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ORIGINAL RESEARCH

RETRACTED ARTICLE: Silencing of Long Non-Coding RNA Colon Cancer-Associated Transcript 2 Inhibits the Growth and Metastasis of Gastric Cancer Through Blocking mTOR Signaling

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Purpose: This study aimed to evaluate the specific role of colon cancer-associated transcript 2 (CCAT2) on gastric cancer (GC), and reveal the potential regulatory mechanism relating to mammalian target of rapamycin (mTOR) signaling.

Methods: The expression of CCAT2 was detected in GC tissues and cells by quantitative real-time PCR (qRT-PCR), and its relation with the pathologic characteristics of GC patients was analyzed. HGC-27 and SGC-7901 cells were transfected with siRNA-CCAT2 to silence CCAT2, and HGC-27 cells were then treated with an mTOR agonist Leucine (Leu) to activate mTOR signaling. The cell proliferation was evaluated by cell viability and colony formation. The cell cycle and apoptosis, and the migration and invasion abilities were detected by Flow cytometry, and Transwell assay, respectively. The expression of PCNA (proliferation marker), Snail, N-cadherin, E-cadherin (invasion markers), P53, Caspase-8, Bcl-2 (apoptosis markers), LC3-II/LC3-I, ATG3, p62 (autophagy makers), phosphorylated mTOR (p-mTOR), p-AKT, and p-p70S6K (mTOR signaling markers) were detected by Western blot.

Results: CCAT2 was upregulated in GC tissues and cells, and positively associated with the maximum tumor diameter, lymphatic metastasis, TNM staging, and low overall survival rate ($P < 0.05$). siRNA-CCAT2 transfection significantly inhibited the viability, colony formation, and migration and invasion abilities, blocked the cell cycle in G0/G1 phase, and promoted the apoptosis and autophagy of SGC-7901 and HGC-27 cells ($P < 0.05$). In addition, siRNA-CCAT2 transfection significantly upregulated P53, Caspase-8, LC3-II/LC3-I and ATG3, and downregulated PCNA, Bcl-2, p62, p-mTOR, p-AKT and p-p70S6K in SGC-7901 and HGC-27 cells ($P < 0.05$). siRNA-CCAT2 reversed the tumor-promoting effect of mTOR signaling activation on HGC-27 cells ($P < 0.05$).

Conclusion: Silencing of CCAT2 inhibited the proliferation, migration and invasion, and promoted the apoptosis and autophagy of GC cells through blocking mTOR signaling.

Keywords: colon cancer-associated transcript 2, gastric cancer, mammalian target of rapamycin, apoptosis, autophagy

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Introduction

Gastric cancer (GC) develops from the lining of the stomach is one of the most common lethal malignancies worldwide.[1] Complete surgical resection is the most effective therapeutic strategy for GC, while more than 50% patients are accompanied with unresectable, recurrent or metastatic GC.[2] Although adjuvant therapeutic

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strategies, such as chemotherapy and radiotherapy greatly improve the prognosis of GC patients, the 5-year overall survival rate is still relatively low (<30% worldwide, and <40% in China).[3,4] The discovery of novel therapeutic targets against GC is urgently needed.

Long non-coding RNAs (LncRNAs) are a class of non-coding RNAs with more than 200 nucleotides.[5] LncRNAs play important regulatory roles in diverse cellular processes, such as the proliferation, apoptosis, differentiation, and invasion.[6] Noteworthily, increasing evidences have proved that a large number of lncRNAs are involved in the tumorigenesis, metastasis, prognosis and drug resistance of GC.[7] Colon cancer-associated transcript 2 (CCAT2) is a novel lncRNA that upregulated in GC.[8,9] It has been reported that CCAT2 is an independent poor prognostic factor of GC, which positively correlated with lymph node and distance metastasis, and negatively correlated with overall and progression-free survival times.[9] In addition, previous studies have found that CCAT2 promotes the proliferation, migration, and invasion of GC cells, while silencing of CCAT2 inhibits the migration and invasion, and promotes the apoptosis of GC cells.[8,10,11] Although the tumor-promoting role of CCAT2 on GC cells has been identified in previous studies, the specific regulatory mechanisms of CCAT2 in GC are not fully revealed.

Mammalian target of rapamycin (mTOR) is a central regulatory kinase that considered as a therapeutic target for GC.[12] The inhibition of mTOR inhibits the proliferation of GC cells in vitro and the tumor progression in animal models. In clinical practice, the mTOR inhibitor everolimus is active and well-tolerated in patients with chemotherapy-refractory metastatic GC.[13] In addition, previous studies have found the expression of phosphorylated mTOR (p-mTOR) is positively correlated with tumor stage and lymph node metastasis, and negatively correlated with relapse-free, disease-free and overall survival.[14,15] However, whether the regulatory role of CCAT2 on GC is associated with mTOR signaling is still unclear.

In this study, the expression of CCAT2 was detected in both GC tissues and GC cells. The relation between CCAT2 expression and pathologic characteristics of GC patients was analyzed. Then, CCAT2 was silenced by siRNA-CCAT2 transfection. The specific roles of siRNA-CCAT2 on the proliferation, migration, invasion, apoptosis and autophagy of GC cells were evaluated, and the potential-regulatory mechanism relating to mTOR signaling was investigated. Our findings may reveal a novel therapeutic target against GC, and provide a new insight into the underlying mechanisms.

Materials and Methods

Clinical Specimens

A total of 60 GC patients (32 males and 28 females, 60.7 ± 11.65 years old) were screened from our hospital from January 2013 to December 2013. The pathologic characteristics of GC patients, including the age, gender, maximum tumor diameter, lymphatic metastasis, and TNM staging were recorded. The tumor tissues (tumor, N = 60) and adjacent normal tissues (non-tumor, N = 60) were collected from these patients prior to administering any adjuvant treatments by surgical resection. This study was approved by the local Institutional Review Board, and informed consents were obtained from all subjects.

Cell Culture

Human gastric epithelial cell line GES-1 and RGM-1 were purchased from Bogoo Biotechnology Co., Ltd. (Shanghai, China). Human GC cell line SGC-7901 (moderately differentiated GC cells), SNU-1 (low-differentiated GC cells), and HGC-27 (non-differentiated GC cells) were purchased from Cell Bank of Chinese Academy of Sciences (Shanghai, China). Cells were cultured in Dulbecco's Modified Eagle Medium (DMEM) (Gibco, USA) containing 10% fetal bovine serum (FBS) (HyClone, USA), and maintained in a humidified incubator at 37°C with 5% CO_2. Cells in logarithmic growth phase were used for further assays.

Cell Transfection

HGC-27 and SGC-7901 cells were digested with 0.25% trypsin (Gibco), and seeded in 12-well plates at a density of 4×10^5/well. Followed by 24 h of culturing, HGC-27 and SGC-7901 cells were transfected with siRNA-CCAT2 (Generay, Shanghai, China) using lipofectamine 2000 (Thermo Fisher Scientific, USA) according to the manufacturer's instruction. Cells transfected with siRNA-negative control (siRNA-NC) were considered as the NC, and cells without transfection were considered as the blank control (Control). After the transfection for 48 h, HGC-27 cells in the siRNA-NC and siRNA-CCAT2 groups were treated with 10 mM mTOR agonist, L-Leucine (Leu) (Sigma, USA) for another 48 h.

