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ORIGINAL RESEARCH

RETRACTED ARTICLE: TRIM11 Promotes Proliferation, Migration, Invasion and EMT of Gastric Cancer by Activating β-Catenin Signaling

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Introduction: Gastric cancer (GC) is the sixth most common malignant tumor and the third leading cause of cancer-related death in the world. Studies have shown that TRIM protein can regulate transcription factor activity and is associated with many cancers. However, the role of TRIM11 in gastric cancer remains unclear.

Methods: TRIM11 protein levels were examined in 36 cases of GC tissues and 4 gastric cancer cell lines. TRIM11 overexpression and knockdown cells were constructed in MGC-803, HGC-27 and SGC-7901 respectively. The biological roles and mechanisms of TRIM11 were examined using CCK8, colony formation, transwell migration assay, invasion assay, Western blotting, Immunohistochemistry and in vivo nude mice experiments.

Results: We found that TRIM11 was upregulated in gastric cancer tissues and gastric cancer cell lines. Functionally, TRIM11 overexpression increased growth rate, colony formation, invasion and migration ability, EMT and β-catenin protein level and its downstream proteins such as CyclinD1 and c-myc, while TRIM11 knockdown shows the opposite effects.

Conclusion: In summary, our data show that TRIM11 is overexpressed in GC. TRIM11 promotes proliferation, migration, invasion and EMT of gastric cancer by activating β-catenin signaling.

Keywords: TRIM11, gastric cancer, proliferation, migration, invasion, EMT

Introduction

Gastric cancer (GC) is the sixth most common malignant tumor and the third leading cause of cancer-related death in the world.[1] In China, the incidence of gastric cancer in the northwest and east coastal areas is significantly higher than that in the south.[2] Although the comprehension of etiology and molecular mechanisms had improved and the morbidity and mortality had declined, the 5-year overall survival of GC patients remains disappointing[3]. Among the many reasons that lead to the low survival rate of gastric cancer patients, high recurrence rate and distant metastasis are the main obstacles to improving the survival of gastric cancer patients.[4]

Tumor metastasis is a complex process that involves epithelial-mesenchymal transition, through which the gastric cancer cells acquire invasive mesenchymal properties, which leads to decreased adhesion and cell polarity and increased mobility and invasiveness, and finally results in metastasis from the primary tumor tissue to the adjacent tissues or even remote sites.[5–8] The Wnt/β-catenin signaling pathway has been widely recognized as a regulator of cell growth, migration and stem-like

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phenotype.[9] The biological processes that EMT participates in are regulated by many signal transduction pathways including Wnt/β-catenin pathway.[10,11] More and more evidences show that the classical Wnt pathway negatively regulates E-cadherin and induces EMT by preventing the important factor β-catenin from degraded by proteasome.[12,13]

It is reported that the deregulation of ubiquitin ligase is related to various biological processes of diseases.[14–16] Tripartite motif containing (TRIM) proteins are a family of proteins that containing a RING-finger domain, 1 or 2 B box, and a coiled-coil domain.[17] Most of TRIM family proteins, including TRIM11, can function as E3 ubiquitin ligases due to its RING-finger domain.[17–19] Studies have shown that TRIM protein can regulate transcription factor activity and is associated with many cancers.[20] TRIM11 has been reported to be associated with prognosis of several cancer patients such as liver, lung and breast cancer and so on.[21–23] In addition, TRIM11 is reported to be an oncogene in lymphomas, which is involved in the activation of the β-catenin signaling pathway and the ubiquitination and degradation of Axin1.[24]

In this study, we found that TRIM11 is upregulated in GC tissues compared to adjacent normal tissue. Overexpression of TRIM11 in GC cells leads to increase of β-catenin, C-myc, CyclinD1 and vimentin and significantly promoted proliferation, migration and invasion. Conversely, TRIM11 knockdown resulted in opposite effects. In addition, we found a significant decrease in tumor growth in nude mice bearing TRIM11-knockdown HGC-27 cells, accompanied by a reduced β-catenin expression. In conclusion, we found that TRIM11 regulates EMT through the β-catenin signaling pathway, providing a potential drug target for the treatment of gastric cancer and the prevention of metastasis of gastric cancer.

Materials and Methods

Human Tissue Specimens

A total of 36 paired gastric tumor and normal tissues were obtained from Renmin Hospital of Wuhan University and then sent to Wuhan Iwill Technology Company for tissue array chips production. This study was approved by the Ethics Committee of Renmin Hospital of Wuhan University and performed under the Declaration of Helsinki. All participants provided informed consent to have their tissues used in this study.

Cell Lines and Cell Culture

Human gastric cancer cell lines (MGC-803, AGS, SGC-7901, HGC-27) and human normal gastric epithelial cell GES-1 were obtained from China Center for Type Culture Collection and cultured in DMEM/F12 (Hyclone, USA). HEK 293T cells were obtained from China Center for Type Culture Collection and cultured in high-glucose DMEM (Hyclone, USA). Those medium supplemented with 10% FBS (Gibco, USA) and 1% penicillin and streptomycin (Beyontime, China) were used to culture cells in the incubator containing 5% CO2 and temperature of 37°C.

Construction and Transfection of Lentiviral Plasmid

Full length of TRIM11 CDS was cloned to the pLVX-Puro lentiviral vector with a HA tag tag. The sequences of TRIM11-shRNA (GCTTCTTAAGATGGCCGAGATT) were cloned into the lentiviral vector pLVshRNA-EGFP (2A) puro. The HEK293T cells were seeded into a 10-cm dish. After incubation overnight and the cell density reached 40%-60%, 7.5ug of psPAX2, 5ug of pMD2.G and 10ug of purpose plasmid were diluted in 500ul of OPTI-MEM, 25ul of the Lipo2000 transfection agent was also added and mixed for incubation of 20min at room temperature before added to the dish. The lentiviral supernatants were harvested to infect gastric cancer cell lines. After 48h of infection, 1mg/mL of puromycin was added into the plate for selection of stably transfected GC cells.

