

TargetID	RefSeq	EntrezID	Symbol	FC	adj.P.Val	PredictedTF	KEGG	GO_Biological_Process
ri 1810010H13 R000022C24 AK007420 1588-S	NR_003518	66776	4933439C20Rik	3.11	0.0018	-	-	-
scl52455.6.1_68-S	NM_030703	93721	Cpn1	2.62	0.0369	-	-	proteolysis (GO:0006508)
scl52728.6.1_56-S	NM_183190	269063	Ms4a5	1.99	0.0369	-	-	signal transduction (GO:0007165)
scl19223.5.1_16-S	NM_008100	14526	Gcg	2.02	0.0369	-	-	regulation of insulin secretion (GO:0050796)
ri 4931440N24 PX00017H21 AK029921 3407-S	NM_008935	19126	Prom1	2.02	0.0369	-	-	-
scl31608.7.1_161-S	NM_181593	233011	Itpkc	1.74	0.037	-	-	-
scl37713.12.428_61-S	NM_145365	208677	Creb3l3	2.42	0.045	TF	Melanogenesis (04916) Prostate cancer (05215)	transcription (GO:0006350) regulation of transcription, D--dependent (GO:0006355) response to unfolded protein (GO:0006986)