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Supplemental Information

hsa_circ_0092306 Targeting miR-197-3p

Promotes Gastric Cancer Development

by Regulating PRKCB in MKN-45 Cells

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Table S1 Correlation of relative hsa_circ_0092306 expression with the clinicopathological characteristics of 45 patients with gastric cancer

Parameters	Group	Cases	hsa_circ_0092306 expression				<i>P</i> -value
			Low	%	High	%	
Gender	Male	30	12	40.00	18	60.00	0.5273
	Female	15	8	53.33	7	46.67	
Age at surgery (year)	< 60	16	9	56.25	7	43.75	0.3484
	≥ 60	29	11	37.93	18	62.07	
Tumor size (cm)	< 3	19	12	63.16	7	36.84	0.0389
	≥ 3	26	8	30.77	18	69.23	
Histological grade	Well	27	8	29.63	19	70.37	0.0307
	Moderately and poorly	18	12	66.67	6	33.33	
TNM stage	I, II	19	13	68.42	6	31.58	0.0076
	III, IV	26	7	26.92	19	73.08	
Lymph node metastasis	Absent	22	15	68.18	7	31.82	0.0027
	Present	23	5	21.74	18	78.26	

Notes: the mean value of hsa_circ_0092306 expression is set as cutoff value to differentiate the low expression or the high expression of hsa_circ_0092306.

Table S2 shRNA sequence

Name	Sequence (5'-3')
sh-hsa_circ_0092306	
Top Strand	CACCACAGGACCCGATGCAGAACATCGAAATGTTC TGCATCGGGTCCTG
Bottom Strand	AAAACAGGACCCGATGCAGAACATTCGATGTTCTG CATCGGGTCCTGT
sh-PRKCB	
Top Strand	CACCGCGGTATGATACGTCTCTTGGCGAACCAAGAG ACGTATCATACCGC
Bottom Strand	AAAAGCGGTATGATACGTCTCTTGGTTCGCCAAGAG ACGTATCATACCGC
sh-NC	
Top Strand	CACCTTCTCCGAACGTGTCACGTTTCAAGAGAACGT GACACGTTTCGGAGAATTTTTTG
Bottom Strand	GATCCAAAAAATTCTCCGAACGTGTCACGTTCTCTT GAAACGTGACACGTTTCGGAGAA

Table S3 primer sequence for qRT-PCR

Name	Sequence (5'-3')
hsa_circ_0092306	
Forward Primer	GACACAGCAAAGGAAGGGTC
Reverse Primer	CAACCTCCACCTCCTGAGTT
miR-197-3p	
Forward Primer	ACACTCCAGCTGGGTTACCCACCTTCTCCA
Reverse Primer	TCGTGGAGTCGGCAATTCAGTTGAGGCT
PRKCB	
Forward Primer	AGCCCCACGTTTTGTGACC
Reverse Primer	GCTGGGAACATTCATCACGC
GAPDH	
Forward Primer	TGTGGGCATCAATGGATTTGG
Reverse Primer	ACACCATGTATTCCGGGTCAAT
U6	
Forward Primer	CTCGCTTCGGCAGCACA
Reverse Primer	AACGCTTCACGAATTTGCGT

A

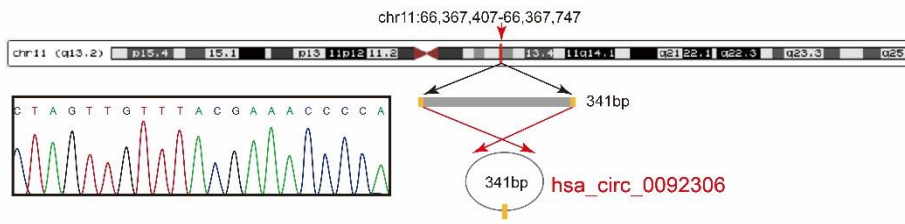


Figure S1 (A) The ideograph got from UCSC Genome Browser showed that the hsa_circ_0092306 originated from chromosome 11 and matured into 341 bp circle.

