

# circHIPK3 Promotes Cell Proliferation and Migration of Gastric Cancer by Sponging miR-107 and Regulating BDNF Expression

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Juan Wei<sup>1,2</sup>  
Hanfeng Xu<sup>2</sup>  
Wei Wei<sup>3</sup>  
Zhaojing Wang<sup>4</sup>  
Qijia Zhang<sup>2</sup>  
Wei De<sup>5</sup>  
Yongqian Shu<sup>1</sup>

<sup>1</sup>Department of Oncology, The First Affiliated Hospital of Nanjing Medical University, Nanjing, Jiangsu, People's Republic of China; <sup>2</sup>Department of Oncology, The Second Hospital of Nanjing, Nanjing University of Chinese Medicine, Nanjing, Jiangsu, People's Republic of China; <sup>3</sup>Department of Gastrosurgery, Jiangsu Cancer Hospital & Jiangsu Institute of Cancer Research & Nanjing Medical University Affiliated Cancer Hospital, Nanjing, Jiangsu, People's Republic of China; <sup>4</sup>Department of Digestive Oncology Surgery, Jiangsu Province Hospital of Traditional Chinese Medicine, Nanjing, Jiangsu, People's Republic of China; <sup>5</sup>Department of Biochemistry and Molecular Biology, Nanjing Medical University, Nanjing, Jiangsu, People's Republic of China

**Background:** Circular RNAs (circRNAs) play important regulatory roles in cancer development. However, the mechanisms by which circRNAs regulate gene expression in gastric cancer (GC) remain unclear.

**Methods:** Human GC samples and their matched normal adjacent tissues were obtained from 30 patients to assess the expression of circHIPK3 and its relationship with GC proliferation and migration. A series of in vitro and in vivo functional experiments were carried out to elucidate the role of circHIPK3 in GC proliferation and migration, and its underlying molecular mechanisms.

**Results:** Using a circRNA microarray we found a circRNA termed circHIPK3 that performed a significant regulatory role in GC. circHIPK3 was further confirmed to be upregulated in all GC tissues and cells tested. Furthermore, circHIPK3 levels were associated with Tumor & Lymph Node & Metastasis (TNM) stage ( $P = 0.032$ ). The area under the receiver operating characteristic curve (ROC) was 0.743 (95% confidence interval 0.615–0.872;  $P = 0.001$ ). CCK-8, colony formation, Transwell and EdU assays were performed to evaluate the effects of circHIPK3 on cell proliferation and migration in GC. Moreover, circHIPK3 was identified as a sponge of miR-107, and as such it regulated brain-derived neurotrophic factor (BDNF), which plays a pivotal role in the development of GC.

**Conclusion:** circHIPK3 represents a novel potential biomarker and therapeutic target of GC.

**Keywords:** circHIPK3, miR-107, BDNF, proliferation, migration, gastric cancer

## Introduction

Gastric cancer (GC) is a leading cause of tumor-associated morbidity and mortality worldwide. China is one of the countries with the highest incidence of GC.<sup>1</sup> Although the diagnosis and therapy of GC have gradually improved, GC patients have a poor prognosis due to tumor metastasis and recurrence. One important reason is the lack of effective diagnostic markers and molecular targets.

In recent years, circular RNA (circRNA), rather than linear RNA, molecules have been found to play fundamental roles in different cellular physiological processes and may be involved in the process of tumor development.<sup>2</sup> circRNAs, a class of noncoding RNAs derived from exons, introns or intergenic regions, have a closed loop structure without 5' and 3' ends, display cell or tissue specific expression and are conserved and stable due to resistance to RNase.<sup>3,4</sup> circRNAs are predominantly localized in the cytoplasm and their function is only beginning to be understood.<sup>3,5</sup> Recent evidence suggests that more circRNAs harbor multiple miRNA binding sites and interact with

Correspondence: Yongqian Shu  
Department of Oncology, The First Affiliated Hospital of Nanjing Medical University, Nanjing, Jiangsu, People's Republic of China  
Email yongqian\_shu@126.com

Wei De  
Department of Biochemistry and Molecular Biology, Nanjing Medical University, Nanjing, Jiangsu, People's Republic of China  
Email dewei\_njmu@sina.com

RNA binding proteins (RBPs) involved in tumorigenesis.<sup>6</sup> And Some circRNA code for proteins eg circZFN609.<sup>7</sup> Studies have shown that circRNAs can be implicated in the progression of gastric cancer, lung cancer, colorectal cancer, glioblastoma and esophageal squamous cell carcinoma as competing endogenous RNAs (ceRNAs). However, the underlying mechanisms by which circRNAs adsorb miRNAs with regulatory roles are still largely unknown.

We examined the expression profile of circRNAs in GC with a microarray and found a significantly overexpressed circRNA called circHIPK3 (circRNA ID: hsa\_circRNA\_100782). circHIPK3 is derived from exon 2 of the HIPK3 gene. circHIPK3 has been identified as a critical regulator in cancers. In our study, we determined that circHIPK3 was upregulated in GC and correlated with clinical stage and grade of GC. Moreover, we discovered that circHIPK3 knockdown suppressed GC cell proliferation and migration. Mechanistically, we found that circHIPK3, as a ceRNA for miR-107, promoted tumorigenesis possibly via the circHIPK3/miR-107/BDNF signaling pathway in GC.

## Materials and Methods

### Patients and Sample Collection

A total of 30 GC tissues and paired adjacent normal tissues were collected from patients who had undergone surgery at the Department of Gastroscopy, Jiangsu Cancer Hospital, in 2017. None of these patients had received adjuvant chemotherapy or radiotherapy before surgery. All specimens were immediately frozen in liquid nitrogen after removal. According to the tumor-node-metastasis (TNM) (V.8.2016) staging system of the International Union against Cancer, all tumors were staged accurately. Written informed consent was obtained from all enrolled subjects, and the study was approved by the Ethics Committee of The Second Hospital of Nanjing, in accordance with the Declaration of Helsinki.

### Cell Culture Procedures

The normal human gastric epithelial cell line GES-1 and GC cell lines (SGC-7901, MKN45, MGC-803, AGS, and BGC-823) were purchased from Shanghai Institutes for Biological Sciences (Shanghai, China). GES-1 and SGC-7901 cells were cultured in DMEM (Gibco, Grand Island, NY) supplemented with 10% heat-inactivated fetal bovine serum (FBS) (Gibco), 100 U/mL penicillin, and 100 µg/mL streptomycin (HyClone). MKN45, MGC-803, AGS, and BGC-823 cells were cultured in RPMI-1640 (Gibco)

containing 10% FBS with 100 units/mL penicillin and 100 mg/mL streptomycin. Cells were grown in a humidified atmosphere of 5% CO<sub>2</sub> at 37°C.