CCK8 Cell Viability Assay

Cell proliferation was detected by Cell Counting Kit-8 (CCK8) (Beyotime, China). Briefly, gastric cancer cells were planted into a 96-well plate at the concentration of 5000 cells per well. The absorbances of cells at 24, 48, 72, 96h were examined according to the manufactures' instructions.

Colony Formation Assay

Gastric cancer cells were seeded into a 6-well plate at the concentration of 500 cells per well. The culture medium was replaced every 3 days. On day 10, colonies were stained with Giemsa for 15min after the fixation by 4% formaldehyde for 10 min. The colonies were counted and analyzed.

Cell-Cycle Detection

Cell cycle was detected by keyGENE reagent test kit (keyGENE, China). Briefly, gastric cancer cells were

planted into a 6-well plate at the concentration of 30,000 cells per well. After 24h of starvation treatment, all GC cells were fed with DMEM/F12 supplemented with 10% FBS. After 24h of culture, GC cells were fixed in 70% Ethanol at 4 °C for 10h. GC cells were then incubated by propidium iodide (PI) and RNAse at dark for 30min. Finally, the red fluorescence at 488 nm was determined by flow cytometry (CytoFLEX, Beckman Coulter), and the cell-cycle progression was analyzed using the CytExpert software.

Cell Migration and Invasion Assays

Transwell chambers from Corning Costar Corp were used to perform the cell migration and invasion assays. A total of 2×10^4 cells in 100ul FBS free DMEM/F12 medium were seeded on the upper chamber and then incubated in the 37°C for 36h. For the invasion assay, the chambers were coated with 100ul of 1:8-diluted Matrigel purchased from BD Biosciences and 1×10^5 cells in 100ul FBS free DMEM/F12 medium were seeded on the upper chamber and then incubated in the 37°C for 36h. The lower chambers were filled with 600ul DMEM/F12 medium containing 25% FBS. After incubation, cells that invaded to the lower surface of the chamber were fixed by 4% formaldehyde for 10 min and stained by Giemsa for 15 min. Migrated and invaded cells were counted at 400-fold magnification in five random visual fields. The experiment was performed three times.

Antibodies and Reagents

The antibodies used are listed below: anti-TRIM11 (#A13887, Abclonal, China), anti-E-cadherin (#A11492, Abclonal, China), anti-Vimentin (#A19607, Abclonal, China), anti-β-catenin (#51,067-2-AP, Proteintech, China), anti-C-myc (#10,828-1-AP, Proteintech, China), anti-Axin2 (#A2413, Abclonal, China), anti-CyclinD1 (#2978, Cell Signaling Technology, USA), anti-GAPDH (#2118, Cell Signaling Technology, USA).

Western Blotting

Total proteins of GC cells were extracted using RIPA lysis buffer containing PMSF and cocktail and the concentration was detected by BCA kits (Beyotime, China). Protein samples were separated by SDS-PAGE and then transferred to PVDF membranes. Membranes were blocked by TBS containing 5% non-fat milk for 1h at room temperature and then incubated with primary antibody at 4 °C overnight. After three times of washing with TBST, membranes were incubated with secondary antibody for 1h at room temperature. Wash the membranes three times again and scan the membranes with an LI-COR Odyssey infrared imaging system (LI-COR Bioscience).

Immunohistochemistry

Immunohistochemistry (IHC) staining was conducted as previously described.[25] Briefly, tissue sections were deparaffinized and rehydrated in graded ethanol solutions. Then, the deparaffinized tissue specimens were boiled in 10mM citrate buffer (pH 6.0) for 2 min for antigen retrieval. Subsequently, the endogenous peroxidase activity was blocked by incubating with 3% H_2O_2 solution. The tissue sections were then incubated with specific antibody (1:300 dilution). The sections were developed using 3, 3′- diaminobenzidine (DAB) and counterstained with hematoxylin. The negative control sections were incubated in parallel with the immunoglobulin IgG (1:300). H-scores were calculated according to the following formula:[26,27]

[1 × (% cells 1+) + 2 × (% cells 2+) + 3 × (% cells 3+)].

All viable tumor cells within the biopsy were taken into account when applying the semi-quantitative scoring system.

Immunofluorescence

GC cells were seeded in a 24-well plate (1.0 × 104 cells/well) and allowed to adhere overnight. Cells were fixed with 4% paraformaldehyde for 30 min, permeabilized with 0.2% Triton X-100 (Beyotime, China) for 20 min, blocked with 5% bovine serum albumin (BSA, Beijing Solarbio Science and Technology co., ltd.) for 30 min and incubated with primary antibodies against β-catenin (1:100) at 4◦C overnight. The next day, cells were washed and incubated with cy3-labeled fluorescent secondary antibodies (1:100) at room temperature for 1 h. Then, the sections were stained with DAPI (Beyotime, China). Observations were performed with a laser scanning confocal microscope (Olympus, Japan, #FV1200).

Xenograft Tumor Experiment in Nude Mice

All procedures, which complied with the National Institutes of Health guide for the care and use of laboratory animals (NIH Publications No. 8023, revised 1978), were

approved by the Animal Care and Use Committees of Renmin Hospital of Wuhan University. Four to five weeks old male BALB/c nude mice were obtained from Beijing Vital River Laboratory Animal Technology Company (China). All animals were maintained at a specific pathogen-free environment. Twelve mice were randomly assigned into two groups: HGC-27 scramble, HGC-27 shTRIM11. GC cells were harvested from 10-cm dish, washed by serum-free medium, suspended in 100ul ice-cold PBS, then subcutaneously injected to the dorsum of each mice. Tumors were measured every 3 days in two dimensions using vernier caliper. Tumor volumes were defined as 0.5 x length x width^2. Thirty days later, mice were sacrificed and subcutaneous tumors were harvested for further experiment.

