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ORIGINAL RESEARCH

RETRACTED ARTICLE: LncRNA FTX Promotes Proliferation and Invasion of Gastric Cancer via miR-144/ZFX Axis

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Background: Long non-coding RNAs are important regulators in cancer cell tumorigenesis. We have demonstrated in a prior study that lncRNA FTX is dysregulated in gastric cancer (GC). In this study, we aim to report gastric cancer-related lncRNA FTX is a main regulator in GC development and progression.

Methods: In vitro and in vivo assays of FTX alterations have been performed to reveal a complex integrated phenotype affecting cell growth, migration, and invasion. lncRNA FTX expression levels in gastric cancer cells and normal cells were measured by RT-PCR. Luciferase reporter assays, Western blotting, and many immune, microscopy technologies were utilized to investigate the expressions of FTX-related proteins and RNAs. The functional role of FTX in cell growth, migration, and invasion were observed in vitro and in vivo.

Results: We explored the underlying mechanisms of FTX in GC development, and the microRNAs' relationship with FTX. We found that FTX promoted cell proliferation, migration, and invasion as well as tumor growth, and this effect could latterly be attenuated by miR-144. ZFX attenuated the effects of FTX/miR-144 axis by sponging with miR-144.

Conclusion: In summary, the above results support a model in which the FTX/miR-144/ZFX act as important effectors in GC tumorigenesis and progression, indicating new therapeutic methods in GC.

Keywords: gastric cancer, LncRNA FTX, proliferation, invasion, miR-144/ZFX axis

Introduction

Gastric cancer (GC) is a member of the top causes of cancer-induced death. Due to its poor prognosis and high malignancy, there are around 700,000 people who die from GC every year.[1–3] Therefore, it is important and urgent to develop new and reliable diagnostic and therapeutic strategies. Accumulative evidences suggest that non-coding RNAs (lncRNAs) and microRNAs (miRNAs) play critical roles in tumor biology.[4–6] This combination has attracted lots of attention and has been proved to be a useful prognostic biomarker.[7]

MiRNAs have been unveiled and found to play important roles in human cancer.[9] MiR-144, an important member of microRNAs that are related to promotion/regulation in some cancers, is attracting more and more interest in the tumorigenesis of GC.[10] The down-regulation of miR-144 was found to suppress the tumor development. For example, in 2012, Iwaya has revealed that the down-regulation of miR-144 is related to the progression of colorectal cancer through the activation of mTOR signaling pathway.[11] The abnormal expression of miR-144 has been found to be related to the occurrence and development of gastric cancer.[11] Liu et al have found the clinical importance

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of miR-144-ZFX, which could inhibit the metastasis of gastric cancer, through the regulation of MET expression.[12] It functions through the changing of oncogenes' expressions, and the up-regulation or down-regulation of tumor mediators, which could affect the tumor cell proliferation and invasion. However, the biological molecular mechanism of miR-144 in GC is very complicated, and needs further investigations.

The participation and investigation of lncRNAs and microRNAs let us unveil the masks of many cancers' progression, invasion, and development. Only limited pairs of lncRNA and miRNA have been found in gastric cancers, such as miRNA-144+lncRNA-TUG1.[13] Most importantly, the clinical application for the combination of lncRNA FTX and miR-144 in gastric cancer also remains blank. Zinc finger protein X-linked (ZFX) is a zinc finger transcription factor encoded on the X chromosome. Previous studies have found that miR-144 could target ZFX and function as the cell growth inhibition factors.[14] In 2013, Wu et al revealed that ZFX expressions were greatly promoted in gastric cancer cell lines and tissues. The knockdown of ZFX could induce great cell apoptosis and cell cycle arrest.[15] However, as far as we know, there has been no report that has addressed the issue of lncRNA-FTX, miR-144, and ZFX in gastric cancer.

We aim to investigate the functions and associations between lncRNA FTX and miR-144/ZFX. To the best of our knowledge, we are the first to unveil the masks of these two RNAs in their combined working mechanism for gastric cancer's proliferation and invasion.