### Total RNA Extraction, Reverse Transcription and Quantitative Real-Time Polymerase Chain Reaction (qRT-PCR)

Total RNA was extracted from GC tissues and GC cells using TRIzol reagent (Invitrogen, Karlsruhe, Germany) according to the manufacturer's instructions. For circRNA, total RNA was reverse transcribed to cDNA, and qPCR was conducted by using a SYBR Green PCR kit (Takara). For miRNA, expression levels were obtained by stem-loop primer SYBR Green quantitative real time-PCR (RiboBio, Guangzhou, China). Then, the correlation of the obtained  $2^{-\Delta\Delta C_t}$  values was determined. The sequences of the circHIPK3 divergent primers were as follows: Forward, 5'-TATGTTGGTGGATCCTGTT CGGCA-3' and Reverse, 5'-TGGTGGGTAGACCAAGAC TTGTGA-3'. Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) was used as a control with the following primers: Forward, 5'-GGGAGCCAAAAGGGTCAT-3' and Reverse, 5'-GAGTCCTTCCACGATACCAA-3'. We used the following siRNA sequences: siRNA-1 for circHIPK3 sense, 5'-GUACUACAGGUAUGGCCUCTT-3'; antisense, 5'-GAG GCCAUACCUGUAGUACTT-3' and siRNA-2 for circHIPK3 sense, 5'-GGUACUACAGGUAUGGCCUTT-3'; antisense, 5'-UCCCAAUCAACAUUCGGTT-3'. The primers were synthesized by Primer Bank.

### circRNA Microarray Analysis

Three GC tissues and paired nontumor tissues were used for microarray analysis. The microarray experiment was performed by Kangcheng Bio-tech Inc(Shanghai, China).

### Actinomycin D and RNase R Treatment

Total RNA (2 µg) was incubated for 40 min at 37°C with 3 U/µg of RNase R. An RNeasy MinElute cleaning Kit (Qiagen) was used to purify the resulting RNA.

### Fluorescence in situ Hybridization (FISH)

The RNA fluorescence in situ hybridization assay was performed by using a Fluorescent In Situ Hybridization Kit (RiboBio, Guangzhou, China) according to the manufacturer's instructions. Cy3-labeled circHIPK3 probes were designed and synthesized by RiboBio, and the cells were visualized by confocal microscopy.

## CCK-8 Assay

The Cell Counting Kit-8 (Dojindo Chemical Laboratory, Kumamoto, Japan) assay was used to assess GC cell proliferative ability according to the manufacturer's instructions. A total of  $5 \times 10^3$  cells were seeded into 96-well plates and cultured for 24 h. Then, 10  $\mu$ L of CCK-8 solution was added to each well, and the plate was incubated at 37°C for 2 h. Then, the OD450 was obtained at a wavelength of 450 nm using a microplate reader.

## 5-Ethynyl-20-Deoxyuridine (EdU) Incorporation Assay

The EdU assay was performed with a Cell-Light EdU DNA Cell Proliferation Kit (RiboBio, Guangzhou, China) according to the manufacturer's protocol. After incubation with 50 mM EdU for 2 h, BGC-823 and MKN45 cells were fixed in 4% paraformaldehyde and stained with Apollo Dye Solution for proliferating cells, followed by staining with Hoechst 33342. Then, the EdU-positive cells were imaged and counted under a DMI3000B microscope (Leica, Wetzlar, Germany) in five randomly selected fields.

## Transwell Migration Assay

A total of  $5 \times 10^4$  BGC-823 and MKN45 cells were resuspended in 300  $\mu$ L serum-free DMEM and seeded into the upper chambers of transwell plates (8  $\mu$ m size, Corning, NY, USA) after transfection for 48 h. The lower chamber contained 700  $\mu$ L DMEM with 10% FBS. After incubation for 24 h at 37°C in a culture incubator, the nonmigrated cells were removed. Cells that had migrated to the bottom of the membrane were fixed with methanol for 10 min, followed by staining with crystal violet. Then, the stained cells were counted in at least three randomly selected fields under a DMI3000B microscope (Leica, Wetzlar, Germany).

## Western Blot Assay

BGC-823 and MKN45 cells were lysed with RIPA extraction reagent (Beyotime) supplemented with a protease inhibitor cocktail (Roche). Cell protein lysates were separated by 10% sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) and incubated with the primary antibodies anti- $\beta$ -actin and anti-BDNF, which were purchased from Abcam (Hong Kong, China).

## RNA Immunoprecipitation (RIP)

For RNA immunoprecipitation, we used the EZMagna RIP Kit (Millipore, Billerica, MA, USA) according to the

manufacturer's protocol. GC cells were lysed in complete RIP lysis buffer, and the cell extract was incubated with magnetic beads conjugated with anti-Ago2 or control anti-IgG antibody (Millipore) for 6 h at 4°C. The beads were washed with wash buffer and then incubated with 0.1% SDS/0.5 mg/mL Proteinase K for 30 min at 55°C to remove proteins. Finally, immunoprecipitated RNA was subjected to qRT-PCR analysis.

## Xenograft Study

Male BALB/c nude mice (Four-week-old) were obtained from Model Animal Research Center of Nanjing University. All animal-related experiments and animal care were approved by Nanjing Medical University Experimental Animal Care Commission, and strictly followed the commission guidelines for laboratory animals. A total of  $5 \times 10^6$  si-circHIPK3-treated or control BGC-823 cells were injected into the flanks of each mouse. Tumor size was measured every week by caliper to determine tumor volume. Six weeks later, the mice were sacrificed, and the xenografts were removed.