Statistical Analysis

Statistical analysis was conducted by SPSS 20.0 software. Measurement data were subject to normal distribution and are expressed as mean ± SD. Comparisons between CC and adjacent normal tissues were analyzed using a paired *t*-test, while comparisons between the other two groups were conducted with an independent sample *t*-test. Comparisons among multiple groups were analyzed by one-way ANOVA and tested by a Tukey's test afterward. Data at different time points among multiple groups were compared using repeated-measurement ANOVA. $P < 0.05$ was considered to be indicative of statistical signif

Results

TRIM11 is Upregulated in Gastric Cancer Samples and Correlate with Poor Survival in GC Patients

To determine the expression level of TRIM11 in GC, we first analyzed microarray datasets in TCGA database. As shown in Figure 1A, expression level of TRIM11 messenger RNA (mRNA) is significantly increased in GC tissues compared to gastric normal tissues. What is more, survival analysis show that patients with higher mRNA expression level of TRIM11 displayed shorter overall survival time than patients with lower expression level of TRIM11 (Figure 1B). These data suggested that there is correlation between TRIM11 and GC.

To confirm results obtained from microarray datasets, we conducted immunohistochemical staining for TRIM11 on primary tumor tissues and adjacent normal tissues from a cohort of 32 GC patients. Table 1 shows the clinical characteristic of these patients and TRIM11 expression was correlated with T stage. Semiquantitative analysis shows that the intensity of TRIM11 staining is significantly increased in GC than normal tissues (Figure 1C and D).

TRIM11 Promotes GC Cell Proliferation in vitro

We examined the expression level of TRIM11 in 4 gastric cancer cell lines (MGC-803, AGS, SGC-7901, HGC-27) and 1 human gastric normal tissue cell line (GES-1). As shown in Figure 2A, TRIM11 protein levels are higher in GC cell lines than that of GES-1.

In order to explore the biological function of TRIM11 in GC, we generated knockdown and overexpression TRIM11 cell lines by lentivirus transfection. We selected three cell lines, HGC-27 and SGC-7901 for TRIM11 knockdown, and MGC-803 for TRIM11 overexpression. We conducted CCK8 assay to determine whether TRIM11 takes effect on the growth of GC cells. As shown in Figure 3A, cell proliferation was significantly suppressed by TRIM11 RNA interference in HGC-27 and SGC-7901 cells, and it was enhanced by overexpression of TRIM11 in MGC-803 cells. In addition, colony formation assay shows that overexpression of TRIM11 facilitated clone forming capability of MGC-803 cells, while knockdown of TRIM11 inhibited clone formation in HGC-27 and SGC-7901 cells (Figure 3B and C). In addition, knockdown of TRIM11 significantly stalled cell-cycle progression in the G1 phase and reducing S/G2 phase cells, while overexpression of TRIM1 showed the opposite effects (Figure 3D).

TRIM11 Promotes GC Cell Migration, Invasion and EMT in vitro

To further assess the impact of TRIM11 on cell migration and invasion, we performed transwell migration and invasion assay and results show that knockdown of TRIM11 significantly inhibited the migration and invasion of HGC-27 and SGC-7901 cells, while overexpression of TRIM11 had the opposite effects on MGC-803 cells (Figure 4A and B). These data implied that downregulation of TRIM11 inhibited proliferation, migration and invasion of GC in vitro. Next, we examined whether there is correlation between TRIM11 and EMT in GC. As shown in Figure 2C, the protein levels of vimentin were increased, while E-cadherin was decreased in TRIM11 overexpression MGC-803 cells compared to vector control treated MGC-803 cells, while knockdown of TRIM11 displayed the opposite tendency (Figure 2B and D).

