	2.16	3.87E-02	1.62	1.15E-02
215334_at	EFR3B	1.86	4.70E-02	1.61	2.87E-02
240052_at	ITPR1	2.02	4.52E-02	1.61	4.38E-02
216892_at	IGHG1	2.03	1.07E-02	1.61	2.01E-02
242993_at	---	1.98	8.89E-03	1.60	6.52E-03
1562306_at	---	1.74	2.58E-02	1.60	3.99E-02
220655_at	TNIP3	1.97	4.29E-02	1.60	1.54E-02
206298_at	ARHGAP22	1.98	3.68E-02	1.59	4.29E-02
227544_at	TMEM229B	2.01	4.11E-02	1.58	9.35E-03
237153_at	---	1.99	4.93E-02	1.58	4.68E-02
1558167_a_at	MGC16275	1.89	4.41E-02	1.58	1.14E-02
221293_s_at	DEF6	2.06	4.67E-02	1.57	2.42E-02
207746_at	POLQ	1.99	9.43E-03	1.57	7.21E-03
219748_at	TREML2	1.78	4.36E-02	1.57	3.18E-02
232175_at	ARF1	2.29	2.55E-03	1.56	3.00E-02
242381_x_at	---	2.29	1.88E-03	1.55	4.08E-02
239701_at	---	2.19	1.04E-02	1.55	3.82E-02
1557669_at	LOC100132005	1.94	3.57E-02	1.54	3.25E-02
1552637_at	PTPN11	2.13	1.52E-02	1.52	4.78E-02
221924_at	ZMIZ2	1.94	3.59E-02	1.52	8.91E-03
240238_at	---	1.91	1.91E-02	1.51	1.93E-02

Supplemental Table 2. Probe sets indicating decreased expression of genes in anterior orbit tissues from subjects with GPA compared to uninflamed control tissues.

Probe Set	Gene Symbol	Fold Difference	FDR P-value	Fold Difference	FDR P-value
209613_s_at	ADH1B	-68.60	2.24E-04	-129.19	1.75E-06
205913_at	PLIN1	-143.00	1.25E-04	-121.91	1.11E-05
209612_s_at	ADH1B	-105.20	5.19E-05	-110.27	8.66E-06
226304_at	HSPB6	-13.64	1.57E-03	-80.10	9.01E-06
1565162_s_at	MGST1	-37.42	1.95E-04	-69.65	8.09E-07
205478_at	PPP1R1A	-54.07	5.49E-05	-69.20	3.00E-06
214767_s_at	HSPB6	-15.37	2.29E-03	-69.19	9.95E-06
207175_at	ADIPOQ	-91.04	2.35E-04	-67.65	2.89E-05
224918_x_at	MGST1	-15.45	7.38E-05	-56.82	1.08E-05
201540_at	FHL1	-25.32	6.97E-04	-55.33	2.54E-05
231736_x_at	MGST1	-19.60	9.21E-05	-55.13	4.83E-06
219398_at	CIDEC	-47.89	3.18E-05	-52.73	1.65E-05
209283_at	CRYAB	-10.13	2.11E-03	-46.48	4.25E-05
203980_at	FABP4	-43.92	4.28E-04	-44.16	9.18E-05
209699_x_at	AKR1C2 /// LOC101060798	-33.58	5.20E-06	-42.33	1.65E-05
204151_x_at	AKR1C1	-17.12	3.04E-05	-40.77	1.76E-05
212097_at	CAV1	-14.11	7.32E-04	-39.56	6.29E-05
225420_at	GPAM	-48.61	8.73E-05	-38.56	9.04E-05
211356_x_at	LEPR	-24.20	4.22E-04	-37.59	4.87E-06
203324_s_at	CAV2	-12.07	5.31E-03	-35.52	2.89E-06
222513_s_at	SORBS1	-10.64	1.67E-03	-34.00	8.86E-05
222124_at	HIF3A	-18.41	5.96E-03	-31.88	6.02E-05
221796_at	NTRK2	-18.69	2.24E-04	-30.75	1.31E-05
210299_s_at	FHL1	-17.45	1.24E-03	-29.40	9.02E-05
211355_x_at	LEPR	-20.35	6.21E-04	-28.82	1.27E-05
229476_s_at	THRSP	-20.58	2.24E-04	-28.73	4.43E-05
228766_at	CD36	-27.10	3.70E-04	-28.58	8.81E-05
203407_at	PPL	-17.08	8.92E-06	-27.81	1.11E-06
211354_s_at	LEPR	-17.91	8.46E-04	-27.27	7.88E-06
209555_s_at	CD36	-34.54	1.22E-03	-27.21	2.79E-04
219140_s_at	RBP4	-23.29	6.10E-06	-27.16	1.87E-05
216594_x_at	AKR1C1	-16.78	8.65E-06	-27.11	2.07E-05
202036_s_at	SFRP1	-31.23	1.21E-05	-27.05	2.42E-07
218087_s_at	SORBS1	-11.54	1.36E-02	-26.96	1.30E-05
228854_at	---	-8.76	2.75E-02	-26.56	2.93E-05
212230_at	PPAP2B	-13.57	1.30E-03	-26.03	7.54E-06
221748_s_at	TNS1	-9.92	2.77E-04	-25.36	9.14E-04
201432_at	CAT	-10.70	1.20E-03	-25.30	2.14E-05

213524_s_at	G0S2	-13.65	4.73E-03	-24.89	1.41E-04
211653_x_at	AKR1C2 /// LOC101060798	-31.90	6.16E-06	-24.69	1.16E-04
205498_at	GHR	-19.66	1.40E-04	-24.45	7.97E-06
222835_at	THSD4	-13.50	2.27E-03	-24.22	6.56E-05
222484_s_at	CXCL14	-5.60	4.36E-02	-23.53	1.30E-03
204894_s_at	AOC3	-30.59	2.46E-04	-22.59	2.55E-05
225207_at	PDK4	-13.50	1.04E-02	-21.80	8.69E-05
214505_s_at	FHL1	-8.35	1.62E-03	-21.64	2.30E-03
202016_at	MEST	-19.57	2.23E-04	-21.60	9.30E-06
202037_s_at	SFRP1	-21.29	1.77E-04	-21.04	5.91E-08
228224_at	PRELP	-6.57	1.93E-02	-21.02	7.12E-06
209894_at	LEPR	-16.24	5.24E-04	-20.75	2.80E-06
1555740_a_at	MRAP	-19.05	3.34E-04	-20.58	4.22E-05
203851_at	IGFBP6	-9.38	1.10E-03	-20.16	3.77E-06
212226_s_at	PPAP2B	-8.97	4.23E-04	-19.72	5.17E-04
209763_at	CHRDL1	-16.42	9.03E-04	-19.39	6.03E-06
243585_at	ATP13A5	-14.16	3.23E-04	-19.16	6.14E-06
212071_s_at	SPTBN1	-6.58	2.51E-03	-19.02	4.42E-04
201525_at	APOD	-4.64	7.20E-03	-18.85	1.02E-03
204719_at	ABCA8	-21.77	7.39E-04	-18.77	8.67E-06
206488_s_at	CD36	-27.27	7.16E-04	-18.61	8.01E-04
225975_at	PCDH18	-16.49	1.15E-04	-18.31	3.06E-06
229477_at	THRSP	-22.67	5.94E-05	-18.25	3.47E-04
210963_s_at	GYG2	-20.66	4.64E-04	-18.21	6.38E-05
211959_at	IGFBP5	-9.01	9.98E-03	-18.21	1.56E-04
206243_at	TIMP4	-9.02	4.52E-03	-18.13	5.55E-05
221795_at	NTRK2	-9.57	5.88E-03	-18.08	6.62E-06
212741_at	MAOA	-16.69	1.37E-04	-18.01	2.38E-06
203323_at	CAV2	-14.34	1.64E-04	-17.94	5.28E-06
219789_at	NPR3	-15.40	4.13E-04	-17.67	7.73E-07
227646_at	EBF1	-9.45	2.29E-03	-17.15	1.28E-05
203571_s_at	ADIRF	-7.67	2.98E-04	-16.93	3.89E-05
235978_at	FABP4	-23.77	9.51E-05	-16.39	2.18E-04
200696_s_at	GSN	-4.78	3.27E-04	-16.37	5.03E-05
201427_s_at	SEPP1	-9.47	9.21E-03	-16.37	2.19E-03
228409_at	PLIN4	-14.73	1.07E-04	-16.29	4.83E-04
209355_s_at	PPAP2B	-11.09	1.63E-04	-16.23	3.47E-04
49452_at	ACACB	-20.14	2.54E-05	-16.09	2.90E-04
207276_at	CDR1	-15.60	5.33E-04	-16.05	4.85E-06
214040_s_at	GSN	-4.44	1.42E-03	-15.89	1.22E-04
212148_at	PBX1	-10.84	2.62E-03	-15.89	1.68E-05
216048_s_at	RHOBTB3	-10.85	8.91E-04	-15.60	3.07E-04
203680_at	PRKAR2B	-8.95	1.59E-03	-15.17	3.02E-05

212713_at	MFAP4	-9.68	9.32E-04	-15.09	2.06E-05
212667_at	SPARC	-7.00	4.12E-02	-14.91	1.49E-03
204223_at	PRELP	-4.63	2.90E-02	-14.82	1.32E-04
43427_at	ACACB	-14.13	2.32E-05	-14.76	9.21E-05
201150_s_at	TIMP3	-5.74	2.11E-02	-14.75	1.46E-03
201785_at	RNASE1	-5.99	8.03E-04	-14.62	4.10E-04
204141_at	TUBB2A	-9.16	9.21E-03	-14.58	1.45E-04
212509_s_at	MXRA7	-5.00	1.31E-02	-14.57	9.87E-05
217889_s_at	CYBRD1	-4.89	5.15E-03	-14.49	9.50E-05
202035_s_at	SFRP1	-21.78	3.17E-05	-14.48	2.99E-05
203065_s_at	CAV1	-11.12	1.07E-04	-14.18	2.87E-04
236565_s_at	LARP6	-6.56	4.87E-03	-14.16	5.83E-06
226834_at	---	-9.44	3.72E-03	-14.15	6.59E-05
209210_s_at	FERMT2	-7.11	3.37E-02	-14.09	1.16E-04
200672_x_at	SPTBN1	-4.99	1.76E-03	-14.06	2.35E-04
229839_at	SCARA5	-22.63	4.47E-04	-14.04	1.15E-06
1555997_s_at	IGFBP5	-5.21	3.01E-02	-14.04	1.41E-03
201348_at	GPX3	-5.71	3.51E-02	-13.78	5.07E-03
212336_at	EPB41L1	-9.10	7.17E-04	-13.76	4.23E-05
205392_s_at	CCL14 /// CCL15 /// CCL15-CCL14	-8.76	3.15E-04	-13.76	5.18E-05
215096_s_at	ESD	-9.81	1.30E-02	-13.71	2.57E-03
213800_at	CFH	-12.71	1.38E-03	-13.53	6.60E-07
214680_at	NTRK2	-9.11	1.02E-04	-13.44	4.79E-06
209686_at	S100B	-9.86	1.05E-04	-13.43	4.16E-06
222722_at	OGN	-7.60	3.15E-02	-13.28	1.02E-03
214110_s_at	LOC654342	-8.51	3.65E-04	-13.28	7.43E-07
225424_at	GPAM	-14.23	2.30E-04	-13.10	1.42E-04
210298_x_at	FHL1	-11.14	1.51E-03	-13.08	4.08E-03
226806_s_at	NFIA	-17.02	2.22E-05	-12.97	1.10E-06
1556919_at	LEPR	-15.45	2.42E-04	-12.79	1.03E-04
203002_at	AMOTL2	-10.15	7.58E-04	-12.74	1.57E-05
200602_at	APP	-7.37	4.11E-02	-12.61	1.36E-02
202481_at	DHRS3	-5.28	1.38E-02	-12.60	1.54E-04
205382_s_at	CFD	-15.92	1.05E-05	-12.43	8.42E-06
226625_at	TGFBR3	-16.33	3.27E-04	-12.33	4.79E-06
217731_s_at	ITM2B	-9.24	2.84E-02	-12.30	2.41E-03
218736_s_at	PALMD	-5.98	1.25E-03	-12.30	3.42E-05
205330_at	MN1	-8.13	2.48E-03	-12.28	6.18E-05
214584_x_at	ACACB	-23.62	9.70E-05	-12.12	2.46E-04
201425_at	ALDH2	-10.58	1.05E-05	-12.08	8.50E-04
203549_s_at	LPL	-9.08	3.95E-02	-12.05	4.58E-04
1556069_s_at	HIF3A	-5.76	4.36E-02	-12.02	3.37E-04
204154_at	CDO1	-7.63	1.53E-03	-12.01	1.57E-05

207761_s_at	METTL7A	-6.70	2.09E-02	-11.93	1.55E-03
213397_x_at	RNASE4	-10.31	2.54E-03	-11.91	1.96E-06
219059_s_at	LYVE1	-10.55	9.36E-03	-11.89	6.88E-05
228949_at	WLS	-6.57	2.17E-02	-11.88	1.20E-04
235849_at	SCARA5	-10.45	1.06E-03	-11.87	1.28E-06
219304_s_at	PDGFD	-6.06	4.98E-02	-11.85	8.86E-05
216191_s_at	TRDV3	-8.36	4.40E-03	-11.63	1.75E-06
204388_s_at	MAOA	-15.06	1.23E-04	-11.52	1.35E-05
210964_s_at	GYG2	-8.72	3.38E-03	-11.49	8.82E-05
219153_s_at	THSD4	-13.06	3.11E-04	-11.44	3.18E-04
201984_s_at	EGFR	-8.49	2.64E-03	-11.37	9.87E-05
219295_s_at	PCOLCE2	-6.36	1.04E-02	-11.35	3.31E-05
229487_at	EBF1	-8.93	6.65E-04	-11.32	9.63E-06
218730_s_at	OGN	-8.11	1.86E-02	-11.32	1.23E-03
203425_s_at	IGFBP5	-3.51	1.12E-02	-11.31	6.97E-04
207057_at	SLC16A7	-8.94	3.94E-03	-11.21	6.70E-04
200718_s_at	SKP1	-6.74	1.43E-02	-11.21	6.53E-03
222453_at	CYBRD1	-4.92	1.28E-02	-11.18	1.31E-05
201149_s_at	TIMP3	-3.15	4.32E-02	-11.12	2.90E-03
214143_x_at	RPL24	-3.56	3.65E-02	-11.10	8.95E-03
227400_at	NFIX	-5.68	2.92E-03	-11.00	3.52E-05
211458_s_at	GABARAPL1 /// GABARAPL3	-7.09	1.22E-02	-10.83	7.64E-04
225627_s_at	CACHD1	-17.82	1.93E-05	-10.80	1.40E-06
238718_at	---	-11.76	4.33E-04	-10.74	1.89E-06
203430_at	HEBP2	-7.31	1.91E-03	-10.72	5.91E-05
210946_at	PPAP2A	-8.98	7.87E-03	-10.71	2.54E-04
202260_s_at	STXBP1	-6.54	8.32E-05	-10.61	1.28E-05
201885_s_at	CYB5R3	-4.38	3.33E-03	-10.54	9.36E-04
201983_s_at	EGFR	-9.23	4.16E-04	-10.48	1.18E-05
202336_s_at	PAM	-5.20	4.99E-02	-10.48	4.66E-04
217800_s_at	NDFIP1	-8.02	8.82E-03	-10.46	1.15E-03
1560698_a_at	TRHDE-AS1	-13.69	1.29E-03	-10.38	6.53E-05
202973_x_at	FAM13A	-6.11	2.60E-02	-10.36	9.81E-07
224435_at	FAM213A	-7.63	1.46E-03	-10.35	9.09E-05
204755_x_at	HLF	-7.55	1.69E-03	-10.32	5.45E-07
205236_x_at	SOD3	-3.62	1.25E-03	-10.32	1.39E-04
214003_x_at	RPS20 /// SNORD54	-3.14	4.11E-02	-10.31	1.45E-02
1556427_s_at	LRRN4CL	-12.47	6.15E-03	-10.31	5.84E-07
209488_s_at	RBPMS	-9.83	1.40E-03	-10.28	4.96E-03
217890_s_at	PARVA	-5.97	2.84E-03	-10.28	1.16E-04
209160_at	AKR1C3	-10.26	2.21E-04	-10.25	5.44E-04
224975_at	NFIA	-7.00	1.20E-02	-10.23	1.18E-04
202409_at	IGF2	-7.85	8.62E-04	-10.22	1.95E-03

215039_at	LOC339524	-12.69	9.07E-04	-10.16	1.62E-06
209543_s_at	CD34	-8.02	3.06E-04	-10.14	6.14E-06
211958_at	IGFBP5	-4.21	3.83E-03	-10.10	9.25E-05
221814_at	GPR124	-5.02	1.26E-02	-10.09	1.44E-03
235708_at	KLB	-12.62	8.31E-05	-10.05	1.97E-05
223623_at	C2orf40	-11.33	5.22E-03	-10.01	3.18E-04
226377_at	NFIC	-5.32	9.73E-03	-9.98	1.56E-04
224743_at	IMPAD1	-6.59	2.37E-03	-9.94	8.99E-04
226763_at	SESTD1	-4.89	8.02E-03	-9.87	1.07E-04
232712_at	---	-9.34	1.18E-03	-9.85	8.88E-08
209289_at	NFIB	-5.94	3.90E-02	-9.83	1.56E-04
225202_at	RHOBTB3	-8.41	6.84E-03	-9.82	6.70E-05
229563_s_at	RPL10A	-3.68	3.71E-02	-9.77	1.89E-02
207302_at	SGCG	-11.05	1.84E-04	-9.76	9.87E-05
201061_s_at	STOM	-4.42	2.20E-02	-9.74	3.08E-03
220037_s_at	LYVE1	-15.82	8.59E-03	-9.72	8.43E-04
200845_s_at	PRDX6	-6.94	9.68E-03	-9.69	4.03E-04
201963_at	ACSL1	-11.03	6.22E-03	-9.63	5.70E-04
203400_s_at	TF	-11.21	7.87E-03	-9.60	3.34E-03
227530_at	AKAP12	-8.30	1.34E-02	-9.60	1.29E-05
205083_at	AOX1	-14.68	3.46E-03	-9.60	3.86E-06
202017_at	EPHX1	-7.02	1.05E-05	-9.53	1.90E-04
219747_at	NDNF	-11.52	2.43E-03	-9.52	1.40E-05
218175_at	CCDC92	-4.27	4.48E-02	-9.49	2.36E-04
228155_at	FAM213A	-6.51	7.50E-04	-9.35	1.70E-04
1555854_at	AKR1C1 /// AKR1C2 /// LOC101060798	-5.90	1.51E-02	-9.34	8.72E-06
204731_at	TGFBR3	-12.78	8.46E-04	-9.34	2.44E-05
205410_s_at	ATP2B4	-4.86	2.70E-02	-9.26	4.47E-04
202565_s_at	SVIL	-5.26	1.46E-02	-9.23	8.54E-05
213348_at	CDKN1C	-10.90	5.91E-04	-9.22	2.58E-05
204753_s_at	HLF	-6.40	1.14E-02	-9.21	1.12E-06
221016_s_at	TCF7L1	-13.39	1.32E-05	-9.21	1.79E-05
212339_at	EPB41L1	-6.13	4.33E-04	-9.15	7.06E-06
217525_at	OLFML1	-5.16	1.40E-02	-9.09	1.01E-05
227334_at	USP54	-5.35	8.63E-03	-9.02	1.97E-06
214629_x_at	RTN4	-5.63	1.86E-02	-9.02	5.24E-03
210139_s_at	PMP22	-6.14	2.79E-02	-9.02	2.56E-04
209541_at	IGF1	-6.54	4.61E-02	-9.01	3.73E-03
211110_s_at	AR	-8.37	4.75E-04	-9.01	4.28E-05
225381_at	MIR100HG	-8.52	1.49E-02	-9.00	6.97E-05
209343_at	EFHD1	-8.03	1.50E-03	-9.00	7.50E-06
201429_s_at	RPL37A	-2.92	3.61E-02	-8.98	1.93E-02
213855_s_at	LIPE	-11.72	2.10E-04	-8.91	4.72E-04

