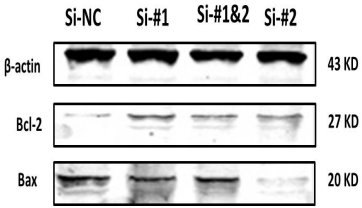
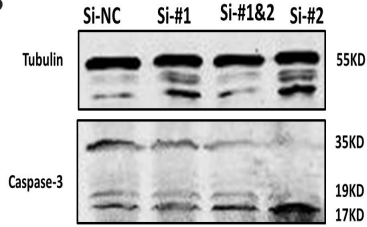
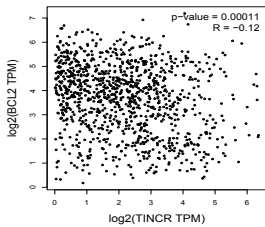
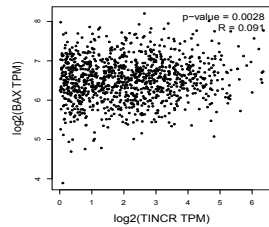
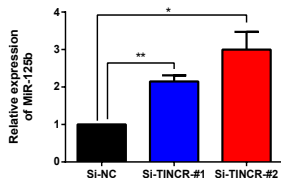


A**B****C****D****E**

label	Category	Gene	Item	FC (Gene)	Q (Gene)	% Differ (Gene)
GO:BP	GOBP	cytoskeleton reorganization	KEGG	7	4.1	3.6E-3
GO:BP	GOBP	positive regulation of cell motility	KEGG	3	1.8	5.6E-3
GO:BP	GOBP	establishment of skin barrier	KEGG	3	1.8	5.6E-3
GO:BP	GOBP	cytokeratin-dependent cell-cell adhesion via plasma membrane cell-cell adhesion molecules	KEGG	3	1.8	5.2E-3
GO:BP	GOBP	mitotic cohesions	KEGG	3	1.8	2.3E-2
GO:BP	GOBP	cell-cell adhesion	KEGG	7	4.1	2.3E-2
GO:BP	GOBP	transcription from the adenovirus II promoter	KEGG	10	5.8	2.4E-2
GO:BP	GOBP	cytoskeletal transport	KEGG	2	1.2	2.4E-2
GO:BP	GOBP	cytoskeleton-mediated ubiquitin-dependent proteolysis	KEGG	6	3.5	2.5E-2
GO:BP	GOBP	epithelial cell proliferation	KEGG	7	4.2	3.6E-2
GO:BP	GOBP	angiogenic sprouting, cellular cell adhesion pathway	KEGG	4	2.3	3.9E-2
GO:BP	GOBP	cytoskeletal homeostasis maintenance	KEGG	2	1.2	4.0E-2
GO:BP	GOBP	RNA secondary structure formation	KEGG	3	1.8	4.4E-2
GO:BP	GOBP	protein complex assembly	KEGG	2	1.2	5.3E-2
GO:BP	GOBP	protein reorganization	KEGG	3	1.8	5.4E-2
GO:BP	GOBP	regulation of neural precursor cell proliferation	KEGG	2	1.2	6.3E-2
GO:BP	GOBP	regulation of cell proliferation	KEGG	5	2.8	6.4E-2
GO:BP	GOBP	regulation of cellular amino acid metabolic process	KEGG	3	1.8	6.4E-2
GO:BP	GOBP	ubiquitin-dependent cell invasion, cell extension	KEGG	2	1.2	7.1E-2
GO:BP	GOBP	protein ubiquitination	KEGG	7	4.1	7.2E-2
GO:BP	GOBP	positive regulation of canonical Wnt signaling pathway	KEGG	4	2.3	7.4E-2
GO:BP	GOBP	positive regulation of cellular protein metabolic process	KEGG	2	1.2	8.2E-2
GO:BP	GOBP	protein recruitment and recruitment of cytoskeletal proteins via RHO class 1 GTP-dependent	KEGG	3	1.8	8.2E-2
GO:BP	GOBP	cytoskeleton assembly	KEGG	2	1.2	9.3E-2
GO:BP	GOBP	MAPK1 signaling pathway	KEGG	3	1.8	1.1E-1

F

Position 360-385 of PLAC2 3' UTR	5' ...AATCCCGGTT-GGAGAGCTTCAAGG... : : :	7mer-m8
hsa-miR-125a	3' ...GUGUCCAAUUCUUGAGAGUCCU...	
Position 360-385 of PLAC2 3' UTR	5' ...AATCCCGGTT-GGAGAGCTTCAAGG... : : :	7mer-m8
hsa-miR-125b	3' ...AGTGTGTCG-AATCCCGAGUCCU...	
Position 1000-1029 of PLAC2 3' UTR	5' ...GCCUGAGCCCAAGGAGGAGUUCAGGGAC... : : :	7mer-1A
hsa-miR-125a	3' ...GUGUCC-AATUUC-CGAG-AGUCCU...	
Position 1004-1029 of PLAC2 3' UTR	5' ...AGGCGCCAG-GAGGUTGACGGGAC... : : :	7mer-1A
hsa-miR-125b	3' ...AGUUGUUGAUGCCAGAGUCCU...	
Position 1130-1159 of PLAC2 3' UTR	5' ...CCUUAUUUCCUUGU-GCAUUAUCAGGGAC... : : :	7mer-1A
hsa-miR-125b	3' ...AGUU----UUGAUGCCAGAGUCCU...	
Position 1133-1159 of PLAC2 3' UTR	5' ...CCUUAUUUCCUUGU-GCAUUAUCAGGGAC... : : :	7mer-1A
hsa-miR-125a	3' ...GUGUCCAAUUCUUGAGAGUCCU...	

G**H**