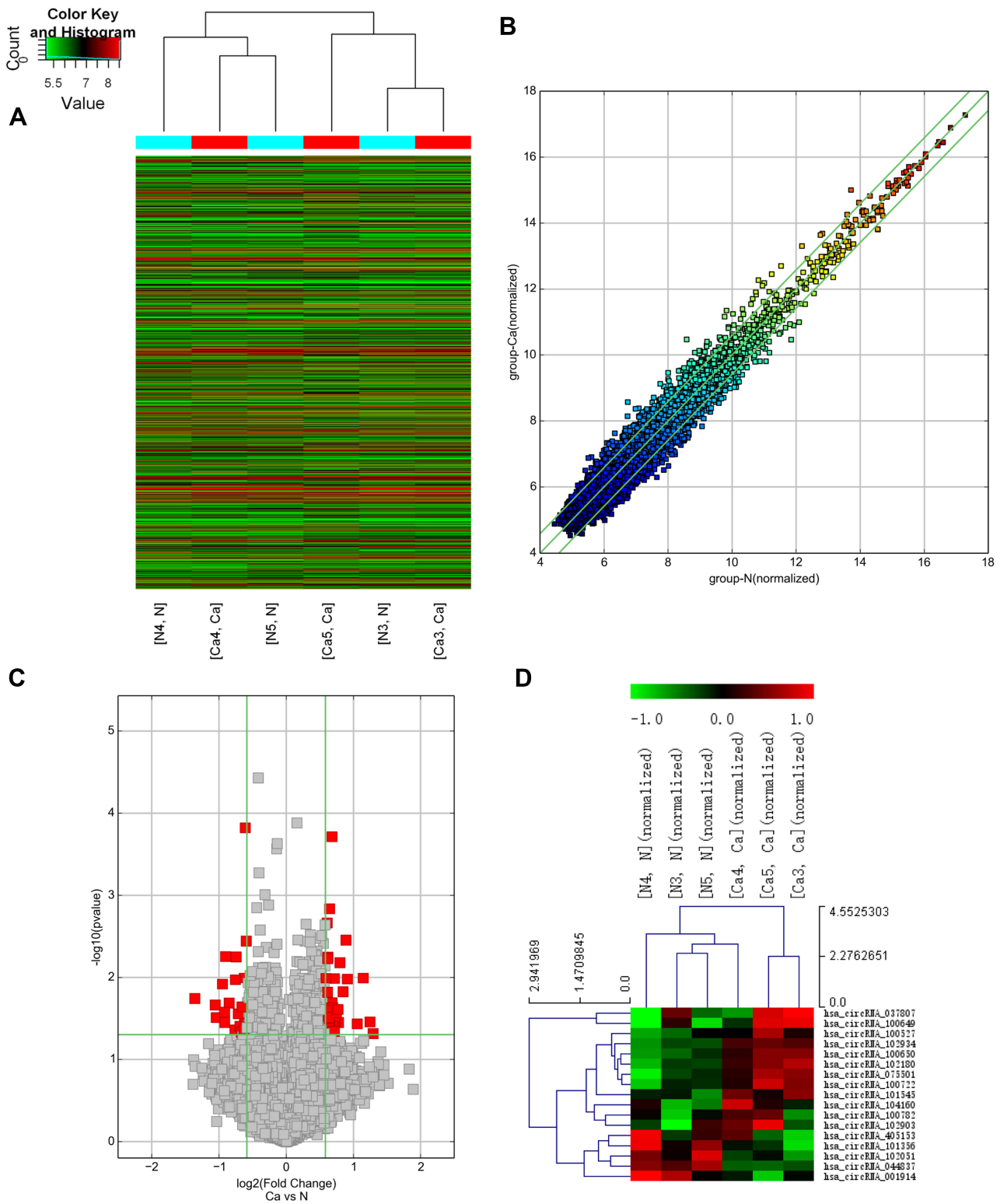
## Statistical Analysis

All statistical data were analyzed using GraphPad Prism 6.0 (GraphPad Software, La Jolla, CA). The differences in levels of circHIPK3 between gastric cancer tissues and paired adjacent nontumorous tissues were assessed using the *t*-test for paired data. The correlations between circHIPK3 levels and clinicopathological factors were further analyzed by one-way analysis of variance (ANOVA). A receiver operating characteristic (ROC) curve was established to evaluate the diagnostic value of circHIPK3. For all results,  $P < 0.05$  was considered statistically significant.

## Results

### circRNA Expression Profiles in Gastric Cancer Tissues and Paired Normal Gastric Tissues

Hierarchical clustering of all expressed circRNAs revealed the circRNA expression profiles in GC and paired adjacent normal tissue samples (Figure 1A). The scatter and volcano plots showed the variation of circRNA expression between GC and paired adjacent normal tissue samples (Figure 1B and C). In total, 61 differentially expressed circRNAs with fold-changes greater than 1.5 were identified. Of these, 23 circRNAs were upregulated and 38 were downregulated. A clustered heatmap showed upregulation and downregulation of