1552509_a_at	CD300LG	-9.30	6.31E-03	-8.89	3.52E-03
205960_at	PDK4	-7.93	1.25E-02	-8.88	1.00E-03
221747_at	TNS1	-7.71	3.30E-04	-8.83	1.17E-04
206481_s_at	LDB2	-10.29	4.23E-03	-8.77	2.38E-06
227373_at	ATXN1L	-8.46	1.14E-02	-8.74	2.08E-04
215726_s_at	CYB5A	-7.44	6.54E-04	-8.68	2.24E-03
239262_at	OTTHUMG00000167230 /// RP11-736K20.4	-6.81	5.69E-04	-8.65	1.08E-05
229800_at	DCLK1	-7.83	2.06E-02	-8.62	1.61E-04
211922_s_at	CAT	-6.00	1.46E-03	-8.60	8.47E-05
203424_s_at	IGFBP5	-5.71	2.79E-03	-8.59	1.04E-03
224996_at	ASPH	-6.03	3.93E-02	-8.58	4.74E-04
211945_s_at	ITGB1	-4.96	4.23E-02	-8.55	4.53E-02
223727_at	KCNIP2	-4.66	9.43E-03	-8.52	1.86E-05
200878_at	EPAS1	-6.22	1.27E-02	-8.46	4.58E-03
201034_at	ADD3	-6.64	3.05E-02	-8.42	3.97E-03
221246_x_at	TNS1	-5.13	1.51E-04	-8.41	3.65E-03
1554574_a_at	CYB5R3	-3.35	3.44E-03	-8.36	4.98E-04
228347_at	SIX1	-9.09	1.37E-04	-8.35	2.75E-06
224895_at	YAP1	-8.10	1.88E-03	-8.35	9.95E-04
211726_s_at	FMO2	-5.62	2.07E-02	-8.33	1.52E-04
213706_at	GPD1	-5.55	6.79E-04	-8.33	3.27E-04
227561_at	DDR2	-7.57	9.61E-04	-8.32	2.87E-06
206767_at	RBMS3	-6.04	2.44E-03	-8.25	2.84E-05
225442_at	DDR2	-6.45	9.16E-04	-8.24	3.99E-05
211819_s_at	SORBS1	-7.15	2.99E-03	-8.22	5.18E-04
201539_s_at	FHL1	-9.72	2.54E-03	-8.21	2.99E-03
209807_s_at	NFIX	-4.98	6.75E-04	-8.19	1.54E-04
202935_s_at	SOX9	-8.21	1.31E-03	-8.17	4.05E-05
201106_at	GPX4	-3.31	5.28E-04	-8.13	4.58E-05
209487_at	RBPMS	-9.26	1.05E-03	-8.10	1.20E-04
242197_x_at	CD36	-10.76	2.63E-02	-8.06	6.21E-03
202976_s_at	RHOBTB3	-7.77	2.03E-03	-8.06	6.12E-04
207275_s_at	ACSL1	-5.49	2.10E-02	-8.04	7.78E-03
204688_at	SGCE	-5.99	8.27E-03	-8.03	1.74E-04
1555230_a_at	KCNIP2	-11.41	4.02E-03	-8.02	3.10E-04
219064_at	ITIH5	-5.71	1.18E-03	-8.02	4.27E-04
212650_at	EHBP1	-5.49	5.83E-03	-8.02	2.05E-03
235570_at	RBMS3	-7.15	5.77E-03	-8.00	9.30E-06
1558647_at	SH3D19	-5.80	1.56E-03	-7.95	1.08E-05
213068_at	DPT	-4.40	2.35E-02	-7.93	1.98E-03
221012_s_at	TRIM8	-4.99	6.94E-03	-7.89	1.02E-04
227899_at	VIT	-8.95	2.48E-03	-7.85	7.39E-06

205908_s_at	OMD	-6.72	2.65E-02	-7.80	6.69E-05
226632_at	CYGB	-6.63	2.63E-03	-7.79	3.73E-05
203632_s_at	GPRC5B	-6.42	2.05E-03	-7.74	1.18E-04
201542_at	SAR1A	-5.39	1.83E-02	-7.74	2.22E-03
208695_s_at	RPL39	-3.77	1.49E-02	-7.73	4.62E-02
211066_x_at	PCDHGA1 /// PCDHGA10 /// PCDHGA11 /// PCDHGA12 /// PCDHGA2 /// PCDHGA3 /// PCDHGA4 /// PCDHGA5 /// PCDHGA6 /// PCDHGA7 /// PCDHGA8 /// PCDHGA9 /// PCDHGB1 /// PCDHGB2 /// PCDHGB3 /// PCDHGB4 /// PCDHGB5 /// PCDHGB6 /// PCDHGB7 /// PCDHGC3 /// PCDHGC4 /// PCDHGC5	-3.48	3.88E-02	-7.72	1.58E-04
243368_at	---	-6.18	3.95E-02	-7.70	3.66E-03
225016_at	APCDD1	-4.62	7.88E-03	-7.69	1.81E-06
212218_s_at	FASN	-4.35	4.30E-04	-7.68	3.87E-02
201308_s_at	11-Sep	-6.56	3.16E-03	-7.64	3.01E-04
200872_at	S100A10	-2.91	4.32E-02	-7.61	2.63E-03
204955_at	SRPX	-5.79	1.65E-02	-7.58	2.29E-04
209079_x_at	PCDHGA1 /// PCDHGA10 /// PCDHGA11 /// PCDHGA12 /// PCDHGA2 /// PCDHGA3 /// PCDHGA4 /// PCDHGA5 /// PCDHGA6 /// PCDHGA7 /// PCDHGA8 /// PCDHGA9 /// PCDHGB1 /// PCDHGB2 /// PCDHGB3 /// PCDHGB4 /// PCDHGB5 /// PCDHGB6 /// PCDHGB7 /// PCDHGC3 /// PCDHGC4 /// PCDHGC5	-3.72	2.06E-02	-7.54	1.33E-04
232204_at	EBF1	-8.59	8.78E-03	-7.54	7.32E-05
212151_at	PBX1	-4.49	1.89E-02	-7.51	1.70E-04
222116_s_at	TBC1D16	-6.36	2.53E-04	-7.51	1.13E-07
214363_s_at	MATR3 /// SNHG4	-6.44	4.76E-02	-7.49	3.45E-02
209154_at	P2RX5-TAX1BP3 /// TAX1BP3	-4.43	4.93E-02	-7.47	2.14E-02
212670_at	ELN	-5.88	1.92E-03	-7.47	8.38E-04
230319_at	---	-11.85	7.39E-04	-7.46	2.64E-05
207040_s_at	ST13	-3.43	4.16E-02	-7.45	4.39E-03
225162_at	SH3D19	-5.81	2.12E-02	-7.44	2.16E-05
200949_x_at	RPS20 /// SNORD54	-2.59	2.63E-02	-7.44	1.37E-02
204112_s_at	HNMT	-6.10	5.06E-03	-7.39	3.52E-04
226169_at	SBF2	-7.50	7.84E-03	-7.37	2.68E-04
212419_at	ZCCHC24	-6.06	3.14E-04	-7.37	1.67E-05
217892_s_at	LIMA1	-6.21	1.54E-02	-7.35	4.08E-03
211026_s_at	MGLL	-5.90	7.18E-05	-7.33	1.42E-03
208383_s_at	PCK1	-14.29	5.66E-03	-7.33	1.77E-03
212372_at	MYH10	-6.62	2.54E-03	-7.32	4.46E-05
222423_at	NDFIP1	-3.35	6.73E-03	-7.31	6.59E-06
224881_at	VKORC1L1	-6.29	1.48E-03	-7.31	3.65E-05

209687_at	CXCL12	-4.53	3.33E-02	-7.31	8.75E-04
219689_at	SEMA3G	-8.96	8.38E-04	-7.30	8.18E-05
226018_at	C7orf41	-7.13	3.93E-03	-7.26	8.63E-06
209581_at	PLA2G16	-8.51	2.61E-04	-7.25	6.94E-05
1566472_s_at	LOC100996506 /// RETSAT	-7.60	1.24E-04	-7.23	4.10E-04
228728_at	CPED1	-4.55	3.78E-02	-7.19	1.31E-04
220736_at	SLC19A3	-10.23	2.55E-03	-7.19	3.95E-03
219779_at	ZFHX4	-6.29	1.57E-02	-7.14	6.09E-04
218665_at	FZD4	-4.85	5.61E-03	-7.14	2.40E-04
204235_s_at	GULP1	-5.90	1.20E-03	-7.14	4.28E-06
207092_at	LEP	-3.90	1.00E-02	-7.13	8.40E-03
209047_at	AQP1	-4.94	7.18E-03	-7.12	1.21E-02
214761_at	ZNF423	-5.75	1.47E-02	-7.09	2.05E-05
229357_at	ADAMTS5	-6.56	3.27E-02	-7.08	3.28E-05
201324_at	EMP1	-6.39	2.12E-02	-7.08	5.17E-04
213075_at	OLFML2A	-5.68	2.64E-02	-7.06	3.28E-05
218656_s_at	LHFP	-5.17	4.75E-02	-7.04	2.24E-05
213347_x_at	RPS4X	-3.23	3.40E-02	-7.03	1.63E-02
224822_at	DLC1	-6.47	1.81E-03	-7.01	3.48E-05
204041_at	MAOB	-7.79	4.20E-05	-7.00	1.04E-04
218864_at	TNS1	-4.92	3.37E-03	-7.00	4.44E-04
201116_s_at	CPE	-4.31	3.13E-02	-6.99	9.18E-05
237351_at	LOC100652994	-6.81	9.10E-05	-6.98	8.56E-06
203088_at	FBLN5	-5.76	3.21E-03	-6.97	1.08E-04
233571_x_at	PPDPF	-2.42	4.70E-02	-6.97	5.76E-03
205779_at	RAMP2	-4.40	3.70E-03	-6.97	1.59E-05
200026_at	RPL34	-2.90	4.03E-02	-6.97	4.09E-02
224970_at	NFIA	-5.89	3.12E-03	-6.96	1.67E-05
205883_at	ZBTB16	-5.86	4.32E-03	-6.93	3.59E-04
229319_at	OTTHUMG00000175939 /// RP3-425C14.4	-5.49	8.80E-03	-6.89	1.55E-05
215617_at	SPATS2L	-3.96	4.49E-02	-6.88	5.18E-05
216321_s_at	NR3C1	-6.98	2.11E-02	-6.88	3.69E-03
220751_s_at	FAXDC2	-3.30	5.80E-03	-6.87	5.09E-06
209513_s_at	HSDL2	-4.67	4.21E-03	-6.86	1.76E-06
224597_at	LINC00657	-5.06	4.46E-02	-6.86	3.52E-04
204424_s_at	LMO3	-7.61	2.21E-04	-6.85	4.08E-05
201036_s_at	HADH	-4.06	7.07E-03	-6.84	5.89E-05
230418_s_at	GALNT16	-9.87	9.80E-03	-6.84	1.36E-04
219563_at	LINC00341	-5.05	5.28E-04	-6.83	1.15E-05
223349_s_at	BOK	-6.87	6.81E-05	-6.83	3.38E-04
211453_s_at	AKT2	-3.27	6.63E-03	-6.82	1.33E-04
58780_s_at	ARHGEF40	-5.36	1.05E-02	-6.81	3.47E-05
202921_s_at	ANK2	-6.76	1.08E-02	-6.81	6.45E-04

204971_at	CSTA	-5.28	2.22E-02	-6.80	1.82E-03
205082_s_at	AOX1	-4.79	2.74E-02	-6.79	5.44E-05
1559388_a_at	LYNX1	-4.26	5.81E-03	-6.78	9.22E-05
223276_at	SMIM3	-6.43	6.52E-03	-6.76	1.54E-03
207030_s_at	CSRP2	-4.40	3.19E-02	-6.76	3.51E-04
200673_at	LAPTM4A	-4.55	1.05E-02	-6.75	7.69E-03
211698_at	EID1	-5.20	2.40E-02	-6.71	2.89E-03
223601_at	OLFM2	-6.23	9.44E-04	-6.70	2.63E-03
224604_at	C4orf3	-3.51	4.43E-02	-6.70	1.53E-04
212158_at	SDC2	-5.63	3.43E-02	-6.70	1.21E-04
201828_x_at	FAM127A	-3.20	2.67E-02	-6.69	6.37E-04
225534_at	SMIM19	-5.31	2.09E-02	-6.68	8.65E-04
202551_s_at	CRIM1	-5.61	3.16E-02	-6.67	4.35E-04
210519_s_at	NQO1	-4.50	2.54E-03	-6.66	7.05E-05
227041_at	SESTD1	-4.64	1.07E-02	-6.65	1.47E-05
207764_s_at	HIPK3	-3.66	2.72E-02	-6.64	1.55E-02
207076_s_at	ASS1	-6.25	2.95E-04	-6.62	1.82E-04
200795_at	SPARCL1	-4.76	1.47E-02	-6.56	4.38E-02
227529_s_at	AKAP12	-7.47	3.80E-03	-6.56	8.67E-05
228082_at	CLMP	-5.52	5.39E-03	-6.55	2.58E-03
205717_x_at	PCDHGA1 /// PCDHGA10 /// PCDHGA11 /// PCDHGA12 /// PCDHGA2 /// PCDHGA3 /// PCDHGA4 /// PCDHGA5 /// PCDHGA6 /// PCDHGA7 /// PCDHGA8 /// PCDHGA9 /// PCDHGB1 /// PCDHGB2 /// PCDHGB3 /// PCDHGB4 /// PCDHGB5 /// PCDHGB6 /// PCDHGB7 /// PCDHGC3 /// PCDHGC4 /// PCDHGC5	-4.49	1.46E-02	-6.54	1.48E-04
213004_at	ANGPTL2	-4.33	2.56E-02	-6.51	6.71E-04
205168_at	DDR2	-6.50	4.96E-04	-6.49	8.89E-05
202410_x_at	IGF2 /// INS-IGF2	-6.63	1.09E-03	-6.46	5.43E-03
201022_s_at	DSTN	-4.61	2.34E-02	-6.46	4.20E-03
1559840_s_at	TBX18	-5.56	8.29E-03	-6.45	7.06E-06
200758_s_at	NFE2L1	-2.96	2.75E-02	-6.45	9.33E-04
222725_s_at	PALMD	-8.79	2.10E-04	-6.44	5.58E-05
223044_at	SLC40A1	-6.39	4.24E-02	-6.42	2.17E-02
200025_s_at	RPL27	-3.11	4.70E-02	-6.42	4.00E-02
45297_at	EHD2	-5.20	4.84E-04	-6.41	8.29E-05
219549_s_at	RTN3	-4.51	4.96E-03	-6.40	1.06E-03
220298_s_at	SPATA6	-4.81	3.82E-03	-6.38	2.14E-06
211730_s_at	POLR2L	-2.47	5.63E-03	-6.38	3.62E-04
210996_s_at	YWHAE	-3.48	2.52E-02	-6.38	2.82E-02
212653_s_at	EHBP1	-7.82	1.81E-04	-6.34	2.06E-05
242541_at	ABCA9	-6.35	1.02E-02	-6.32	6.04E-04

200637_s_at	PTPRF		-7.29	1.51E-05	-6.32	6.09E-04
212759_s_at	TCF7L2		-4.59	5.49E-03	-6.31	1.02E-03
202975_s_at	RHOBTB3		-6.97	2.23E-03	-6.31	2.49E-03
204115_at	GNG11		-10.68	1.39E-03	-6.30	1.61E-04
203394_s_at	HES1		-8.80	1.78E-03	-6.30	2.21E-03
206101_at	ECM2		-5.50	2.36E-02	-6.29	1.01E-04
201336_at	VAMP3		-3.69	3.65E-02	-6.29	5.12E-03
201366_at	ANXA7		-5.81	2.36E-02	-6.28	1.16E-02
207255_at	LEPR		-7.61	3.12E-04	-6.28	1.17E-04
210990_s_at	LAMA4		-4.51	2.70E-03	-6.26	8.87E-04
224593_at	ZNF664		-7.11	2.88E-03	-6.25	5.05E-04
217837_s_at	CHMP3 /// RNF103-CHMP3		-4.83	5.77E-03	-6.25	4.46E-05
201860_s_at	PLAT		-9.89	2.98E-03	-6.24	4.43E-04
217963_s_at	NGFRAP1		-5.97	1.04E-03	-6.22	1.71E-04
212136_at	ATP2B4		-4.89	4.23E-03	-6.21	4.18E-03
226677_at	ZNF521		-7.71	3.43E-02	-6.21	3.52E-05
227466_at	FAM200B		-3.11	4.68E-02	-6.19	1.35E-03
218245_at	TSKU		-7.85	1.64E-04	-6.17	1.39E-04
221321_s_at	KCNIP2		-11.94	8.17E-04	-6.17	2.31E-04
200007_at	SRP14		-4.20	4.97E-02	-6.16	2.04E-02
226895_at	NFIC		-4.34	2.90E-02	-6.16	6.09E-03
224976_at	NFIA		-6.80	4.37E-04	-6.16	6.45E-04
203813_s_at	SLIT3		-6.78	1.86E-04	-6.16	1.44E-04
209616_s_at	CES1 /// LOC100653057		-7.84	8.10E-04	-6.16	6.44E-03
1552616_a_at	ACACB		-5.90	3.22E-03	-6.15	1.24E-03
223063_at	C1orf198		-5.10	3.52E-04	-6.15	5.30E-06
225274_at	PCYOX1		-5.16	4.12E-03	-6.11	1.35E-04
216339_s_at	LOC101060681 /// TNXA /// TNXB		-6.26	8.03E-04	-6.11	2.95E-03
226448_at	FAM89A /// MIR1182		-4.54	7.90E-04	-6.10	8.74E-06
213151_s_at		7-Sep	-5.45	4.47E-02	-6.08	2.26E-02
238151_at	---		-3.83	1.05E-03	-6.05	7.81E-07
208790_s_at	PTRF		-4.30	7.89E-04	-6.04	2.35E-04
210825_s_at	PEBP1		-3.77	1.58E-02	-6.02	3.12E-04
1555889_a_at	CRTAP /// LOC100653071		-3.44	2.41E-02	-6.02	2.05E-02
213247_at	SVEP1		-4.66	1.73E-03	-6.01	1.86E-05
202920_at	ANK2		-6.02	1.69E-02	-6.01	1.37E-03
208789_at	PTRF		-3.31	6.63E-04	-5.98	2.08E-05
212494_at	TENC1		-2.61	2.62E-02	-5.98	7.88E-06
220477_s_at	TMEM230		-4.75	2.57E-02	-5.98	1.19E-02
213342_at	YAP1		-6.07	5.99E-03	-5.96	1.66E-03
202202_s_at	LAMA4		-6.23	3.46E-03	-5.95	3.91E-04
221478_at	BNIP3L		-5.81	3.57E-03	-5.94	1.67E-03
204389_at	MAOA		-6.70	4.16E-03	-5.93	2.40E-04