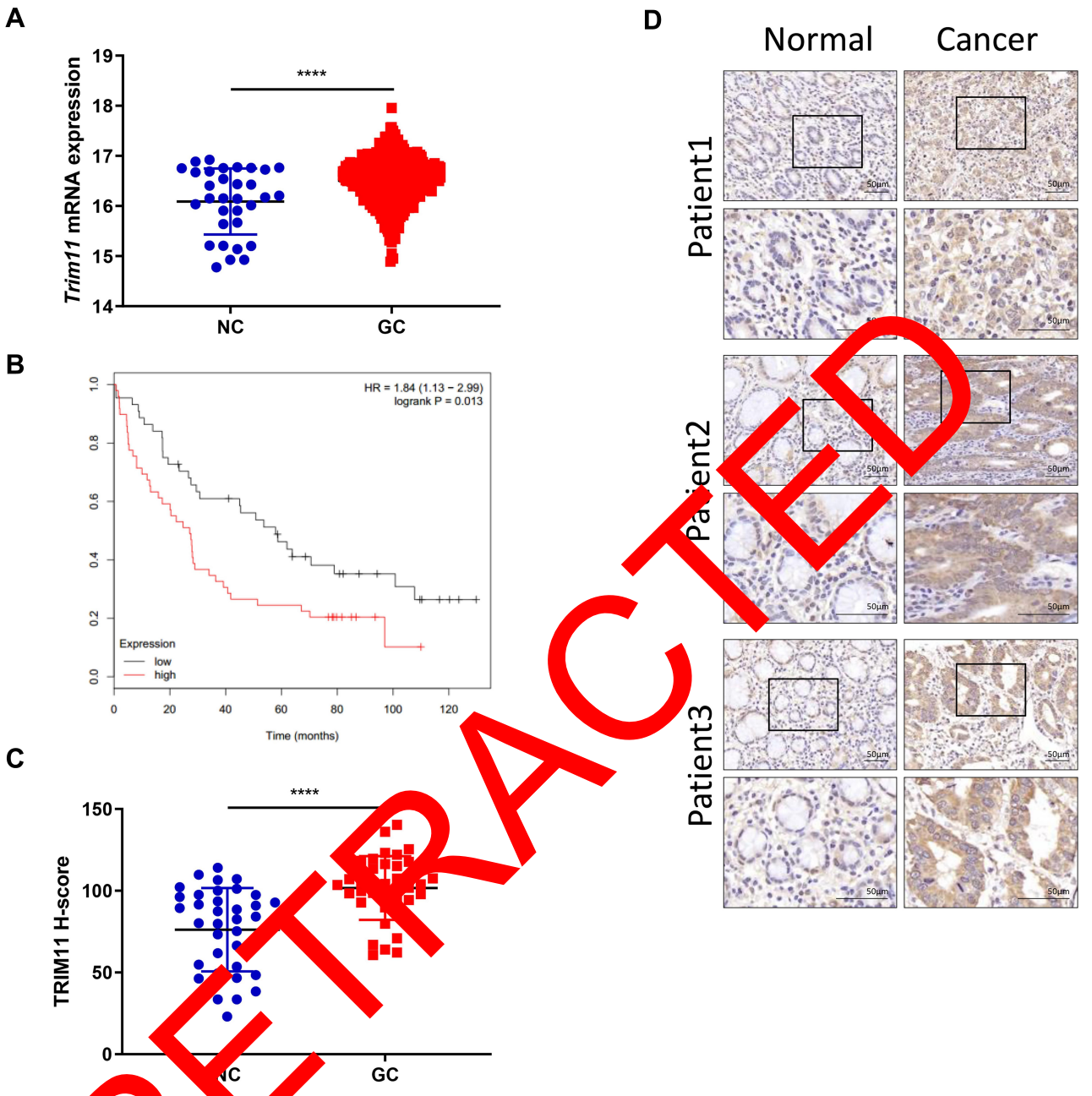

Figure 1 TRIM11 is up-regulated in GC clinical samples and correlated with poor survival in GC patients. (**A**) Analysis from the TCGA database shows that mRNA expression levels of TRIM11 are significantly higher in gastric cancers compared with normal tissues (P<0.0001), 32 normal tissues and 375 cancer tissues were analyzed. (**B**) TRIM11 mRNA expression level negatively correlates with GC patient survival (kmplotter, P=0.013, n=49 in the TRIM11 high mRNA group, n=44 in the TRIM11 low mRNA group). (**C**) Quantitative analysis of TRIM11 staining shows significantly H-score in gastric tumor samples compared with adjacent normal tissues (32 normal tissues and 32 tumor samples). (**D**) Immunohistochemical staining of normal and gastric cancer tissues with anti-TRIM11 antibody. ****P<0.0001.

TRIM11 Regulates Tumor Growth of GC in vivo

To detect the positive role of TRIM11 in gastric cancer progression in vivo, we conducted xenograft tumor assays using HGC-27 cells stably transfected with sh-TRIM11 and scramble shRNA. As shown in Figure 5A–C, tumors from mice bearing shTRIM11 cells grew slowly than that of scramble shRNA cells since injection.

TRIM11 Regulates β-Catenin Pathway in vitro and in vivo

To explore the underlying mechanism by which TRIM11 regulates gastric cancer, we did some literature research

Table 1 Statistical Analysis of the Expression of TRIM11 and Different Clinical Features of Gastric Cancer

Clinical Characteristics	TRIM11 Expression		χ^2	P
	Upregulation	Downregulation		
Gender				
Male	11	12	0.1204	0.7286
Female	7	6		
Age				
55 or older	11	11	0	>0.9999
Younger than 55	7	7		
T stage				
T0+T1	1	7	5.786	0162
T2+T3	17	11		
Lymph node metastasis				
NO	4	9		0.0
YES	14	9		
Lauren's classification				
Intestinal	7	8	0.0622	0.7326
Diffuse	10	8		
Mixed	1	2		

and found that several TRIM proteins can regulate β-catenin pathway, so we hypothesize that TRIM11 may regulate GC through β-catenin pathway. We detected the expression level of β-catenin in TRIM11 overexpression in MGC-803 cells and found that it was increased. Then, we further investigated the expression level of β-catenin

