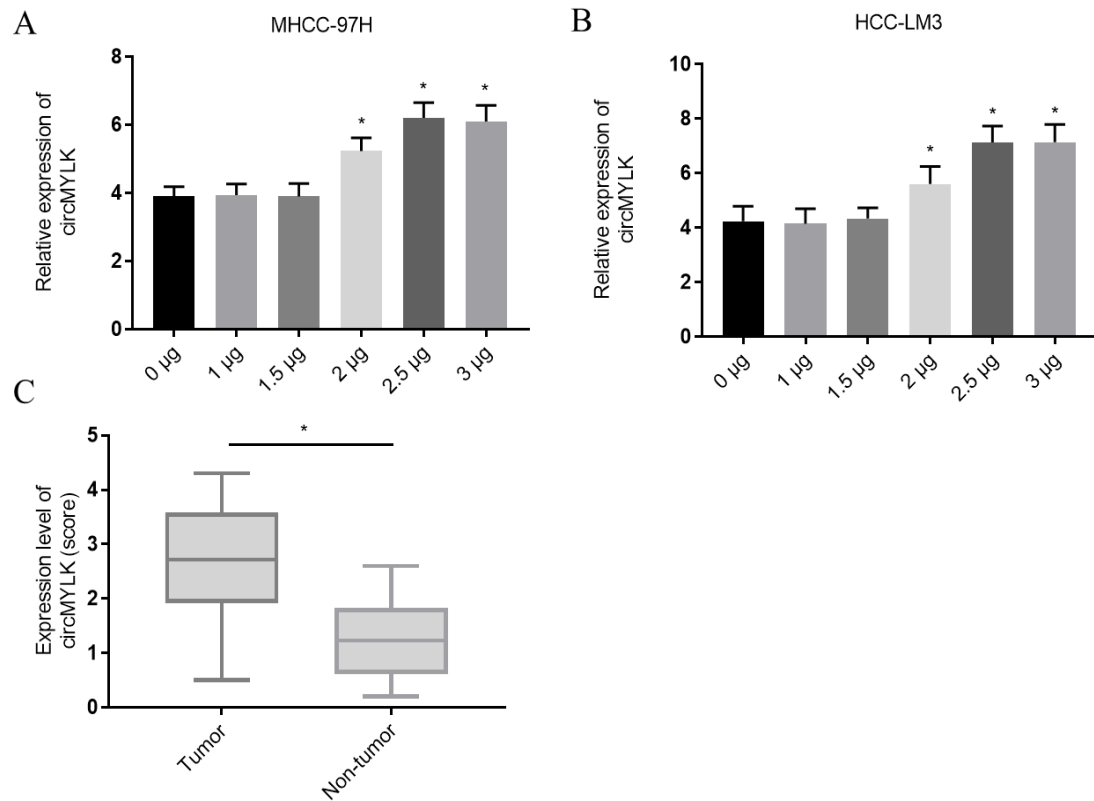
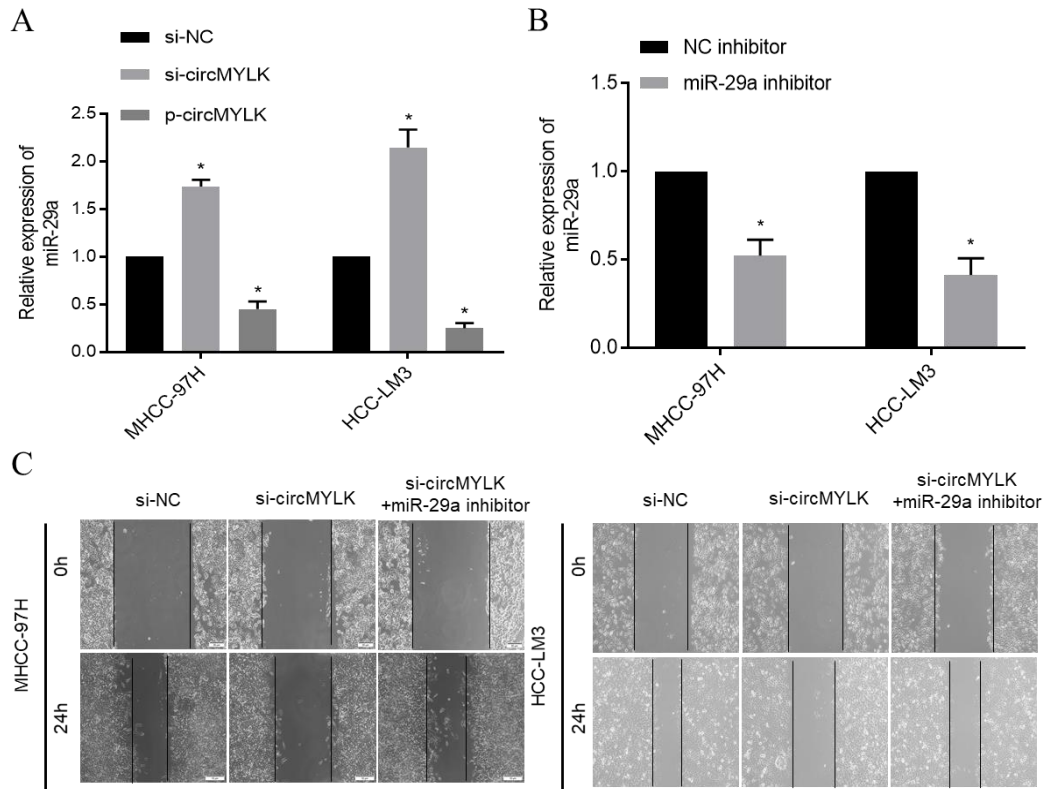