209185_s_at	IRS2	-3.70	4.40E-02	-5.90	1.61E-04
202686_s_at	AXL	-4.69	3.05E-02	-5.90	3.56E-04
212239_at	PIK3R1	-3.65	3.78E-02	-5.89	3.05E-05
212135_s_at	ATP2B4	-3.86	5.03E-03	-5.88	8.06E-03
214433_s_at	SELENBP1	-7.66	1.60E-05	-5.87	2.65E-05
225102_at	MGLL	-5.62	1.92E-05	-5.87	1.45E-04
209348_s_at	MAF	-8.90	1.94E-02	-5.84	2.19E-03
213702_x_at	ASAH1	-4.60	4.12E-02	-5.83	4.29E-02
223132_s_at	TRIM8	-3.59	1.55E-02	-5.82	5.81E-04
1560697_at	TRHDE-AS1	-9.71	1.04E-03	-5.81	1.41E-03
202371_at	TCEAL4	-5.00	2.83E-02	-5.81	9.30E-04
209135_at	ASPH	-3.96	3.31E-02	-5.81	8.87E-04
218010_x_at	PPDPF	-2.41	2.95E-02	-5.80	3.05E-03
1553961_s_at	SNX21	-4.09	6.21E-03	-5.80	2.88E-05
208770_s_at	EIF4EBP2	-3.51	7.70E-03	-5.79	1.80E-03
210869_s_at	MCAM	-6.23	1.44E-03	-5.77	2.23E-03
226932_at	SSPN	-4.13	3.00E-02	-5.76	7.04E-05
212566_at	MAP4	-4.81	2.28E-02	-5.75	1.18E-03
205726_at	DIAPH2	-3.93	2.13E-02	-5.73	1.55E-04
202053_s_at	ALDH3A2	-4.17	2.31E-02	-5.72	3.68E-04
209298_s_at	ITSN1	-5.42	2.91E-02	-5.71	1.63E-03
210896_s_at	ASPH	-3.78	2.04E-02	-5.70	8.60E-04
204537_s_at	GABRE /// MIR224 /// MIR452	-7.42	4.95E-05	-5.69	4.69E-04
1553102_a_at	CCDC69	-4.40	4.88E-02	-5.68	2.40E-03
209309_at	AZGP1	-9.95	2.09E-03	-5.66	3.11E-03
201968_s_at	PGM1	-3.97	3.95E-03	-5.65	2.64E-05
203335_at	PHYH	-5.38	2.28E-03	-5.64	6.47E-05
210517_s_at	AKAP12	-6.65	5.57E-03	-5.64	3.59E-05
213029_at	NFIB	-5.21	6.54E-03	-5.64	9.01E-05
201387_s_at	UCHL1	-4.03	5.59E-03	-5.63	8.39E-05
227419_x_at	PLAC9	-3.58	9.35E-03	-5.63	6.21E-06
1557938_s_at	PTRF	-4.00	8.15E-03	-5.63	4.71E-04
200985_s_at	CD59	-4.15	4.07E-02	-5.62	6.87E-03
223087_at	ECHDC1	-6.19	6.03E-03	-5.60	7.76E-03
214279_s_at	NDRG2	-2.89	2.59E-02	-5.59	9.95E-05
201701_s_at	PGRMC2	-4.81	3.79E-03	-5.55	1.05E-03
205341_at	EHD2	-3.76	4.10E-03	-5.54	1.03E-04
201787_at	FBLN1	-4.02	8.01E-03	-5.52	4.81E-03
204823_at	NAV3	-5.53	1.28E-02	-5.51	1.72E-06
212154_at	SDC2	-3.85	3.62E-02	-5.49	2.07E-03
213032_at	NFIB	-8.79	9.42E-03	-5.48	8.09E-04
209702_at	FTO	-5.02	9.61E-03	-5.47	3.96E-04
224581_s_at	NUCKS1	-4.38	6.71E-03	-5.46	8.91E-04

227957_at	GSN	-2.95	1.62E-02	-5.46	1.26E-05
201812_s_at	C4orf46 /// TOMM7	-3.00	6.50E-03	-5.45	3.36E-04
57588_at	SLC24A3	-4.90	6.10E-03	-5.43	4.31E-05
210881_s_at	IGF2 /// INS-IGF2	-4.87	3.33E-03	-5.42	3.45E-03
227958_s_at	GSN	-4.60	6.10E-03	-5.41	2.38E-05
228186_s_at	RSPO3	-7.67	2.99E-03	-5.40	7.84E-05
208847_s_at	ADH5	-5.62	2.05E-04	-5.39	2.08E-03
206929_s_at	NFIC	-2.33	3.62E-02	-5.38	4.96E-04
208732_at	RAB2A	-3.72	4.06E-02	-5.38	2.58E-04
224999_at	EGFR	-4.27	1.91E-02	-5.35	2.55E-04
213419_at	APBB2	-4.55	2.80E-02	-5.35	5.43E-03
201628_s_at	RRAGA	-4.57	2.07E-02	-5.35	6.80E-03
206930_at	GLYAT	-4.54	2.37E-03	-5.35	4.94E-03
221619_s_at	MTCH1	-3.24	4.36E-02	-5.34	9.00E-03
212646_at	RFTN1	-3.56	2.88E-02	-5.33	4.69E-03
202133_at	WWTR1	-5.18	2.09E-02	-5.32	2.37E-03
205253_at	PBX1	-5.08	1.65E-03	-5.30	2.82E-04
223836_at	FGFBP2	-4.01	4.47E-02	-5.30	3.88E-04
222457_s_at	LIMA1	-4.98	3.26E-02	-5.30	4.34E-03
203562_at	FEZ1	-3.99	9.26E-03	-5.29	3.67E-05
203414_at	MMD	-8.39	1.11E-03	-5.28	3.29E-04
204963_at	SSPN	-5.53	1.19E-02	-5.28	1.86E-05
208660_at	CS	-3.24	3.94E-02	-5.27	3.24E-02
225352_at	SEC62	-4.87	1.13E-02	-5.27	5.69E-04
203336_s_at	ITGB1BP1	-3.87	4.34E-03	-5.26	2.61E-06
39729_at	PRDX2	-4.29	5.72E-03	-5.24	1.07E-03
213895_at	EMP1	-7.16	7.66E-03	-5.24	1.59E-03
224445_s_at	ZFYVE21	-3.47	7.84E-03	-5.23	1.34E-05
206955_at	AQP7 /// LOC100509620	-6.39	2.47E-03	-5.22	3.02E-04
216331_at	ITGA7	-3.74	6.21E-03	-5.22	4.66E-03
202123_s_at	ABL1	-3.95	1.48E-03	-5.21	1.36E-03
209290_s_at	NFIB	-5.41	2.29E-02	-5.21	9.25E-03
229011_at	---	-5.09	1.08E-02	-5.20	3.52E-05
203859_s_at	PALM	-4.14	5.79E-04	-5.19	7.47E-05
201412_at	LRP10	-3.58	2.23E-02	-5.19	2.24E-02
222454_s_at	PARVA	-3.72	1.87E-02	-5.18	6.40E-04
212977_at	CXCR7	-6.04	3.71E-03	-5.17	6.21E-05
201148_s_at	TIMP3	-3.31	1.63E-02	-5.17	3.19E-04
213001_at	ANGPTL2	-3.69	3.10E-02	-5.16	2.06E-04
226694_at	AKAP2 /// PALM2-AKAP2	-5.21	1.24E-02	-5.14	4.16E-03
212690_at	DDHD2	-4.89	2.22E-02	-5.14	3.36E-04
1570202_a_at	MKL2	-3.70	3.12E-02	-5.14	3.83E-03
209106_at	NCOA1	-4.19	1.07E-02	-5.13	2.13E-03

1555240_s_at	GNG12	-3.61	3.29E-02	-5.12	1.31E-06
201403_s_at	LOC100505828 /// MGST3	-3.18	5.30E-03	-5.12	1.41E-03
221870_at	EHD2	-2.79	4.24E-03	-5.11	1.90E-04
218901_at	PLSCR4	-4.89	2.83E-02	-5.11	4.67E-04
222860_s_at	PDGFD	-5.15	2.01E-02	-5.10	1.13E-03
209303_at	NDUFS4	-3.23	3.98E-02	-5.08	4.77E-04
201121_s_at	PGRMC1	-3.19	3.72E-02	-5.07	7.47E-05
222669_s_at	SBDS /// SBDSP1	-3.85	3.79E-02	-5.05	1.11E-05
213156_at	---	-4.23	2.22E-02	-5.05	3.13E-03
219737_s_at	PCDH9	-6.42	7.01E-04	-5.04	5.80E-05
200911_s_at	TACC1	-3.08	4.07E-02	-5.02	1.71E-03
229404_at	TWIST2	-5.65	8.45E-04	-5.01	2.11E-04
227522_at	CMBL	-4.33	7.54E-03	-5.01	2.87E-06
208796_s_at	CCNG1	-4.74	4.70E-02	-5.01	4.40E-03
226192_at	AR	-3.15	4.75E-02	-4.99	1.47E-04
209147_s_at	PPAP2A	-4.22	2.65E-02	-4.99	1.35E-04
1562234_a_at	NAV3	-8.56	7.63E-04	-4.99	1.92E-05
226751_at	CNRIP1	-3.59	1.90E-02	-4.99	1.41E-04
213568_at	OSR2	-6.52	3.68E-03	-4.96	3.45E-04
205141_at	ANG	-3.66	7.28E-03	-4.96	3.84E-04
212761_at	TCF7L2	-4.43	1.90E-02	-4.95	1.22E-02
40665_at	FMO3	-4.15	1.74E-02	-4.94	7.67E-03
203812_at	SLIT3	-4.96	9.53E-04	-4.94	6.44E-05
219561_at	COPZ2	-3.47	1.44E-02	-4.94	1.43E-05
218546_at	C1orf115	-3.59	5.11E-03	-4.93	1.03E-04
200090_at	FNTA	-2.99	4.84E-02	-4.91	1.89E-03
205353_s_at	PEBP1	-3.64	1.43E-02	-4.91	8.86E-04
203131_at	PDGFRA	-5.77	1.55E-02	-4.90	5.39E-03
200844_s_at	PRDX6	-6.23	2.83E-04	-4.90	9.66E-05
202377_at	LEPROT	-4.90	1.92E-02	-4.89	3.42E-03
212987_at	FBXO9	-2.70	4.96E-02	-4.88	7.48E-03
215913_s_at	GULP1	-7.49	1.75E-05	-4.87	1.73E-04
219213_at	JAM2	-3.77	3.65E-02	-4.86	1.00E-03
206030_at	ASPA	-5.53	5.55E-04	-4.86	4.75E-04
215388_s_at	CFH /// CFHR1	-6.08	2.24E-02	-4.84	1.29E-02
219054_at	NPR3	-6.87	7.67E-04	-4.83	1.18E-04
213176_s_at	LTBP4	-4.09	1.00E-03	-4.83	4.31E-05
233375_at	EFCAB2	-3.71	1.95E-02	-4.81	4.33E-04
200711_s_at	SKP1	-4.33	2.04E-02	-4.81	3.59E-05
202399_s_at	AP3S2 /// C15orf38-AP3S2	-3.61	1.81E-02	-4.79	1.15E-03
218418_s_at	KANK2	-4.89	2.20E-03	-4.78	1.88E-04
211467_s_at	NFIB	-3.09	3.29E-02	-4.77	2.81E-03
208848_at	ADH5	-2.92	3.78E-02	-4.77	1.52E-07

235129_at	PPP1R1A	-10.34	5.00E-05	-4.76	2.69E-05
215235_at	SPTAN1	-3.56	2.61E-02	-4.75	1.11E-02
227243_s_at	EBF3	-5.65	5.30E-03	-4.74	2.75E-04
1554044_a_at	MRAP	-3.96	1.05E-02	-4.72	6.44E-04
221983_at	FAM134A	-3.96	6.90E-03	-4.71	5.20E-04
202092_s_at	ARL2BP	-3.51	4.24E-02	-4.71	2.88E-02
210757_x_at	DAB2	-5.13	1.37E-02	-4.71	1.90E-02
201801_s_at	SLC29A1	-6.01	1.65E-04	-4.71	1.20E-03
218552_at	ECHDC2	-3.54	7.03E-03	-4.71	1.62E-04
209357_at	CITED2	-4.61	1.59E-02	-4.68	6.87E-03
224481_s_at	HECTD1	-4.64	2.55E-02	-4.68	9.80E-03
217143_s_at	TRDC /// TRDC	-5.39	6.95E-04	-4.68	1.47E-04
209512_at	HSDL2	-4.54	3.02E-02	-4.67	2.83E-04
200771_at	LAMC1	-4.51	4.33E-02	-4.67	4.81E-03
211340_s_at	MCAM	-4.77	1.78E-03	-4.67	6.22E-04
233889_at	TBX18	-5.70	3.07E-04	-4.67	1.39E-04
209366_x_at	CYB5A	-5.84	1.41E-04	-4.67	3.99E-04
203329_at	PTPRM	-2.84	1.88E-02	-4.67	8.24E-04
215116_s_at	DNM1	-3.73	4.27E-02	-4.67	1.22E-03
213488_at	SNED1	-4.24	4.78E-02	-4.66	3.65E-03
203641_s_at	COBLL1	-5.13	6.48E-04	-4.66	5.96E-04
204039_at	CEBPA	-4.37	1.25E-02	-4.65	1.60E-03
241963_at	ZNF704	-4.14	4.52E-03	-4.64	2.64E-05
213285_at	TMEM30B	-4.44	2.59E-02	-4.64	4.73E-05
226282_at	PTPN14	-3.08	3.61E-02	-4.62	3.77E-04
203803_at	PCYOX1	-5.99	6.41E-03	-4.62	7.48E-04
225914_s_at	CAB39L	-4.25	8.61E-03	-4.62	3.55E-05
202995_s_at	FBLN1	-3.44	3.73E-02	-4.61	2.05E-02
213357_at	GTF2H5	-3.81	3.59E-02	-4.61	1.36E-03
235747_at	LINC00849	-4.50	2.30E-03	-4.61	6.82E-04
231862_at	CBX5	-4.60	4.21E-02	-4.60	2.96E-02
202747_s_at	ITM2A	-5.26	3.59E-02	-4.59	1.17E-02
224690_at	FAM210B	-3.51	1.80E-02	-4.59	4.43E-03
212793_at	DAAM2	-2.92	4.58E-02	-4.59	3.10E-06
218062_x_at	CDC42EP4	-3.88	8.12E-04	-4.58	3.06E-06
224821_at	ABHD14B	-3.64	6.57E-03	-4.58	7.74E-04
219025_at	CD248	-4.34	3.32E-04	-4.58	5.37E-04
217761_at	ADI1	-5.09	1.27E-02	-4.58	2.01E-04
202187_s_at	PPP2R5A	-3.44	4.84E-03	-4.56	7.92E-03
202341_s_at	TRIM2	-6.69	1.59E-03	-4.56	8.84E-05
212093_s_at	MTUS1	-7.00	2.23E-03	-4.55	5.00E-04
202930_s_at	SUCLA2	-4.50	3.26E-02	-4.55	1.26E-03
200879_s_at	EPAS1	-2.96	1.56E-02	-4.54	2.13E-02

218061_at	MEA1	-2.71	3.41E-02	-4.54	2.09E-03
208820_at	PTK2	-4.45	4.14E-02	-4.54	1.50E-03
212675_s_at	CEP68	-3.89	2.76E-02	-4.53	9.59E-05
210010_s_at	SLC25A1	-3.22	2.61E-03	-4.53	1.65E-03
219090_at	SLC24A3	-4.24	6.29E-03	-4.52	8.88E-06
227386_s_at	TMEM200B	-4.70	2.34E-03	-4.51	4.99E-04
219552_at	SVEP1	-5.06	3.63E-03	-4.49	2.00E-04
225080_at	MYO1C	-4.28	3.93E-04	-4.49	6.16E-05
213737_x_at	GOLGA8I /// GOLGA8O	-3.47	4.27E-02	-4.48	8.47E-04
209086_x_at	MCAM	-3.70	3.29E-03	-4.48	3.24E-03
226705_at	FGFR1	-5.01	6.92E-04	-4.47	5.84E-04
204454_at	LDOC1	-3.34	2.37E-02	-4.47	5.72E-05
218651_s_at	LARP6	-5.14	1.47E-03	-4.47	1.58E-05
205723_at	CNTFR	-7.70	1.35E-04	-4.43	1.08E-05
226113_at	ZNF436	-4.89	2.02E-03	-4.43	1.37E-03
201278_at	DAB2	-5.01	2.07E-02	-4.42	3.95E-03
204964_s_at	SSPN	-3.82	1.51E-02	-4.41	1.89E-06
204442_x_at	LTBP4	-3.25	1.12E-02	-4.41	1.92E-05
212169_at	FKBP9	-3.31	2.84E-02	-4.41	4.31E-03
202008_s_at	NID1	-4.35	4.48E-02	-4.40	2.34E-02
212096_s_at	MTUS1	-5.91	3.04E-03	-4.40	5.35E-04
209123_at	QDPR	-3.58	3.12E-04	-4.40	1.08E-04
225677_at	BCAP29	-4.48	9.88E-03	-4.40	7.46E-04
221496_s_at	TOB2	-3.19	1.10E-02	-4.40	2.59E-03
205529_s_at	RUNX1T1	-4.01	4.11E-02	-4.40	5.83E-04
1555754_s_at	ATN1	-1.99	3.79E-02	-4.39	4.56E-03
239220_at	OTTHUMG00000167229 /// RP11-736K20.5	-4.76	9.97E-04	-4.39	3.98E-04
222455_s_at	PARVA	-9.64	1.16E-03	-4.38	1.94E-05
244741_s_at	ZNF667-AS1	-3.77	3.40E-02	-4.37	5.63E-06
213122_at	TSPYL5	-5.52	1.41E-03	-4.37	2.25E-04
215836_s_at	PCDHGA1 /// PCDHGA10 /// PCDHGA11 /// PCDHGA12 /// PCDHGA2 /// PCDHGA3 /// PCDHGA4 /// PCDHGA5 /// PCDHGA6 /// PCDHGA7 /// PCDHGA8 /// PCDHGA9 /// PCDHGB1 /// PCDHGB2 /// PCDHGB3 /// PCDHGB4 /// PCDHGB5 /// PCDHGB6 /// PCDHGB7 /// PCDHGC3 /// PCDHGC4 /// PCDHGC5	-2.63	4.17E-02	-4.37	8.48E-05
202007_at	NID1	-5.42	4.70E-02	-4.37	4.85E-03
218007_s_at	RPS27L	-4.55	1.99E-02	-4.36	2.31E-02
1553644_at	SYNE3	-3.06	1.38E-04	-4.35	8.59E-06
201380_at	CRTAP /// LOC100653071	-3.42	2.32E-02	-4.34	5.94E-04
242137_at	RBMS3	-4.05	2.54E-02	-4.34	5.44E-04
233261_at	EBF1	-4.42	4.34E-02	-4.33	2.27E-03