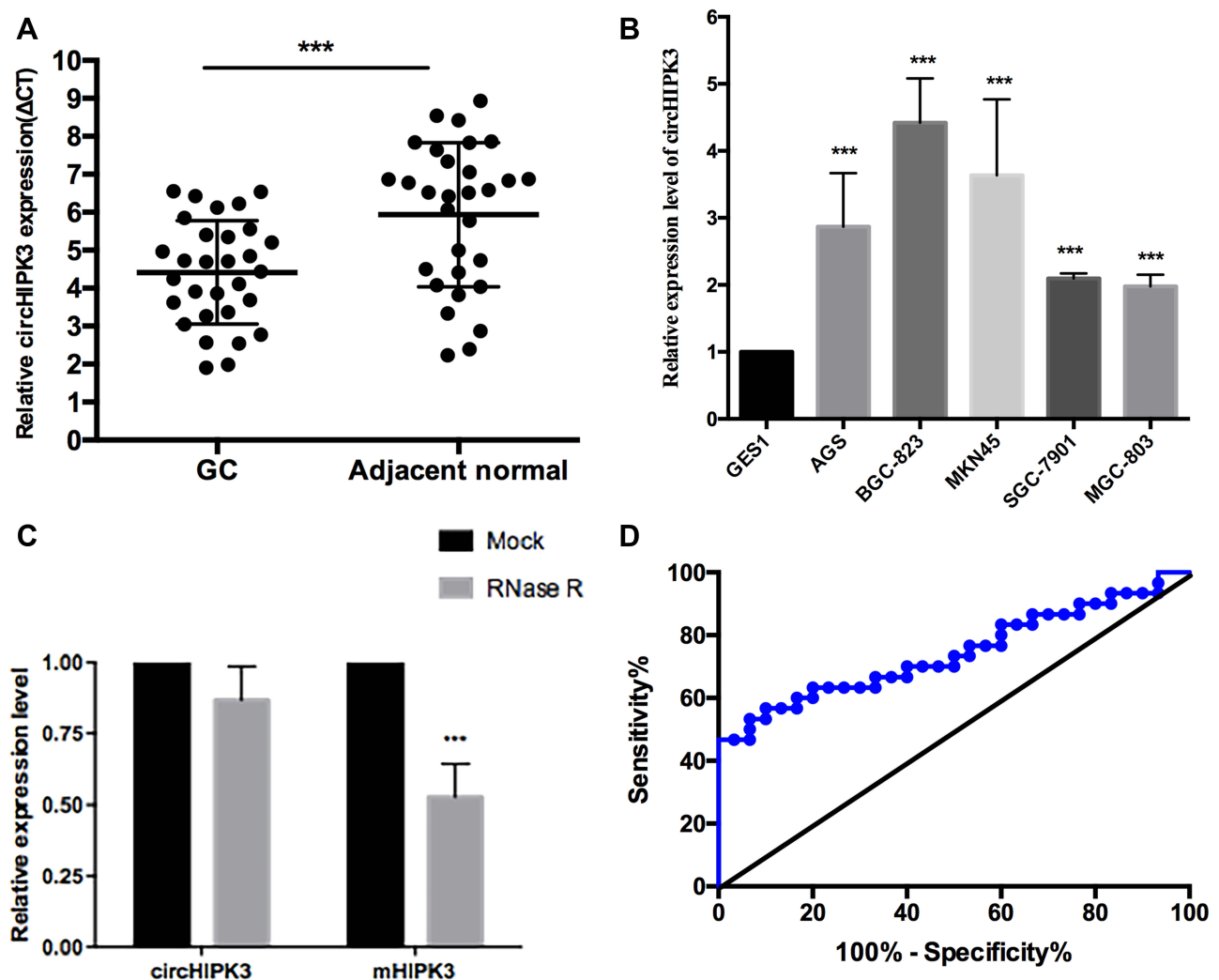
**Figure 1** Expression profile of circRNAs in GC tissue, as determined by microarray analysis. **(A)** The result of hierarchical clustering shows a distinguishable circRNA expression profiling among samples. Each column represents the expression profile of a tissue sample, and each row corresponds to a circRNA. circRNA microarray expression profiles from three sets of matched GC tissue samples (C3–C5) and adjacent normal tissues samples (N3–N5). circRNAs in red indicate overexpression; those in green indicate reduced expression. **(B)** The scatter plot was used for assessing the variation in circRNA expression between GC and adjacent normal tissues samples. The values of x and y axes in the scatter plot were the normalized signal values of the samples (log<sub>2</sub> scaled). The green lines are fold-change lines. The circRNAs above the top green line and below the bottom green line indicated more than 1.5-fold change of circRNAs between the two compared samples. **(C)** Volcano plot analysis based on circRNA expression levels. The vertical green lines correspond to 1.5-fold increased or decreased expression, and the horizontal green line represents P<0.05. Therefore, the red points in the plot represent differentially expressed circRNAs with statistical significance. **(D)** Heat plots of circRNA in GC and adjacent normal tissues. Each column represents the expression profile of a tissue sample, and each row corresponds to a circRNA. “Red” indicates higher expression level, and “green” indicates lower expression level.

circRNAs (Figure 1D). These dysregulated circRNAs may play an important role in tumorigenesis and development. To verify the microarray results, qPCR was performed. In accordance with the microarray results, circHIPK3 was not the most differentially expressed circRNA, but the qRT-PCR results showed that circHIPK3 was relatively stable. Subsequently, circHIPK3 was selected for further study.

### circHIPK3 Was Determined to Be Significantly Upregulated in Gastric Cancer Tissues and Cell Lines

Among the screened upregulated circRNAs, circHIPK3 expression was high and stable, as shown by qRT-PCR results. Therefore, circHIPK3 was selected as a target for

investigating its relationship with gastric cancer. To further test the expression level of the dysregulated circHIPK3, qRT-PCR was used to measure its expression in 30 paired primary cancerous and adjacent noncancerous tissues from GC patients. The results indicated that circHIPK3 expression was significantly upregulated compared with the corresponding noncancerous tissues (Figure 2A). circHIPK3 expression was also examined by qRT-PCR in five human gastric cancer cell lines and the nontumorigenic gastric epithelial cell line GES-1. This experiment showed that the levels of circHIPK3 in the five human gastric cancer cell lines MKN45, SGC-7901, BGC-823, MGC-803 and AGS were higher than the levels in the GES-1 human normal gastric epithelial cell line (Figure 2B). We next determined the stability and localization of circHIPK3.



**Figure 2** The expression levels of circHIPK3 expression in GC tissues and cell lines. (A) The expression levels of circHIPK3 expression in tumor and adjacent normal tissues in 30 GC patients. (B) circHIPK3 was up-regulated in GC cell lines. The expression of circHIPK3 was dramatically higher in BGC-823 and MKN45 cell lines than in other cell lines. (C) qRT-PCR analysis of circHIPK3 and HIPK3 mRNA after treatment with RNase R in GC cells. circHIPK3 was resistant to RNase R treatment. \*\*\* $P < 0.001$ . (D) ROC curve of circHIPK3: The area under the ROC was 0.743 (95% confidence interval = 0.615–0.872;  $P = 0.001$ ).

**Table 1** A Pathological Feature of 30 Primary GC and Nontumor Samples Was Analyzed

Clinicopathological Factor	n	Mean±SEM	P value
Age(Year)			
≥60	15	4.136±1.221	0.739
<60	15	4.761±1.398	
Gender			
Female	10	5.566±1.969	0.397
Male	20	3.890±0.972	
Diameter in cm			
≥5	12	5.079±1.434	0.582
<5	18	4.028±1.209	
Differentiation			
Low/middle	25	4.735±1.080	0.493
High	5	3.015±0.849	
Lymphatic Metastasis			
Yes	17	5.407±1.167	0.237
No	13	3.195±1.432	
TNM Stage			
I+II	12	2.081±0.492	0.032
III+IV	18	6.027±1.380	

Note:  $P < 0.05$  represents statistical significance.

After treatment with RNase R, the linear transcripts of HIPK3 were degraded, while the circular transcripts of circHIPK3 were resistant to RNase R treatment (Figure 2C), indicating that circHIPK3 is highly stable in GC cells. Furthermore, the area under the ROC curve was 0.74 (Figure 2D). The sensitivity and specificity were 0.833 and 0.533, respectively. The ROC is a comprehensive index used to reflect the sensitivity and specificity of continuous variables. When the area under the curve is larger, the diagnostic value of the variable is higher. Due to the limited number of samples of gastric cancer tissues, we only analyzed circHIPK3 expression levels in 30 paired gastric cancer tissue samples. More samples should be analyzed in the future.