Quantitative Real-Time PCR (qRT-PCR)

Total RNAs were extracted from specific tissues/cells by using TRIZOL (Thermo Fisher Scientific). cDNA was synthesized by using cDNA Synthesis Master Kit (Thermo Fisher Scientific). qRT-PCR was performed on ABI7500

(ABI, USA) by using SYBR Green Real-Time PCR Master Kit (Thermo Fisher Scientific). The PCR program included 95°C for 30 s, 30 cycles of 95°C for 5 s and 60°C for 30 s. The special primers were used as followed: CCAT2-F, 5′-CCCTGGTCAAATTGCTTAACCT-3′; CCAT2-R, 5′-TTATTCGTCCCTCTGTTTTATGGAT-3′; β-actin-F, 5′-AGAGGGAAATCGTGCGTGAC-3′; β-actin-R, 5′-CAATAGTGATGACCTGGCCGT-3′. The relative expression level of CCAT2 was calculated using the 2-ΔΔCt method.[16]

Western Blot

Cells were lysed by using RIPA Lysis buffer (Thermo Fisher Scientific). Total proteins were separated by 10% sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE), and transferred to polyvinylidene fluoride (PVDF) membrane (Millipore, USA). After blocked with 5% skim milk in Tris Buffered Saline Tween (TBST) for 2 h, the membrane was incubated with primary antibody (anti-PCNA, -P53, -Bcl-2, -Caspase-8, -LC3-II/LC3-I, -ATG3, -p62, -mTOR, -p-mTOR, p-AKT, p-p70S6K, -E-cadherin, -Snail, -N-cadherin, and -GAPDH; 1: 1000, Cell Signaling Technology, USA) at 4°C overnight. Then the membrane was washed with Tris-buffered saline Tween (TBST) for three times, and incubated with Horseradish peroxidase (HRP)-conjugated secondary antibody (1:5000, Cwbiotech, China) for 1 h at 25°C. The protein bands were visualized and quantified using a Gel Imaging System (Thermo Fisher Scientific).

Cell Viability Assay

The cell viability was detected by using a Cell Counting Kit 8 (CCK-8, Beyotime, China) according to the manufacturer's instruction. Simply, cells of different groups (at 1, 2, 3 and 4 days post-transfection) were seeded in 96-well plates and CCK-8 solution was added into each well. After 2 h of incubation, the absorbance at 450nm (A450) was detected by a microplate reader (Anthos, England).

Colony Formation Assay

Cells of different groups were seeded in 12-well plates at a density of 500/well, and cultured until the colonies could be observed under naked eyes (about 7–10 days). After washed with phosphate buffer saline (PBS) for three times, the colonies were fixed with 4% paraformaldehyde for 10 min and stained with crystal violet for 20 min. The stained colonies were photographed by a digital camera (Olympus, Japan) and counted.

Transwell Assay

Transwell assay was performed by using transwell chambers (Corning, USA). For detection of cell migration, 200μL cells (0.1×10^6) were seeded in the upper chamber, and 600 μL DMEM containing 10% FBS were placed in the lower chamber. After incubated at 37°C for 24 h, cells on the lower chamber were fixed in 1% formaldehyde for 20 min and stained with 0.1% crystal violet for 20 min. Positive stained cells were observed under a microscope (Olympus) and counted at five randomly selected fields. For detection of cell invasion, the upper chamber was precoated with Matrigel, and the remaining steps were the same as those described above.

Flow Cytometry

For detection of cell cycle, cells of different groups were fixed in 70% pre-cooled ethanol and stained with MuseTM Cell Cycle Reagent (Millipore) for 30 min under darkness. The number of cells in different cell cycle phases was detected by a MUSE cell analyzer (Millipore). For detection of cell apoptosis, cells were sequentially stained with Annexin V-Enhanced Green Fluorescent Protein (EGFP) and Propidium Iodide (PI) (Thermo Fisher Scientific). After 15 min of incubation under darkness, the apoptotic rate was detected by a MUSE cell analyzer (Millipore).

Immunofluorescence

Cells were washed with PBS for three times, fixed in 4% paraformaldehyde at 4°C for 1 h, and permeated in 0.1% Triton X-100 at 37°C for 10 min. Cells were then blocked with 3% BSA at 37°C for 1 h, and incubated with primary antibody (anti-LC3, 1:500, Abcam) overnight at 4°C. After 3 times of washing with PBS, cells were incubated with Alexa Fluor 488-conjugated secondary antibody (1:500, Abcam) at 37°C for 1 h, and then stained with DAPI at 37°C for 1 h. Positive stained cells (green fluorescence) were observed under fluorescence microscope (Olympus).

Statistical Analyses

All data were expressed as mean ± standard deviation (SD). Statistical analysis was performed by GraphPad Prism 7.0. Comparison between different groups was determined by one-way ANOVA, followed by Tukey's multiple comparisons test (two groups). The survival rate of patients (with a follow-up until January 2018) was determined by Kaplan-Meier Survival Analysis. A p-value less than 0.05 was considered to be significantly different.

This study was conducted after obtaining local ethical committee approval of The Second Hospital of Shandong University and written informed consent from the patients.

Results

CCAT2 Was Upregulated in Both GC Tissues and GC Cells

The expression of CCAT2 was detected in both GC tissues and GC cells. qRT-RCR showed that the expression of CCAT2 was significantly higher in GC tissues (tumor) than in adjacent normal tissues (non-tumor) ($P < 0.05$) (Figure 1A). In addition, the expression of CCAT2 was significantly higher in SGC-7901 (moderately differentiated GC cells), SNU-1 (low-differentiated GC cells), and HGC-27 (non-differentiated GC cells) cells than in GES-1 and RGM-1 (normal gastric epithelial cells) cells ($P < 0.05$) (Figure 1B).

CCAT2 was silenced in SGC-7901 and HGC-27 cells by siRNA-CCAT2 transfection. As shown in Figure 1C, the expression of CCAT2 was significantly inhibited by siRNA-CCAT2 transfection in both SGC-7901 and HGC-27 cells. The expression of CCAT2 was not significantly influenced by siRNA-NC transfection in SGC-7901 and HGC-27 cells (Figure 1C).

CCAT2 Was Positively Associated with Poor Prognosis

According to the median expression of CCAT2, GC patients were divided into high and low expression group. The relation between CCAT2 expression and pathologic characteristics of GC patients was evaluated. As shown in Table 1, CCAT2 expression was positively associated with the maximum tumor diameter, lymphatic metastasis, and TNM staging ($P <$ [illegible]). However, CCAT2 expression was not significantly associated with the age and gender. Furthermore, survival analysis showed that patients with high CCAT2 expression exhibited significantly lower overall survival rate than those with low CCAT2 expression ($P <$ [illegible]05) (Figure 2).