214890_s_at	FAM149A		-2.97	1.68E-02	-4.33	3.58E-05
201060_x_at	STOM		-3.69	3.53E-02	-4.33	2.07E-02
212701_at	TLN2		-3.52	2.20E-03	-4.32	2.52E-04
217047_s_at	FAM13A		-4.96	1.40E-02	-4.31	7.91E-05
213364_s_at	SNX1		-4.03	1.91E-02	-4.31	1.06E-03
205399_at	DCLK1		-4.39	1.78E-02	-4.31	2.65E-04
225629_s_at	ZBTB4		-3.62	4.43E-02	-4.31	9.45E-05
226188_at	LGALSL		-3.58	1.86E-02	-4.29	1.96E-04
212970_at	APBB2		-6.15	5.78E-05	-4.29	9.69E-05
235281_x_at	AHNAK		-2.82	1.75E-02	-4.29	4.31E-02
232313_at	TMEM132C		-7.85	8.63E-05	-4.29	8.91E-05
209868_s_at	RBMS1		-3.33	4.77E-02	-4.29	3.99E-02
205609_at	ANGPT1		-5.59	6.28E-05	-4.27	2.93E-05
208626_s_at	VAT1		-2.49	6.07E-03	-4.27	2.24E-04
205384_at	FXYD1		-3.66	1.53E-03	-4.27	1.02E-04
206837_at	ALX1		-5.74	2.68E-02	-4.27	2.65E-03
201706_s_at	PEX19		-3.90	9.24E-03	-4.27	7.60E-06
225185_at	MRAS		-3.14	1.54E-02	-4.26	2.12E-05
211986_at	AHNAK		-2.56	2.69E-02	-4.25	2.53E-03
207277_at	CD209		-7.08	1.92E-02	-4.24	1.89E-03
222209_s_at	TMEM135		-5.71	1.78E-03	-4.24	1.44E-03
1557400_at	---		-4.20	2.37E-02	-4.24	5.82E-05
201307_at		11-Sep	-3.11	1.10E-02	-4.24	8.40E-04
225576_at	GINM1		-4.03	1.33E-02	-4.24	1.26E-03
219616_at	ACSS3		-2.76	4.77E-02	-4.23	5.12E-04
224707_at	CYSTM1		-3.71	6.06E-03	-4.23	1.20E-03
227388_at	TUSC1		-5.79	1.47E-03	-4.22	5.85E-05
219935_at	ADAMTS5		-5.17	2.56E-02	-4.21	4.82E-03
1553322_s_at	TEAD1		-4.07	2.36E-02	-4.21	6.51E-05
201009_s_at	LOC101060503 /// TXNIP		-2.54	4.99E-02	-4.20	4.70E-02
209212_s_at	KLF5		-3.82	2.45E-02	-4.19	3.75E-04
200862_at	DHCR24		-2.73	2.95E-02	-4.19	2.75E-03
202564_x_at	ARL2		-2.64	5.66E-03	-4.18	4.81E-05
204997_at	GPD1		-8.07	2.67E-04	-4.18	7.77E-03
218450_at	HEBP1		-3.08	4.81E-02	-4.18	4.94E-03
200671_s_at	SPTBN1		-3.11	3.63E-03	-4.17	3.49E-04
219091_s_at	MMRN2		-3.52	2.45E-02	-4.16	3.98E-03
211607_x_at	EGFR		-3.86	4.81E-03	-4.15	2.88E-04
200923_at	LGALS3BP		-3.13	1.84E-02	-4.15	2.96E-02
209834_at	CHST3		-3.66	2.00E-02	-4.14	4.46E-03
204418_x_at	GSTM2		-2.62	2.17E-02	-4.14	3.88E-04
218259_at	MKL2		-4.94	1.19E-02	-4.14	5.86E-04
203758_at	CTSO		-5.06	4.13E-02	-4.14	2.79E-02

203282_at	GBE1	-4.11	3.57E-02	-4.13	7.93E-04
1557820_at	AFG3L2	-4.65	4.86E-02	-4.13	1.36E-02
228027_at	ARMCX5-GPRASP2 /// GPRASP2	-3.90	4.66E-02	-4.12	3.02E-04
224894_at	YAP1	-4.11	1.14E-02	-4.11	3.35E-05
203245_s_at	LINC00094	-3.17	7.18E-03	-4.11	2.46E-05
225949_at	NRBP2	-3.30	2.63E-02	-4.10	5.11E-04
207843_x_at	CYB5A	-4.70	2.03E-04	-4.10	1.10E-03
200681_at	GLO1	-2.77	4.00E-02	-4.09	1.44E-03
1556056_at	SIK2	-4.04	9.41E-05	-4.09	4.09E-05
223131_s_at	TRIM8	-3.26	8.56E-03	-4.09	1.35E-03
201124_at	ITGB5	-6.23	6.43E-03	-4.09	1.20E-03
215016_x_at	DST	-4.53	1.46E-02	-4.09	3.21E-03
226813_at	NTPCR	-4.63	6.03E-03	-4.09	1.40E-03
202378_s_at	LEPROT	-4.20	1.38E-02	-4.07	9.04E-03
212647_at	RRAS	-3.51	6.06E-04	-4.06	6.19E-05
229127_at	JAM2	-3.47	3.04E-02	-4.06	2.34E-04
213236_at	SASH1	-2.95	1.04E-02	-4.06	6.00E-04
212224_at	ALDH1A1	-5.21	1.77E-03	-4.06	1.14E-03
207937_x_at	FGFR1	-2.90	1.56E-02	-4.05	8.10E-04
218865_at	1-Mar	-5.66	1.00E-03	-4.05	3.74E-03
205200_at	CLEC3B /// EXOSC7	-3.08	2.85E-02	-4.05	3.28E-03
201778_s_at	EFCAB14	-2.93	4.38E-02	-4.03	1.31E-03
212056_at	GSE1	-4.08	2.46E-02	-4.03	2.58E-02
219790_s_at	NPR3	-6.71	3.12E-03	-4.03	2.08E-03
201117_s_at	CPE	-4.52	6.87E-03	-4.02	9.96E-05
213033_s_at	NFIB	-2.84	2.96E-02	-4.02	1.47E-03
224337_s_at	FZD4	-7.06	7.71E-05	-4.01	2.74E-03
237517_at	---	-4.25	4.84E-02	-4.00	1.44E-02
223000_s_at	F11R	-4.73	1.92E-03	-4.00	6.99E-03
209220_at	GPC3	-3.39	2.48E-02	-4.00	5.23E-04
231846_at	FOXRED2	-3.73	2.26E-02	-4.00	3.27E-04
228693_at	CCDC50	-4.39	3.72E-02	-4.00	1.73E-03
224755_at	TM9SF3	-5.37	1.15E-02	-3.99	5.20E-03
208591_s_at	PDE3B	-5.34	2.13E-02	-3.99	2.77E-03
228158_at	LOC100996732 /// LOC100996735 /// LOC101060590 /// LOC645166 /// LOC654342	-5.26	2.19E-03	-3.98	8.70E-04
208944_at	TGFBR2	-4.01	2.11E-02	-3.97	1.98E-03
230071_at	11-Sep	-4.73	1.19E-02	-3.97	2.00E-04
210823_s_at	PTPRS	-2.75	3.33E-03	-3.97	8.22E-05
200636_s_at	PTPRF	-5.07	1.17E-05	-3.97	2.57E-05
218101_s_at	NDUFC2 /// NDUFC2-KCTD14	-4.03	9.52E-03	-3.96	3.66E-03
212062_at	ATP9A	-7.01	5.86E-06	-3.95	1.63E-04

204754_at	HLF	-3.32	3.25E-02	-3.95	1.45E-05
236291_at	RDH5	-3.96	6.19E-03	-3.94	2.02E-03
202136_at	ZMYND11	-4.20	1.29E-02	-3.94	1.73E-03
218494_s_at	SLC2A4RG	-3.75	1.81E-03	-3.93	3.55E-05
225698_at	EPB41L4A-AS1	-2.74	4.20E-02	-3.93	5.31E-06
231452_at	HRASLS5	-4.05	2.12E-02	-3.92	1.89E-03
212240_s_at	PIK3R1	-5.59	2.58E-03	-3.92	1.76E-04
202457_s_at	PPP3CA	-5.85	1.60E-02	-3.91	1.40E-02
212985_at	APBB2	-4.14	3.02E-02	-3.91	8.10E-05
209600_s_at	ACOX1	-4.13	9.93E-03	-3.90	2.67E-03
212558_at	SPRY1	-3.32	4.03E-02	-3.90	1.59E-02
226522_at	PODN	-3.62	2.56E-03	-3.89	2.83E-04
202994_s_at	FBLN1	-4.01	3.54E-02	-3.89	8.97E-03
239370_at	LOC100505633	-3.82	1.19E-02	-3.89	1.20E-03
226165_at	C8orf59	-4.69	3.12E-02	-3.89	4.04E-02
213058_at	TTC28	-3.77	2.52E-02	-3.89	3.63E-04
218487_at	ALAD	-4.70	2.11E-03	-3.88	4.61E-05
212875_s_at	C2CD2	-2.97	7.50E-03	-3.88	2.55E-04
224543_at	SVEP1	-4.42	1.96E-05	-3.87	8.09E-04
202912_at	ADM	-5.54	8.46E-04	-3.87	6.04E-03
212233_at	MAP1B	-5.52	3.54E-02	-3.87	1.31E-03
211717_at	ANKRD40	-3.16	6.69E-03	-3.87	2.24E-03
210984_x_at	EGFR	-4.75	1.49E-04	-3.87	3.97E-04
209663_s_at	ITGA7	-4.88	1.07E-02	-3.87	1.91E-02
214063_s_at	TF	-4.77	2.69E-03	-3.87	3.80E-02
227917_at	LOC100506990	-4.25	1.02E-02	-3.86	1.53E-02
226084_at	MAP1B	-4.63	3.50E-02	-3.86	4.70E-03
211423_s_at	SC5D	-3.12	2.06E-02	-3.86	7.23E-04
227923_at	SHANK3	-4.47	4.77E-03	-3.86	6.86E-03
213352_at	TMCC1	-3.15	2.82E-02	-3.85	5.65E-04
228256_s_at	EPB41L4A	-3.91	2.57E-03	-3.84	2.42E-04
223435_s_at	PCDHA1 /// PCDHA10 /// PCDHA11 /// PCDHA12 /// PCDHA13 /// PCDHA2 /// PCDHA3 /// PCDHA4 /// PCDHA5 /// PCDHA6 /// PCDHA7 /// PCDHA8 /// PCDHA9 /// PCDHAC1 /// PCDHAC2	-3.41	1.89E-02	-3.84	3.30E-07
65718_at	GPR124	-4.47	3.35E-02	-3.83	4.27E-04
202566_s_at	SVIL	-3.42	4.47E-02	-3.82	3.95E-03
235382_at	AQPEP	-4.74	1.40E-02	-3.82	5.57E-03
226820_at	ZNF362	-3.32	4.33E-02	-3.82	1.93E-03
213830_at	YME1L1	-3.66	6.46E-03	-3.82	2.88E-05
228950_s_at	WLS	-4.45	2.29E-03	-3.82	1.67E-04
207191_s_at	ISLR	-3.11	3.27E-02	-3.82	1.42E-03
243880_at	GOSR2	-4.52	1.48E-02	-3.82	3.87E-03

209908_s_at	TGFB2	-6.03	2.68E-03	-3.81	1.43E-04
224689_at	MANBAL	-3.07	6.41E-03	-3.81	1.38E-05
214665_s_at	CHP1	-3.17	2.88E-03	-3.80	3.10E-03
213865_at	DCBLD2	-3.48	3.16E-02	-3.80	2.54E-03
47560_at	LPHN1	-3.70	9.96E-04	-3.80	2.06E-04
205817_at	SIX1	-2.88	5.67E-03	-3.79	5.22E-05
214066_x_at	NPR2	-3.19	8.21E-03	-3.78	3.08E-04
223449_at	SEMA6A	-3.24	3.74E-02	-3.77	2.10E-04
211941_s_at	PEBP1	-2.23	4.26E-02	-3.77	3.14E-03
228411_at	PARD3B	-3.27	2.95E-02	-3.74	6.33E-05
235371_at	GXYLT2	-7.02	3.25E-03	-3.74	1.63E-02
205752_s_at	GSTM5	-4.28	2.30E-02	-3.74	3.18E-04
1563621_at	---	-2.92	2.93E-02	-3.72	7.50E-03
229512_at	FAM120C	-4.49	8.60E-04	-3.72	2.96E-05
218467_at	PSMG2	-4.46	1.12E-02	-3.72	2.81E-02
213005_s_at	KANK1	-3.10	3.93E-02	-3.72	1.65E-03
210168_at	C6	-6.54	2.43E-02	-3.71	1.82E-02
208666_s_at	ST13	-3.71	7.66E-03	-3.71	1.02E-02
218284_at	SMAD3	-3.55	2.77E-03	-3.69	7.89E-05
226095_s_at	ATXN1L	-2.44	4.72E-02	-3.69	4.76E-04
208158_s_at	OSBPL1A	-3.46	2.52E-02	-3.69	1.61E-04
224871_at	TPRG1L	-4.56	2.19E-04	-3.68	5.00E-06
40093_at	BCAM	-3.14	1.89E-02	-3.68	2.32E-03
210832_x_at	PTGER3	-4.53	4.61E-03	-3.68	5.76E-03
225900_at	EXOC6B	-5.49	2.50E-04	-3.67	1.89E-04
40148_at	APBB2	-4.65	7.07E-03	-3.66	5.07E-03
218417_s_at	SLC48A1	-2.98	2.01E-02	-3.65	9.95E-05
221589_s_at	ALDH6A1	-4.12	5.81E-03	-3.65	5.66E-04
226676_at	ZNF521	-4.42	1.53E-02	-3.64	1.62E-04
213451_x_at	LOC101060681 /// TNXA /// TNXB	-4.48	6.65E-03	-3.64	1.44E-03
225941_at	EIF4E3	-3.74	1.04E-02	-3.63	1.28E-03
1558941_at	ZNF704	-5.47	2.01E-04	-3.63	5.78E-04
217802_s_at	NUCKS1	-3.89	2.07E-02	-3.63	2.98E-02
235368_at	ADAMTS5	-4.52	3.95E-02	-3.62	5.69E-04
235538_at	---	-4.22	2.19E-02	-3.62	4.02E-03
232235_at	DSEL	-4.24	3.27E-03	-3.62	1.59E-05
222834_s_at	GNG12	-3.08	4.30E-02	-3.62	1.64E-04
210089_s_at	LAMA4	-2.67	1.14E-02	-3.61	4.77E-04
38918_at	SOX13	-4.92	8.33E-03	-3.61	7.25E-04
1554701_a_at	TBC1D16	-3.94	2.12E-03	-3.61	8.81E-05
204237_at	GULP1	-3.05	3.22E-02	-3.61	2.02E-04
214749_s_at	ARMCX6	-4.72	3.49E-02	-3.60	2.95E-02
1553194_at	NEGR1	-6.99	7.42E-03	-3.60	9.98E-04

228772_at	HNMT	-3.88	8.37E-03	-3.60	1.78E-04
209485_s_at	OSBPL1A	-3.86	8.07E-03	-3.59	1.02E-04
208788_at	ELOVL5	-3.94	3.07E-02	-3.59	3.20E-02
201658_at	ARL1	-4.33	1.79E-02	-3.58	3.06E-03
224903_at	CIRH1A	-3.91	1.95E-02	-3.58	2.25E-03
223983_s_at	C19orf12	-2.91	3.39E-02	-3.58	6.84E-03
201830_s_at	NET1	-4.75	4.44E-02	-3.57	8.56E-03
224812_at	HIBADH	-3.74	2.53E-02	-3.56	4.04E-04
242323_at	PLA2G12A	-4.27	5.38E-03	-3.56	5.11E-04
201612_at	ALDH9A1	-3.83	3.86E-02	-3.56	3.01E-02
212120_at	RHOQ	-3.66	1.36E-02	-3.55	2.34E-02
1562139_a_at	FOXP2	-4.27	9.75E-03	-3.55	2.63E-03
242181_at	---	-2.34	3.38E-02	-3.55	6.83E-05
209909_s_at	TGFB2	-3.98	1.84E-02	-3.55	1.86E-04
225778_at	RBMS2	-3.29	4.13E-02	-3.54	4.22E-04
46270_at	UBAP1	-3.68	2.49E-02	-3.53	6.83E-03
226723_at	CCDC23	-4.04	7.42E-03	-3.52	1.04E-03
1555729_a_at	CD209	-3.23	3.82E-02	-3.52	9.06E-03
212851_at	DCUN1D4	-2.98	4.77E-02	-3.52	8.80E-03
208970_s_at	UROD	-3.99	1.40E-02	-3.52	1.73E-03
200649_at	NUCB1	-2.47	3.30E-02	-3.52	3.93E-02
208186_s_at	LIPE	-2.64	4.55E-02	-3.52	2.34E-02
203631_s_at	GPRC5B	-2.89	4.81E-02	-3.51	2.83E-04
201397_at	PHGDH	-4.78	7.70E-05	-3.51	5.07E-04
217813_s_at	SPIN1	-4.15	1.46E-02	-3.51	1.47E-02
242133_s_at	---	-4.81	2.10E-02	-3.50	1.87E-04
226683_at	SNX18	-3.93	8.45E-03	-3.50	2.47E-02
1569640_s_at	EEPD1	-4.22	8.15E-04	-3.50	1.67E-03
228006_at	PTEN	-3.86	3.71E-02	-3.50	8.33E-04
226388_at	TCEA3	-2.99	7.96E-03	-3.50	1.27E-05
226571_s_at	PTPRS	-4.54	4.68E-04	-3.49	1.68E-04
32259_at	EZH1	-3.72	1.97E-04	-3.49	3.29E-04
202134_s_at	WWTR1	-3.33	2.06E-02	-3.49	3.11E-03
202554_s_at	GSTM3	-5.00	2.34E-03	-3.49	9.74E-04
239185_at	ABCA9	-5.86	1.77E-03	-3.49	2.13E-03
212513_s_at	USP33	-3.86	1.34E-02	-3.49	1.46E-03
237867_s_at	PID1	-3.59	3.56E-03	-3.49	5.51E-05
206355_at	GNAL	-3.76	2.69E-02	-3.48	2.05E-03
223005_s_at	TMEM245	-3.63	2.61E-02	-3.48	5.21E-03
216081_at	LAMA4	-4.05	3.77E-02	-3.47	8.07E-04
202634_at	POLR2K	-2.20	4.58E-02	-3.47	5.93E-04
223193_x_at	FAM162A	-3.27	2.30E-02	-3.47	1.08E-02
202807_s_at	TOM1	-4.64	1.19E-03	-3.46	2.24E-03