Firstly, we were focused to identify the relationship between the expressions of lncRNA-FTX and miR-144 in the same gastric cancer cells. Then, we wanted to know how miR-144 regulated FTX and their inner associations. Next, we hoped to investigate the in vivo and in vitro effects of FTX on the gastric cancer cells. Our results found that 1) FTX promoted cell proliferation, migration, and invasion, as well as tumor growth; 2) FTX promotion effect in cell proliferation could latterly be attenuated by miR-144; and 3) ZFX attenuated the effects of FTX/miR-144 axis by sponging with miR-144. With the above results, our investigations confirmed that the cross-talk among FTX, miR-144, and ZFX serve as critical roles in gastric cancer tumorigenesis and progression.

Methods and Materials
Study Patients' Subjects
Between 2010 and 2011, we obtained 38 pairs of gastric cancer tissues and their adjacent nontumor tissues from patients under surgery at The First Affiliated Hospital of Henan University of Science and Technology. These patients were diagnosed with gastric cancer based on histopathologic evaluation. Before the surgery, they have not received any local or systemic treatment. Immediately, all the collected tissue samples were snap frozen in liquid nitrogen and stored at −80 °C until further required. This study was carried with approval from The First Affiliated Hospital of Henan University of Science and Technology.

Cell Culture
We used the human gastric adenocarcinoma cell lines, including HS746T, BSG823, MGN28, 9811, BGC803, MGC803, and BGC823; and GSEI cell line regarded as normal gastric cell lines (control group). All the cells were purchased from Cell Bank of the Chinese Academy of Sciences (Shanghai, China). After receiving the cell lines, they were expanded and frozen immediately. For the experiment in each time, we would use a new aliquot and get passed every 3–4 months. Cells were cultured in DMEM, which was supplemented with 10% fetal calf serum, penicillin, and streptomycin. The culture conditions were set at 37 °C in an atmosphere containing 5% CO_2. Cells were transiently transfected with FTX overexpression vector, including 1) siRNA FTX, 2) miR-144 mimic, 3) miR144 inhibitor, and 4) ZFX pcDNA plasmid or ZFX shRNA (Genepharma, Shanghai, China). They were treated together with RNAiMax and Lipofectamine LTX with Plus Reagent (Thermo Fisher Scientific).

RNA Preparation and Detection
Firstly, we extracted total RNA through TRIzol reagent (Invitrogen, USA). We measured the quality of total RNA at a ratio of A260/A280 in 1% agarose gel electrophoresis. We used the GoScript Reverse Transcription System (Promega, Madison, Wis) to produce complementary DNA. Real-time RT-PCR was used to amplify the cDNA template, through the SYBR Premix Dimmer Eraser kit (TaKaRa, Dalian, China). Gene expression was normalized to GADPH or U6 expression. We performed the RT-PCRs and calculated their values by the $2^{-\Delta\Delta Ct}$ method.

Luciferase Reporter Assays
We synthesized fragment sequences and inserted them into the pGL3-basic vector (Promega). We verified all vectors through sequencing and evaluated the luciferase activities. The study was conducted in strict compliance with the manufacturer's instructions.

Cell Proliferation and Apoptosis Assays

We examined the cell proliferation capability via a Cell Proliferation Reagent Kit I (MTT; Roche Applied Science). Gastric cancer cells' cloning capability was monitored by colony formation assays.

In vivo Tumor Growth Assays

To perform the in vivo tumor growth assays, we obtained several 4 weeks' female athymic BALB/c nude rats. They were kept in specific pathogen-free environments and processed through manuals with approval from The First Affiliated Hospital of Henan University of Science and Technology Experimental Animal Care Commission. Next, we harvested sh-FTX, FTX overexpression vector, or empty vector transfected BGC823 cells. We injected 10^7 cells subcutaneously into a single side of each mouse to perform tumor formation assay, w. Every three days, we examined the tumor growth and calculated the tumor volumes using the equation of $V = 0.5 \times D \times d^2$ (V is volume; D is longitudinal diameter; and d is latitudinal diameter). We carried this study strictly following the protocols of Guide for the Care and Use of Laboratory Animals of the NIH (Bethesda, MD). This study was conducted with approval from the Ethics of The First Affiliated Hospital of Henan University of Science and Technology.