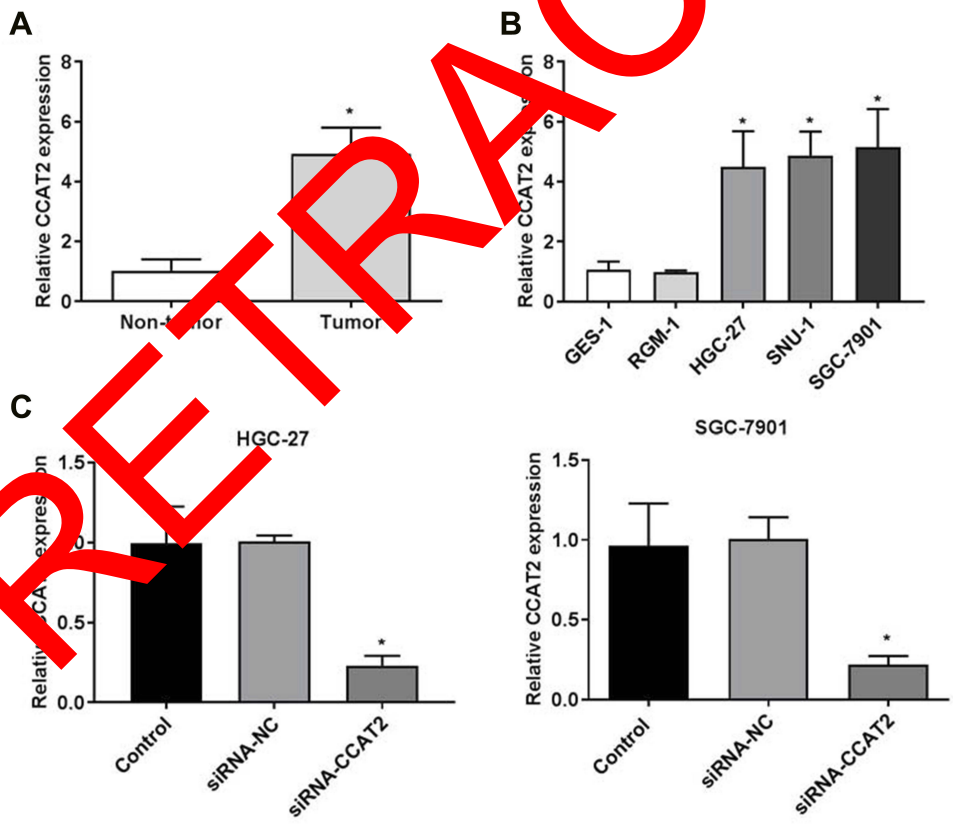

Figure 1 The expression of colon cancer-associated transcript 2 (CCAT2) detected by quantitative real-time PCR (qRT-PCR). (**A**) Relative CCAT2 expression in gastric cancer (GC) tissues (tumor) and adjacent normal tissues (non-tumor) (N = 60); (**B**) Relative CCAT2 expression in SGC-7901 (moderately differentiated GC cells), SNU-1 (low-differentiated GC cells), HGC-27 (non-differentiated GC cells), GES-1 and RGM-1 (normal gastric epithelial cells) cells; (**C**) Relative CCAT2 expression in transfected HGC-27 and SGC-7901 cells. siRNA-CCAT2, cells transfected with siRNA-CCAT2; siRNA-NC, cells transfected with siRNA-negative control; Control, cells without transfection. *P < 0.05 vs (**A**) non-tumor, (**B**) GES-1 and RGM-1, (**C**) Control and siRNA-NC.

Table 1 The Pathologic Characteristics of Gastric Cancer (GC) Patients with High and Low Colon Cancer-Associated Transcript 2 (CCAT2) Expression

Parameters	Numbers	CCAT2 Expression		P value
		High Expression	Low Expression	
Age (years)				0.713
< 60	29	14	15	
≥ 60	41	16	25	
Gender				0.861
Male	32	17	15	
Female	28	15	13	
Maximum tumor diameter (cm)				0.010
< 5cm	29	6	23	
≥ 5cm	31	24	7	
Lymphatic metastasis				0.007
Yes	29	19	10	
No	31	11	20	
TNM staging				0.009
I+II	28	10	18	
III+IV	32	20	12	

Silencing of CCAT2 Inhibited the Proliferation of GC Cells

The effects of siRNA-CCAT2 transfection on the proliferation of HGC-27 and SGC-7901 cells were evaluated by cell viability and colony formation. As shown in Figure 3A, siRNA-CCAT2 transfection significantly inhibited the cell viability in a time-dependent manner ($P < 0.05$) (Figure 3A). siRNA-CCAT2 transfection also significantly decreased the number of colonies ($P < 0.05$) (Figure 3B). The cell viability and colony formation of SGC-7901 and HGC-27 cells were not significantly influenced by siRNA-NC transfection (Figure 3A and B). In addition, Western blot showed that the expression of PCNA (a cell proliferation marker) was significantly downregulated by siRNA-CCAT2 transfection in both SGC-7901 and HGC-27 cells ($P < 0.05$) (Figure 3C).

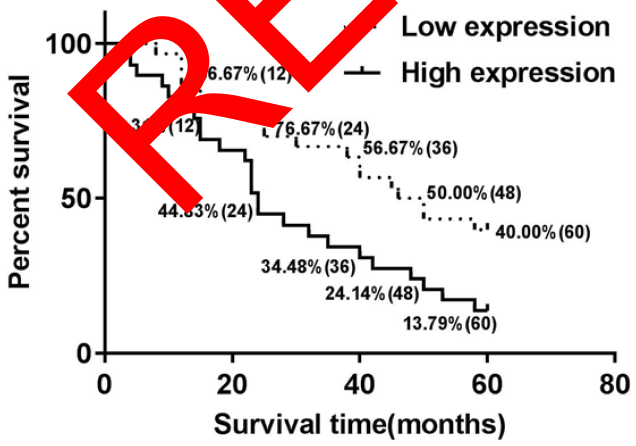

Figure 2 Survival curves of gastric cancer (GC) patients with high and low colon cancer-associated transcript 2 (CCAT2) expression (Kaplan-Meier Survival Analysis).

Silencing of CCAT2 Inhibited the Migration and Invasion of GC Cells

The effects of siRNA-CCAT2 transfection on the migration and invasion of HGC-27 and SGC-7901 cells were detected by Transwell assay. As shown in Figure 4A and B, the numbers of migrated and invasive cells were significantly decreased by siRNA-CCAT2 transfection ($P < 0.05$). The migration and invasion of HGC-27 and SGC-7901 cells were not significantly influenced by siRNA-NC transfection (Figure 4A and B). In addition, the expression of metastasis-related markers was measured by Western blot. As shown in Figure 4C, the expression of E-cadherin was significantly increased, and the expression of N-cadherin and Snail were significantly decreased by siRNA-CCAT2 transfection in HGC-27 and SGC-7901 cells ($P < 0.05$). The expression of E-cadherin, N-cadherin and Snail were not significantly influenced by siRNA-NC transfection in HGC-27 and SGC-7901 cells (Figure 4C).

Silencing of CCAT2 Blocked GC Cells in G0/G1 Phase

The effects of siRNA-CCAT2 transfection on the cell cycle of HGC-27 and SGC-7901 cells were detected by Flow cytometry. As shown in Figure 5, siRNA-CCAT2 transfection significantly increased the percentage of cells in G0/G1 phase, and decreased the percentage of cells in S phase ($P < 0.05$). The percentage of cells in G2/M phase was not significantly changed by siRNA-CCAT2 transfection. In addition, the cell cycles of HGC-27 and SGC-7901 cells were not significantly influenced by siRNA-NC transfection (Figure 5).