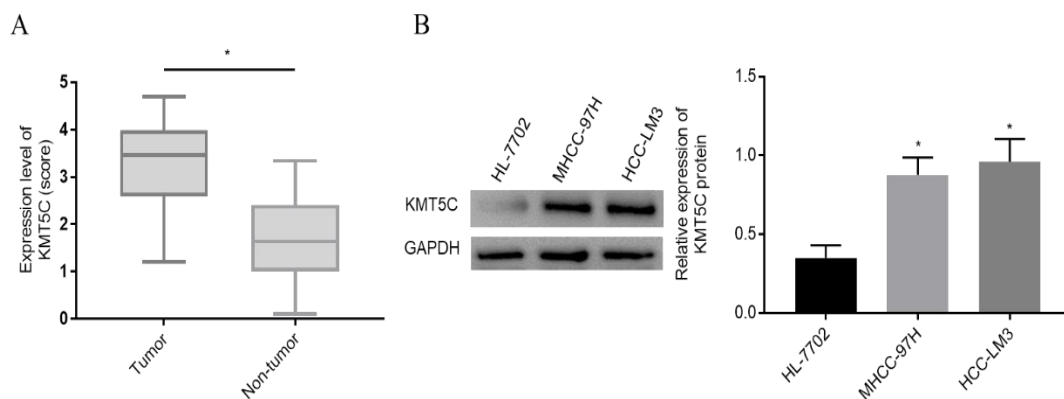
Supplementary Figures



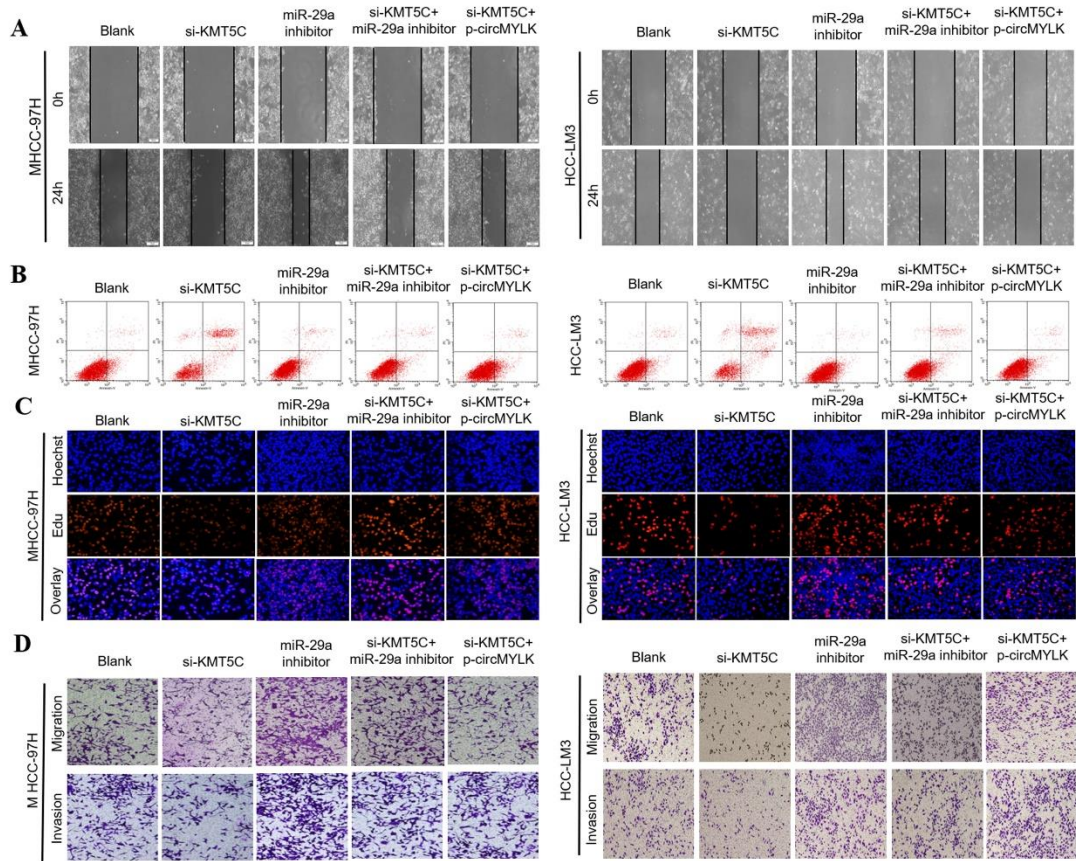
Supplementary Figure 1. (A-B) A dose-process experiment was conducted to determine the amount of RNA circMYLK that can achieve approximately the maximum effect. (C) FISH results of circMYLK level in HCC tissues. n=60. *P<0.05.