Western Blotting, Immunofluorescence Analysis, and Immunocytochemistry

To investigate the protein expressions, we performed Western blot, immunocytochemistry, and immunofluorescence analyses through standard protocols.

Quantification of FTX, ZFX, and miR-144 Expression Levels

We quantified the copy numbers of FTX, ZFX, and miR-144 transcripts through qRT-PCR assay as we described previously.

Statistical Analysis

We performed all the statistical analyses through SPSS 17.0 (Chicago, USA). We presented all data as the mean ± standard deviation from three groups of independent data. The differences between two groups were calculated through Student's *t*-test.

RNA Immunoprecipitation(RIP)

RNA Immunoprecipitation experiments were performed using the Magna RIP RNA-Binding Protein IPKit

(Millipore, Bedford, MA, USA) and the Ago2 antibody (2897; CellSignaling, Danvers, MA, USA). Eventually, purified RNAs in the precipitates were used to determine FTX expression.

Results

Up-Regulation of lncRNA-FTX Expression and Down-Regulation of miR-144 in Gastric Cancer Cell Lines

We firstly used qRT-PCR to detect LncRNA-FTX mRNA expressions in GC tissues and adjacent normal tissues. Figure 1A shows that the expression of LncRNA-FTX in GC tissues was up-regulated compared with those in adjacent normal tissues (p < 0.05). Figure 1B demonstrates the relative miR-144 levels in adjacent tissues and the cancer tissues. Figure 1C illustrates that there was a negative correlation between FTX expression and miR-144 level in GC tissues. Figure 1D shows that LncRNA-FTX expression in HS746T, BSG823, MKN28, N811, BGC803, MGC803, BGC823 cell lines were all up-regulated compared with GSE1 cell line. However, the poorly differentiated gastric cancer MGC803 and BGC823 cell lines had the lowest miR-144 expression, as shown in Figure 1E.