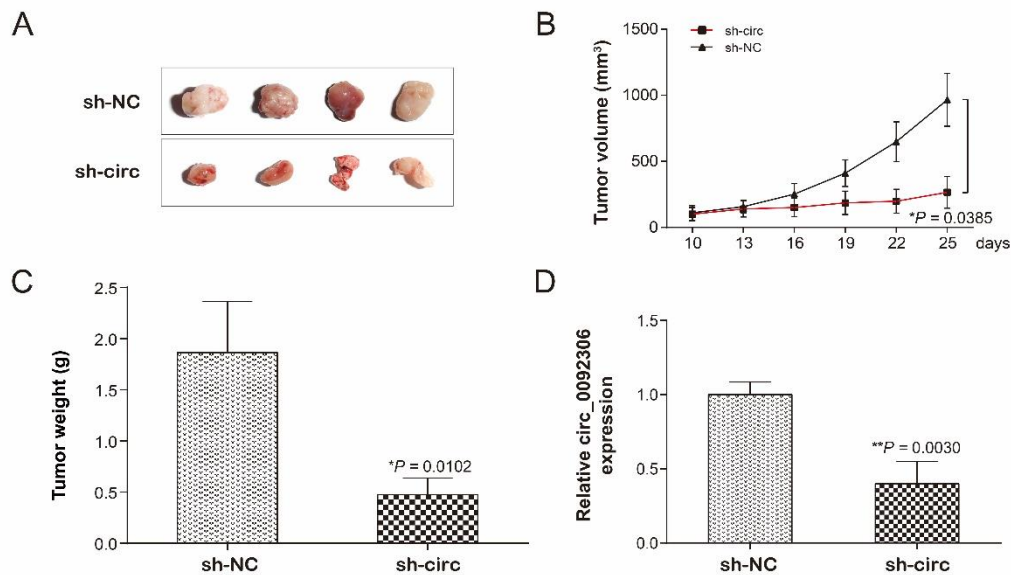


Figure S2 The knockdown of hsa_circ_0092306 inhibited tumor growth *in vivo*. (A) The actual size of the tumor showed smaller size in the hsa_circ_0092306 knockdown group compared with NC group. (B) Tumor growth volume was measured every 3 days after 10 days from transplantation and was significantly reduced in the hsa_circ_0092306 knockdown group. (C) The weight of tumor acquired from day 25 in sh-circ group was significantly decreased. (D) The hsa_circ_0092306 expression in the sh-circ group was lower than that in the sh-NC group. **P* < 0.05 and ***P* < 0.01 meant significant statistical significances.