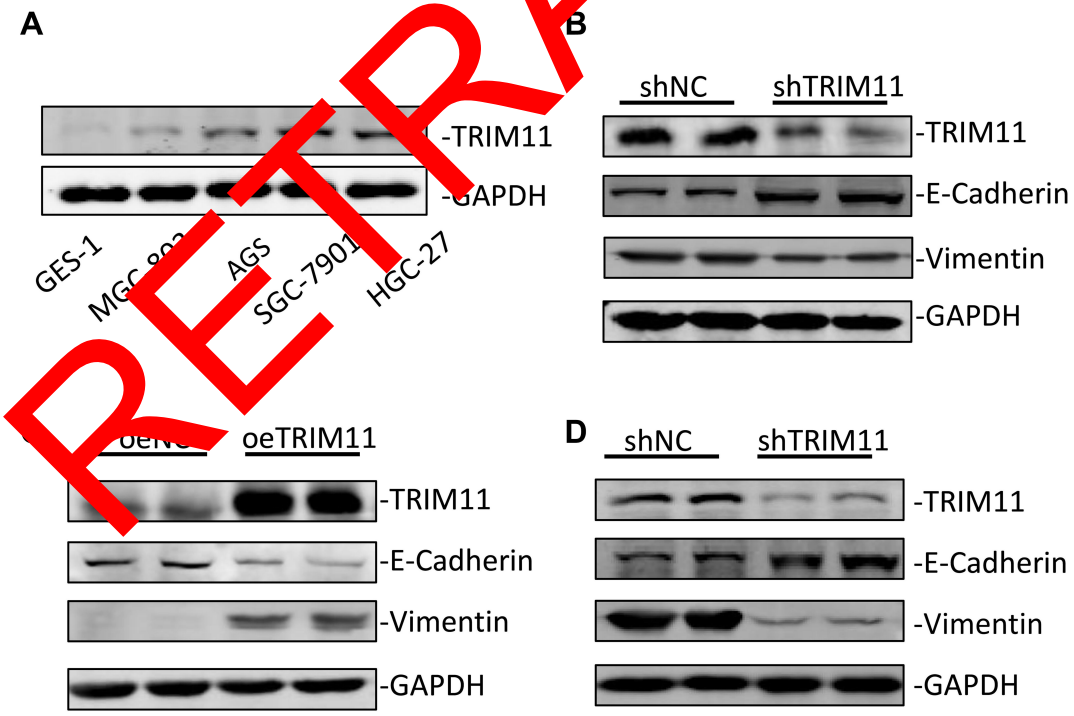

Figure 2 TRIM11 is upregulated in GC cell lines. (**A**) TRIM11 protein levels in a human normal gastric cell line (GES-1) and four GC cell lines (SGC-7901, MGC-823, HGC-27, AGS) were analyzed by Western blotting. (**B**) The protein levels of TRIM11, E-cadherin and vimentin in knockdown of TRIM11 in SGC-7901 cells were analyzed by Western blotting. (**C**) The protein levels of TRIM11, E-cadherin and vimentin in overexpression of TRIM11 in MGC-803 cells were analyzed by Western blotting. (**D**) The protein levels of TRIM11, E-cadherin and vimentin in knockdown of TRIM11 in HGC-27 cells were analyzed by Western blotting.

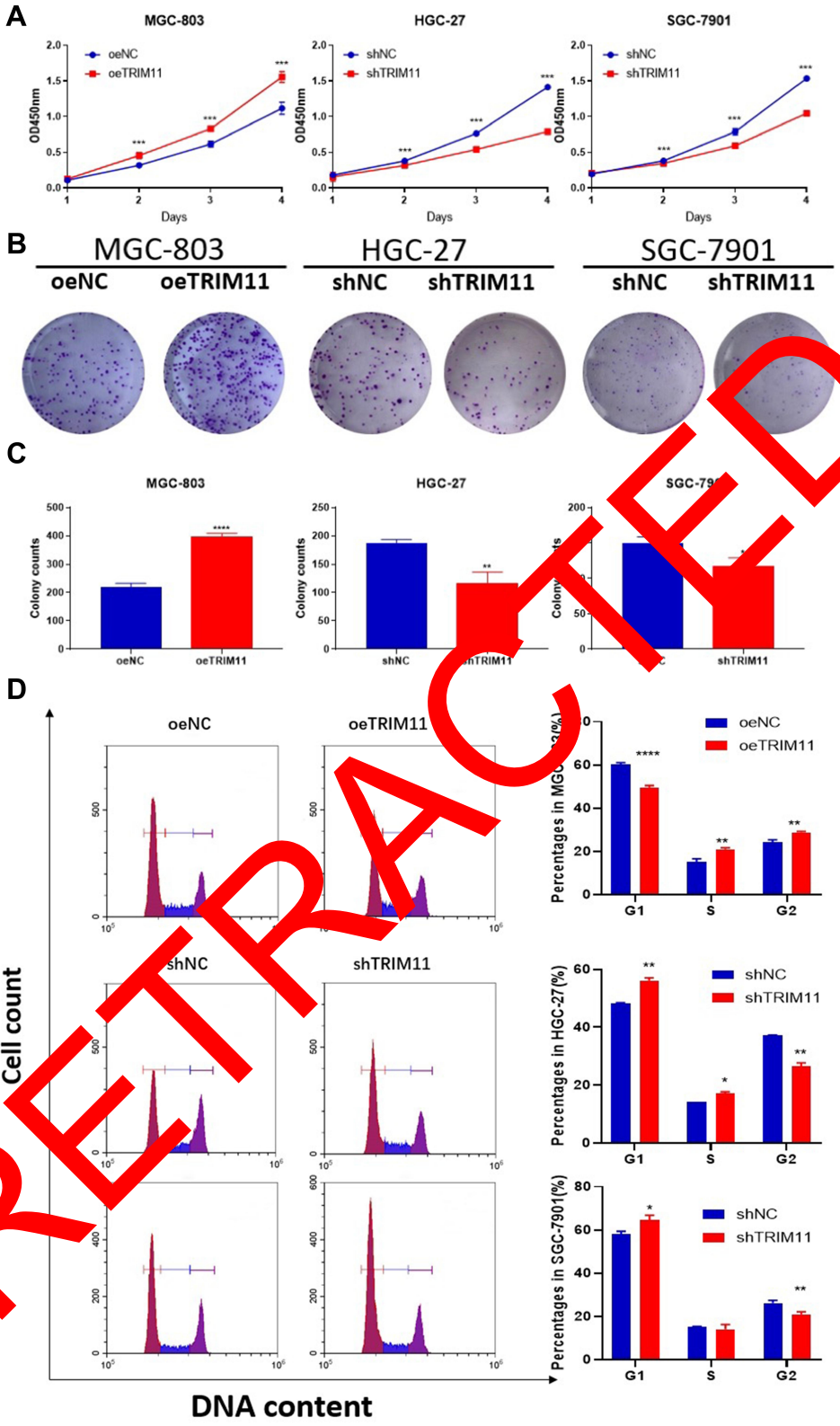

Figure 3 TRIM11 promotes GC cell proliferation in vitro. (**A**) TRIM11 overexpression promotes the proliferation rate of MGC-803 cells, while TRIM11 knockdown reduces the proliferation rate of HGC-27 and SGC-7901 cells. (**B**, **C**) TRIM11 overexpression promotes the capability of clone formation in MGC-803 cell, while TRIM11 knockdown inhibits the capability of clone formation in HGC-27 and SGC-7901 cells. (**D**) Cell-cycle phase proportions were assessed by flow cytometry. **P*<0.05, ***P*<0.01, ****P*<0.001, *****P*<0.0001.