MiR-144 Negatively and Reciprocally Regulates FTX

Next, we aim to determine whether miR-144 negatively and reciprocally regulates FTX. We transfected miR-144 mimic/inhibitor into BGC803 and BGC823 cells. Figure 2A shows the expression of FTX mRNA levels in BGC803 and BGC823 cells transfected with pc-NC, pc-FTX, si-NC, or si-FTX. Figure 2C and D shows a significant suppression of FTX expression by miR-144 mimic. Conversely, Figure 2B illustrates that pcFTX reduced miR-144 expression while siFTX enhanced miR-144 expression. Then, we used the starBase, v2.0 program (http://starbase.sysu.edu.cn) to predict the microRNA sequence that could bind FTX. Figure 2E highlights the shared gene sequence between the target and microRNA. Next, we constructed the luciferase reporter and cotransfected it with miR-144 mimics into GC cells. Figure 2F shows that miR-144 mimics repressed luciferase activity FTX-WT. However, the luciferase activity of constructs containing mutant FTX has similar resultsto that from control cells. Figure 2G reveals RIP assay, and we found that FTX enrichment was highly elevated with input from miR-144, in contrast with IgG and Ago2. As a summary, our data showed a direct interaction between FTX and miR-144.
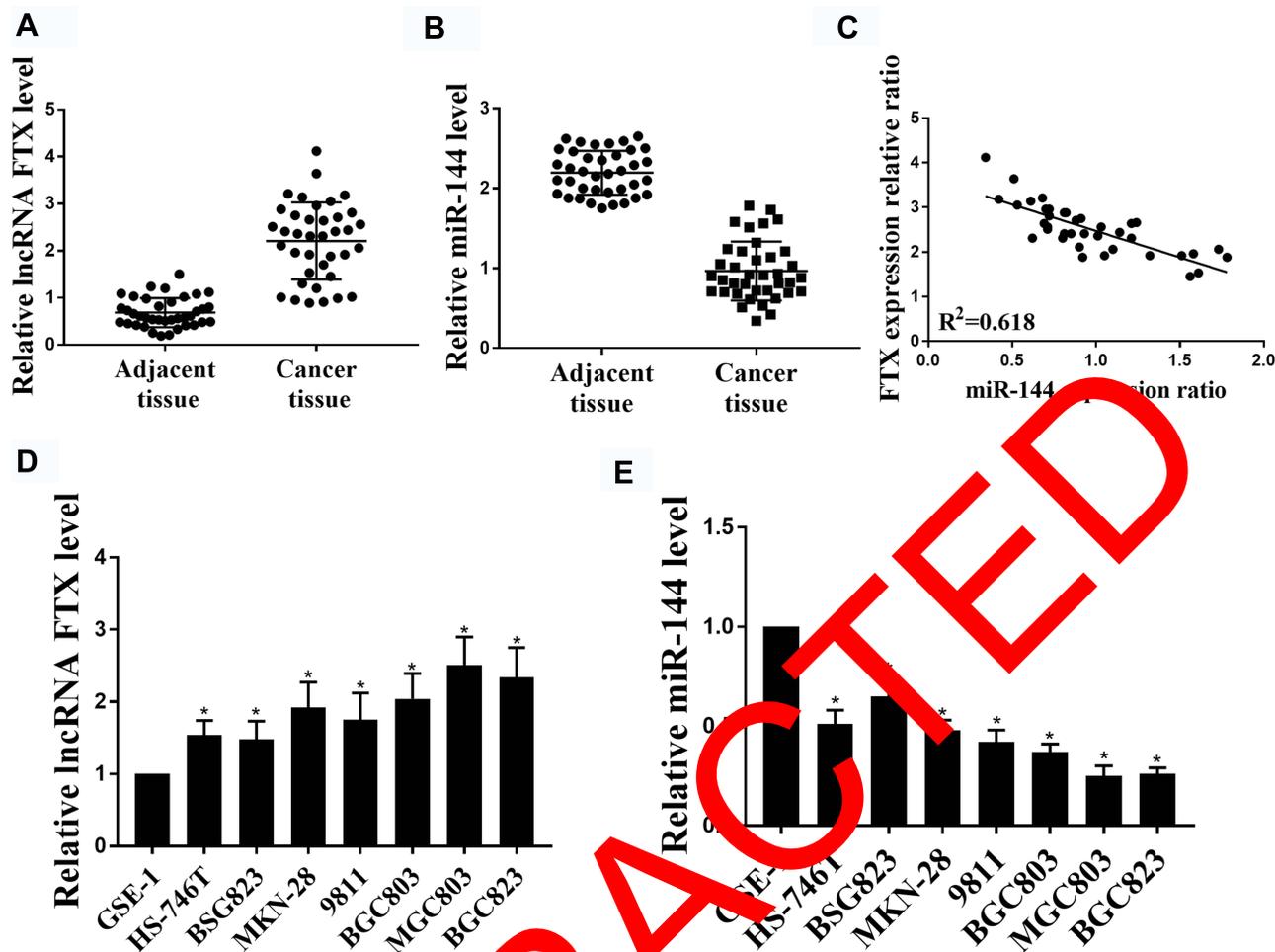
Figure I Expression of LncRNA-FTX and miR-144 in the tissues and gastric cancer cell lines. (A) Relative expression of LncRNA-FTX in GC tissues and adjacent normal tissues (n=38), P<0.05. (B) Relative expression of miR-144 in GC tissues and adjacent normal tissues (n=38), P<0.05. (C) The relationship of FTX and miR-144 expression in GC tissues. (D) The expression of FTX mRNA levels in GC cell lines, P<0.05. (E) The expression of miR-144 mRNA levels in GC cell lines, *p<0.05.