213455_at	FAM114A1		-2.94	2.28E-02	-3.46	9.45E-05
220511_s_at	DLC1		-3.74	2.23E-03	-3.45	2.65E-03
204111_at	HNMT		-2.75	5.27E-03	-3.44	7.16E-05
214721_x_at	CDC42EP4		-4.35	6.24E-04	-3.44	4.14E-05
218718_at	PDGFC		-3.86	4.60E-02	-3.44	9.28E-03
216352_x_at	PCDHGA3		-3.39	5.66E-03	-3.43	4.76E-04
244111_at	KRT222		-3.57	3.15E-02	-3.43	1.16E-04
226731_at	ITGA1		-3.55	1.46E-02	-3.43	6.90E-04
223519_at	ZAK		-4.61	4.85E-02	-3.43	1.62E-02
218773_s_at	MSRB2		-2.91	1.72E-02	-3.43	1.29E-04
223467_at	RASD1		-3.45	4.16E-02	-3.43	4.40E-03
242338_at	TMEM64		-2.76	3.19E-02	-3.42	1.38E-03
215059_at	---		-3.42	3.26E-03	-3.42	1.22E-04
1558101_at	NFIA		-3.01	1.12E-02	-3.42	3.23E-04
206726_at	HPGDS		-2.52	4.71E-02	-3.41	1.28E-04
212249_at	PIK3R1		-4.26	2.92E-03	-3.40	2.09E-04
229106_at	DYNLL2		-2.59	4.11E-02	-3.39	1.40E-03
203426_s_at	IGFBP5		-3.35	6.30E-03	-3.39	1.10E-03
222573_s_at	SAV1		-3.87	2.32E-05	-3.38	1.28E-05
208510_s_at	PPARG		-4.92	5.71E-03	-3.38	1.52E-03
203337_x_at	ITGB1BP1		-4.08	1.49E-02	-3.37	9.04E-03
213198_at	ACVR1B		-3.72	1.54E-02	-3.37	1.96E-02
209614_at	ADH1B		-3.66	2.34E-02	-3.37	2.29E-04
231993_at	ITGBL1		-3.49	4.99E-02	-3.37	1.18E-03
228716_at	THRB		-4.04	4.50E-03	-3.37	1.85E-04
1553960_at	SNX21		-3.37	5.00E-03	-3.36	2.18E-04
210249_s_at	NCOA1		-2.63	4.17E-02	-3.36	7.66E-03
224645_at	EIF4EBP2		-3.38	1.55E-03	-3.36	3.21E-06
220952_s_at	PLEKHA5		-5.75	1.39E-02	-3.35	3.68E-04
226148_at	ZBTB44		-3.95	3.39E-02	-3.35	9.54E-03
224131_at	HCAR1		-4.57	5.75E-05	-3.34	3.23E-04
225977_at	PCDH18		-4.16	1.02E-03	-3.34	1.99E-05
213486_at	COPG2IT1		-3.82	1.02E-02	-3.34	8.14E-03
202245_at	LSS		-2.56	4.44E-03	-3.33	4.18E-03
210762_s_at	DLC1		-3.82	1.29E-02	-3.33	3.12E-03
216333_x_at	LOC101060681 /// TNXA /// TNXB		-4.61	4.38E-03	-3.33	1.09E-03
225924_at	FNIP2		-2.92	4.82E-02	-3.33	9.05E-03
214496_x_at	KAT6B		-3.18	1.49E-02	-3.32	1.25E-04
214383_x_at	KLHDC3		-2.44	4.05E-03	-3.32	1.56E-04
204400_at	EFS		-4.94	6.78E-03	-3.31	3.02E-05
221636_s_at		2-Mar	-3.70	3.79E-02	-3.30	7.80E-03
41644_at	SASH1		-3.68	1.48E-02	-3.30	1.06E-02
218025_s_at	ECI2		-4.02	7.34E-03	-3.29	1.81E-03

202863_at	SP100	-3.78	2.85E-02	-3.29	1.07E-02
201035_s_at	HADH	-5.06	4.29E-04	-3.28	1.36E-03
215870_s_at	PLA2G5	-4.06	2.11E-02	-3.28	4.80E-03
238003_at	HEPACAM /// HEPN1	-2.53	7.46E-03	-3.28	1.72E-04
221928_at	ACACB	-3.76	2.23E-03	-3.28	5.34E-03
212441_at	KIAA0232	-2.17	4.69E-02	-3.27	6.62E-06
218966_at	MYO5C	-3.23	4.54E-02	-3.27	1.89E-03
213675_at	PARVA	-3.69	3.53E-04	-3.27	6.89E-06
228839_s_at	LOC642361	-3.71	1.22E-02	-3.26	1.31E-03
1552476_s_at	PLCD3	-4.23	8.51E-03	-3.25	4.45E-04
225613_at	MAST4	-4.55	5.46E-03	-3.25	5.69E-04
222783_s_at	SMOC1	-4.30	4.01E-03	-3.25	4.79E-04
202562_s_at	C14orf1	-2.19	2.18E-02	-3.24	6.66E-04
225915_at	CAB39L	-3.68	1.81E-02	-3.24	8.39E-04
205499_at	SRPX2	-4.05	7.48E-03	-3.23	2.83E-03
205608_s_at	ANGPT1	-7.21	1.46E-03	-3.23	1.07E-03
218440_at	MCCC1	-4.15	1.18E-02	-3.23	2.71E-03
211874_s_at	KAT6B	-3.32	4.35E-02	-3.22	4.31E-04
48106_at	SLC48A1	-2.48	5.42E-03	-3.22	2.59E-04
213724_s_at	PDK2	-3.34	6.33E-04	-3.22	2.07E-05
207542_s_at	AQP1	-2.95	2.44E-02	-3.21	2.54E-02
201346_at	ADIPOR2	-3.51	8.03E-04	-3.20	2.01E-04
221958_s_at	WLS	-4.09	1.16E-02	-3.20	2.19E-04
212294_at	GNG12	-3.28	2.99E-03	-3.20	1.23E-03
235631_at	DDR2	-3.86	3.83E-03	-3.20	6.09E-05
207808_s_at	PROS1	-4.95	2.63E-02	-3.19	4.78E-04
205079_s_at	MPDZ	-3.53	4.00E-03	-3.19	7.13E-04
1564876_s_at	FOXP2	-3.86	3.27E-03	-3.19	5.08E-03
213617_s_at	TPGS2	-2.60	2.11E-02	-3.18	1.16E-02
209550_at	NDN	-4.33	3.24E-04	-3.18	5.34E-04
234233_s_at	---	-3.38	2.98E-02	-3.17	4.14E-03
208647_at	FDFT1	-2.95	1.74E-02	-3.17	1.07E-03
235076_at	CALCOCO2	-3.94	1.42E-02	-3.14	5.29E-05
39854_r_at	PNPLA2	-2.89	5.39E-04	-3.14	5.39E-03
205011_at	VWA5A	-3.02	3.63E-02	-3.13	8.87E-04
222437_s_at	CHMP3 /// RNF103-CHMP3	-3.67	2.07E-02	-3.13	6.26E-03
217504_at	ABCA6	-4.74	1.31E-02	-3.13	2.37E-02
235201_at	FOXP2	-4.02	8.03E-03	-3.13	4.96E-03
223213_s_at	ZHX1	-3.85	1.41E-02	-3.12	3.83E-04
211569_s_at	HADH	-3.45	3.19E-02	-3.12	1.58E-03
225611_at	MAST4	-3.43	4.40E-03	-3.12	1.27E-03
200693_at	YWHAQ	-3.58	1.15E-02	-3.11	4.45E-03
201276_at	RAB5B	-3.49	6.79E-05	-3.11	1.75E-04

210740_s_at	ITPK1	-2.34	1.25E-02	-3.11	9.82E-03
209386_at	TM4SF1	-4.08	2.48E-02	-3.11	1.34E-02
205315_s_at	SNTB2	-3.93	7.74E-04	-3.11	6.01E-04
206093_x_at	LOC101060681 /// TNXA /// TNXB	-4.41	9.05E-03	-3.11	3.87E-03
238066_at	RBP7	-3.80	1.23E-02	-3.11	2.30E-02
212730_at	SYNM	-4.49	2.47E-02	-3.10	3.51E-02
211954_s_at	IPO5	-2.32	2.47E-02	-3.10	1.05E-04
207071_s_at	ACO1	-6.67	8.22E-05	-3.10	2.12E-02
209087_x_at	MCAM	-4.07	3.47E-03	-3.09	1.85E-02
217891_at	C16orf58	-2.86	2.29E-02	-3.08	4.30E-02
220326_s_at	ARHGEF40	-2.49	3.73E-03	-3.06	2.12E-04
202685_s_at	AXL	-2.23	4.96E-02	-3.06	8.12E-04
217780_at	WDR83OS	-2.34	4.83E-02	-3.06	1.02E-03
212451_at	SECISBP2L	-4.10	3.63E-02	-3.06	2.76E-02
218631_at	AVPI1	-5.14	9.08E-04	-3.05	1.88E-03
221618_s_at	TAF9B	-3.38	3.07E-02	-3.05	2.17E-04
209373_at	MALL	-2.97	4.34E-03	-3.05	3.09E-03
226770_at	MAGI3	-3.97	1.54E-02	-3.04	7.40E-04
228456_s_at	CDS2	-2.35	4.64E-02	-3.04	2.94E-03
203638_s_at	FGFR2	-3.08	6.82E-03	-3.03	1.22E-03
216511_s_at	TCF7L2	-4.36	1.30E-02	-3.03	3.94E-03
218224_at	PNMA1	-4.01	1.87E-03	-3.02	3.96E-04
1557116_at	APOL6	-3.81	1.02E-02	-3.02	1.07E-04
224582_s_at	NUCKS1	-2.43	3.95E-02	-3.01	1.77E-03
228807_at	ASPA	-3.96	3.67E-03	-3.01	6.56E-03
219814_at	MBNL3	-2.67	2.91E-02	-3.01	1.74E-04
226844_at	MOB3B	-3.12	4.26E-02	-3.01	6.12E-03
209830_s_at	SLC9A3R2	-2.59	4.05E-02	-3.01	8.22E-04
218253_s_at	EIF2D	-3.02	2.75E-02	-3.01	6.27E-03
208030_s_at	ADD1	-3.94	2.80E-03	-3.00	1.00E-02
227121_at	---	-2.80	4.57E-02	-3.00	1.48E-03
231015_at	KLF15	-2.46	2.02E-02	-3.00	1.50E-03
202967_at	GSTA4	-3.81	2.54E-04	-2.99	4.35E-05
201575_at	SNW1	-2.50	2.47E-02	-2.99	4.98E-03
212553_at	RPRD2	-3.98	4.55E-03	-2.98	4.55E-03
202646_s_at	CSDE1	-2.36	2.44E-02	-2.98	1.25E-03
203787_at	SSBP2	-4.31	1.71E-02	-2.98	5.43E-03
205158_at	RNASE4	-3.34	2.08E-03	-2.98	1.98E-03
204793_at	GPRASP1	-3.86	3.39E-02	-2.98	7.62E-03
1557241_a_at	OTTHUMG00000175567 /// RP11-524D16__A.3	-4.18	3.20E-03	-2.97	8.24E-04
204290_s_at	ALDH6A1	-3.43	1.52E-02	-2.97	1.54E-03
202443_x_at	NOTCH2	-2.95	2.84E-02	-2.97	2.21E-02

219077_s_at	WWOX	-2.45	3.51E-02	-2.97	1.27E-03
236262_at	MMRN2	-4.13	3.04E-02	-2.97	3.26E-03
224744_at	IMPAD1	-2.57	2.82E-02	-2.96	5.16E-04
212253_x_at	DST	-2.48	2.70E-02	-2.96	5.04E-03
225276_at	GSPT1	-2.82	2.52E-02	-2.95	3.10E-03
229946_at	FAM168B	-2.43	3.03E-02	-2.95	1.11E-02
202561_at	TNKS	-2.99	1.08E-02	-2.95	4.98E-04
242935_at	SBF2	-2.64	4.26E-02	-2.95	1.05E-04
212640_at	PTPLB	-3.04	8.68E-03	-2.94	9.55E-03
219902_at	BHMT2	-3.49	1.44E-02	-2.94	5.33E-03
216268_s_at	JAG1	-3.64	2.98E-02	-2.94	4.66E-03
226342_at	SPTBN1	-4.57	8.47E-04	-2.94	1.47E-03
212104_s_at	RBFOX2	-2.27	4.52E-02	-2.93	1.66E-03
204239_s_at	NNAT	-3.12	2.77E-03	-2.93	1.17E-03
226484_at	ZBTB47	-2.90	4.32E-02	-2.93	4.64E-06
34697_at	LRP6	-3.31	1.89E-02	-2.93	1.05E-03
218667_at	PJA1	-3.24	8.39E-04	-2.93	4.44E-04
32811_at	MYO1C	-2.27	7.21E-04	-2.93	1.18E-03
230174_at	LYPLAL1	-2.73	2.12E-02	-2.92	8.38E-04
221452_s_at	TMEM14B	-3.15	4.05E-02	-2.92	2.52E-03
231762_at	FGF10	-4.58	1.22E-03	-2.92	2.16E-04
225908_at	IAH1	-2.83	3.94E-02	-2.91	1.34E-03
1554485_s_at	TMEM37	-4.31	1.01E-02	-2.90	2.79E-03
48031_r_at	FAXDC2	-3.99	1.27E-03	-2.90	6.78E-04
226190_at	MAP3K13	-3.19	3.56E-02	-2.90	1.11E-02
202630_at	APPBP2	-4.27	2.66E-02	-2.89	1.60E-02
222436_s_at	CHMP3 /// RNF103-CHMP3	-2.88	6.82E-03	-2.89	6.76E-03
209109_s_at	TSPAN6	-3.03	1.39E-02	-2.89	1.33E-02
219576_at	MAP7D3	-3.51	1.09E-03	-2.88	3.41E-04
227326_at	MXRA7	-2.66	3.02E-02	-2.88	6.25E-05
228291_s_at	PLK1S1	-2.99	2.09E-02	-2.88	1.10E-03
225426_at	PPP6C	-3.51	5.96E-03	-2.88	5.21E-04
211076_x_at	ATN1	-1.80	2.11E-02	-2.87	4.69E-02
210554_s_at	CTBP2	-3.22	4.27E-02	-2.87	9.90E-03
224415_s_at	HINT2	-2.98	1.55E-03	-2.87	4.47E-05
208335_s_at	DARC	-2.96	8.80E-03	-2.87	2.00E-03
202544_at	GMFB	-3.22	4.33E-02	-2.86	1.48E-02
200939_s_at	RERE	-2.55	3.65E-02	-2.86	7.78E-04
202003_s_at	ACAA2	-3.31	8.93E-03	-2.85	4.11E-03
202908_at	WFS1	-2.30	1.65E-02	-2.85	3.18E-04
223075_s_at	AIF1L	-3.71	4.24E-03	-2.85	2.69E-03
227962_at	ACOX1	-3.00	1.34E-02	-2.84	1.74E-04
227792_at	ITPRIPL2	-3.27	4.05E-02	-2.84	2.31E-02

223126_s_at	C1orf21	-3.00	1.92E-02	-2.84	6.67E-05
1562102_at	---	-3.78	1.37E-02	-2.84	1.66E-02
225860_at	MMP24-AS1	-2.35	1.00E-02	-2.83	3.71E-04
214889_at	FAM149A	-2.72	7.18E-03	-2.83	3.37E-04
228182_at	ADCY5	-2.80	3.69E-02	-2.83	6.49E-03
238353_at	RASL11A	-2.66	2.77E-02	-2.83	5.79E-03
228824_s_at	PTGR1	-2.87	4.74E-02	-2.82	2.90E-03
206178_at	PLA2G5	-3.57	2.40E-03	-2.82	2.20E-03
227997_at	IL17RD	-3.91	2.19E-02	-2.82	2.18E-03
211042_x_at	MCAM	-2.58	1.03E-02	-2.81	2.55E-03
200940_s_at	RERE	-5.51	4.23E-03	-2.81	1.16E-02
226989_at	RGMB	-2.75	1.34E-02	-2.81	3.52E-06
235471_at	VSTM4	-3.55	2.70E-02	-2.81	3.85E-03
224564_s_at	RTN3	-2.25	3.74E-02	-2.80	1.02E-02
201580_s_at	TMX4	-2.69	4.87E-02	-2.80	2.97E-02
229948_at	---	-3.11	1.48E-03	-2.80	9.21E-05
203054_s_at	TCTA	-2.44	2.96E-02	-2.80	4.43E-03
206363_at	MAF	-4.37	1.69E-02	-2.80	1.65E-02
1554758_a_at	CD99L2	-2.72	1.01E-02	-2.80	5.04E-03
228770_at	GPR146	-3.39	6.07E-04	-2.80	4.54E-04
1558420_at	C14orf180	-4.08	4.29E-04	-2.79	5.67E-03
232501_at	---	-2.18	4.35E-02	-2.79	2.33E-04
215963_x_at	RPL3	-1.98	3.27E-02	-2.79	4.05E-02
201707_at	PEX19	-4.05	1.30E-05	-2.79	1.25E-04
223468_s_at	RGMA	-2.89	2.53E-02	-2.79	1.02E-03
1565358_at	RARA	-2.95	1.42E-02	-2.78	7.15E-03
1555881_s_at	LZTS2	-2.53	6.29E-03	-2.78	5.35E-04
241866_at	SLC16A7	-3.88	2.76E-03	-2.78	5.03E-04
226657_at	C17orf103	-2.01	4.98E-02	-2.77	4.57E-04
211876_x_at	PCDHGA10 /// PCDHGA11 /// PCDHGA12 /// PCDHGA3 /// PCDHGA5 /// PCDHGA6 /// PCDHGC3	-2.67	1.12E-02	-2.77	3.60E-03
207069_s_at	SMAD6	-3.88	2.14E-02	-2.77	1.94E-04
226216_at	INSR	-3.76	2.67E-02	-2.76	9.40E-03
242736_at	---	-4.96	1.55E-03	-2.76	2.09E-02
203222_s_at	TLE1	-3.42	2.38E-02	-2.75	4.95E-03
205125_at	PLCD1	-1.87	1.91E-02	-2.75	6.33E-07
206132_at	MCC	-2.97	2.67E-02	-2.75	5.16E-03
233849_s_at	ARHGAP5	-2.90	3.70E-02	-2.74	7.99E-04
213010_at	PRKCDBP	-3.25	2.63E-02	-2.74	1.10E-03
215537_x_at	DDAH2	-2.55	1.12E-03	-2.73	1.31E-04
202623_at	EAPP	-3.77	2.22E-02	-2.73	1.78E-03
202762_at	ROCK2	-2.99	4.47E-02	-2.73	1.69E-02