## Correlation Between circHIPK3 Expression and Clinical Characteristics of GC Patients

The expression of circHIPK3 was detected in 30 pairs of primary GC and adjacent nontumor tissues using qRT-PCR. circHIPK3 was highly overexpressed in GC samples. We next evaluated the association between circHIPK3 and clinical and pathological parameters. The circHIPK3 level was

related to TNM stage ( $P=0.032$ , Table 1). However, we found no association between circHIPK3 expression levels and other clinicopathological factors, such as age, gender, diameter, differentiation, and lymphatic metastasis.

## Identification and Characterization of circHIPK3 in GC Cells

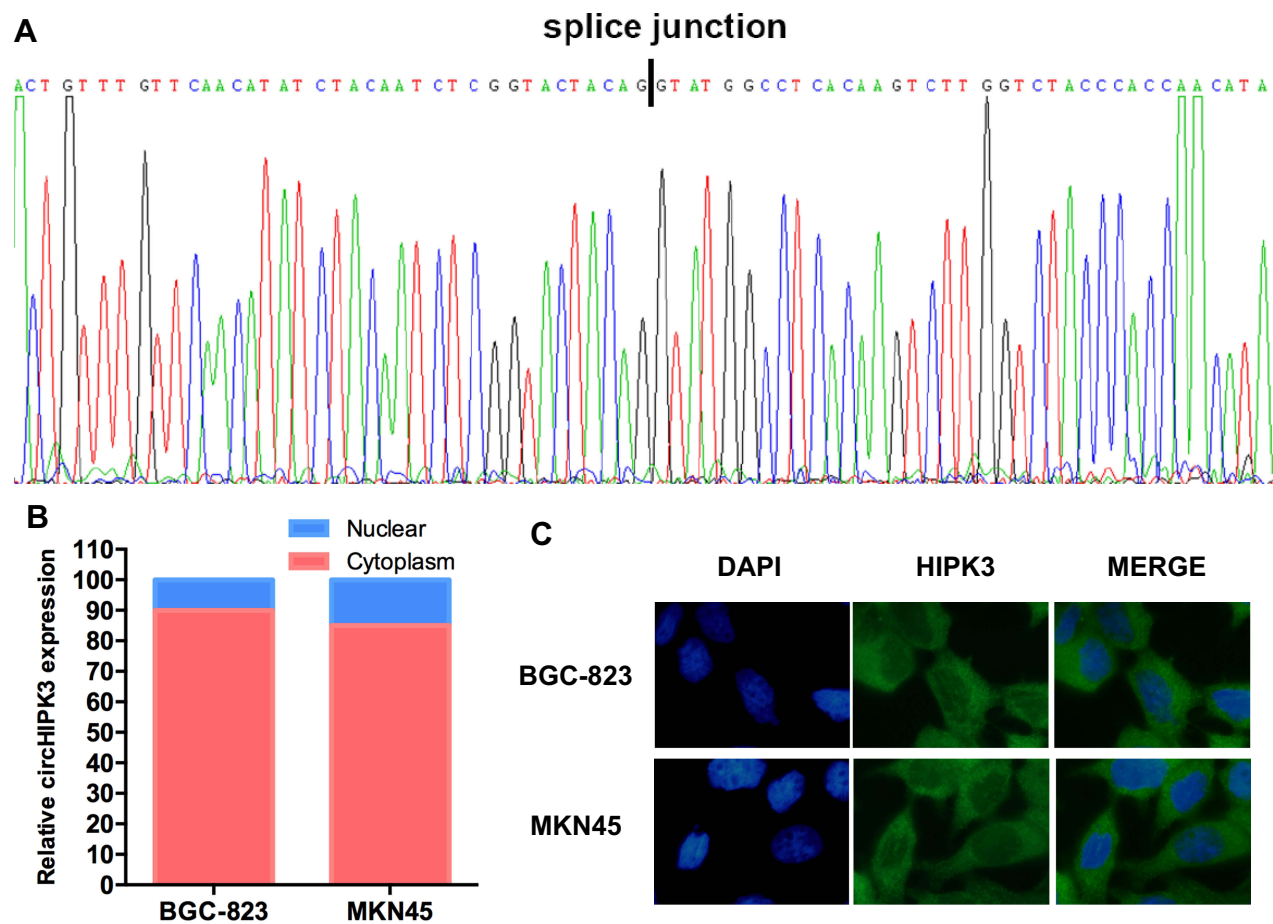
circHIPK3 is located in chr11: 33307958–33309057 and is generated from exon 2 of the HIPK3 gene. Sanger sequencing confirmed the splice junction of circHIPK3 (Figure 3A). The nuclear mass separation assay and fluorescence in situ hybridization (FISH) analysis showed that more than 90% of circHIPK3 was present in the cytoplasm (Figure 3B and C). Collectively, these results suggest that circHIPK3 is highly stable and mostly localizes to the cytoplasm.

## The Effects of circHIPK3 on GC Cell Proliferation and Migration in vitro

To investigate the biological function of circHIPK3, we designed circHIPK3 siRNA, which specifically targeted the back-splice junction site of circHIPK3. Compared to that in the negative control (NC) siRNA cells, the expression of circHIPK3 was downregulated by si-circHIPK3 (Figure 4A). Using a Cell Counting Kit-8 (CCK-8), colony formation, and 5-ethynyl-2'-deoxyuridine (EdU) proliferation assays, we determined that knockdown of circHIPK3 greatly impaired the proliferation ability of MGC-823 and MKN45 cells, while ectopic expression of circHIPK3 promoted cell proliferation (Figure 4B–D). Transwell assays demonstrated that cell migration capacity was decreased by si-circHIPK3 (Figure 4E).

## circHIPK3 Serves as a miRNA Sponge for miR-107

Given that circRNAs can act as a miRNA sponge and circHIPK3 is stable in the cytoplasm, we determined whether circHIPK3 may also bind to miRNAs as a sponge and regulate the miRNA targets via a competitive endogenous RNA (ceRNA) mechanism. To identify the miRNAs that bind to circHIPK3, we performed a circRNA-miRNA interaction network prediction on the CircInteractome database. The 5 highest-ranking candidate miRNAs (hsa-miR-17-3p, hsa-miR-30d-3p, hsa-miR-107, hsa-miR-103a-3p, hsa-miR-338-3p) and 378 corresponding target mRNAs were predicted to interact with circHIPK3 in this study (Figure 5A). We screened miRNAs that may have binding sites targeting the circHIPK3 sequence based on the circBase ([www.circbase.org](http://www.circbase.org)) database



**Figure 3** (A) Sanger sequence showing the back-splice junction of circHIPK3. (B) The majority of circHIPK3 was present in the cytoplasm according to the nuclear mass separation assay. (C) The majority of circHIPK3 was present in the cytoplasm according to FISH.

and found that miR-107 had a binding site on circHIPK3 (Figure 5B). To determine the expression of miR-107 in GC, we analyzed miR-107 levels by qRT-PCR and found that miR-107 was significantly downregulated and relatively stable in GC cells (Figure 5C). It is well known that miRNAs usually silence gene expression by binding to Argonaute 2 (Ago 2) protein and forming the RNA-induced silencing complex (RISC). Based on previous studies, in the context of the ceRNA mechanism, it might be common for Ago2 to bind with both circRNAs and miRNAs.<sup>8,9</sup> We therefore conducted an RNA immunoprecipitation (RIP) assay to pull down RNA transcripts that bind to Ago2 in BGC-823 and MKN45 cells. Endogenous circHIPK3 was efficiently pulled down by anti-Ago2 (Figure 5D).