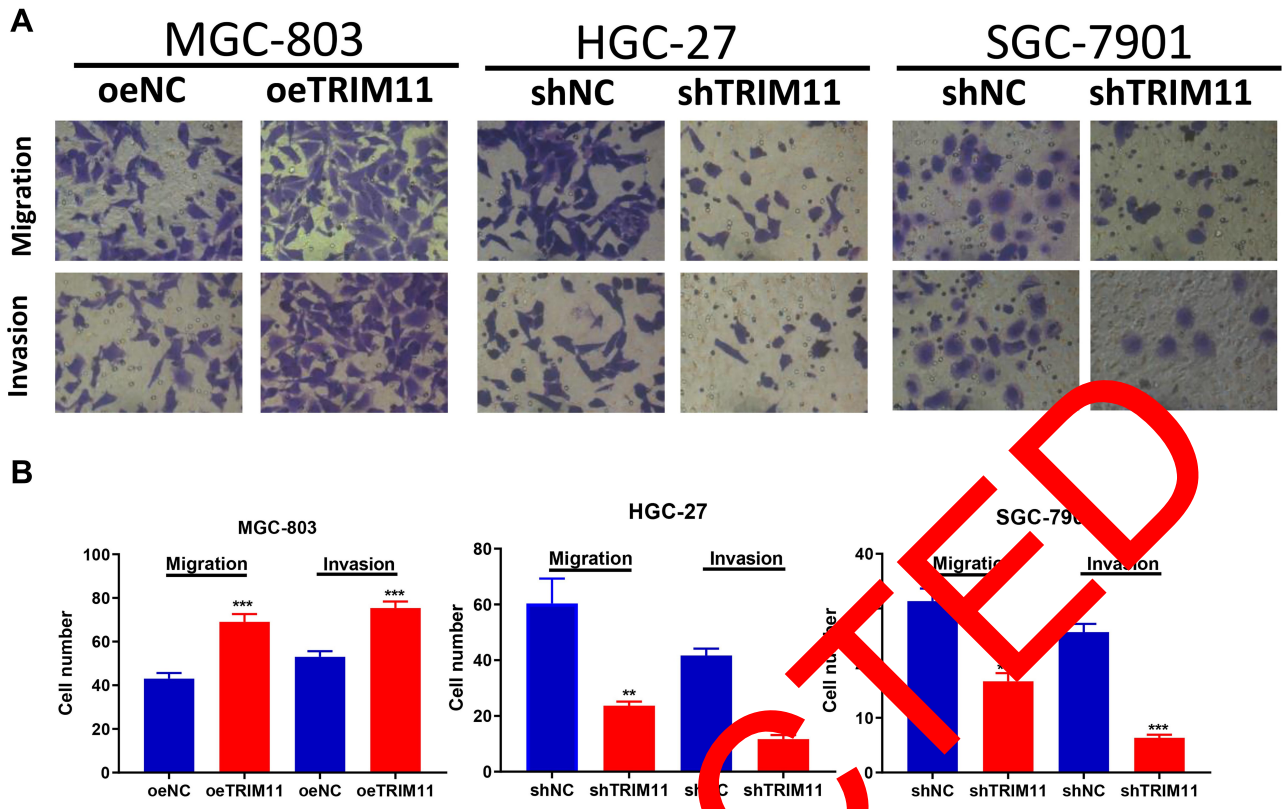

Figure 4 TRIM11 promotes GC cell migration and invasion in vitro. (**A**, **B**) TRIM11 overexpression inhibited MGC-803 cell migration and invasion, whereas TRIM11 knockdown exerts the opposite effect in HGC-27 and SGC-7901 cells. ***P*<0.01, ****P*<0.001.

downstream molecules and found that Cyclin D1 and C-myc were upregulated and Axin2 were downregulated (Figure 6A) in overexpression of TRIM11 in MGC-803 cells, while knockdown of TRIM11 in HGC-27 cells displayed the opposite results (Figure 6B). We also found that the protein level of β-catenin in shTRIM11 xenograft tumors was significantly lower than that of shNC xenograft tumors (Figure 6C). What is more, we also analyzed the protein level of β-catenin in cell nucleus and cytoplasm by Western blotting and immunofluorescence. Results show that overexpression of TRIM11 promotes the transfer of β-catenin protein from cytoplasm to nucleus (Figure 6D and E). These data suggest that TRIM11 may exert its oncogenic effect through β-catenin pathway.

Discussion

In this present study, we aimed to identify new biomarkers that can help improve the long-term outcomes of GC patients. Results show that TRIM11 is upregulated in GC tissues compared to adjacent normal tissues and overexpression of TRIM11 in GC cells leads to significantly promoted proliferation, migration and invasion, while TRIM11 knockdown showed the opposite effects. These data suggested that TRIM11 may function as an oncogene in GC and TRIM11 knockdown may be related to better outcomes of GC, which have a guiding role in GC treatment.