Silencing of CCAT2 Promoted the Apoptosis of GC Cells

The effects of siRNA-CCAT2 transfection on the apoptosis of HGC-27 and SGC-7901 cells were detected by Flow cytometry. As shown in Figure 6A, siRNA-CCAT2 transfection significantly increased the percentage of

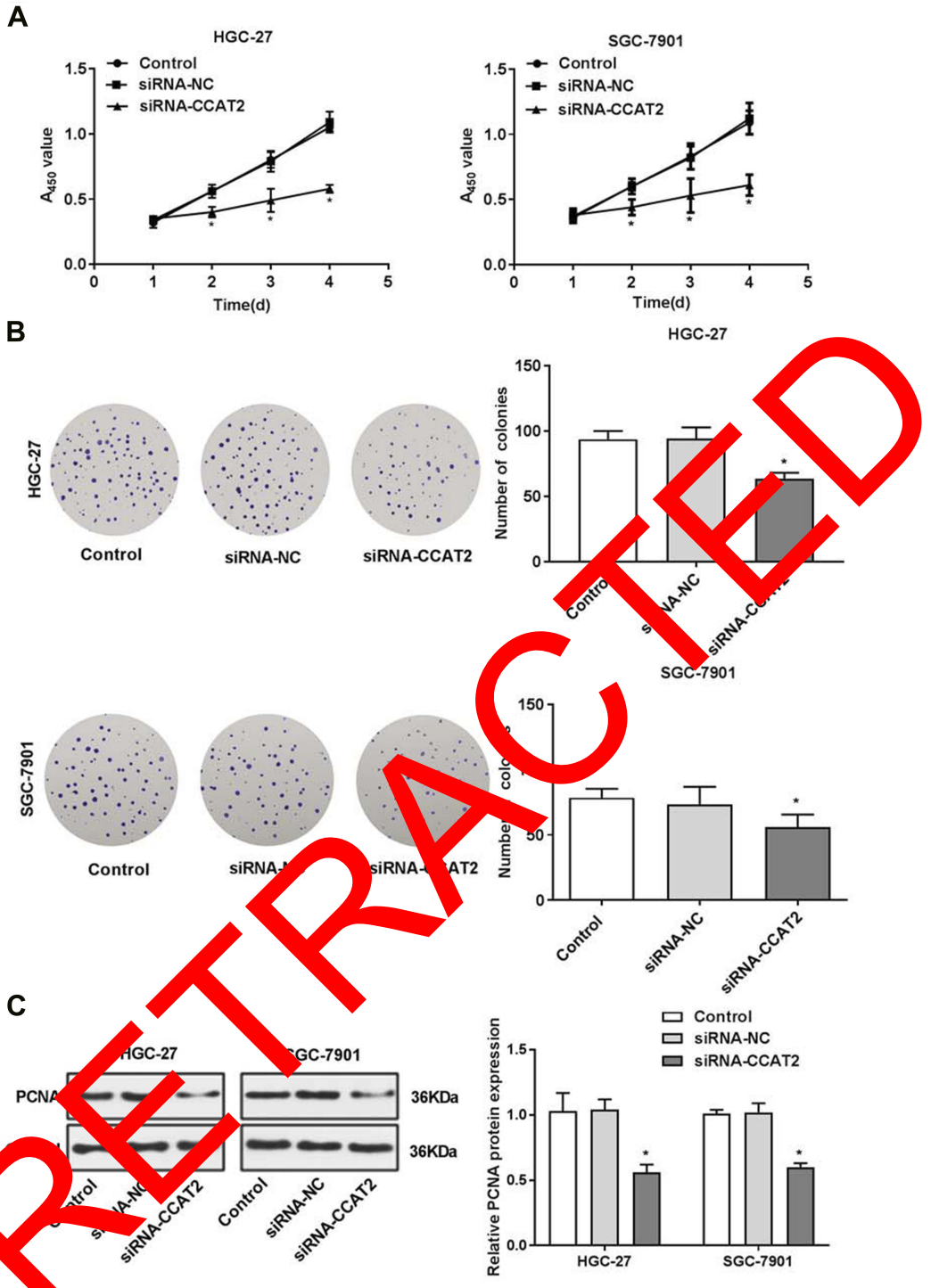

Figure 3 The effects of siRNA-colon cancer-associated transcript 2 (siRNA-CCAT2) transfection on the proliferation of HGC-27 and SGC-7901 cells. (**A**) Cell viability (A_{450}); (**B**) Colony formation (number); (**C**) Relative PCNA expression (Western blot). siRNA-CCAT2, cells transfected with siRNA-CCAT2; siRNA-NC, cells transfected with siRNA-negative control; Control, cells without transfection. *P < 0.05 vs Control and siRNA-NC.

apoptotic cells (P < 0.05). The percentage of apoptotic cells was not significantly changed by siRNA-NC transfection (Figure 6A). In addition, Western blot showed that siRNA-CCAT2 transfection significantly upregulated P53 and Caspase-8, and downregulated Bcl-2 (P < 0.05). The expression of the above apoptosis markers were not significantly influenced by siRNA-NC transfection (Figure 6B).