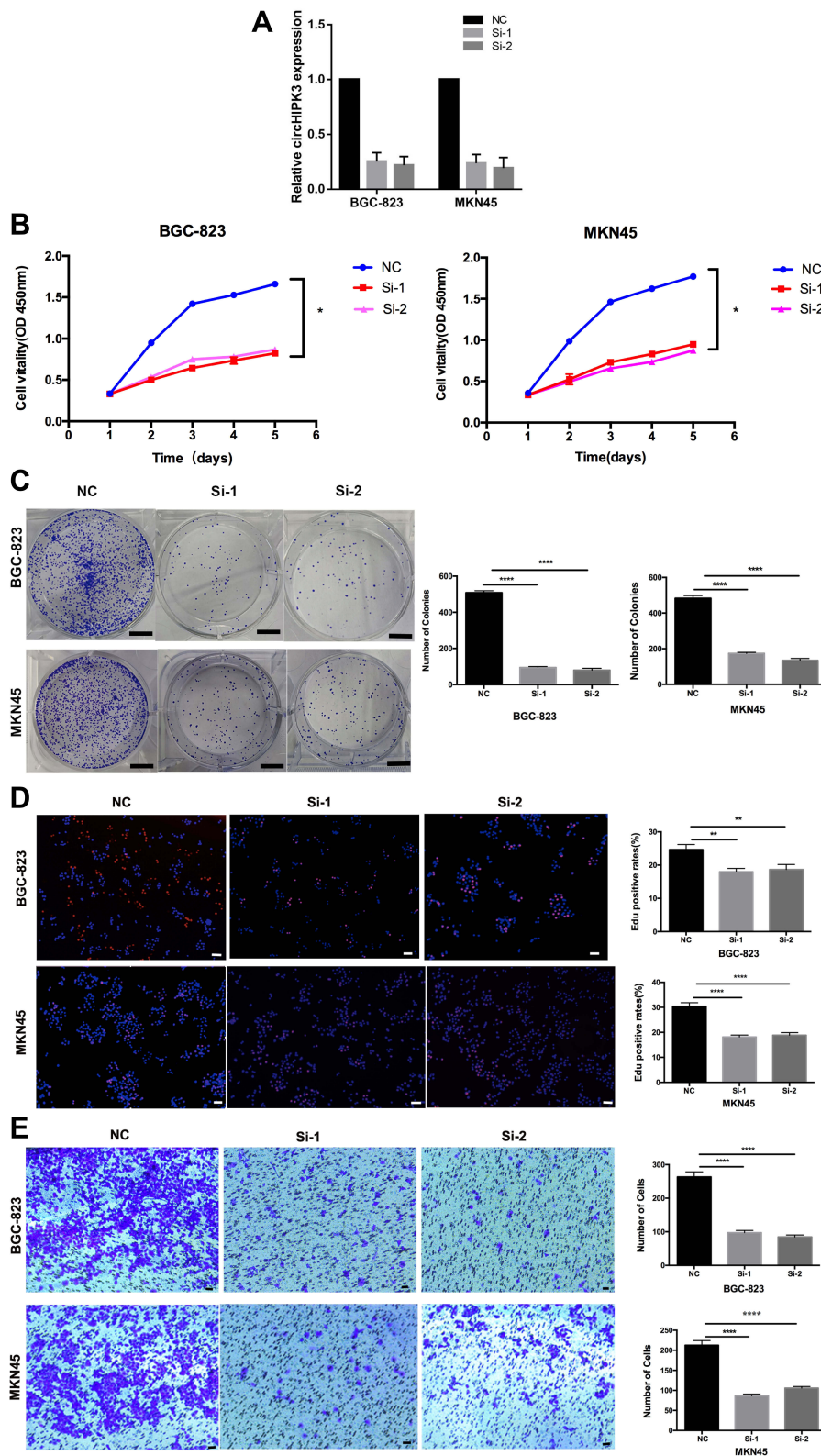
### miR-107 Exerts Its Role by Regulating BDNF Expression in GC

A review of the literature found that miR-107 suppresses GC development through the downregulation of brain-

derived neurotrophic factor (BDNF).<sup>10</sup> We predicted that circHIPK3 exerts its functions via the miR-107/BDNF axis. Western blotting showed that si-circHIPK3 reduced the protein levels of BDNF and that coectopic expression of miR-107 and circHIPK3 increased the levels of BDNF in GC cells (Figure 6). These results confirm that miR-107 is sponged by circHIPK3, which subsequently upregulates BDNF protein expression. Taken together, these data indicated that miR-107 could directly downregulate BDNF and regulate its downstream signaling.