225494_at	DYNLL2	-2.49	3.28E-02	-2.73	1.57E-02
223136_at	AIG1	-4.03	9.06E-03	-2.71	8.75E-04
203249_at	EZH1	-2.81	3.83E-03	-2.70	7.30E-03
228151_at	ARL15	-3.94	2.41E-02	-2.70	1.86E-02
217849_s_at	CDC42BPB	-2.30	4.60E-02	-2.70	3.77E-02
204134_at	PDE2A	-3.01	2.31E-02	-2.70	1.31E-02
1320_at	PTPN21	-2.82	6.43E-03	-2.70	6.81E-05
208615_s_at	PTP4A2	-3.59	2.57E-02	-2.70	3.59E-02
226845_s_at	MYEOV2	-4.72	2.05E-03	-2.69	1.04E-02
218032_at	SNN	-2.33	1.12E-02	-2.69	3.87E-05
212590_at	RRAS2	-2.86	3.83E-02	-2.69	1.00E-02
226408_at	TEAD2	-3.02	3.40E-02	-2.69	5.65E-03
222911_s_at	CXorf36	-3.46	2.17E-02	-2.69	2.02E-02
32099_at	SAFB2	-2.30	4.21E-02	-2.67	2.71E-03
225863_s_at	C19orf12	-3.05	1.03E-02	-2.67	1.56E-02
210106_at	BLOC1S1-RDH5 /// RDH5	-3.04	8.68E-03	-2.66	3.88E-03
219374_s_at	ALG9	-2.82	3.60E-02	-2.66	3.51E-02
221295_at	CIDEA	-6.62	3.02E-03	-2.65	7.19E-03
228594_at	NADK2	-2.85	3.56E-02	-2.65	1.15E-03
202734_at	TRIP10	-2.78	1.35E-02	-2.65	8.41E-05
221430_s_at	RNF146	-2.37	4.11E-02	-2.65	4.27E-03
217830_s_at	NSFL1C	-2.14	4.40E-02	-2.65	1.51E-04
223886_s_at	RNF146	-3.36	2.74E-02	-2.65	2.57E-02
224813_at	WASL	-2.98	2.87E-02	-2.65	1.35E-02
201810_s_at	SH3BP5	-3.64	1.75E-02	-2.64	9.11E-03
212186_at	ACACA	-2.16	4.60E-02	-2.64	6.22E-03
212504_at	DIP2C	-2.79	1.74E-03	-2.64	2.07E-03
209468_at	LRP5	-2.33	4.07E-02	-2.64	1.41E-04
218354_at	TRAPPC2L	-2.47	2.31E-02	-2.64	1.20E-03
218561_s_at	LYRM4	-2.39	3.93E-02	-2.64	8.18E-04
219929_s_at	ZFYVE21	-3.29	1.02E-02	-2.63	3.36E-04
214608_s_at	EYA1	-3.15	1.46E-02	-2.63	1.43E-02
225203_at	PPP1R16A	-2.53	4.64E-03	-2.63	4.29E-03
216215_s_at	RBFOX2	-2.67	1.64E-03	-2.63	1.67E-05
201056_at	GOLGB1	-2.44	2.84E-02	-2.63	4.50E-03
201802_at	SLC29A1	-2.16	5.71E-03	-2.63	2.64E-04
205528_s_at	RUNX1T1	-3.53	1.76E-02	-2.63	4.96E-03
205756_s_at	F8	-3.74	4.63E-02	-2.63	1.91E-03
205139_s_at	UST	-3.72	2.92E-02	-2.63	6.70E-04
213543_at	SGCD	-2.95	4.73E-02	-2.63	1.98E-03
216840_s_at	LAMA2	-3.24	3.55E-02	-2.62	8.82E-03
214259_s_at	AKR7A2	-2.65	5.79E-03	-2.62	8.70E-04
235344_at	PPM1A	-4.43	4.96E-03	-2.62	2.55E-03

1558421_a_at	C14orf180	-3.16	1.42E-02	-2.62	4.11E-03
207044_at	THRB	-2.75	8.54E-03	-2.62	3.69E-05
241381_at	CXorf36	-4.38	2.12E-03	-2.61	5.43E-03
226028_at	ROBO4	-4.00	1.29E-03	-2.61	1.51E-02
205503_at	PTPN14	-2.52	2.95E-02	-2.61	4.29E-03
210544_s_at	ALDH3A2	-3.70	1.42E-03	-2.61	6.30E-04
1553572_a_at	CYGB	-2.79	4.92E-03	-2.61	2.33E-03
218739_at	ABHD5	-2.88	1.49E-02	-2.61	1.16E-02
222422_s_at	NDFIP1	-3.30	7.21E-03	-2.60	6.03E-03
213071_at	DPT	-2.39	3.27E-02	-2.60	6.00E-03
208562_s_at	ABCC9	-3.47	2.75E-02	-2.60	4.68E-03
223283_s_at	TSHZ1	-3.29	2.52E-02	-2.60	1.41E-03
212796_s_at	TBC1D2B	-2.44	1.40E-02	-2.60	2.96E-02
235110_at	PLA2G16	-3.27	1.49E-03	-2.60	3.44E-03
227195_at	ZNF503	-3.69	3.83E-03	-2.58	8.90E-04
219599_at	EIF4B	-3.48	1.91E-02	-2.58	4.59E-02
218356_at	FTSJ2	-3.05	3.91E-02	-2.58	9.93E-03
213518_at	PRKCI	-2.52	3.74E-02	-2.58	8.52E-03
201865_x_at	NR3C1	-2.73	1.22E-02	-2.57	7.51E-03
229024_at	---	-4.45	1.80E-04	-2.57	3.09E-02
220102_at	FOXL2	-4.63	1.55E-03	-2.57	4.04E-03
201223_s_at	RAD23B	-3.21	1.84E-02	-2.57	3.26E-02
228088_at	SESTD1	-3.02	1.59E-02	-2.56	1.46E-04
223279_s_at	UACA	-2.97	3.65E-02	-2.56	8.05E-03
235836_at	MXRA7	-2.54	1.44E-02	-2.56	6.13E-04
232837_at	KIF13A	-2.38	1.86E-02	-2.56	8.45E-04
202262_x_at	DDAH2	-2.51	1.76E-03	-2.55	6.67E-05
225729_at	C6orf89	-3.14	5.03E-04	-2.55	2.39E-03
229764_at	LOC101060141 /// TPRG1	-3.38	2.97E-02	-2.55	1.94E-03
211955_at	IPO5	-2.71	3.31E-02	-2.54	4.73E-03
212343_at	YIPF6	-3.39	1.10E-02	-2.54	1.65E-04
221543_s_at	ERLIN2	-2.76	2.14E-02	-2.54	2.53E-04
203910_at	ARHGAP29	-4.21	4.75E-02	-2.54	4.97E-03
235335_at	ABCA9	-2.84	3.70E-02	-2.54	2.95E-03
202811_at	STAMBP	-3.63	2.87E-04	-2.54	4.89E-04
227190_at	TMEM37	-3.30	3.14E-02	-2.54	1.79E-02
216080_s_at	FADS3	-2.24	2.67E-02	-2.52	9.20E-03
218471_s_at	BBS1	-2.99	2.66E-02	-2.52	6.69E-03
243358_at	IGF1R	-4.59	5.10E-03	-2.52	5.43E-03
224879_at	C9orf123	-2.78	2.14E-02	-2.51	4.50E-03
225974_at	TMEM64	-2.56	3.85E-02	-2.51	1.74E-04
214909_s_at	DDAH2	-2.25	7.99E-03	-2.51	3.74E-04
212101_at	KPNA6	-2.63	3.37E-02	-2.51	4.15E-02

1553679_s_at	VKORC1L1	-3.03	2.98E-02	-2.51	1.46E-02
222456_s_at	LIMA1	-3.71	5.88E-03	-2.51	2.62E-03
225928_at	VTI1B	-2.77	9.76E-03	-2.51	2.50E-03
221274_s_at	LMAN2L	-2.82	4.03E-03	-2.51	2.04E-02
207537_at	PFKFB1	-3.75	2.71E-03	-2.51	1.93E-02
229984_at	DTWD1	-4.63	8.84E-04	-2.50	3.72E-02
202631_s_at	APPBP2	-3.57	9.71E-03	-2.50	1.42E-03
217973_at	DCXR	-2.19	4.56E-02	-2.50	5.99E-03
226638_at	ARHGAP23	-3.43	4.17E-03	-2.49	6.97E-03
212052_s_at	TBC1D9B	-2.43	2.61E-02	-2.49	5.87E-03
201522_x_at	PAR-SN /// SNORD107 /// SNRPN /// SNURF	-2.45	4.40E-02	-2.49	3.23E-02
222760_at	ZNF703	-2.02	3.09E-02	-2.49	3.86E-04
242414_at	QPRT	-2.56	2.38E-02	-2.49	1.11E-03
228384_s_at	PYROXD2	-2.66	4.41E-03	-2.48	7.32E-04
226992_at	NOSTRIN	-3.09	2.51E-03	-2.48	1.02E-02
201092_at	RBBP7	-2.67	3.19E-02	-2.47	2.60E-05
227536_at	ZC3H13	-2.40	2.67E-02	-2.46	1.40E-03
205545_x_at	DNAJC8	-2.77	2.16E-02	-2.46	2.27E-03
213298_at	NFIC	-2.53	4.67E-03	-2.46	1.02E-04
212423_at	ZCCHC24	-3.28	4.38E-04	-2.45	5.90E-03
206263_at	FMO4	-2.41	2.55E-02	-2.45	1.03E-02
202019_s_at	LANCL1	-2.76	1.06E-02	-2.44	9.81E-03
203733_at	DEXI	-2.41	2.97E-02	-2.44	6.10E-05
225133_at	KLF3	-4.03	1.85E-02	-2.44	1.81E-03
201328_at	ETS2	-2.83	2.02E-02	-2.44	3.34E-03
209409_at	GRB10	-2.39	3.38E-02	-2.44	2.69E-03
226506_at	THSD4	-2.55	2.75E-02	-2.44	1.26E-02
205606_at	LRP6	-3.07	1.11E-02	-2.43	2.22E-03
217874_at	SUCLG1	-2.38	4.19E-02	-2.43	1.99E-02
215918_s_at	SPTBN1	-3.84	2.02E-02	-2.43	8.08E-03
212771_at	FAM171A1	-4.26	1.87E-03	-2.42	7.09E-03
214239_x_at	PCGF2	-3.27	1.40E-02	-2.42	5.38E-04
212609_s_at	AKT3	-2.48	3.77E-02	-2.42	3.18E-04
222995_s_at	RHBDD2	-2.52	7.74E-03	-2.42	2.44E-03
225772_s_at	COX14	-2.67	1.26E-03	-2.41	4.20E-03
209002_s_at	CALCOCO1	-2.76	3.42E-03	-2.41	3.24E-03
201567_s_at	GOLGA4	-2.35	4.74E-02	-2.41	4.29E-03
207836_s_at	RBPMS	-3.13	6.66E-03	-2.41	7.66E-03
203768_s_at	STS	-2.98	1.84E-03	-2.41	1.25E-03
203588_s_at	TFDP2	-3.38	1.22E-03	-2.40	1.04E-03
206068_s_at	ACADL	-2.81	6.43E-03	-2.40	1.40E-02
222418_s_at	TMEM43	-2.86	2.11E-02	-2.40	2.63E-02

223430_at	SIK2	-3.69	1.57E-03	-2.39	7.72E-04
231050_at	HRASLS5	-3.72	2.09E-02	-2.39	2.10E-02
238062_at	GPIHBP1	-3.84	2.51E-03	-2.39	3.75E-02
203220_s_at	TLE1	-3.56	2.84E-03	-2.39	6.90E-04
209576_at	GNAI1	-3.53	3.24E-02	-2.39	4.22E-02
205824_at	HSPB2	-3.38	3.22E-03	-2.38	3.80E-03
229394_s_at	ARHGAP35	-2.78	4.84E-02	-2.38	7.73E-03
203767_s_at	STS	-2.48	4.18E-02	-2.38	1.50E-03
234936_s_at	CC2D2A	-2.83	2.01E-02	-2.38	1.48E-03
40489_at	ATN1	-2.18	1.68E-02	-2.38	5.01E-03
226485_at	VSIG10	-3.67	1.04E-02	-2.38	1.07E-02
202936_s_at	SOX9	-3.37	2.89E-03	-2.38	7.95E-04
32625_at	NPR1	-3.08	6.31E-03	-2.37	6.14E-03
224280_s_at	MTFR1L	-3.00	3.00E-02	-2.37	1.86E-04
211535_s_at	FGFR1	-2.68	1.44E-02	-2.37	1.77E-03
201897_s_at	CKS1B	-3.06	1.10E-03	-2.37	3.15E-03
218149_s_at	ZNF395	-4.23	4.37E-03	-2.37	2.57E-03
218909_at	RPS6KC1	-3.85	3.30E-02	-2.36	4.80E-02
215088_s_at	SDHC	-2.47	2.44E-02	-2.36	1.46E-02
218124_at	RETSAT	-4.55	7.10E-04	-2.36	1.08E-02
232977_x_at	MYH14	-2.95	7.51E-03	-2.36	3.64E-03
223170_at	TMEM98	-2.42	2.44E-02	-2.36	1.38E-02
1563560_at	AHNAK	-2.03	2.30E-02	-2.35	9.41E-04
206856_at	LILRB5	-5.40	3.23E-03	-2.35	2.29E-03
222269_at	APOOL	-3.05	3.33E-02	-2.35	1.66E-03
208336_s_at	TECR	-2.09	3.09E-02	-2.35	1.26E-03
225354_s_at	SH3BGRL2	-2.88	1.44E-02	-2.35	3.42E-03
214843_s_at	USP33	-2.70	1.03E-02	-2.34	1.55E-02
208316_s_at	OCRL	-3.26	6.86E-03	-2.34	7.52E-04
212798_s_at	ANKMY2	-2.66	4.42E-02	-2.34	1.47E-02
217726_at	COPZ1	-3.04	6.19E-03	-2.33	1.32E-02
200635_s_at	PTPRF	-2.90	6.32E-03	-2.33	3.09E-03
212705_x_at	PNPLA2	-2.80	2.20E-03	-2.33	6.87E-03
210006_at	ABHD14A	-2.30	1.29E-02	-2.33	1.48E-04
218204_s_at	FYCO1	-3.21	9.27E-03	-2.32	1.82E-04
205383_s_at	ZBTB20	-2.60	2.31E-02	-2.32	4.99E-04
237217_at	ADAMTSL1	-3.15	1.17E-02	-2.32	2.01E-02
224653_at	EIF4EBP2	-2.75	4.13E-03	-2.32	5.44E-03
223007_s_at	TMEM245	-2.58	3.65E-02	-2.32	1.75E-02
204980_at	CLOCK	-2.82	1.33E-02	-2.32	2.21E-02
218910_at	ANO10	-2.01	4.44E-02	-2.32	5.12E-03
213181_s_at	MOCS1	-2.86	9.19E-03	-2.31	2.51E-03
222998_at	MAF1	-2.05	3.20E-02	-2.31	1.36E-02

228568_at	GCOM1 /// MYZAP	-2.18	2.39E-02	-2.31	8.58E-03
242888_at	PRRT3-AS1	-3.63	2.01E-03	-2.31	2.55E-03
230972_at	ANKRD9	-3.35	1.24E-02	-2.30	1.83E-03
240112_at	---	-4.68	1.36E-02	-2.30	3.41E-02
237326_at	LINC00310	-3.61	1.38E-03	-2.30	1.14E-02
214564_s_at	PCDHGC3	-2.39	1.60E-02	-2.29	5.58E-03
205379_at	CBR3	-2.14	4.64E-02	-2.29	3.40E-04
221599_at	AAMDC	-2.57	1.39E-02	-2.29	2.62E-03
214585_s_at	VPS52	-2.43	2.91E-02	-2.28	4.92E-02
221142_s_at	PECR	-2.85	3.04E-03	-2.28	5.11E-03
209099_x_at	JAG1	-2.74	4.57E-02	-2.28	1.41E-03
239273_s_at	MMP28	-2.98	2.07E-02	-2.28	1.44E-02
227657_at	RNF150	-2.53	2.07E-02	-2.28	1.71E-02
224750_at	RNF185	-2.25	4.96E-02	-2.27	2.29E-04
244043_at	TFDP2	-2.39	4.10E-03	-2.27	7.29E-04
235279_at	PARVA	-3.34	3.72E-03	-2.26	5.23E-04
212153_at	POGZ	-4.01	5.35E-03	-2.26	2.12E-02
203589_s_at	TFDP2	-3.30	7.77E-03	-2.26	1.14E-03
219175_s_at	SLC41A3	-2.47	2.83E-03	-2.26	1.98E-02
229910_at	SHE	-2.73	2.36E-02	-2.26	1.03E-02
216954_x_at	ATP5O	-2.06	1.50E-02	-2.26	4.25E-02
213792_s_at	INSR	-2.16	1.62E-02	-2.25	4.50E-04
208871_at	ATN1	-1.99	2.09E-02	-2.25	6.94E-03
202749_at	WRB	-2.88	4.92E-02	-2.25	3.47E-03
40562_at	GNA11	-2.45	1.38E-02	-2.25	8.81E-04
201032_at	BLCAP	-3.96	1.24E-04	-2.24	1.58E-03
204045_at	TCEAL1	-2.48	3.05E-02	-2.24	1.14E-02
228345_at	CHIC1	-3.07	3.79E-02	-2.23	2.00E-02
224522_s_at	DCAKD	-2.89	2.90E-03	-2.23	4.40E-03
211621_at	AR	-2.89	3.40E-02	-2.22	4.61E-03
218194_at	REXO2	-3.24	3.07E-02	-2.22	2.72E-02
242532_at	---	-3.43	1.53E-02	-2.22	2.90E-02
224993_at	MLLT1	-2.42	1.98E-02	-2.21	4.76E-02
208769_at	EIF4EBP2	-4.02	6.70E-03	-2.21	1.22E-03
209206_at	---	-2.31	3.27E-02	-2.21	5.81E-03
214480_at	ETV3	-2.54	1.05E-02	-2.21	1.82E-02
1555270_a_at	WFS1	-2.12	4.80E-02	-2.21	2.00E-03
227692_at	GNAI1	-4.31	1.33E-04	-2.20	4.38E-02
228813_at	HDAC4	-1.84	2.74E-02	-2.20	7.25E-04
221473_x_at	SERINC3	-2.05	3.94E-02	-2.20	3.08E-02
208093_s_at	NDEL1	-2.46	4.43E-02	-2.19	1.51E-02
212872_s_at	MED20	-2.45	3.67E-02	-2.19	4.44E-02
207230_at	CDON	-3.35	8.84E-03	-2.19	2.87E-02