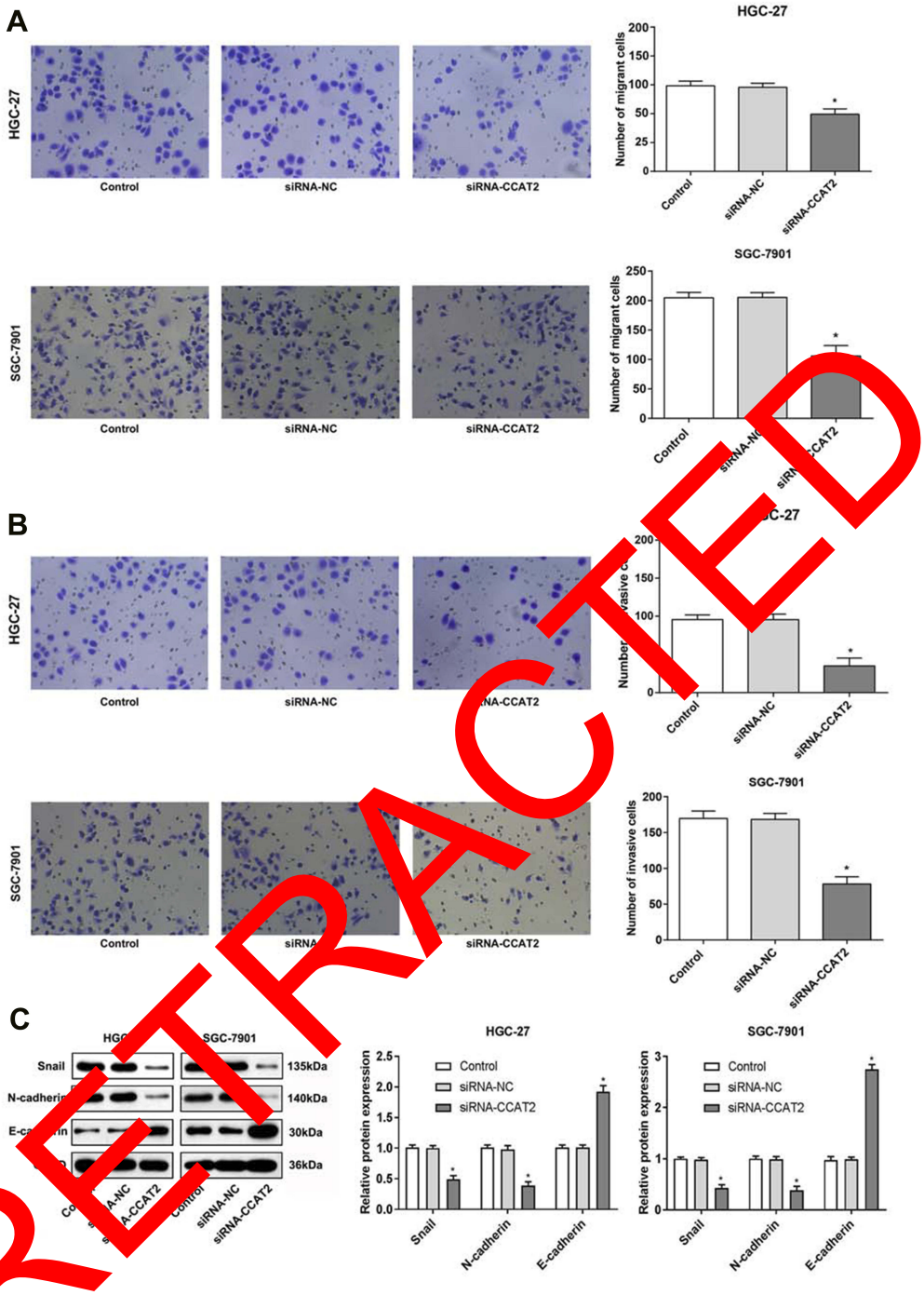

Figure 4 The effects of siRNA-colon cancer-associated transcript 2 (siRNA-CCAT2) transfection on the migration and invasion of HGC-27 and SGC-7901 cells. (**A**) The number of migrant cells (×200); (**B**) The number of invasive cells (×200). (**C**) Relative expression of E-cadherin, N-cadherin and Snail (Western blot). siRNA-CCAT2, cells transfected with siRNA-CCAT2; siRNA-NC, cells transfected with siRNA-negative control; Control, cells without transfection. *P < 0.05 vs Control and siRNA-NC.

Silencing of CCAT2 Promoted the Autophagy of GC Cells

The effects of siRNA-CCAT2 transfection on the autophagy of HGC-27 and SGC-7901 cells were evaluated. As shown in Figure 7A, siRNA-CCAT2 transfection significantly upregulated LC3-II/LC3-I and ATG3, and downregulated p62 in HGC-27 and SGC-7901 cells ($P < 0.05$). In addition, immunofluorescence showed that the LC3 positive rate was significantly higher in siRNA-CCAT2 group than in siRNA-NC and Control group ($P < 0.05$) (Figure 7B). The

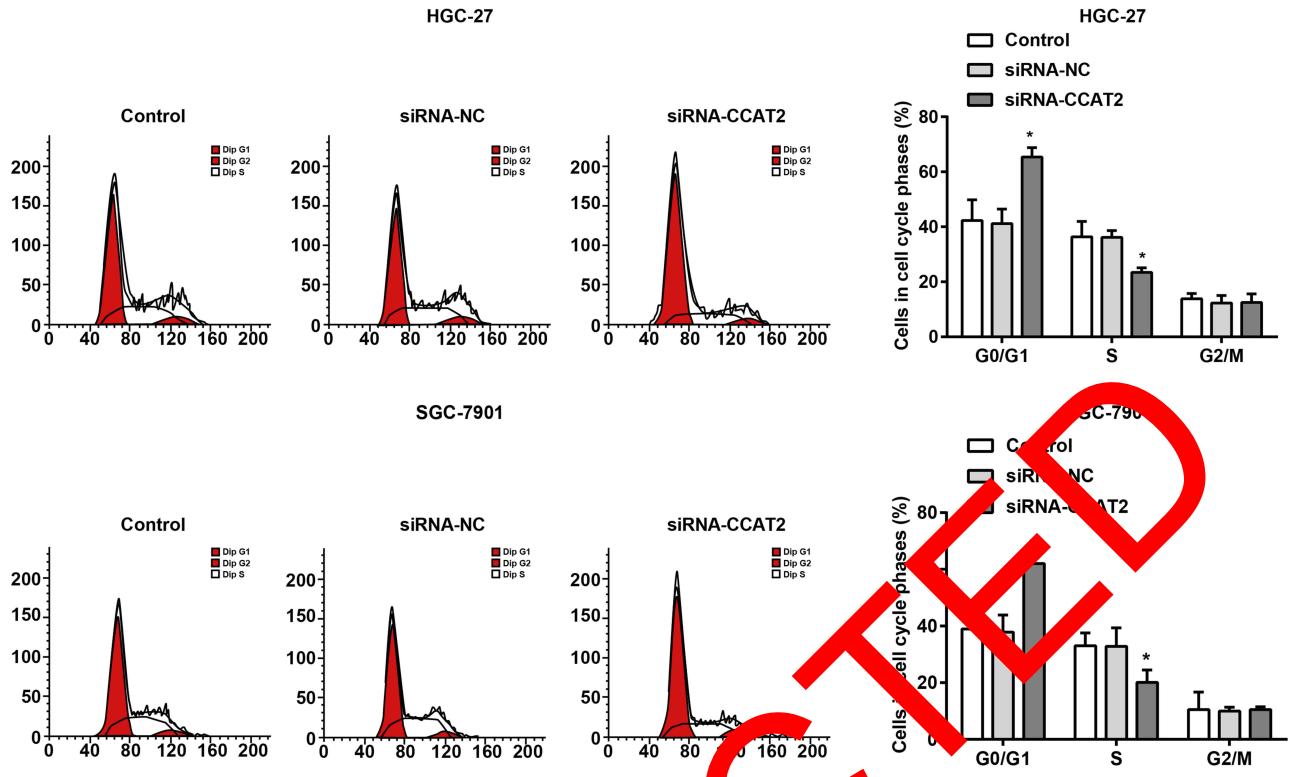

Figure 5 The effects of siRNA-colon cancer-associated transcript 2 (siRNA-CCAT2) transfection on the cell cycle of HGC-27 and SGC-7901 cells (the percentage of cells in G0/G1, S, and G2/M phase). siRNA-CCAT2, cells transfected with siRNA-CCAT2; siRNA-NC, cells transfected with siRNA-negative control; Control, cells without transfection. *P < 0.05 vs Control and siRNA-NC.

expression of autophagy markers, and LC3 positive rate and p-p70S6K in Leu-treated HGC-27 cells (P < 0.05) were not significantly influenced by siRNA-NC transfection (Figure 9A). In addition, the intervention of Leu significantly increased the number of colonies, the number of migrant and invasive cells, and decreased the apoptotic cells and LC3-positive rate in HGC-27 cells (P < 0.05). The transfection of siRNA-CCAT2 significantly abolished the effects of Leu on the proliferation, migration, invasion, and autophagy of HGC-27 cells (P < 0.05) (Figure 9B–F).

Silencing of CCAT2 Blocked mTOR Signaling in GC Cells

The specific effect of CCAT2 on mTOR signaling was evaluated by Western blot. As shown in Figure 8, the expression of p-mTOR, p-AKT and p-p70S6K were significantly downregulated by siRNA-CCAT2 transfection in HGC-27 and SGC-7901 cells (P < 0.05). The mTOR signaling was not significantly influenced by siRNA-NC transfection (Figure 8).