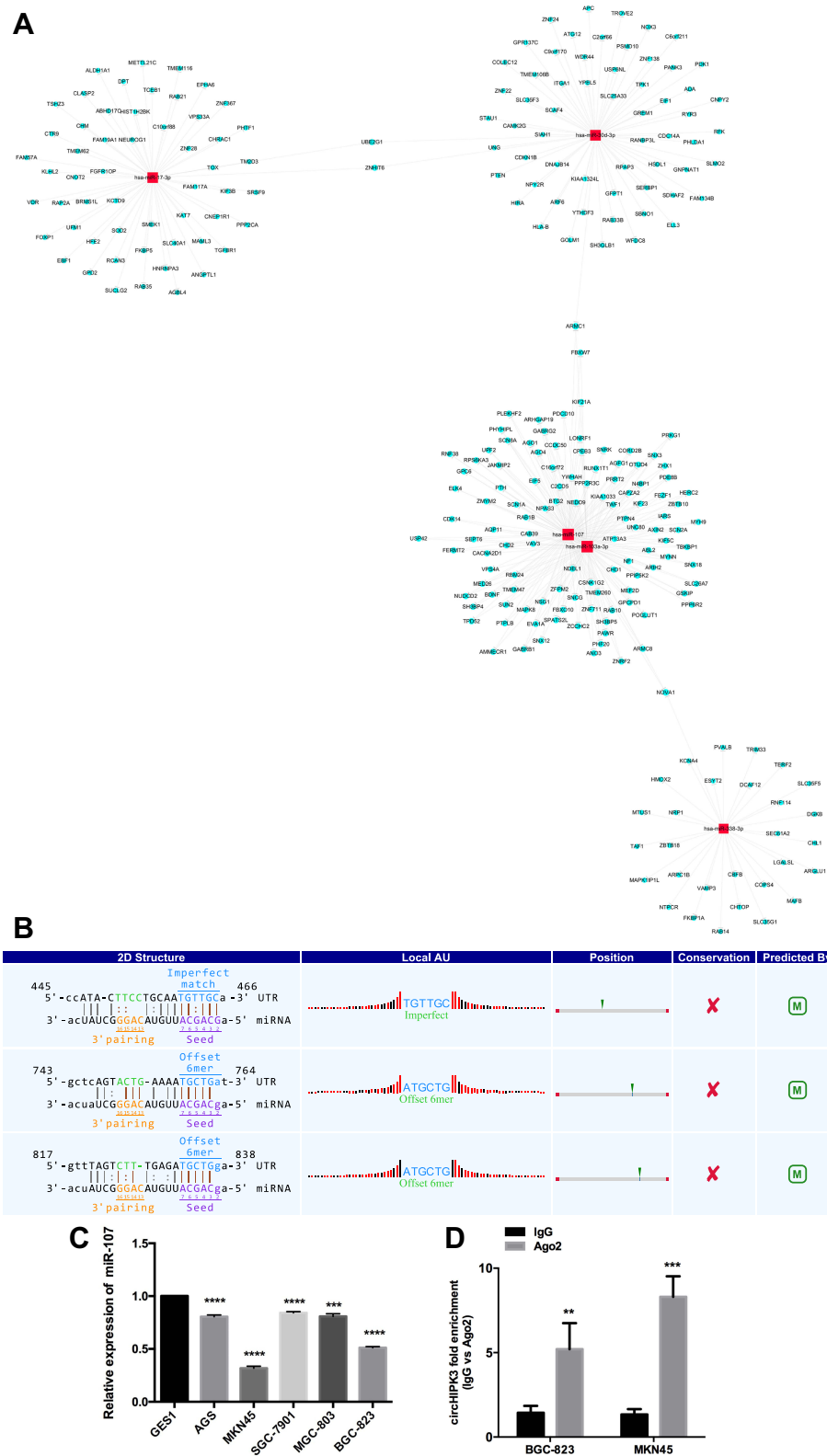
### circHIPK3 Promotes GC Tumorigenesis in vivo and Acts as a Potential Therapeutic Target

To investigate the biological function of circHIPK3 in vivo, we established a xenograft tumor model in nude mice. BGC-823 cells transfected with si-circHIPK3 or a control siRNA were subcutaneously injected into nude mice. Tumor volume was measured every week for 6 weeks. The mice were killed

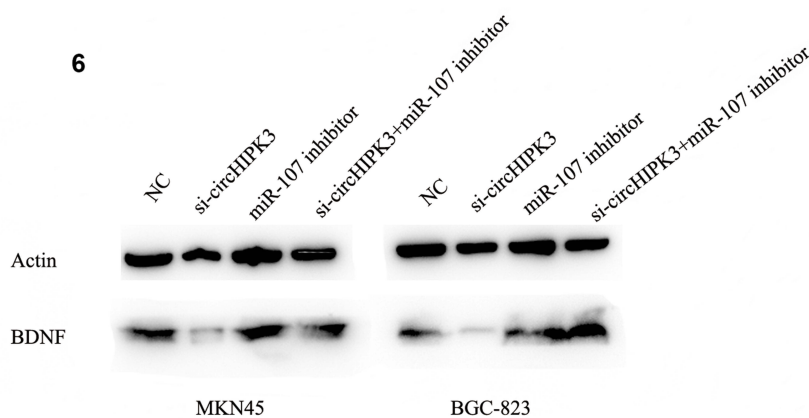


**Figure 4** circHIPK3 regulated the proliferation and migration of GC cells. **(A)** Knockdown efficacy of circHIPK3 in BGC-823 and MKN45 cells was determined by qRT-PCR. **(B)** circHIPK3 promotes the proliferation of BGC-823 and MKN45 cells shown by the CCK8 assays. **(C)** Clone formation shows that circHIPK3 promotes the proliferation of BGC-823 and MKN45 cells. Scale bar, 15mm. **(D)** Observation of DNA synthesis of BGC-823 and MKN45 cells transfected with si-circHIPK3 vectors by EdU assay. Scale bar, 100µm. **(E)** Determination of cell invasive potential of BGC-823 and MKN45 cells transfected with si-circHIPK3 vectors by Transwell assay. Data are the means±SD of three experiments. \*P<0.05; \*\*P<0.01; \*\*\*P<0.0001. Scale bar, 100µm.





**Figure 5 (A)** The predicted circHIPK3 targeted miRNA and mRNA network. **(B)** The interaction of circHIPK3/miR-107 was predicted based on TargetScan and miRanda. **(C)** qRT-PCR analysis shows the expression levels of miR-107 in GC. **(D)** RIP assay using an antibody against Ago2. \*\* $P < 0.01$ ; \*\*\* $P < 0.001$ ; \*\*\*\* $P < 0.0001$ .