FTX Promoted Gastric Cancer Cell Tumor Growth in vivo

Figure 3A–C shows the results that tumors grown from FTX stable knockdown cells were smaller than tumors grown from control cells. Figure 3A displays representative images of mice bearing tumors from shNC and sh-FTX, and we found tumors from sh-FTX were much smaller. Figure 3B presents the tumor growth curves after injection, with sh-FTX growing much slower. Figure 3C shows the FTX levels in tumors from mice by qRT-PCR, and the sh-FTX group was lower. Conversely, Figure 3D–F illustrates that tumors grown from FTX-overexpressing cells were larger than tumors grown from control cells. Moreover, Figure 3G shows that the tumor tissues collected from the Ki67-positive cells had more

cells than that from FTX knockdown group, but the FTX overexpression group maintained more Ki67-positive cells than that from the control group. The above results confirmed that the knockdown of FTX inhibited gastric cancer cell tumor growth in vivo.

FTX Promoted Cell Proliferation, Migration, and Invasion

We performed the MTT and colony formation assays. Figure 4A and B shows the cell viability in 0, 2, 4, and 6 days, in BCG803 and BCG823, respectively. We found that pcFTX showed the highest viability while siFTX group showed the lowest value. Figure 4C displays the number of colonies in both BCG803 and BCG823, which had consistent results with Figure 4A and B. These results
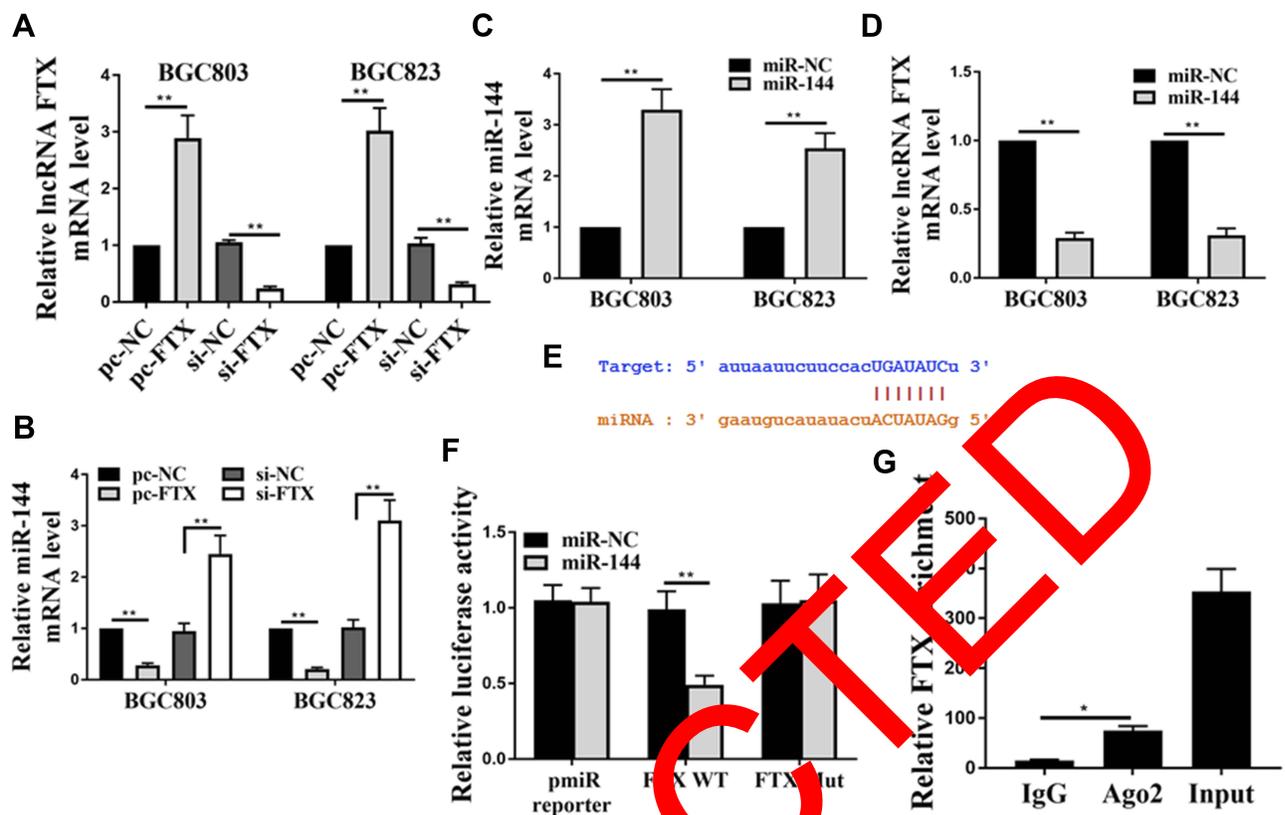
Figure 2 Reciprocal repression of FTX and miR144. (**A**) The expression of FTX mRNA levels in BGC803 and BGC823 cells transfected with pc-NC, pc-FTX, si-NC or si-FTX. (**B**) The expression of miR-144 mRNA levels in BGC803 and BGC823 cells transfected with pc-NC, pc-FTX, si-NC or si-FTX. (**C**) The expression of miR-144 mRNA levels in BGC803 and BGC823 cells transfected with miR-NC or miR-144 mimic. (**D**) The expression of lncRNA-FTX mRNA levels in BGC803 and BGC823 cells transfected with miR-NC or miR-144 mimic. (**E**) The putative target sequence for miR-144 on the 3′-UTR of FTX. (**F**) The luciferase activity was detected by luciferase reporter assay. (**G**) RIP assay reveals that FTX enrichment is highly elevated with input from miR-144, in contrast with IgG and Ago2. p<0.05; **p<0.01.