TRIM11 has been reported to be an oncogene in several cancers. In lung cancer, TRIM11 promotes proliferation, migration and invasion of lung cancer through PI3K/AKT signaling pathway.[21] In addition, TRIM11 promotes tumor angiogenesis via activation of STAT3/VEGFA signaling in lung adenocarcinoma.[28] In breast cancer, TRIM11 was increased in breast cancer tissues promoted proliferation by participating in the metabolism of glycolysis.[29] TRIM11 promotes breast cancer cell proliferation by stabilizing estrogen receptor α.[23] In liver cancer, TRIM11 is overexpressed in HCC tissues and downregulation of TRIM11 inhibited HCC cell proliferation and invasion as well as suppressed the epithelial–mesenchymal transition (EMT) process.[22] In glioma, TRIM11 is found to be overexpressed in gliomas and has an oncogenic function mediated through the EGFR signaling pathway.[30] TRIM11 was also found to be upregulated in lymphomas and knockdown of TRIM11 inhibited cell proliferation by suppressing β-catenin signaling.[24] In consistent with these

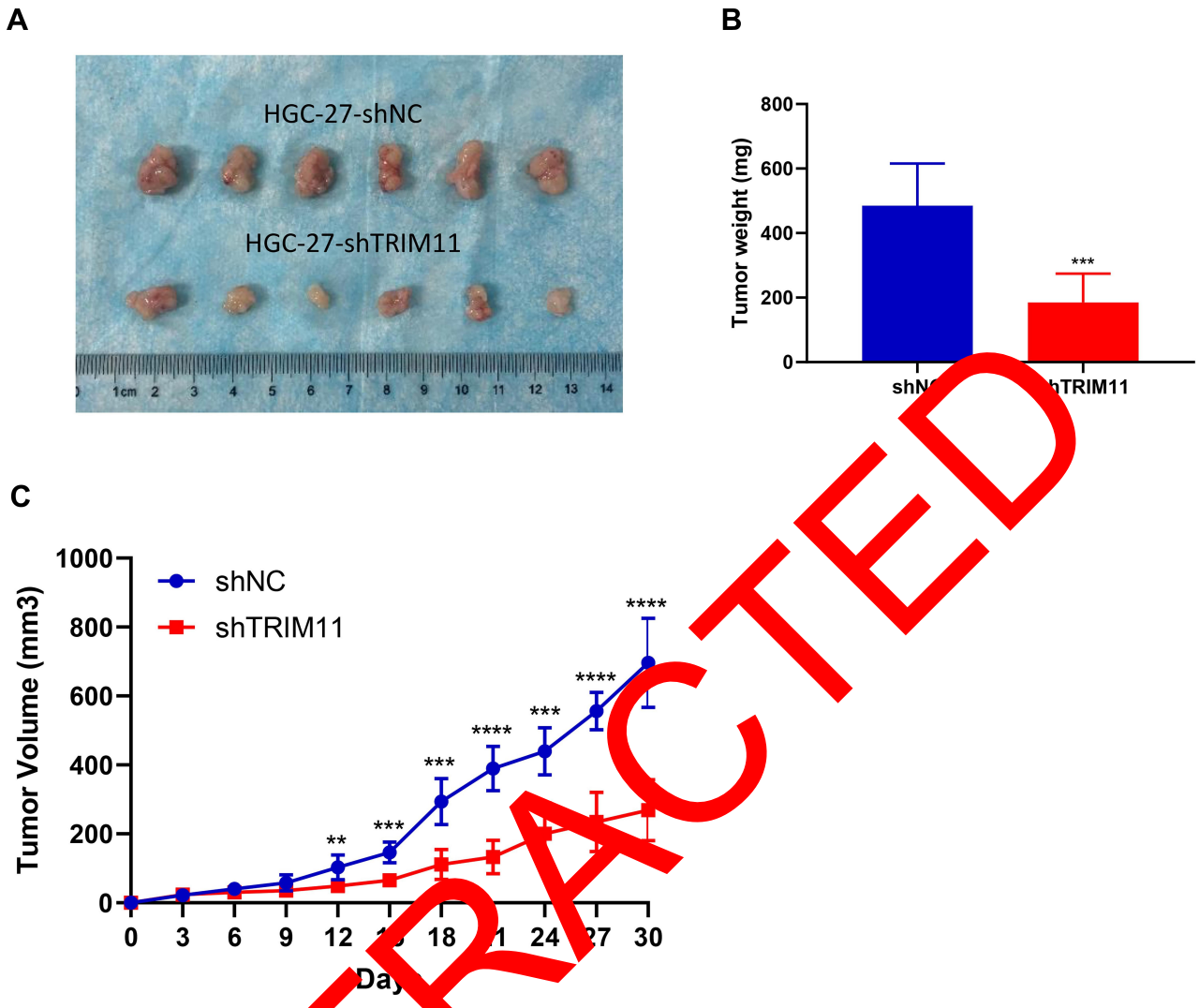

Figure 5 TRIM11 promotes GC cell p[illegible]er[illegible]n in vivo. (**A**) [illegible]M11 gene silencing by shRNA resulted in suppressed tumorigenicity of HGC-27 cells in vivo. (**B**, **C**) Reduced tumor volumes and weights [illegible] xenogra[illegible]enerated by HGC-27 cells transfected with TRIM11-shRNA. **P<0.01, ***P<0.001, ****P<0.0001.

previous studies, t[illegible] cur[illegible]t study showed that TRIM11 overexpressio[illegible]enhan[illegible] gastric[illegible]ancer cell proliferation, migration[illegible]and [illegible]vasion, [illegible]ile TRIM11 knockdown showe[illegible]the opp[illegible]ite effects. All these data may suggest the carcin[illegible]ic effect of TRIM11 in gastric cancer.

EMT is a[illegible]early event of tumor metastasis, which is characterized by downregulation of epithelial cell markers (E-cadherin, γ-catenin and claudin-1) and upregulation of mesenchymal cell markers (vimentin, fibronectin, and N-cadherin).[31,32] Here, we revealed that TRIM11 overexpression results in an increase in vimentin expression and a decrease in E-cadherin expression. Knockdown of TRIM11 showed the opposite results. These data demonstrated that TRIM11 overexpression may promote GC metastasis by inducing EMT.

