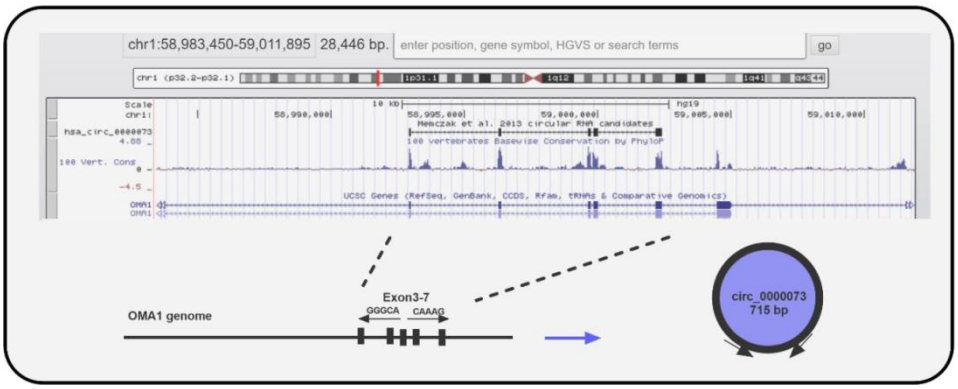
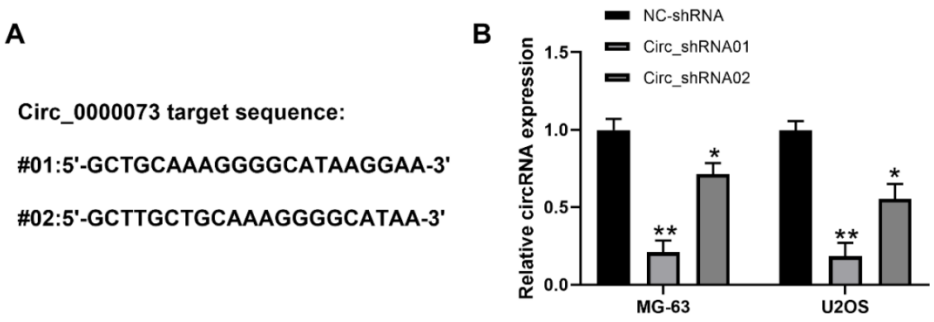
SUPPLEMENTARY FIGURES



Supplementary Figure 1. The scheme of hsa_circ_0000073.

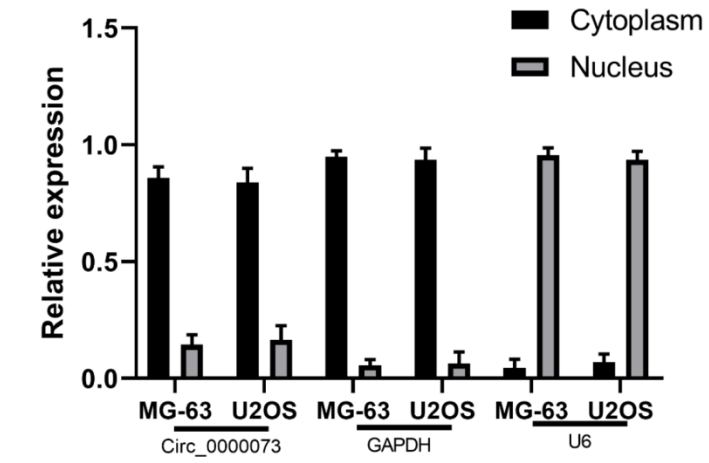


Supplementary Figure 2. (**A**) Circ_0000073 target sequence for shRNA design. (**B**) The silenced efficiencies of circ_0000073 knock down plasmids were qualified by a qRT-PCR assays, and Circ_shRNA-01 was selected in the following RNAi experiments.

A

Transcript id	Exon information			
NM_145243	Spliced_len	Exon Number	Exon Sizes	Exon Offsets
	715	5	75, 129, 108, 174, 229	0, 3340, 6692, 6897, 9252
Protein coding potential				
IRES Elements	Parameter Index			
	Position (start--end)		R Score	With Pseudoknot (Y/N)
	273--409		1.583801	Y
	636--712		1.485804	Y
Open Reading Frame (ORF)	Start Position		End Position	Protein Length
	233		1r+36	172 aa
	MEEFKNDMLT EKDARYLAVK EVLCHLIECN KDVPGISQIN WVIHVVDSPI INAFVLPNGQ MFVFTGFLNS VTDIHQLSFL LGHEIAHAVL GHAAEKAGMV HLLDFLGMIF LTMIWAICPR DSLALLCQWI QSKLQEYMFN RPYSRKLEAE ADKIGLLLAA KGHKEMVAGT SS*			
	Note: (1). nr represents n rounds(n<3); (2). * represents a stop codon.			
Protein Features	The possibility of encoding protein is relatively low(R<1.6 or it has no open reading frame), so no protein features was predicted!			

B



Supplementary Figure 3. (**A**) CircDB database showed that there was no translation function in hsa_circ_0000073. (**B**) The expression of circ_0000073 in U2OS cells by in-situ hybridization assay.