confirmed that the knockdown of FTX impaired gastric cancer cell proliferation, whereas FTX overexpression promoted cell proliferation in vitro. Furthermore, we performed transwell assays to check the role of FTX on GC cell migration ability. Figure 4D and E shows that the knockdown of FTX dramatically decreased cell migration, while FTX overexpression promoted cell migration. Figure 4F and G shows the cell apoptosis rate, and we noticed that si-FTX greatly elevated the apoptosis rate of BGC803 cells and BGC823 cells.

The Promotion of Cell Proliferation and Migration in GC Cells by FTX Were Attenuated by miR-144

Figure 5A–C shows the MTT and colony formation assays. We found that FTX overexpression promoted cell proliferation in vitro, and miR-144 mimic reduced cell proliferation. However, co-transfection miR-144 with pcFTX could reduce cell proliferation that was induced with FTX overexpression.

Furthermore, we performed transwell assays to investigate the effect of FTX, on which the gastric cancer cell migration ability was attenuated by miR-144 mimic. Figure 5D and E shows that the miR-144 mimic remarkably reduced cell migration, while FTX overexpression increased cell migration and this effected was attenuated by co-transfected miR-144 mimic. Figure 5F and G demonstrates cell apoptosis rate for cells transfected with control, pcFTX, miR-144, or pcFTX+miR144. It was obvious that miR-144 greatly elevated the cell apoptosis, but pcFTX attenuated this effect.