Supplementary Figure 2. (A) qRT-PCR results showed that in both cell lines, circMYLK knockdown led to a significant increase in miR-29a expression, while circMYLK overexpression displayed the exact opposite role. (B) MiR-29a expression were significantly reduced in both cell lines, indicating that it has a good transfection efficiency. (C) Wound healing experiment indicated that HCC cells co-transfected with the miR-29a inhibitor and si-circMYLK improved migration ability, compared with si-circMYLK group, and no obvious difference compared with the si-NC group. *P<0.05.



Supplementary Figure 3. (A) Immunofluorescence assay revealed that KMT5C was overexpressed in HCC tissues. n=60. (B) Western blot analysis revealed that the KMT5C protein expression levels in HCC cell lines was higher than that in the human normal liver cell line. *P<0.05.



Supplementary Figure 4. (A) Wound healing assays showed cell migration ability of HCC-LM3 and MHCC-97H cells in each group. (B) Flow cytometry revealing the rates of apoptosis in HCC cells in each group. (C) EdU proliferation assay demonstrating the HCC cell growth in each group. (D) Migration and invasion assays indicating the migration and invasion abilities of MHCC-97H and HCC-LM3 cells in each group. * $P < 0.05$.

Supplementary Table S1. Clinicopathologic characteristics in 60 HCC cases and their correlation between circRNA-MYLK levels

clinicopathologic characteristics	Number	circ-MYLK expression		P value
		Highexpression	Lowexpression	
Age(years)				0.635
≤60	24	13	11	
>60	36	17	19	
Gender				0.561
Male	46	24	22	
Female	14	6	8	
Tumor size (cm)				0.0028
≤5	22	5	17	
>5	38	25	13	
TNM stage				0.0034
I - II	29	5	24	
III -IV	31	25	6	
Tumor number				0.658
Solitary	26	14	12	
Multiple	34	16	18	
Tumor capsular				0.337
Incomplete	2	2	0	
Complete	58	28	30	
Differentiation grade				<0.001
Well	8	0	8	
Moderate	26	9	17	
Poorly	26	21	5	
AFP (ng/mL)				0.572
≤400	38	14	24	
>400	22	16	6	

NOTE:

The median expression level was served as the cutoff. Data were conducted by chi-squared test. P<0.05 was considered statistically significant
Abbreviations:AFP, alpha fetoprotein; TNM, tumor-node-metastasis.

Supplemental Table S2. The siRNA sequences of circMYLK and KMT5C

Gene	Sequence
si-circMYLK	5'-GUUGACAGUAGAAGACCAUTT -3'
NC-1	5'-UUCUCCGAACGUGUCACGUTT-3'
si-KMT5C	5'-GCTACTCCATGGAGACCAA-3'
NC-2	5'-TTCTCCGAACGTGTCACGT-3'

Supplementary Table S3. Primer sequences for qRT-PCR

Gene	Primer	Sequence
CircMYLK	Forward	5'-GGACTTTCAGCCTTGTGATTCA-3'
	Reverse	5'-GGAAATGTGTGACGAGGCAA-3'
MiR-29a	Forward	5'-TGCCTAGCACCATCTGAAAT-3'
	Reverse	5'-CAGTGCAGGGTCCGAGGT-3'
KMT5C	Forward	5'-GTTTGACGAGAGCCGAAGGAG-3'
	Reverse	5'-TCGCACAGTTCTCGTGCTGTC-3'
GAPDH	Forward	5'-CAGGGCTGCTTTTAACTCTGGT -3'
	Reverse	5'-GATTTTGGAGGGATCTCGCT-3'
U6	Forward	5'-CTCGCTTCGGCAGCACA-3'
	Reverse	5'-AACGCTTCACGAATTTGCGT-3'