

Probe Set ID	p-value (T T regulation (FCAbsolute (T Test paired p-value P <= 0.05)	Gene Symbol
201791_s_at	0.0337666 down	2.318062	DHCR7
202913_at	0.0469508 down	1.158668	ARHGEF11
204794_at	0.0215535 down	2.7998335	DUSP2
206192_at	0.0163132 down	1.136272	CDSN
207693_at	0.0337915 down	3.0389533	CACNB4
210032_s_at	0.0485447 down	1.1124951	SPAG6
210210_at	0.0054842 down	1.2910166	MPZL1
211112_at	0.0143194 down	1.1930116	SLC12A4
212411_at	0.0433504 down	1.6341357	IMP4
218188_s_at	0.044928 down	1.6450179	TIMM13
218295_s_at	0.0120693 down	1.5705556	NUP50
218455_at	0.0134561 down	1.639495	NFS1
221293_s_at	0.0245022 down	1.3287699	DEF6
221716_s_at	0.032513 down	1.0570351	ACSBG2
221915_s_at	0.027576 down	1.2325428	RANBP1
222583_s_at	0.00755 down	1.5436001	NUP50
222640_at	0.0215691 down	1.3852891	DNMT3A
223562_at	0.028505 down	1.279317	PARVG
224462_s_at	0.0020432 down	1.1757898	CHCHD6
225998_at	0.036424 down	1.6894983	GAB1
226002_at	0.0167066 down	1.8293827	GAB1
226659_at	0.0061151 down	2.4969766	DEF6
229114_at	0.0392223 down	2.091971	GAB1
239717_at	0.0056531 down	1.159967	CHRNA10
240261_at	0.0087418 down	1.2117853	TOM1L1
204647_at	0.0017942 up	1.3780755	HOMER3
205841_at	0.0300821 up	1.5812043	JAK2
205842_s_at	0.041865 up	1.7036841	JAK2
207408_at	0.043678 up	1.1099343	SLC22A14
209941_at	0.0164631 up	1.4054135	RIPK1
215489_x_a	0.0044821 up	1.6441947	HOMER3
216322_at	0.0401626 up	1.1204196	CD58
222222_s_at	0.0026712 up	1.2481266	HOMER3
226395_at	0.03712 up	1.5592209	HOOK3
226551_at	0.0061458 up	1.6044394	RIPK1
227056_at	0.0298988 up	1.2771562	KIAA0141
1555483_x_	0.027397 up	1.554966	FBLIM1

Gene Symbol	Primer 1	Primer 2
ARHGEF11	TCTCCCAGAGAAGACAGGCT	GATTCTGGAACCGTGGAGAC
CACNB4	GGCCTGCTTGTGTAGGAATC	GCCTTGAAAGAGGTGCTCTG
CD58	GCACATTGCTTGGTACATGG	GTCCTCAGCGTGGTCTGC
CDSN	TCGTTAGGGGAGGTGATACG	CTGCTGGCTGGTCTCCTC
CHCHD6	TCTTCCTCTCAATACGCTCCA	GAGGAGCAGAAGTCAGTCCG
CHRNA10	GGACCACGTTGGTGCTG	CTATGGTGGCCTGGATGC
DEF6	GTATCCCTGGCTGGACACAG	GTCTCCAAGTCCCAGCTCAA
DHCR7	GACTCTTGGCTTTGGGAATG	AACTTTTAAGGGGCCGGT
DNMT3A	CTTTCAGGCTACGATCCACG	TACTTCCAGAGCTTCAGGGC
DUSP2	GCAGGTCTGACGAGTGACTG	GACTCCAGGGCTCCTGTCTA
GAB1	TGGATCTCCAGTTAAACGGC	GGTGGTGAAGTGGTCTGCTC
HOMER3	GCCATCCTGAGATTTCTCCC	GCTTTGCCTCTGAACAGCAT
HOOK3	TCAGTTTTGATTCTGTTTAGCCA	GCCAGACCGTGGGAAGATTTA
IMP4	GACCCCTGTAAGGCCAGAG	CTCAGCCCAGGAGAGGAAG
JAK2	CCATTCCCATGCAGAGTCTT	CAGAAGCAGGCAACAGGAAC
MPZL1	GGATATCCGCATACACCACAG	TCTGCCTTCTGGATCTCACC
NFS1	GGCTGCTTCACTCCAATCTC	CCTACCTCCCAGTGCAGAAG
NUP50	CCTCCAGAAGGTACCACCAA	CATGGCCAGTGAGGAAGTCT
PARVG	TGGCATCCTTGTTACGATA	CCTCACTCCCACTCTCCTG
RANBP1	CAGAGGCAAATCGGAACAGT	AGTCCAACCATGACCCTCAG
RIPK1	TCACAACCTGCATTTTCGTTTG	CATTTCTGGCATTGAAGAAA
SLC12A4	CTCCAAGGGGGAAAGAAAAG	CTCAGTTGGGTGGACTACGG
SLC22A14	CCTCCTTACCTTCCCTTTC	GGTGGGTGGGATACTTGTGA
SPAG6	TGTTGAATTGTTGGGACCAC	GCGACTAGACCCCAAACAT
TIMM13	GAGTTGTAGGCGCGAGACA	TGTATAGGGAAACCTGGGGG
TOM1L1	GCATCTCCCGACCTGTTTTA	TGATGTCCGCCATATTGATG