ZFX Is a Direct miR-144 Target

Figure 6A highlights the putative target sequence for miR-144 on the 3′-UTR of ZFX. ZFX was predicted to be a target of miR-144. It was reported that ZFX is a direct target of miR-144, and regulation is achieved through a single miR-144 binding sequence in its 3′UTR. Figure 6B and C shows that the reporter assays in 293T cells revealed miR-144-dependent repression of the
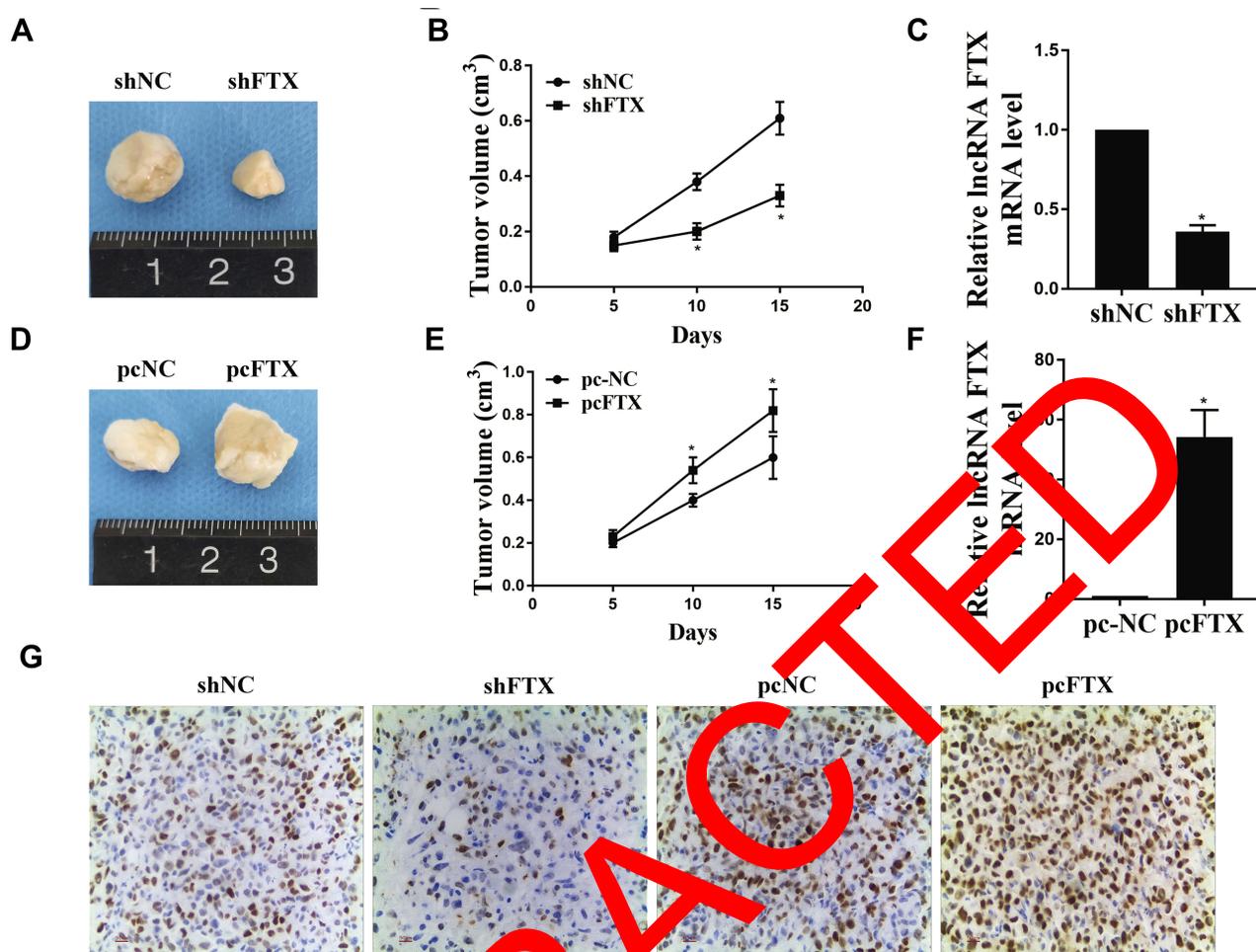
Figure 3 FTX promoted gastric cancer growth in vivo. (**A**) pictures of mice with tumors from shNC and sh-FTX. (**B**) Tumor growth curves. (**C**) FTX levels in tumors through qRT-PCR. (**D**) Mice tumors from pcNC and pcFTX groups. (E) Tumor growth curves after injections. (**F**) FTX levels from pcNC and pc-FTX groups. G, Ki-67 immunostaining of tumor samples from different groups. *p<0.05, n=6.

ZFX-WT 3′UTR. Consistent with the reporter assay, Figure 6D displays that ZFX protein expression was decreased in the presence of miR-144 mimic in GC cells. Conversely, ZFX levels increased after treatment with miR-144 inhibitor. These results indicate that ZFX is a direct target of miR-144. According to the ceRNA concept, lncRNA could act as ceRNA to exert its regulatory functions.[16] We next hoped to verify that FTX interacted with miR-144 to regulate the activity of ZFX. We examined the protein levels of ZFX by Western blot analysis. Figure 6E shows that the upregulation of FTX significantly promoted ZFX protein expression, which was significantly attenuated by the overexpression of miR-144. In contrast to ZFX, pcFTX suppressed the expressions of cyto c and casp3, but miR-144 attenuated this effect. The above results strongly indicated that FTX regulated ZFX expression in a miR-144-dependent manner.