220911_s_at	NYNRIN	-2.22	2.28E-02	-2.19	1.09E-02
216308_x_at	GRHPR	-2.31	2.74E-02	-2.19	3.72E-03
218697_at	NCKIPSD	-2.69	7.76E-03	-2.18	1.95E-02
204506_at	PPP3R1	-2.63	1.40E-02	-2.18	3.38E-03
201904_s_at	CTDSPL	-2.49	1.49E-02	-2.18	4.06E-03
36553_at	ASMTL	-2.43	4.74E-02	-2.17	1.63E-03
227780_s_at	ECSCR	-2.67	4.34E-02	-2.17	4.17E-04
202365_at	UNC119B	-2.67	8.29E-03	-2.17	3.83E-03
223459_s_at	C1orf56	-2.70	1.92E-03	-2.16	6.09E-04
219067_s_at	NSMCE4A	-2.67	2.58E-02	-2.15	1.64E-02
207129_at	CA5B	-3.85	5.13E-03	-2.15	2.76E-03
213351_s_at	TMCC1	-2.65	3.53E-02	-2.15	2.00E-02
226112_at	SGCB	-2.57	4.48E-02	-2.15	1.28E-03
1552923_a_at	PITPNM2	-2.69	4.62E-02	-2.15	2.65E-02
218957_s_at	PAAF1	-2.78	3.04E-02	-2.14	8.30E-03
221864_at	ORAI3	-2.37	2.72E-02	-2.13	4.34E-04
1555668_a_at	PARK2	-2.42	2.04E-02	-2.13	8.28E-03
1557380_at	AGAP11	-2.72	2.73E-02	-2.13	2.19E-02
223266_at	STRADB	-2.39	3.31E-02	-2.13	1.20E-02
209605_at	TST	-2.28	1.99E-02	-2.12	1.44E-03
35685_at	RING1	-1.95	4.55E-02	-2.12	1.96E-02
226157_at	TFDP2	-2.79	2.11E-02	-2.12	4.31E-03
219072_at	BCL7C	-1.92	2.32E-02	-2.11	4.44E-04
212739_s_at	NME4	-2.23	1.46E-02	-2.11	1.28E-03
1556116_s_at	TNPO1	-2.66	1.60E-02	-2.11	3.20E-02
229698_at	SHANK3	-2.35	4.92E-02	-2.11	4.97E-02
53991_at	DENND2A	-2.80	1.92E-03	-2.11	1.45E-02
203035_s_at	LOC101060431 /// PIAS3	-2.39	4.18E-02	-2.10	1.09E-02
205854_at	TULP3	-2.94	1.28E-02	-2.10	9.29E-03
213264_at	PCBP2	-2.17	3.13E-02	-2.10	7.34E-03
227022_at	GNPDA2	-2.59	1.79E-02	-2.09	5.09E-03
226207_at	RILPL1	-2.98	3.37E-02	-2.09	6.23E-04
233882_s_at	SEMA6D	-3.05	6.31E-03	-2.09	7.31E-03
235293_at	---	-2.98	9.80E-04	-2.09	7.37E-04
233825_s_at	CD99L2	-2.43	1.93E-02	-2.08	8.05E-03
204310_s_at	NPR2	-2.21	3.33E-02	-2.08	3.00E-03
237777_at	PFKFB1	-2.58	2.07E-02	-2.07	3.85E-02
219825_at	CYP26B1	-2.40	1.01E-02	-2.07	1.88E-02
229410_at	SLC35E1	-2.47	3.02E-02	-2.07	9.33E-03
220170_at	FHL5	-4.06	2.80E-02	-2.07	4.44E-02
226049_at	ERC1	-1.89	1.26E-02	-2.07	1.96E-03
243691_at	---	-4.27	4.05E-04	-2.06	2.81E-03
208869_s_at	GABARAPL1	-2.51	9.78E-04	-2.06	1.05E-04

222734_at	WARS2	-3.41	1.04E-02	-2.06	1.40E-02
219137_s_at	MFF	-2.71	3.61E-02	-2.06	4.35E-02
220261_s_at	ZDHHC4	-2.23	1.37E-02	-2.05	2.26E-02
201732_s_at	CLCN3	-2.82	3.44E-02	-2.04	1.18E-02
205120_s_at	SGCB	-2.52	3.10E-02	-2.04	7.91E-04
226257_x_at	MRPS22	-2.38	3.02E-03	-2.04	3.60E-02
225389_at	BTBD6	-2.43	3.70E-03	-2.03	2.28E-02
228730_s_at	SCRN2	-2.14	1.24E-02	-2.03	1.12E-02
219713_at	SHPK	-3.03	7.57E-04	-2.03	1.92E-02
226114_at	ZNF436	-2.73	3.77E-02	-2.03	2.33E-03
1557954_at	TXLNG	-3.25	2.44E-02	-2.03	2.25E-02
216210_x_at	TRIOBP	-2.02	4.02E-02	-2.03	2.35E-02
232570_s_at	ADAM33	-5.62	3.70E-03	-2.03	2.41E-02
224197_s_at	C1QTNF1	-2.70	2.67E-02	-2.02	3.25E-02
222425_s_at	POLDIP2	-1.97	2.46E-02	-2.02	8.15E-03
210790_s_at	SAR1A	-2.57	3.38E-02	-2.02	2.62E-02
223191_at	COX16	-3.06	2.11E-02	-2.02	2.75E-02
200083_at	USP22	-2.45	5.06E-03	-2.02	2.98E-02
201120_s_at	PGRMC1	-2.91	1.25E-02	-2.02	3.16E-02
242264_at	---	-3.03	3.08E-03	-2.01	9.91E-03
210473_s_at	GPR125	-3.08	2.99E-02	-2.01	1.99E-02
209256_s_at	KLHDC10	-3.49	2.84E-03	-2.01	1.16E-02
225844_at	POLE4	-1.92	1.64E-02	-2.01	1.87E-03
211596_s_at	LRIG1	-3.57	4.83E-03	-2.01	3.03E-02
202915_s_at	FAM20B	-2.76	4.59E-02	-2.00	2.00E-02
234312_s_at	ACSS2	-1.85	2.05E-02	-2.00	4.43E-02
201325_s_at	EMP1	-2.96	4.38E-02	-2.00	1.31E-02
224685_at	MLLT4	-2.38	4.28E-02	-2.00	2.26E-02
213627_at	MAGED2	-2.44	3.36E-02	-2.00	4.98E-03
35846_at	THRA	-1.96	4.55E-02	-1.99	2.09E-03
239210_at	OTTHUMG00000184145 /// RP11-477H21.2	-3.29	1.18E-02	-1.99	4.28E-03
211928_at	DYNC1H1	-2.34	4.44E-02	-1.99	3.33E-02
228740_at	OTTHUMG00000172945 /// RP11-999E24.3	-2.74	2.52E-02	-1.99	6.34E-03
226656_at	CRTAP	-2.17	1.60E-02	-1.99	9.75E-04
33736_at	STOML1	-1.96	1.40E-02	-1.99	1.57E-03
219097_x_at	SMIM7	-2.21	1.87E-02	-1.98	2.04E-02
226087_at	LZIC	-2.07	2.42E-02	-1.98	1.42E-03
225968_at	PRICKLE2	-2.20	1.53E-02	-1.98	6.13E-04
231546_at	---	-2.91	4.61E-02	-1.98	3.77E-02
203450_at	CBY1	-2.20	2.00E-03	-1.97	1.89E-03
241986_at	BMPER	-2.45	3.68E-02	-1.97	1.51E-02

44696_at	TBC1D13	-1.85	1.52E-02	-1.97	1.42E-03
212912_at	RPS6KA2	-3.82	1.28E-02	-1.97	4.52E-02
212992_at	AHNAK2	-2.70	1.40E-02	-1.96	2.31E-02
203581_at	RAB4A /// SPHAR	-2.16	4.45E-02	-1.96	2.18E-02
1552627_a_at	ARHGAP5	-3.34	4.16E-04	-1.96	2.60E-02
203860_at	PCCA	-2.75	7.19E-03	-1.96	6.33E-03
214531_s_at	SNX1	-2.62	1.48E-02	-1.96	6.38E-03
230644_at	LRFN5	-2.82	1.18E-03	-1.95	1.59E-02
217707_x_at	SMARCA2	-2.94	2.25E-02	-1.95	9.82E-03
219205_at	SRR	-2.25	2.63E-02	-1.95	3.86E-03
215192_at	PMS2P4	-2.86	9.60E-03	-1.95	3.44E-02
219418_at	NHEJ1 /// SLC23A3	-2.10	3.99E-02	-1.95	7.07E-03
224792_at	TNKS1BP1	-2.54	3.26E-03	-1.94	2.32E-03
217246_s_at	DIAPH2	-3.65	5.43E-03	-1.94	2.56E-02
224704_at	TNRC6A	-2.62	2.81E-02	-1.94	2.55E-02
215735_s_at	TSC2	-2.24	1.54E-02	-1.93	4.17E-02
203006_at	INPP5A	-2.59	2.03E-02	-1.93	1.65E-02
225590_at	SH3RF1	-2.10	2.76E-02	-1.93	1.60E-03
1554424_at	FIP1L1	-3.05	6.00E-03	-1.92	1.69E-02
229461_x_at	NEGR1	-2.76	1.51E-02	-1.92	6.39E-03
212157_at	SDC2	-3.94	2.59E-03	-1.91	1.41E-02
217025_s_at	DBN1	-2.49	4.11E-02	-1.91	7.00E-03
220032_at	CPED1	-2.58	5.21E-03	-1.91	7.76E-03
201361_at	TMEM109	-1.91	6.72E-03	-1.91	2.34E-02
202261_at	VPS72	-2.44	3.45E-02	-1.91	4.09E-02
225660_at	SEMA6A	-3.61	2.23E-03	-1.91	2.77E-02
228942_s_at	DAB2IP	-2.25	4.99E-02	-1.91	9.53E-03
205188_s_at	SMAD5	-1.99	3.95E-02	-1.90	1.32E-03
228299_at	KCTD20	-2.27	2.48E-02	-1.90	1.75E-02
203197_s_at	C1orf123	-2.19	5.40E-03	-1.90	2.31E-02
226931_at	TMTC1	-2.66	3.04E-02	-1.90	2.00E-02
207842_s_at	CASC3	-2.49	4.98E-03	-1.90	7.06E-03
213272_s_at	TMEM159	-2.30	2.10E-02	-1.90	1.99E-02
1555864_s_at	PDHA1	-2.60	3.70E-03	-1.90	2.67E-02
238032_at	---	-2.37	6.69E-03	-1.89	1.52E-02
210078_s_at	KCNAB1	-2.39	3.53E-02	-1.89	2.47E-03
212677_s_at	CEP68	-2.31	3.73E-02	-1.89	3.70E-02
232693_s_at	FBXO16 /// ZNF395	-2.23	4.43E-03	-1.88	1.81E-02
224886_at	JMJD8	-1.74	4.38E-02	-1.88	3.88E-03
208941_s_at	SEPHS1	-2.26	7.75E-03	-1.88	1.34E-02
206352_s_at	PEX10	-2.31	3.89E-04	-1.88	1.03E-03
215945_s_at	TRIM2	-2.96	2.74E-03	-1.88	2.83E-02
201570_at	SAMM50	-2.57	1.17E-02	-1.88	1.78E-02

201256_at	COX7A2L	-2.24	4.38E-02	-1.87	2.79E-02
230326_s_at	C11orf73	-3.06	2.48E-03	-1.87	2.82E-02
209242_at	PEG3	-2.45	1.99E-02	-1.87	9.13E-03
40016_g_at	MAST4	-2.39	4.11E-03	-1.87	2.35E-02
203367_at	DUSP14	-1.92	9.97E-03	-1.86	2.34E-02
229844_at	FOXP1	-2.77	2.66E-02	-1.86	3.22E-02
227625_s_at	STUB1	-1.85	3.09E-02	-1.86	3.98E-02
203187_at	DOCK1	-2.40	8.89E-03	-1.86	9.00E-04
214736_s_at	ADD1	-1.90	1.79E-02	-1.85	4.21E-03
204829_s_at	FOLR2	-2.57	3.69E-02	-1.85	3.25E-02
237154_at	OTTHUMG00000036478 /// RP1-28O10.1	-2.96	5.03E-04	-1.85	3.87E-02
242590_at	---	-3.22	2.98E-02	-1.85	3.72E-03
201080_at	PIP4K2B	-1.99	4.35E-02	-1.85	1.38E-03
210276_s_at	TRIOBP	-2.15	1.02E-02	-1.85	2.77E-03
206684_s_at	ATF7	-2.63	1.11E-03	-1.85	2.96E-03
223066_at	SNAPIN	-2.13	4.50E-02	-1.84	2.44E-03
223311_s_at	MTA3	-2.35	8.54E-04	-1.83	1.82E-02
206649_s_at	TFE3	-2.10	3.83E-02	-1.83	1.19E-03
226728_at	SLC27A1	-2.11	1.84E-02	-1.83	3.00E-03
206870_at	PPARA	-2.50	1.65E-02	-1.82	5.53E-03
204505_s_at	DMTN	-2.46	2.64E-03	-1.82	1.10E-02
234937_x_at	ZFP28	-3.22	1.69E-02	-1.82	1.76E-02
1554429_a_at	DMWD	-1.85	4.31E-02	-1.82	2.05E-02
202032_s_at	MAN2A2	-1.95	3.06E-02	-1.81	4.65E-04
214582_at	PDE3B	-2.98	2.28E-02	-1.81	3.19E-02
213501_at	ACOX1	-2.49	2.80E-02	-1.81	1.35E-02
222481_at	TIMM10B	-1.86	2.87E-02	-1.81	1.25E-02
221964_at	TULP3	-1.90	2.53E-02	-1.81	3.27E-03
212482_at	RMND5A	-1.99	4.13E-02	-1.81	6.72E-03
201905_s_at	CTDSPL	-1.91	1.23E-02	-1.81	7.07E-03
210438_x_at	TROVE2	-2.55	1.10E-02	-1.81	1.63E-02
223216_x_at	FBXO16 /// ZNF395	-2.13	5.13E-03	-1.80	2.20E-03
218208_at	PQLC1	-1.94	1.16E-02	-1.80	8.33E-03
207050_at	CACNA2D1	-2.38	4.58E-02	-1.80	2.71E-02
222841_s_at	TIMM22	-2.01	2.70E-02	-1.79	1.46E-03
202590_s_at	PDK2	-2.72	1.24E-03	-1.79	7.51E-03
211599_x_at	MET	-2.84	1.19E-02	-1.79	3.15E-02
227063_at	TMEM256	-2.60	7.96E-03	-1.78	5.45E-03
225422_at	CDC26	-2.74	3.59E-02	-1.78	1.68E-02
227151_at	SNX33	-2.13	2.18E-02	-1.78	2.59E-04
231963_at	ANKRD33B	-1.91	2.80E-02	-1.78	1.50E-02
225816_at	PHF17	-2.83	3.16E-02	-1.78	2.08E-02
212126_at	CBX5	-1.93	3.84E-02	-1.78	1.71E-02

212655_at	ZCCHC14	-2.37	3.94E-02	-1.77	1.45E-02
204306_s_at	CD151	-2.04	2.58E-02	-1.77	8.94E-03
227727_at	MRGPRF	-2.03	4.81E-02	-1.76	2.22E-02
223321_s_at	FGFRL1	-1.93	3.40E-02	-1.76	3.61E-03
207469_s_at	PIR	-2.28	4.99E-02	-1.76	9.94E-03
213103_at	STARD13	-2.05	4.85E-02	-1.76	2.63E-02
242034_at	FBXL17	-3.67	1.75E-02	-1.75	2.26E-02
222921_s_at	HEY2	-2.46	3.54E-02	-1.75	4.16E-02
220753_s_at	CRYL1	-2.55	6.47E-03	-1.75	8.66E-03
226360_at	ZNRF3	-3.05	2.78E-02	-1.74	2.92E-02
220454_s_at	SEMA6A	-2.25	4.68E-02	-1.74	2.78E-02
209522_s_at	CRAT	-2.14	3.35E-02	-1.74	1.84E-02
204227_s_at	TK2	-2.18	7.03E-03	-1.72	2.20E-03
208446_s_at	ZFYVE9	-2.32	2.43E-03	-1.72	2.89E-02
223366_at	ZNF704	-1.97	3.83E-02	-1.71	3.50E-02
204168_at	MGST2	-2.20	4.09E-02	-1.71	2.29E-02
214082_at	CA5B	-1.95	4.03E-02	-1.71	1.36E-02
212522_at	PDE8A	-1.92	8.50E-03	-1.70	4.56E-02
221123_x_at	FBXO16 /// ZNF395	-2.81	1.75E-04	-1.70	1.91E-02
205981_s_at	ING2	-2.17	4.17E-02	-1.69	2.59E-02
212134_at	PHLDB1	-2.30	9.71E-03	-1.69	1.92E-02
231826_at	RALGAPA2	-2.51	1.29E-02	-1.69	1.07E-02
202227_s_at	BRD8	-2.78	9.21E-03	-1.67	4.77E-02
200759_x_at	NFE2L1	-2.24	6.82E-03	-1.67	4.12E-02
209482_at	POP7	-2.11	1.42E-02	-1.67	1.83E-02
218882_s_at	WDR3	-1.93	2.93E-02	-1.66	2.32E-02
223305_at	TMEM216	-2.40	1.31E-02	-1.66	2.43E-03
204800_s_at	DHRS12	-1.96	1.20E-02	-1.66	1.08E-02
225511_at	GPRC5B	-2.79	2.96E-03	-1.66	2.45E-02
225972_at	TMEM64	-1.93	3.32E-02	-1.62	2.47E-02
228605_at	UBXN2A	-2.61	2.64E-03	-1.62	2.78E-02
202177_at	GAS6	-1.95	2.24E-02	-1.61	3.18E-02
52005_at	WIZ	-1.79	3.79E-02	-1.61	3.01E-02
226139_at	CCDC149	-2.67	2.73E-03	-1.60	1.53E-02
222711_s_at	RHBDF1	-1.94	2.21E-02	-1.60	2.17E-02
202012_s_at	EXT2	-2.20	3.24E-02	-1.60	6.68E-03
226850_at	SUMF1	-2.52	2.14E-03	-1.60	1.81E-02
218262_at	RMND5B	-1.72	2.87E-02	-1.60	3.81E-02
223703_at	C10orf11	-2.08	3.26E-02	-1.59	1.38E-02
215198_s_at	CALD1	-2.44	2.40E-02	-1.59	1.79E-02
201851_at	SH3GL1	-2.36	3.75E-03	-1.58	2.22E-02
564_at	GNA11	-2.43	4.23E-03	-1.58	4.66E-02
32836_at	AGPAT1	-1.82	4.00E-02	-1.58	6.62E-03

227054_at	N6AMT2	-1.90	3.16E-02	-1.57	3.39E-02
225958_at	PHC1	-1.86	4.26E-02	-1.57	4.27E-02
227113_at	ADHFE1	-1.88	2.81E-02	-1.56	3.31E-02
218100_s_at	IFT57	-2.40	2.12E-02	-1.56	2.44E-02
219013_at	GALNT11	-2.65	1.58E-02	-1.54	3.88E-02
225489_at	TMEM18	-2.23	8.35E-03	-1.53	4.85E-02
203538_at	CAMLG	-2.88	3.26E-03	-1.51	3.32E-02

Supplemental Table 3. Probe sets indicating increased expression of genes in anterior orbit tissues from subjects with GPA compared to tissues from subjects with sarcoidosis.