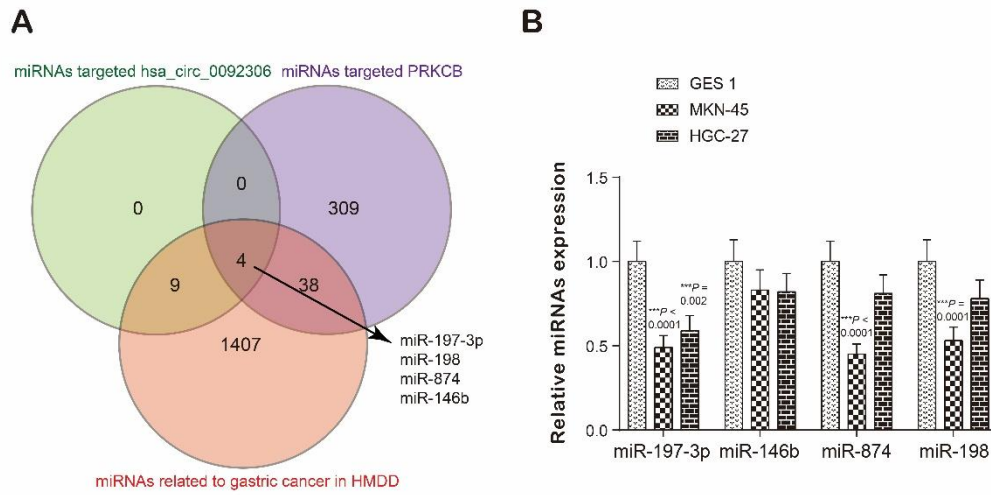


Figure S3 MiR-197-3p was screened out for further investigation. (A) The four miRNAs were screened out in miRNAs who targeted hsa_circ_0092306 and PRKCB, and related to GC in HMDD. (B) MiR-197-3p expression detected by qRT-PCR was both lower in MKN-45 and HGC-27 cells than that in GSE 1 cells. *** $P < 0.001$ meant significant statistical significances.

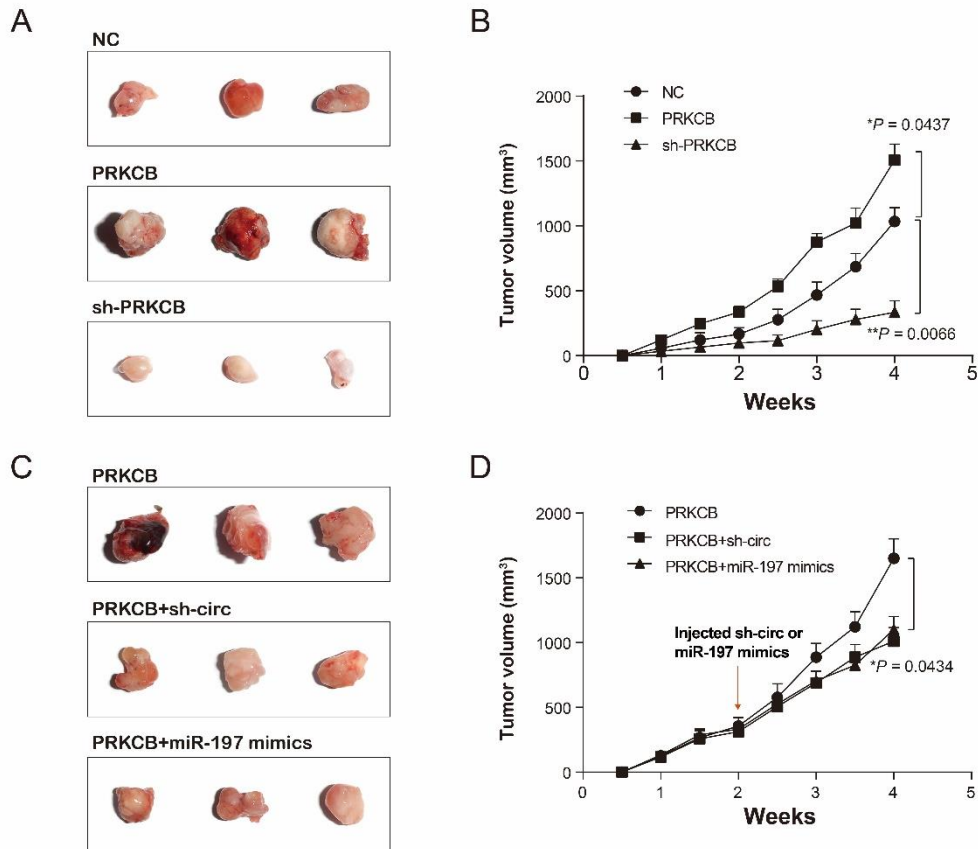


Figure S4 Hsa_circ_0092306 inhibited GC growth through regulating miR-197-3p/PRKCB.

(A-B) Tumor actual sizes and tumor growth volume curve showed PRKCB promoted GC growth *in vivo*. (C-D) Hsa_circ_0092306 knockdown or miR-197-3p mimics injection attenuated the growth of tumors induced by the PRKCB overexpression *in vivo*. The red arrow represented the inject time of sh-circ and miR-197-3p mimics. *P < 0.05 and **P < 0.01, compared with NC or PRKCB overexpression group, meant significant statistical significances.