

Gene Symbol	Probeset	Description	Q Value	mutant mean (log2)	SD	wildtype mean (log2)	SD	Relative expression (mutant/wildtype)	Gene location
Regulators of G-protein signaling (no known intervening genes)									
<i>Rgs5</i>	1420942_s_at	regulator of G-protein signaling 5	0.014	6.91	0.13	7.31	0.35	0.76	1:171,585,632-171,625,944
<i>Rgs4</i>	1416286_at	regulator of G-protein signaling 4	0.009	7.61	0.16	7.84	0.15	0.85	1:171,671,807-171,677,773
Potassium channel subunits (no known intervening genes)									
<i>Kctd3</i>	1459353_at	potassium channel tetramerisation domain containing 3	0.040	7.22	0.08	7.01	0.24	1.16	1:190,794,977-190,831,719
<i>Kcnk2</i>	1449158_at	potassium channel, subfamily K, member 2	0.005	8.63	0.22	8.88	0.07	0.84	1:191,031,810-191,167,711
alpha 2,6-Sialyltransferases (no known intervening genes)									
<i>St6galnac5</i>	1419420_at	alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	0.027	8.00	0.22	8.27	0.26	0.83	3:152,482,850-152,645,174
<i>St6galnac3</i>	1457125_at	alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3	0.040	5.48	0.15	5.65	0.16	0.89	3:152,865,473-153,388,026
C1q complement components (no known intervening genes)									
<i>C1qb</i>	1417063_at	complement component 1, q subcomponent, beta polypeptide	0.005	7.26	0.21	7.67	0.17	0.75	4:136,436,048-136,442,028
<i>C1qc</i>	1449401_at	complement component 1, q subcomponent, C chain	0.005	6.71	0.23	7.07	0.17	0.78	4:136,445,724-136,448,808
<i>C1qa</i>	1417381_at	complement component 1, q subcomponent, alpha polypeptide	0.018	7.09	0.20	7.29	0.13	0.87	4:136,451,833-136,454,684
Type 3 Semaphorins (one intervening gene [<i>Speer3</i>], not expressed)									
<i>Sema3a</i>	1420416_at	semaphorin 3A	0.014	8.08	0.10	8.27	0.13	0.88	5:13,396,784-13,602,559
<i>Sema3e</i>	1442226_at	semaphorin 3E	0.036	5.74	0.29	6.04	0.13	0.81	5:14,025,276-14,256,688
Gaba receptor subunits (one intervening gene, not probed)									
<i>Gabra2</i>	1455444_at	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 2	0.014	6.20	0.32	6.55	0.18	0.78	5:71,352,296-71,487,088
<i>Gabra4</i>	1433707_at	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 4	0.005	6.26	0.34	6.64	0.22	0.77	5:71,960,973-72,049,547
<i>Gabbr1</i>	1419719_at	gamma-aminobutyric acid (GABA-A) receptor, subunit beta 1	0.032	6.29	0.19	6.50	0.15	0.87	5:72,091,255-72,528,467

Beta globin locus (set of four genes, no known intervening genes)									
<i>Hbb-b1</i> ///		hemoglobin, beta adult major, minor							
<i>Hbb-b2</i>	1417184_s_at	chains	0.005	13.18	0.20	13.43	0.09	0.84	7:110,961,038-110,962,510
<i>Hbb-b2</i>	1427866_x_at	hemoglobin, beta adult minor chain	0.014	5.39	0.27	5.85	0.30	0.74	7:110,975,048-110,976,610
		hemoglobin Z, beta-like embryonic							
<i>Hbb-bh1</i>	1437990_x_at	chain	0.005	7.15	0.31	8.49	0.51	0.39	7:110,990,150-110,991,678
		hemoglobin Y, beta-like embryonic							
<i>Hbb-y</i>	1436717_x_at	chain	0.097	13.55	0.08	13.61	0.07	0.95	7:111,000,272-111,001,721
Type VI collagen chains (no known intervening genes)									
<i>Col6a2</i>	1452250_a_at	collagen, type VI, alpha 2	0.018	8.17	0.39	8.59	0.30	0.75	10:76,058,507-76,086,072
<i>Col6a1</i>	1448590_at	collagen, type VI, alpha 1	0.014	7.22	0.46	7.70	0.32	0.72	10:76,171,537-76,188,789
Small leucine-rich repeat proteoglycans (set of four genes; one [<i>Kera</i>] not probed; <i>Epyc</i> levels close to background)									
<i>Dcn</i>	1449368_at	decorin	0.036	8.92	0.54	9.34	0.29	0.75	10:96,942,245-96,980,777
<i>Lum</i>	1423607_at	lumican	0.027	9.11	0.58	9.72	0.38	0.65	10:97,028,437-97,035,337
<i>Epyc</i>	1421114_a_at	epiphycan	0.384	4.99	0.25	5.14	0.48	0.90	10:97,106,702-97,144,534
Alpha globin locus (set of three genes, one [<i>Hbq</i>] not probed)									
		hemoglobin X, alpha-like embryonic							
<i>Hba-x</i>	1448716_at	chain	0.005	11.00	0.22	11.35	0.21	0.78	11:32,176,602-32,178,113
<i>Hba-a1</i> ///									
<i>Hba-a2</i>	1452757_s_at	hemoglobin alpha, adult chain	0.005	13.55	0.10	13.69	0.07	0.91	11:32,183,678-32,184,486
Gap junction proteins (set of three genes, one [<i>Gja3</i>] not probed)									
<i>Gjb2</i>	1423271_at	gap junction protein, beta 2	0.014	6.99	0.44	7.42	0.22	0.74	14:57,717,451-57,723,539
<i>Gjb6</i>	1448397_at	gap junction protein, beta 6	0.005	6.04	0.40	6.72	0.27	0.63	14:57,742,141-57,752,103
Protocadherins (two intervening genes, not probed)									
<i>Pcdh8</i>	1447825_x_at	protocadherin 8	0.027	10.11	0.13	10.27	0.11	0.90	14:80,166,592-80,171,107
<i>Pcdh17</i>	1436920_at	protocadherin 17	0.040	7.55	0.57	8.27	0.61	0.61	14:84,843,370-84,936,867
Protocadherin beta cluster (see Figure 8)									
Sorcs family receptors (no known intervening genes)									
		sortilin-related VPS10 domain							
<i>Sorcs3</i>	1425111_at	containing receptor 3	0.005	6.81	0.23	7.05	0.11	0.84	19:48,280,515-48,879,995
		VPS10 domain receptor protein							
<i>Sorcs1</i>	1425864_a_at	SORCS 1	0.005	6.23	0.10	6.46	0.12	0.85	19:50,218,430-50,752,975