SiRNA-CCAT2 Reversed the Tumor-Promoting Effect of mTOR Signaling Activation on HGC-27 Cells

To further explore the regulatory relationship between CCAT2 and mTOR signaling, Leu was used to activate mTOR signaling in HGC-27 cells. Western blot showed that Leu significantly upregulated p-mTOR and p-p70S6K in HGC-27 cells (P < 0.05). The transfection of siRNA-CCAT2 significantly downregulated p-mTOR

Discussion

CCAT2, firstly discovered as an oncogene in colon cancer is a novel lncRNA located in the 8q24 genomic region.[17] The oncogenic role of CCAT2 has also been identified in GC.[18] Previous studies have proved that CCAT2 is upregulated in GC tissues, and positively correlated with tumor stage, lymphatic metastasis, and poor survival.[8,9] In consistent with previous studies, we found that the expression of CCAT2 was significantly higher in GC tissues than in adjacent normal tissues. The expression of CCAT2 was positively associated with the maximum tumor diameter, lymphatic metastasis, TNM staging, and low overall

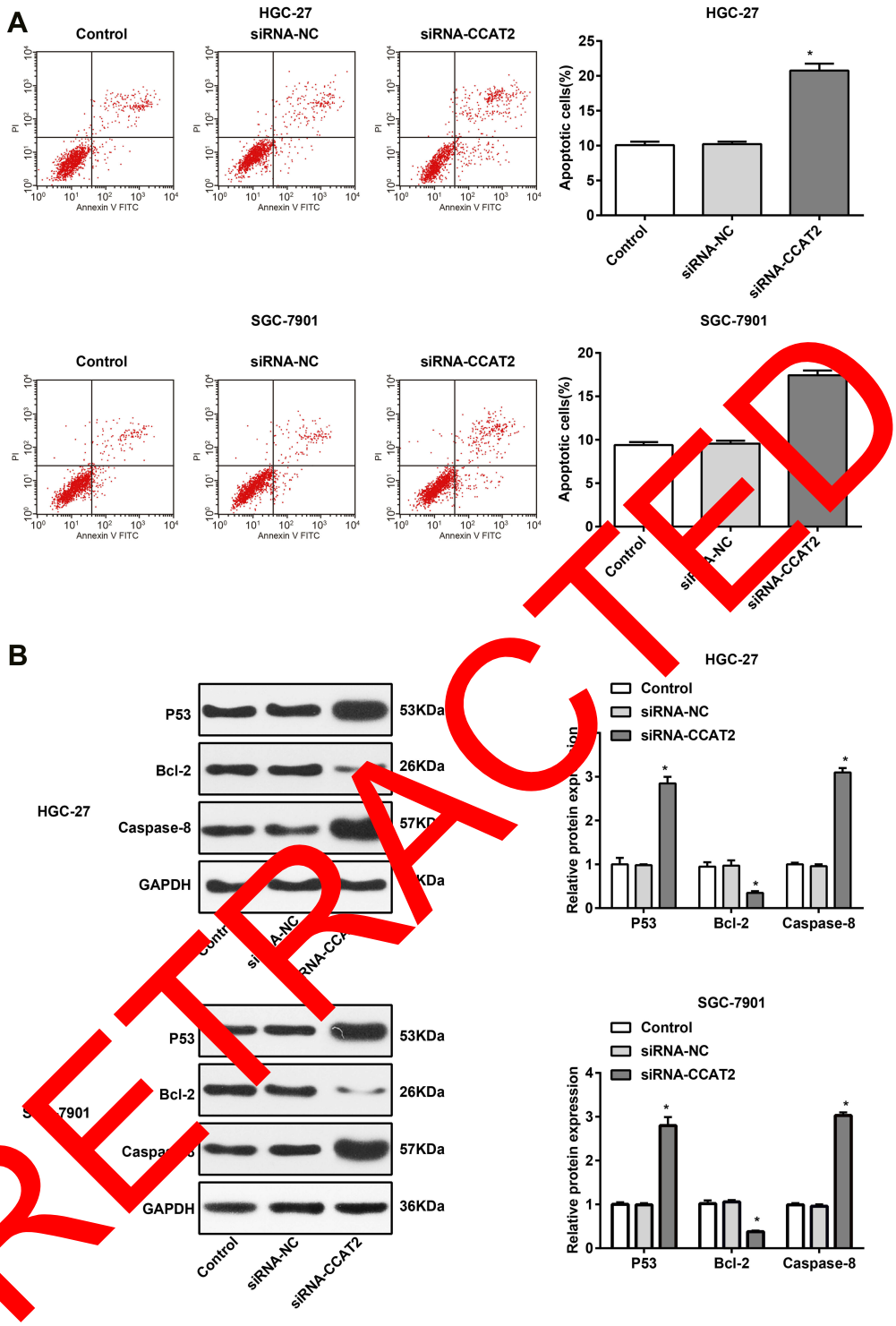

Figure 6 The effects of siRNA-colon cancer-associated transcript 2 (siRNA-CCAT2) transfection on the apoptosis of HGC-27 and SGC-7901 cells. (**A**) The percentage of apoptotic cells; (**B**) Relative expression of P53, Caspase-8, and Bcl-2 (Western blot). siRNA-CCAT2, cells transfected with siRNA-CCAT2; siRNA-NC, cells transfected with siRNA-negative control; Control, cells without transfection. *P < 0.05 vs Control and siRNA-NC.

survival rate. Our findings further illustrate that CCAT2 serves as an oncogenic lncRNA in GC.

Since CCAT2 was significantly upregulated in GC cells (SGC-7901, SNU-1, and HGC-27) with different degrees of differentiation, non-differentiated HGC-27 cells and moderately differentiated SGC-7901 cells were used for further assays. By silencing CCAT2 in HGC-27 and SGC-7901 cells via siRNA-CCAT2 transfection, we