When β-catenin accumulates to a certain concentration in the cytoplasm, it will transfer to the nucleus and form a complex to stimulate the expression of Wnt targeted genes such as CyclinD1 and c-Myc.[33,34] The increase of cyclin CyclinD1 can promote the development of the cell cycle by allowing the cell to enter the S phase, thereby promoting cell proliferation.[35,36] Studies have shown that knockdown of TRIM11 in the lymphoma cells decreased the expression of β-catenin, Cyclin D1 and c-Myc. The study pointed out that TRIM11 may degrade Axin2 through ubiquitination to promote β-catenin to enter the nucleus, combine with transcription factors TCF/LEFS, promotes the expression of CyclinD1 and C-myc, and ultimately promotes the progression of lymphoma.[24] In this study, we found that TRIM11 promotes the expression of CyclinD1 and C-myc by promoting β-

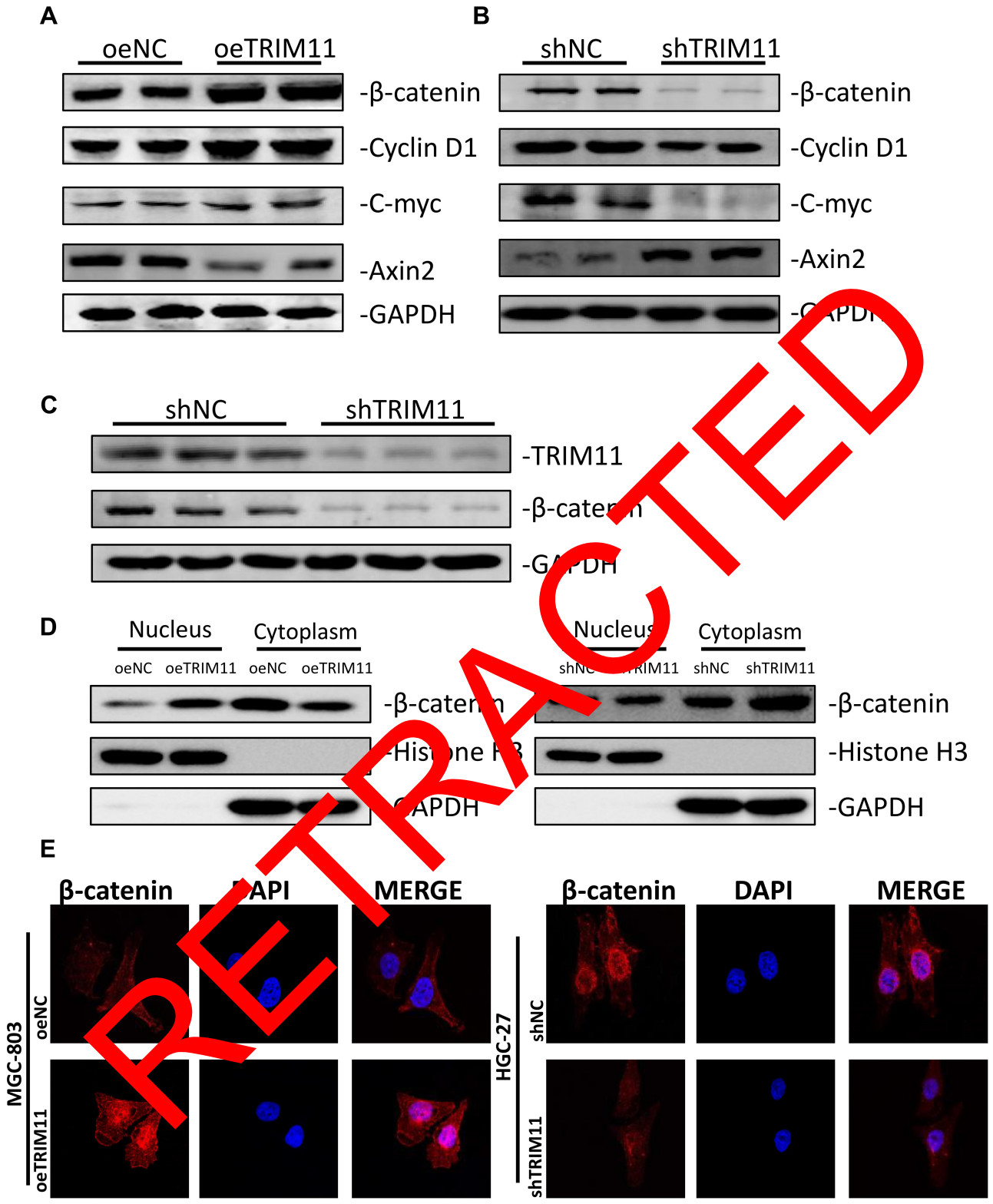

Figure 6 TRIM11 regulates β-catenin signaling in GC. (**A**) The protein levels of β-catenin, Cyclin D1, C-myc and Axin2 in overexpression of TRIM11 in MGC-803 cells were analyzed by Western blotting. (**B**) The protein levels of β-catenin, Cyclin D1, C-myc and Axin2 in knockdown of TRIM11 in HGC-27 cells were analyzed by Western blotting. (**C**) Analysis of β-catenin protein level in xenograft tumors by Western blotting. (**D**) Analysis of β-catenin protein level in cell nucleus and cytoplasm by Western blotting. (**E**) Analysis of β-catenin protein level in cell nucleus and cytoplasm by Immunofluorescence.

catenin entering the nucleus, and ultimately promoting the development of gastric cancer. This is consistent with previous research, but the specific mechanism of how TRIM11 affect β-catenin needs to be further explored.

Our study has limitations. First of all, the sample size of this study is too small and more patients need to be included in the future to verify the conclusions obtained by this study. Moreover, the underlying mechanism of how TRIM11 acting on the β-catenin signaling needs further research to reveal.

In brief, the current study identified the overexpression of TRIM11 in clinical GC tissues and GC cell lines for the first time. Results from in vitro and vivo assays suggested that TRIM11 displayed positive effects on GC cell proliferation, migration and invasion through regulating EMT and β-catenin signaling pathway. Our research proposed the carcinogenic effect of TRIM11 in GC, and targeting TRIM11 represents a promising therapeutic target for GC, while it still needs more detailed research.

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Disclosure

The authors report no conflicts of interest in this work.

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