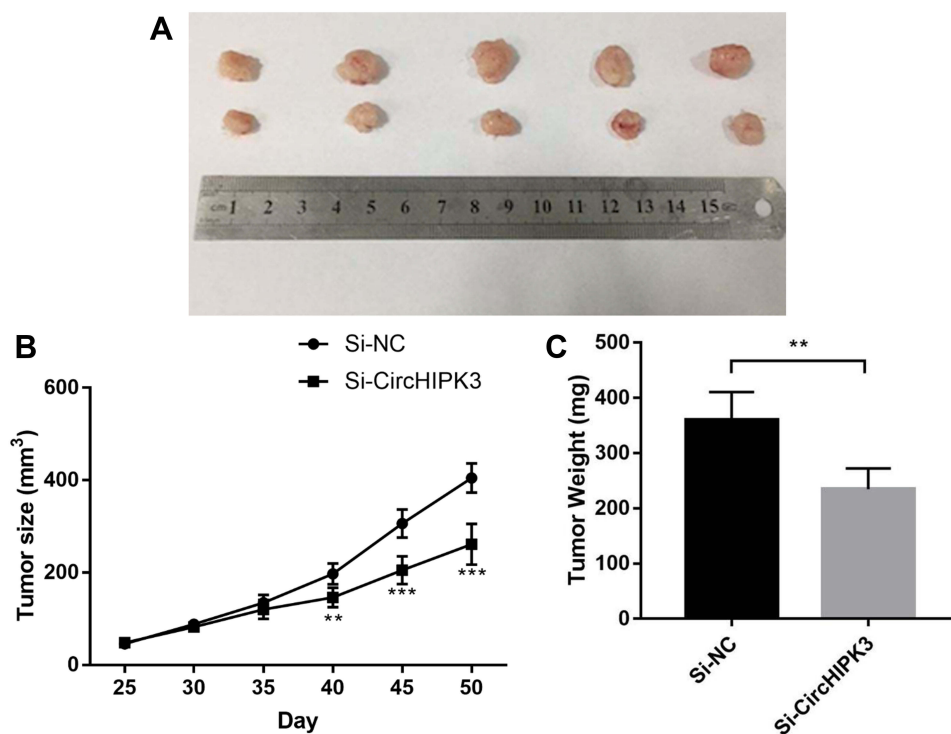
**Figure 6** Western blot analysis of the protein of BDNF in MKN45 and BGC-823 cells.

by anesthesia and xenografts were removed for further analyses (Figure 7). In accordance with the in vitro results, circHIPK3 depletion suppressed BGC-823 xenograft growth in vivo.

### Discussion

circRNAs, a recently discovered RNA type, were thought to be only a byproduct of splicing errors. Due to the advancements in high-throughput sequencing, many circRNAs have been identified from various animal genomes, and many of

them are fairly stable and significantly expressed. circRNAs have been reported to be dysregulated in diverse cancer types, such as lung cancer,<sup>11</sup> oral cancer,<sup>12</sup> bladder cancer,<sup>13</sup> hepatocellular carcinoma,<sup>14</sup> and esophageal squamous cell carcinoma.<sup>15</sup> A previous study revealed that these differentially expressed circRNAs play important roles in the process of gene expression.<sup>16–19</sup> In our research, we found that 61 circRNAs were differentially expressed between GC and adjacent normal tissues. Of these, 23 circRNAs were up-regulated. Subsequently, circHIPK3 was selected for further



**Figure 7** circHIPK3 promotes GC tumorigenesis in vivo and is a potential therapeutic target. (A) circHIPK3 knockdown markedly repressed tumor growth in nude mice. (B) Si-CircHIPK3 significantly reduced tumor size compared with si-NC. (C) Si-CircHIPK3 significantly reduced tumor weight. \*\**P* <0.01, \*\*\**P* <0.001.

study. circHIPK3 was not the most differentially expressed circRNA, but qRT-PCR showed that circHIPK3 was relatively stable.

CircRNAs are generated from diverse genomic locations, and most of them are important players in the regulation of posttranscriptional gene expression.<sup>20</sup> We demonstrated that circHIPK3, which is an exonic circRNA originating from exon 2 of the HIPK3 gene, was upregulated in GC tissues and predominantly localized in the cytoplasm. Exon 2 of the HIPK3 gene is large (1099 bp) and flanked by long introns on both sides, which contain many complementary Alu repeats to further promote its circularization.<sup>21</sup>

Stable transcripts with a host of miRNA-binding sites or miRNA response elements (MREs) can function as miRNA sponges, and exonic circRNAs also contain certain MREs. Moreover, with the decreasing MRE polymorphisms, exonic circRNAs become more efficient miRNA sponges.<sup>22</sup> One extreme case is CDR1as, which contains over 70 binding sites for miR-7 and significantly suppresses the activity of miR-7.<sup>23</sup> Many reports have indicated that circHIPK3 exerts oncogenic or anticancer roles in different cancers, such as hepatocellular carcinoma,<sup>14</sup> bladder cancer,<sup>24</sup> colorectal cancer,<sup>25</sup> ovarian cancer,<sup>26</sup> glioma<sup>27</sup> and lung cancer.<sup>28</sup> Chen et al<sup>14</sup> found that circHIPK3 might be a new marker for HCC and may regulate HCC through a circHIPK3/miR-124/AQP3 axis. Jin et al<sup>27</sup> reported that circHIPK3 was upregulated in glioma and that circHIPK3 could influence the malignant behaviors of glioma cells via the circHIPK3/miR-654/IGF2BP3 axis. Li et al<sup>24</sup> demonstrated that overexpression of circHIPK3 can effectively inhibit aggressiveness and metastasis of bladder cancer cells by targeting the miR-558/HPSE network. Chen et al<sup>29</sup> illustrated that circHIPK3-mediated miR-193a-3p/MCL1 signaling promoted prostate cancer occurrence and development. These results suggest that circHIPK3 is involved in complex regulatory networks and has multifunctional roles in diseases.

Indeed, the role of circHIPK3 in GC remains unclear; thus, we aimed to reveal the function of circHIPK3 in GC. In our study, we found that circHIPK3 was significantly upregulated in GC. Then, knockdown of circHIPK3 inhibited GC cell proliferation and migration and suppressed GC growth and metastasis in vivo. Bioinformatics analysis demonstrated that circHIPK3 may sponge miR-107. A previous study revealed that miR-107 suppresses GC development through the downregulation of BDNF.<sup>12</sup> BDNF, a member of the neurotrophin family, has been shown to be involved in the initiation and development of various cancers.<sup>30</sup> We investigated the

associated mechanism involving circHIPK3, miR-107 and BDNF in GC cells by Western blot. Our data indicated that circHIPK3 regulates the proliferation and migration of GC cells via the miR-107/BDNF axis. An in vivo study confirmed that circHIPK3 knockdown suppressed xenograft tumor growth. Further understanding of the circHIPK3/miR-107/BDNF axis may provide a novel therapeutic strategy for GC in the future. In addition, we will investigate the underlying molecular mechanism in future studies.

In summary, our findings suggest that circHIPK3 serves as a novel oncogenic circRNA by sponging miR-107, as well as a promising prognostic biomarker in GC. Our data also show that targeting the circHIPK3/miR-107/BDNF axis is a potential treatment strategy for treating GC.

## Acknowledgments

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## Disclosure

The authors report no conflicts of interest in this work.

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