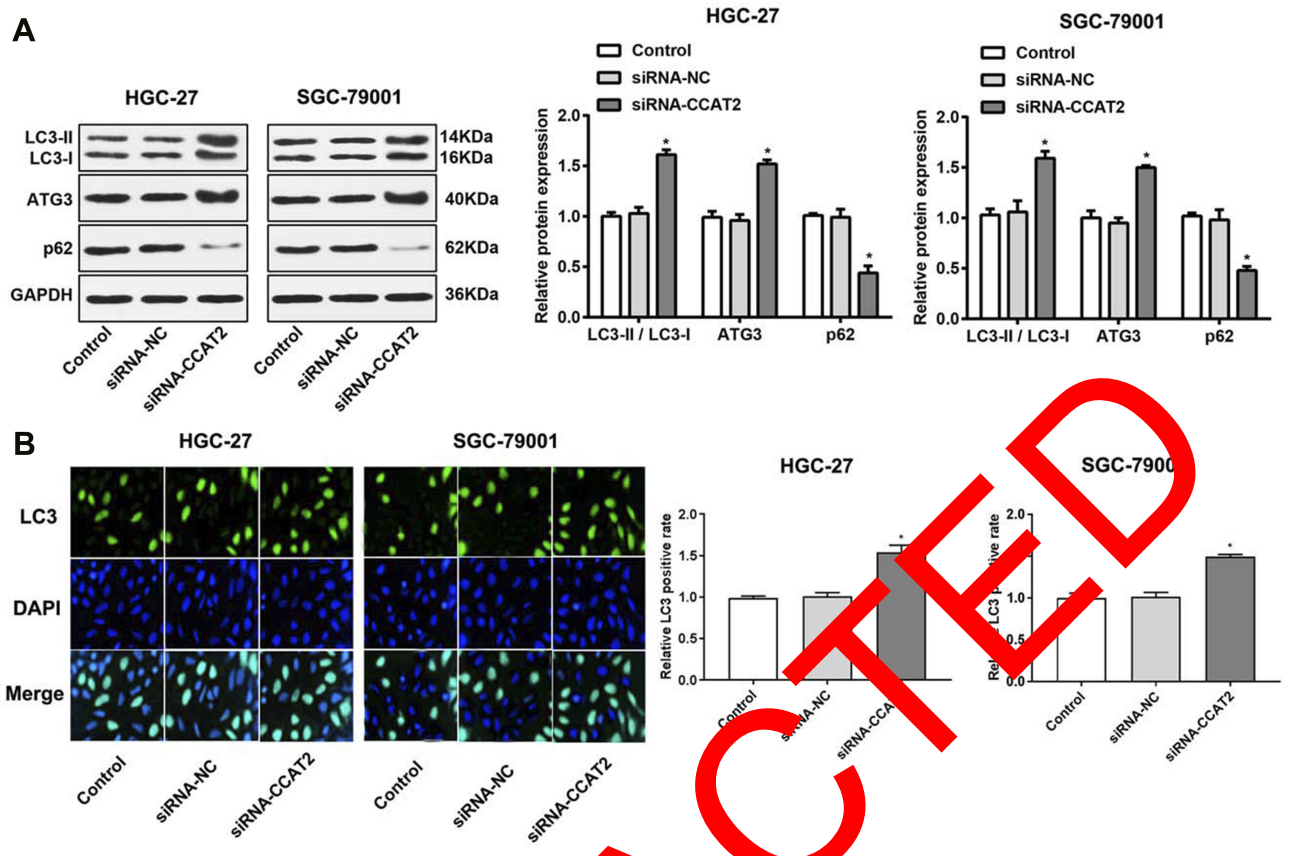

Figure 7 The effects of siRNA-colon cancer-associated transcript 2 (siRNA-CCAT2) transfection on the autophagy of HGC-27 and SGC-7901 cells. (**A**) Relative expression of LC3-II/LC3-I, ATG3, and p62 detected by Western blot, (**B**) Relative LC3-positive rate detected by Immunofluorescence. siRNA-CCAT2, cells transfected with siRNA-CCAT2; siRNA-NC, cells transfected with siRNA-negative control; Control, cells without transfection. *P < 0.05 vs Control and siRNA-NC.

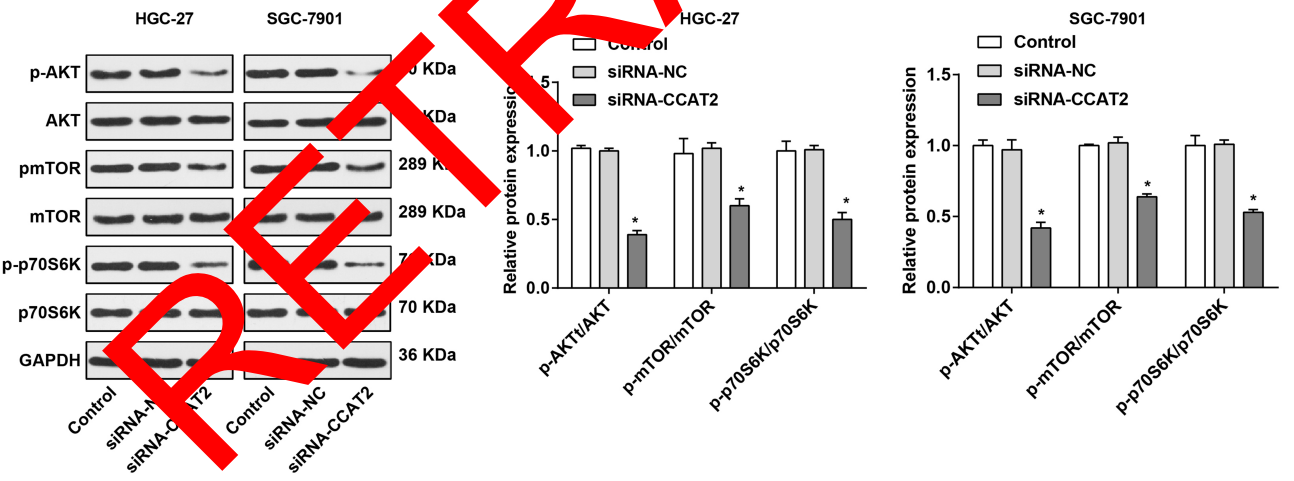

Figure 8 The expression of phosphorylated mammalian target of rapamycin (p-mTOR), p-AKT, and p-p70S6K in HGC-27 and SGC-7901 cells detected by Western blot. siRNA-CCAT2, cells transfected with siRNA-CCAT2; siRNA-NC, cells transfected with siRNA-negative control; Control, cells without transfection. *P < 0.05 vs Control and siRNA-NC.

found that siRNA-CCAT2 transfection significantly inhibited the cell viability in a time-dependent manner. This result is just consistent with previous studies that CCAT2 knockdown significantly inhibits the growth ability and survival rate of BGC-823 cells.[10,11] We also found that siRNA-CCAT2 transfection significantly inhibited the colony formation, and downregulated PCNA in HGC-27 and SGC-7901 cells. These results

