A
Up-regulated genes induced by miR-24-1
regulation of transcription
regulation of cellular biosynthetic process
regulation of macromolecule biosynthetic process
regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
regulation of gene expression
regulation of transcription, DNA-dependent
regulation of RNA metabolic process
protein modification process
negative regulation of transcription, DNA-dependent
negative regulation of RNA metabolic process
-log p-value
B
Down-regulated genes
Up-regulated genes
Target number
P=9.68X10-5
P=7.35X10-5
P=1.06X10-8
P=1.00X10-15
P=1.97X10-14
Miranda
microCosm
DIANA-MICROT
PITA
union target
miRNA Target Prediction Method
C
Motif E-Value=8.7e-003
Bits
miR-24-3p seed sequence
GGCUCAG
D
P=2.5298e-117
Percentage of regions containing seed sequence of miR-24-3p (%)
Peak
Mock
E
Ctrl
miR-24-1
Microarray
Fold change of normalized intensity
qPCR
Relative expression
CAPG
DUSP16
MVP
ENO3
C19orf57
F
Chr12
20 kb
hg19
DUSP16
miR-24-1 RNA-seq
Ctrl RNA-seq
Predicted miR-24-1 target
2 kb
UCSC Layered H3K27Ac
UCSC Layered H3K4me1
UCSC Layered H3K4me3
miR-24-1 H3K27ac
Ctrl H3K27ac
miR-24-1 H3K4me1
Ctrl H3K4me1
miR-24-1 Pol II
Ctrl Pol II
miR-24-1 H3K9me3
Ctrl H3K9me3
G
Chr17
50 kb
MINK1
ENO3
200 bases
500 bases
100 bases
H
Ctrl
miR-24-1 antagomir
Relative expression
DUSP16
ENO3
I
Sanger sequencing the PCR products of TALEN targeted mixture cells
Left TALEN pair target
miR-24-1 target site
Right TALEN pair target
J
Sanger sequencing the PCR products of single clone cell
miR-24-1 target site
K
M
WT
miR-24-1 target site deletion
1500bp
1000bp
900bp
800bp
700bp
600bp
500bp
400bp
300bp
200bp
100bp