LncRNA APOC1P1-3 promoting anoikis-resistance of breast cancer cells

Ping Zhou*

Supplementary

Table S1. Verification of the non-coding characteristics of lncRNA-APOC1P1-3.

Label	Strand	Frame	Start	Stop	Length(bp/aa)
ORF6	-	2	453	286	168/55
ORF8	-	3	380	297	84/27
ORF3	+	3	51	125	75/24
ORF2	+	2	428	493	66/21
ORF4	+	3	240	302	63/20
ORF5	-	1	52	＞2	51/16
ORF7	-	2	264	214	51/16
ORF1	+	1	379	420	42/13

LncRNA-APOC1P1-3 has 8 ORFs, each is less than 200nt. All ORFs labeled "+" after BLAST and these short peptides have no homologous proteins.

Table S2. Comparison of the target microRNAs with different databases.

Names	Total	Elements
PITA **Kangcheng**	**8**	**hsa-miR-193a-5p** **hsa-miR-587** **hsa-miR-566** **hsa-miR-483-5p** **hsa-miR-188-3p** **hsa-miR-369-5p** **hsa-miR-502-5p** **hsa-miR-1290**
Miranda **PITA**	**2**	**hsa-miR-204** **hsa-miR-211**
Kangcheng **miRDB4** **PITA**	**1**	**hsa-miR-188-3p**

There are 8 cross results among PITA database and chip results (Kangcheng). PITA and Miranda have 2 cross results, and miRDB4, PITA and Kangcheng have 1 cross result.

Table S3. 20 sets of random mutations for binding sites, and its thermodynamics.

NO.	Mutant sequences	mfe(kcal/mol)
1	AGTGAAGTTCGTGGCAAGATCTGCGAT	-18.6
2	AGTGAGCTTCATACCAAGGTGTGGAAT	-18.9
3	AGTGAATTTGCTGGCAAGCTGTAGGAT	-19.4
4	**AGTGAGCTTCGTGCCAAGGTGGGGTAT**	**-25.4**
5	AGTGAGCTTCGTGCCAAGGTGGGGCAT	-25.3
6	AGTGAGCTTCTTGGCAAGGTGTAGGAT	-20.7
7	AGTGGACTTTCTACCAAGCTGTGAGAT	-17.5
8	AGTGGACTTCCGGCCAAGGTGGGCGAT	-22.3
9	AGTGAATTTCATGGCAAGGTGTAGGAT	-18.3
10	AGTGAGCTTACTGTCAAGACGTGCGAT	-17.3
11	AGTGGACTTACTACCAAGGTGCGGGAT	-17.6

Table S4. The primer sequences are described in table S4.

Gene name	Forward primer(5'-3')	Reverse primer(5'-3')
APOC1P1-3 Primer1	GGTCCTGGTGGTGGTTCTGTC	CTCCTTCACTTTCCGAAATGTCTC
APOC1P1-3 Primer2	AGGATTCAGGTTGGTGCCC	TCTGTGTGATGCGGTTGATGA
GAPDH	GGGAAACTGTGGCGTGAT	GAGTGGGTGTCGCTGTTGA
β-actin	GGTGGCTTTTAGGATGGCAAG	ACTGGAACGGTGAAGGTGACAG

Figure S1. Thermodynamic analysis of the predicted binding sites by BiBiServ-RNAhybrid.

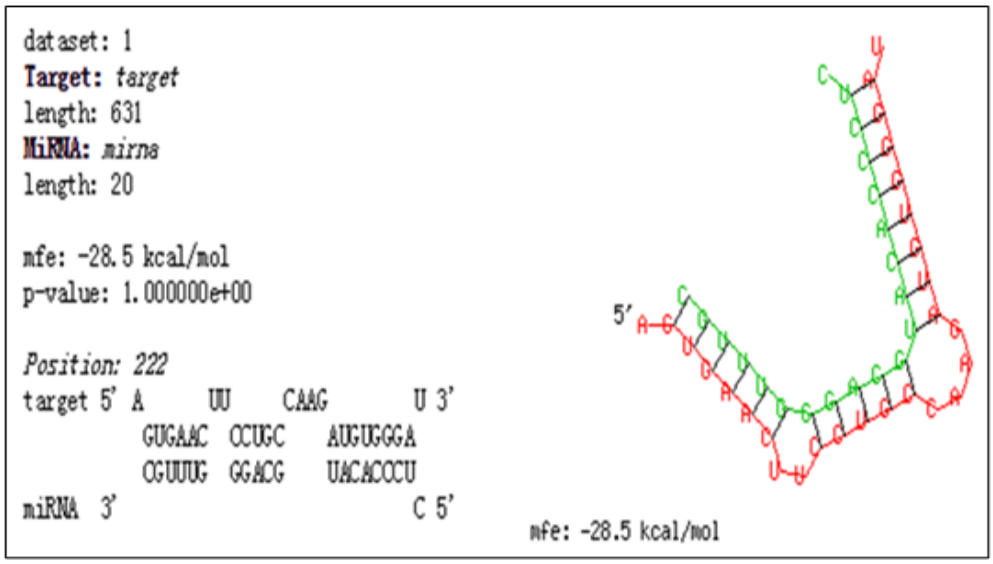

Figure S2. Site-directed mutation in pmirGLO-APOC1P1-3'UTR plasmid.