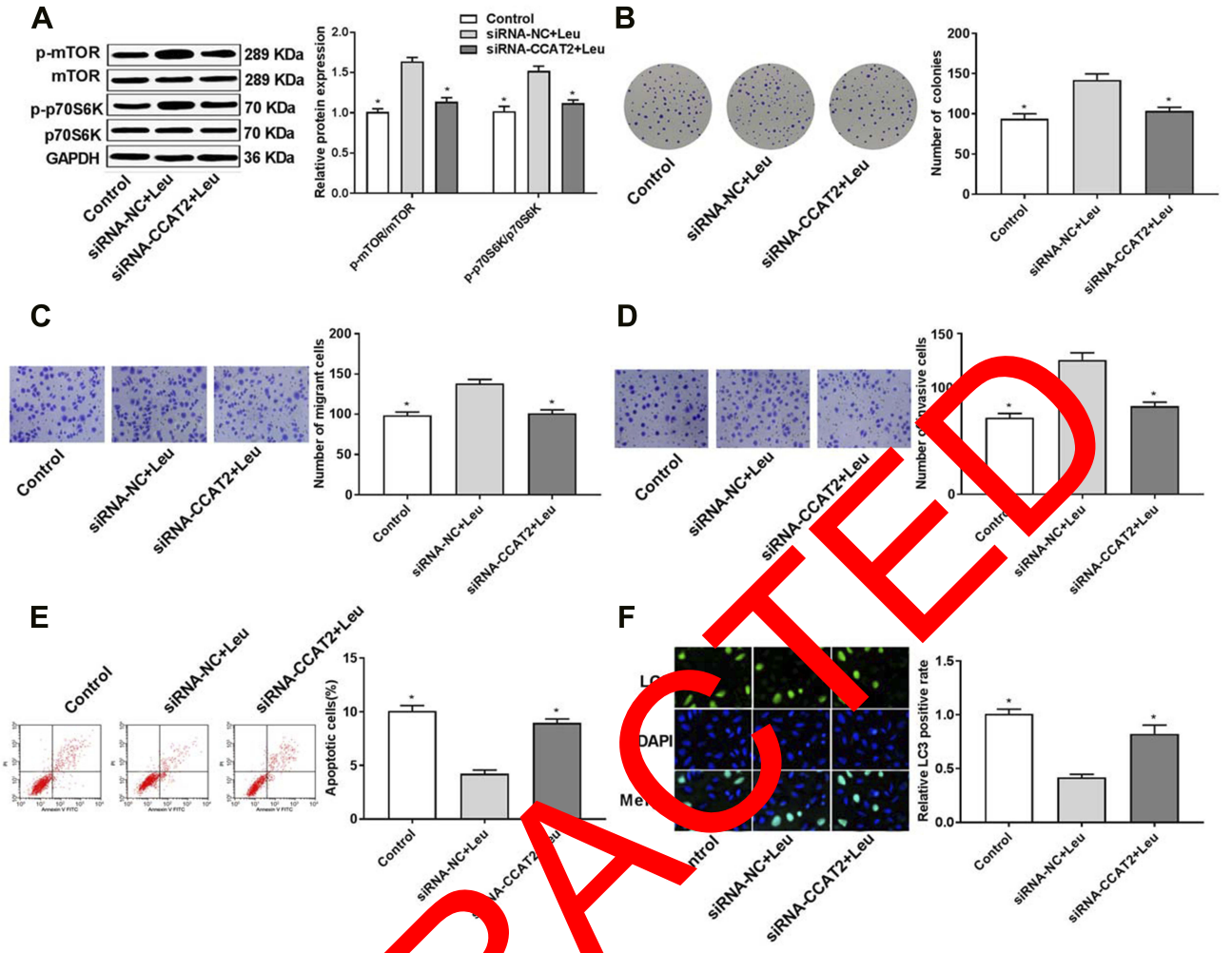

Figure 9 The effect of siRNA-colon cancer-associated transcript 2 (siRNA-CCAT2) transfection on the tumor-promoting role of mTOR pathway in HGC-27 cells. (**A**) The expression of p-mTOR, p-AKT, and p-p70S6K in HGC-27 cells detected by Western blot; (**B**) Colony formation (number); (**C**) The number of migrant cells (×200); (**D**) The number of invasive cells (×200); (**E**) The percentage of apoptotic cells; (**F**) Relative LC3-positive rate detected by Immunofluorescence. siRNA-CCAT2 + Leu, cells transfected with siRNA-CCAT2 and treated with Leucine (Leu, mTOR agonist); siRNA-NC + Leu, cells transfected with siRNA-negative control and treated with Leu; Control, cells without transfection and treatment. $^{*}P < 0.05$ vs siRNA-NC + Leu.

further illustrate that silencing of CCAT2 inhibits the proliferation of GC cells. In order to reveal the intrinsic mechanism of inhibited proliferation, the cell cycle of siRNA-CCAT2-transfected cells was further detected. The results showed that siRNA-CCAT2 transfection significantly increased the percentage of cells in G0/G1 phase, and decreased the percentage of cells in S phase. These results indicate that silencing of CCAT2 arrests cell cycle at G0/G1 phase, thereby inhibiting proliferation. In addition to the proliferation, a previous study has proved that the apoptotic index of BGC-823 cells is significantly increased by silencing of CCAT2.[11] In consistent with previous study, we found that siRNA-CCAT2 transfection significantly increased the percentage of apoptotic cells. In addition, siRNA-CCAT2 transfection significantly upregulated P53 and Caspase-8, and downregulated Bcl-2 in HGC-27 and SGC-7901 cells. Since P53 and Caspase-8 are known as apoptogenic factors, and Bcl-2 is known as an apoptosis inhibitory factor,[19] our findings further illustrate that silencing of CCAT2 promotes the apoptosis of GC cells.

Tumor metastasis directly contributes to the poor prognosis of GC.[20] Previous studies have proved that CCAT2 knockdown significantly inhibits the migration and invasion of MKN45 cells (GC),[10] LCC9/MCF-7 cells (breast cancer),[21] and HEC-1-A/RL95-2 cells (endometrial cancer).[22] In this study, we found that siRNA-CCAT2 transfection significantly decreased the numbers of migrant and invasive cells. Our findings are just consistent with previous studies, and further illustrate that silencing of CCAT2

inhibits the migration and invasion of GC cells. On the other hand, autophagy, an adaptive cell response plays an important role in the development of tumors.[23] LC3, ATG3, and p62 are important markers for autophagy.[24,25] During autophagy, LC3-phosphatidylethanolamine conjugate (LC3-II) formed by cytosolic LC3 (LC3-I) is recruited to autophagosomal membrane, and lysosomal turnover of the autophagosomal marker LC3-II can reflect the autophagic activity.[26] E2-like enzyme ATG3 is involved in the binding of LC3 to phosphatidylethanolamine.[27] p62 is one of the selective substrates for autophagy that plays a key role in the formation of cytoplasmic proteinaceous inclusion.[28] The expression of p62 is usually decreased during autophagy and is negatively correlated with autophagic activity.[29] In this study, we found that siRNA-CCAT2 transfection significantly upregulated LC3-II/LC3-I and ATG3, downregulated p62, and increased LC3-positive rate in HGC-27 and SGC-7901 cells. Our results indicate that silencing of CCAT2 promotes the autophagy of GC cells. Previous studies have proved that β-Elemene, Matrine, and Celastrol induce both the apoptosis and autophagy of GC cells.[30–32] We suspected that the autophagy may be activated in GC cells to protect against apoptosis.

The action mechanisms of CCAT2 on tumors are complex, which involve diverse regulatory factors, such as E-cadherin/LATS2,[10] P15,[33] GSK3β/β-catenin, Wnt/β-catenin,[35] and TGF-β.[21] In this study, the specific regulatory relationship between CCAT2 and mTOR signaling was evaluated. We found that siRNA-CCAT2 transfection significantly downregulated p-mTOR, p-AKT and p-p70S6K in HGC-27 and SGC-7901 cells. In addition, siRNA-CCAT2 transfection also significantly reversed the tumor-promoting effect of mTOR signaling activation on HGC-27 cells. mTOR is known as a central-regulatory kinase that involved in the regulation of cell proliferation, differentiation, metabolism, and angiogenesis.[3] mTOR has been recognized as a therapeutic target for GC. It has been reported that silibinin significantly inhibits the proliferation of MGC-803 cells through suppressing the phosphorylation of mTOR.[36] Carnosine inhibits the proliferation, induce the cell cycle arrest in G0/G1 phase, and promotes the apoptosis of SGC-7901 and MKN-45 cells through suppressing the phosphorylation of mTOR. Therefore, we suspect that silencing of CCAT2 may inhibit the proliferation, migration and invasion, and promote the apoptosis of GC cells through blocking mTOR signaling.

Conclusions

In conclusion, CCAT2 was upregulated in both GC tissues and GC cells. The upregulation of CCAT2 was positively associated with the maximum tumor diameter, lymphatic metastasis, TNM staging, and low overall survival rate of GC patients. In addition, silencing of CCAT2 inhibited the proliferation, migration and invasion, induced the cell cycle arrest in G0/G1 phase, and promoted the apoptosis and autophagy of GC cells. The anti-tumor effect of siRNA-CCAT2 on GC cells was closely associated with the inhibition of mTOR signaling. Silencing of CCAT2 may be a promising therapeutic target against GC. However, this study is still limited in the cellular level. Further researches on the specific role of CCAT2 on animal models are still needed.

Ethics Approval and Consent to Participate

This study was conducted after obtaining local ethical committee approval of The Second Hospital of Shandong University. All patients signed informed consent, and this was conducted in accordance with the Declaration of Helsinki.

Author Contributions

All authors contributed to data analysis, drafting or revising the article, gave final approval of the version to be published, and agree to be accountable for all aspects of the work.

Disclosure

The authors report no funding and no conflicts of interest in this work.

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