Probe Set	**Gene Symbol**	**Fold Difference**	**FDR p-value**
210393_at	LGR5	1.95	4.73E-02
239461_at	GALNT15	1.89	4.42E-02
205968_at	KCNS3	1.84	3.60E-02
210331_at	HECW1	1.84	2.26E-02
214424_s_at	ALDOB	1.83	4.43E-02
1558803_at	---	1.78	3.40E-02
1563590_at	---	1.77	2.51E-02
220244_at	LINC00312	1.75	1.35E-02
1554580_a_at	WWP2	1.75	1.42E-02
202895_s_at	SIRPA	1.72	3.83E-02
1564251_at	EMID1	1.72	2.32E-02
243955_at	---	1.72	6.36E-03
1561676_at	PRICKLE2-AS3	1.71	1.11E-02
1555225_at	C1orf43	1.70	3.02E-02
1561961_at	PHF2P1	1.69	4.88E-02
1554946_at	LOC100506465	1.69	2.38E-03
231621_at	MPZL1	1.68	2.61E-02
1564000_at	ANKRD31	1.67	5.85E-04
204738_s_at	KRIT1	1.67	5.21E-03
231355_at	CACNG8	1.67	2.83E-02
207309_at	NOS1	1.67	4.41E-02
232768_at	CCNB2	1.66	4.50E-03
1555332_at	TPH2	1.63	1.47E-02
1552458_at	MBD3L1	1.63	2.32E-02
230055_at	KHDC1	1.63	4.31E-02
236543_at	---	1.62	3.43E-02
241030_at	---	1.61	4.04E-03
234683_at	KRTAP4-11 /// KRTAP4-6 /// LOC100134267	1.61	3.08E-02
241733_at	C18orf54	1.59	2.61E-02
1562821_a_at	DSCAM-AS1	1.59	3.81E-02
1557615_a_at	ARHGAP19	1.59	2.80E-02
210957_s_at	AFF2	1.58	3.62E-02
232956_at	---	1.58	2.60E-02
234546_at	AC003973.4 /// OTTHUMG00000182925	1.58	3.78E-02
233858_at	OTTHUMG00000173031 /// RP11-25E2.2	1.57	2.15E-02
1564758_at	LOC643659	1.57	4.47E-02
228116_at	---	1.57	2.25E-02
207268_x_at	ABI2	1.56	3.86E-02

243839_s_at	---	1.55	6.46E-03
1557837_a_at	ELMOD2	1.55	2.00E-02
228235_at	MIR503HG	1.55	2.46E-02
219722_s_at	GDPD3	1.55	2.17E-02
236470_at	---	1.54	6.65E-03
238289_at	---	1.54	4.98E-02
1557513_a_at	---	1.54	4.77E-02
201915_at	SEC63	1.54	4.38E-02
1557280_s_at	ITSN1	1.53	3.80E-02
1557709_at	OTTHUMG00000175952 /// RP1-140C12.2	1.53	2.92E-02
230153_at	NEK9	1.53	4.59E-02
244299_at	---	1.50	4.76E-02
223304_at	SLC37A3	1.50	2.56E-02
229762_at	---	1.50	4.06E-02
243484_x_at	---	1.50	4.77E-02
1566181_at	---	1.50	4.50E-02

Supplemental Table 4. Probe sets indicating decreased expression of genes in anterior orbit tissues from subjects with GPA compared to tissues from subjects with sarcoidosis.

Probe Set	Gene Symbol	Fold Difference	FDR p-value
218404_at	SNX10	-9.19	5.73E-03
1555745_a_at	LYZ	-8.86	1.37E-02
209396_s_at	CHI3L1	-8.67	1.99E-02
32128_at	CCL18 /// LOC101060271	-8.18	4.74E-02
209395_at	CHI3L1	-8.08	9.95E-04
203915_at	CXCL9	-7.65	3.41E-02
206227_at	CILP	-7.62	4.86E-04
1558034_s_at	CP	-7.61	1.48E-02
206134_at	ADAMDEC1	-7.57	1.49E-02
212671_s_at	HLA-DQA1 /// HLA-DQA2 /// LOC100509457	-7.30	1.13E-02
200887_s_at	STAT1	-7.22	4.58E-03
204846_at	CP	-6.97	2.84E-02
209924_at	CCL18 /// LOC101060271	-6.90	4.46E-02
1566342_at	SOD2	-6.79	2.01E-02
336_at	TBXA2R	-6.77	1.17E-03
215891_s_at	GM2A	-6.70	1.10E-03
1567628_at	CD74	-6.65	4.02E-03
223484_at	C15orf48	-6.51	6.70E-03
201141_at	GPNMB	-6.43	3.84E-02
205676_at	CYP27B1	-6.16	3.85E-03
211470_s_at	SULT1C2	-6.14	1.34E-02
208168_s_at	CHIT1	-6.08	1.25E-02
208691_at	TFRC	-5.86	3.69E-02
202269_x_at	GBP1	-5.82	2.47E-02
201201_at	CSTB	-5.65	1.41E-02
215223_s_at	LOC100129518 /// SOD2	-5.53	1.26E-02
209969_s_at	STAT1	-5.45	1.01E-02
210982_s_at	HLA-DRA	-5.26	1.29E-02
225647_s_at	CTSC	-5.23	4.01E-02
206420_at	IGSF6	-5.16	1.47E-03
209696_at	FBP1	-5.16	7.31E-04
214211_at	FTH1	-4.81	1.81E-02
202902_s_at	CTSS	-4.69	1.72E-02
215193_x_at	HLA-DRB1 /// HLA-DRB3 /// HLA-DRB4 /// LOC100507709 /// LOC100507714	-4.69	6.75E-03
201137_s_at	HLA-DPB1	-4.67	3.94E-02
209823_x_at	HLA-DQB1 /// LOC101060835	-4.63	5.84E-03
208864_s_at	TXN	-4.59	3.28E-02
205633_s_at	ALAS1	-4.44	1.10E-02

203922_s_at	CYBB	-4.38	2.12E-02
200628_s_at	WARS	-4.35	9.73E-03
212998_x_at	HLA-DQB1 /// LOC101060835	-4.31	3.42E-02
209312_x_at	HLA-DRB1 /// HLA-DRB4 /// HLA-DRB5 /// LOC100507709 /// LOC100507714	-4.31	2.98E-02
223502_s_at	TNFSF13B	-4.31	4.33E-02
200629_at	WARS	-4.27	1.06E-02
202953_at	C1QB	-4.21	4.94E-02
224399_at	PDCD1LG2	-4.19	4.31E-03
212737_at	GM2A	-4.15	6.17E-05
218232_at	C1QA	-4.11	3.43E-02
222868_s_at	IL18BP	-4.07	1.00E-02
202901_x_at	CTSS	-4.07	9.15E-03
206214_at	PLA2G7	-4.06	5.47E-03
227253_at	CP	-4.02	4.98E-02
207332_s_at	TFRC	-3.97	3.12E-02
208306_x_at	HLA-DRB1 /// LOC100507709 /// LOC100507714	-3.92	1.85E-03
217933_s_at	LAP3	-3.89	3.43E-02
209727_at	GM2A	-3.85	2.95E-04
1553706_at	HTRA4	-3.84	4.94E-03
220049_s_at	PDCD1LG2	-3.84	1.24E-02
217388_s_at	KYNU	-3.80	1.21E-02
201850_at	CAPG	-3.76	3.69E-04
203936_s_at	MMP9	-3.73	2.42E-02
226878_at	HLA-DOA	-3.64	1.31E-02
232617_at	CTSS	-3.56	4.43E-02
235706_at	CPM	-3.55	3.99E-02
1555565_s_at	TAPBP	-3.53	2.71E-02
209230_s_at	NUPR1	-3.52	3.86E-03
203920_at	NR1H3	-3.45	3.48E-02
201118_at	PGD	-3.45	1.02E-02
205342_s_at	SULT1C2	-3.45	1.31E-02
221266_s_at	DCSTAMP	-3.37	2.10E-03
210152_at	LILRB4	-3.36	3.24E-02
218424_s_at	STEAP3	-3.29	9.53E-04
35820_at	GM2A	-3.19	3.75E-04
1559776_at	---	-3.17	1.17E-02
237215_s_at	TFRC	-3.16	1.93E-02
220423_at	PLA2G2D	-3.16	4.88E-02
211138_s_at	KMO	-3.12	1.10E-02
211656_x_at	HLA-DQB1 /// LOC101060835	-3.11	3.18E-02
208680_at	PRDX1	-3.10	3.32E-02
203828_s_at	IL32	-3.08	1.69E-02

217373_x_at	MDM2	-3.07	3.89E-02
235678_at	GM2A	-3.07	6.42E-04
213198_at	ACVR1B	-3.04	1.69E-02
219648_at	MREG	-3.03	3.25E-02
223451_s_at	CKLF	-3.01	1.40E-02
205404_at	HSD11B1	-3.01	1.11E-02
225171_at	ARHGAP18	-2.97	4.09E-02
217995_at	SQRDL	-2.97	1.34E-02
211991_s_at	HLA-DPA1	-2.96	1.69E-02
221875_x_at	HLA-F	-2.93	4.44E-02
227265_at	FGL2	-2.93	2.68E-02
211529_x_at	HLA-G	-2.92	1.01E-02
218454_at	PLBD1	-2.92	3.59E-03
212862_at	CDS2	-2.91	1.48E-02
225924_at	FNIP2	-2.91	8.89E-03
209545_s_at	RIPK2	-2.81	1.42E-02
203932_at	HLA-DMB	-2.79	1.80E-02
202411_at	IFI27	-2.78	8.28E-03
1553151_at	ATP6V0D2	-2.75	2.96E-03
216041_x_at	GRN	-2.74	5.84E-03
226460_at	FNIP2	-2.74	4.19E-02
206100_at	CPM	-2.72	3.91E-02
226255_at	ZBTB33	-2.70	4.58E-02
204493_at	BID	-2.69	3.81E-02
205306_x_at	KMO	-2.68	1.62E-02
223640_at	HCST	-2.66	1.24E-02
209166_s_at	MAN2B1	-2.59	1.89E-02
206313_at	HLA-DOA	-2.59	1.46E-02
211582_x_at	LST1	-2.58	2.03E-02
211528_x_at	HLA-G	-2.58	4.72E-02
200678_x_at	GRN	-2.57	7.96E-03
202679_at	NPC1	-2.54	2.00E-02
239598_s_at	LPCAT2	-2.51	2.02E-02
209329_x_at	HIGD2A	-2.47	4.92E-02
1553043_a_at	CD300LF	-2.46	1.37E-02
225956_at	CREBRF	-2.45	3.46E-02
207809_s_at	ATP6AP1	-2.45	3.28E-02
204961_s_at	NCF1 /// NCF1B /// NCF1C	-2.43	4.85E-02
214390_s_at	BCAT1	-2.42	4.32E-02
214430_at	GLA	-2.41	3.18E-03
221561_at	SOAT1	-2.41	2.27E-02
202071_at	SDC4	-2.40	4.23E-02
221983_at	FAM134A	-2.39	3.73E-02

201272_at	AKR1B1	-2.39	4.43E-02
205174_s_at	QPCT	-2.37	1.75E-02
203096_s_at	RAPGEF2	-2.36	3.61E-02
222816_s_at	ZCCHC2	-2.35	3.23E-02
1555416_a_at	ALOX15B	-2.35	1.83E-03
202675_at	SDHB	-2.35	4.70E-02
235643_at	SAMD9L	-2.30	3.35E-02
203454_s_at	ATOX1	-2.30	3.19E-02
211284_s_at	GRN	-2.29	8.22E-04
223501_at	TNFSF13B	-2.29	4.21E-02
221524_s_at	RRAGD	-2.29	2.37E-02
215536_at	HLA-DQB2	-2.27	4.10E-03
213415_at	CLIC2	-2.23	3.24E-02
227135_at	NAAA	-2.23	2.50E-02
212658_at	LHFPL2	-2.22	3.83E-02
208002_s_at	ACOT7	-2.22	7.81E-04
201551_s_at	LAMP1	-2.21	9.74E-03
222550_at	ARMC1	-2.21	2.83E-02
220832_at	TLR8	-2.19	2.74E-02
208608_s_at	SNTB1	-2.15	8.48E-03
213246_at	TMEM251	-2.13	3.17E-02
206991_s_at	CCR5	-2.12	4.74E-02
209164_s_at	CYB561	-2.11	1.33E-02
214992_s_at	DNASE2	-2.11	8.08E-03
1554508_at	PIK3AP1	-2.11	4.71E-02
235059_at	RAB12	-2.08	3.95E-02
219593_at	SLC15A3	-2.08	3.79E-03
204084_s_at	CLN5	-2.08	4.79E-02
203619_s_at	FAIM2	-2.08	5.61E-03
211832_s_at	MDM2	-2.08	3.45E-02
202896_s_at	SIRPA	-2.07	1.70E-02
223465_at	COL4A3BP	-2.07	4.34E-02
209749_s_at	ACE	-2.07	2.61E-05
204638_at	ACP5	-2.06	1.15E-02
1555153_s_at	FCHO2	-2.06	4.17E-02
219525_at	SLC47A1	-2.04	4.03E-03
209831_x_at	DNASE2	-2.03	3.44E-03
205153_s_at	CD40	-2.02	4.91E-02
225057_at	SLC15A4	-2.01	3.48E-02
205627_at	CDA	-1.98	9.73E-03
1555736_a_at	AGTRAP	-1.98	2.62E-02
209911_x_at	HIST1H2BD	-1.97	3.60E-02
201037_at	PFKP	-1.97	3.10E-02

221503_s_at	KPNA3	-1.96	3.12E-02
200901_s_at	M6PR	-1.96	1.30E-02
235354_s_at	RSRC1	-1.95	4.21E-02
225390_s_at	KLF13	-1.94	4.70E-02
205921_s_at	SLC6A6	-1.93	4.76E-02
227712_at	LYRM2	-1.93	1.45E-02
222143_s_at	MTMR14	-1.92	8.24E-03
212802_s_at	GAPVD1	-1.91	3.67E-02
204385_at	KYNU	-1.91	2.98E-03
206637_at	P2RY14	-1.88	2.52E-02
232682_at	MREG	-1.88	8.90E-03
212500_at	ADO	-1.87	3.68E-02
226550_at	SLC9A7	-1.86	2.73E-02
206714_at	ALOX15B	-1.86	4.39E-02
206050_s_at	RNH1	-1.85	4.10E-02
224689_at	MANBAL	-1.83	2.43E-02
233936_s_at	GGNBP2	-1.82	1.82E-02
203971_at	SLC31A1	-1.81	2.04E-02
220731_s_at	NECAP2	-1.79	1.35E-02
201411_s_at	PLEKHB2	-1.79	3.46E-02
227970_at	GPR157	-1.78	3.71E-02
219788_at	PILRA	-1.77	1.79E-02
217976_s_at	DYNC1LI1	-1.77	4.49E-02
210841_s_at	NRP2	-1.76	4.66E-02
224871_at	TPRG1L	-1.76	2.06E-02
209571_at	CIR1	-1.75	2.33E-02
200752_s_at	CAPN1	-1.75	4.66E-02
211495_x_at	TNFSF12 /// TNFSF12-TNFSF13 /// TNFSF13	-1.75	2.84E-02
201198_s_at	PSMD1	-1.74	4.66E-02
225965_at	DDHD1	-1.74	2.85E-02
244154_at	DDHD1	-1.72	4.01E-02
207565_s_at	MR1	-1.71	3.82E-02
235710_at	VPS53	-1.71	2.08E-02
200052_s_at	ILF2	-1.71	8.24E-03
222993_at	MRPL37	-1.69	3.98E-02
226679_at	SLC26A11	-1.68	4.98E-02
217625_x_at	LINC00963	-1.68	2.06E-02
216095_x_at	MTMR1	-1.68	3.74E-02
1558371_a_at	---	-1.67	3.32E-02
232490_s_at	PRUNE	-1.67	4.05E-02
229597_s_at	WDFY4	-1.66	1.68E-02
212648_at	DHX29	-1.66	3.72E-02
204543_at	RAPGEF1	-1.65	3.19E-02

31874_at	GAS2L1	-1.65	4.34E-02
210838_s_at	ACVRL1	-1.64	2.05E-02
209375_at	XPC	-1.64	4.77E-02
236108_at	EPG5	-1.63	3.96E-02
219053_s_at	VPS37C	-1.62	4.62E-02
222157_s_at	WDR48	-1.62	2.58E-02
204316_at	RGS10	-1.61	2.32E-02
208830_s_at	SUPT6H	-1.60	3.52E-02
218567_x_at	DPP3	-1.59	2.44E-02
209553_at	LOC100505729 /// VPS8	-1.59	2.93E-02
231913_s_at	BRCC3	-1.58	1.98E-02
208021_s_at	RFC1	-1.58	7.23E-03
227463_at	ACE	-1.58	9.30E-03
203912_s_at	DNASE1L1	-1.57	3.05E-02
202703_at	DUSP11	-1.56	1.55E-03
203291_at	CNOT4	-1.56	3.43E-02
209523_at	TAF2	-1.56	2.86E-02
205248_at	DOPEY2	-1.55	2.22E-02
209629_s_at	NXT2	-1.55	4.74E-02
1554780_a_at	PHTF2	-1.55	4.02E-02
205746_s_at	ADAM17	-1.54	3.42E-02
212497_at	MAPK1IP1L	-1.54	2.89E-02
214941_s_at	PRPF40A	-1.54	3.21E-02
217808_s_at	MAPKAP1	-1.53	1.29E-02
204601_at	N4BP1	-1.53	4.08E-02
207847_s_at	MUC1	-1.53	2.89E-02
36566_at	CTNS	-1.53	2.96E-02
213039_at	ARHGEF18	-1.52	3.83E-02
214708_at	SNTB1	-1.52	4.09E-02
241068_at	---	-1.51	1.38E-02
238539_at	HPS3	-1.51	3.58E-02
209093_s_at	GBA /// GBAP1	-1.51	2.24E-02

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Supplemental Table 5. Probe sets indicating decreased expression in GPA versus normal controls that are common to both our study of anterior orbit and a published study of leukocytes (Alcorta D, et al. Microarray studies of gene expression in circulating leukocytes in kidney diseases. Experimental Nephrology. 2002;10:139-49; Alcorta DA, et al. Leukocyte gene expression signatures in antineutrophil cytoplasmic autoantibody and lupus glomerulonephritis. Kidney International. 2007;72:853-64).

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Probe Set	**Gene Symbol**	**Gene Title**
207275_s_at	ACSL1	acyl-CoA synthetase long-chain family member 1
202912_at	ADM	adrenomedullin
220326_s_at 58780_s_at	ARHGEF40	Rho guanine nucleotide exchange factor (GEF) 40
210896_s_at 209135_at 224996_at	ASPH	aspartate beta-hydroxylase
224707_at	CYSTM1	cysteine-rich transmembrane module containing 1
201328_at	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)
227466_at	FAM200B	family with sequence similarity 200, member B
223836_at	FGFBP2	fibroblast growth factor binding protein 2
204115_at	GNG11	guanine nucleotide binding protein (G protein), gamma 11
209409_at	GRB10	growth factor receptor-bound protein 10
209185_s_at	IRS2	insulin receptor substrate 2
202747_s_at	ITM2A	integral membrane protein 2A
200923_at	LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein
202032_s_at	MAN2A2	mannosidase, alpha, class 2A, member 2
223044_at	SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1
202863_at	SP100	SP100 nuclear antigen
216191_s_at	TRDV3	T cell receptor delta variable 3
217143_s_at	YME1L1	YME1-like 1 (S. cerevisiae)