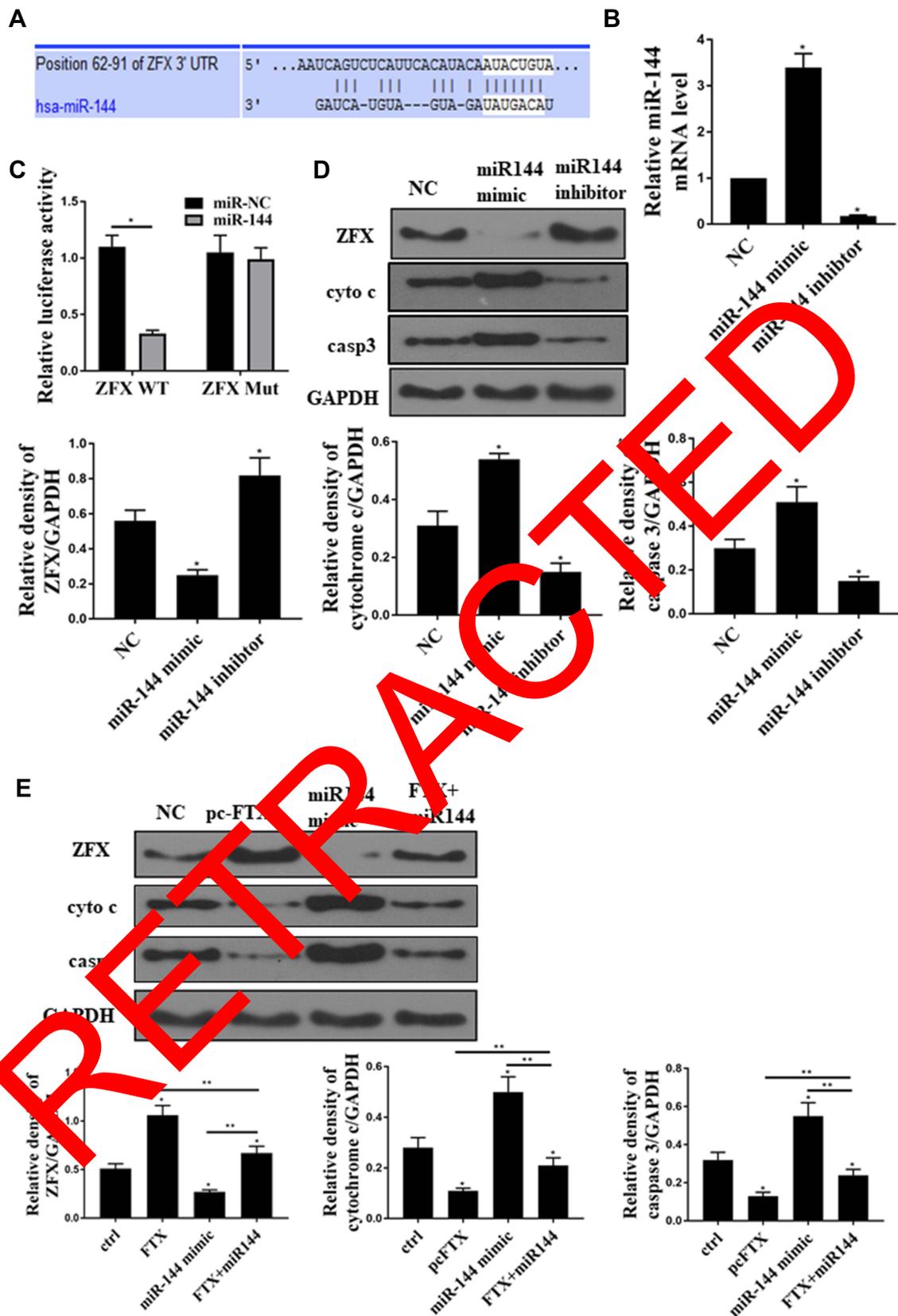## ZFX Attenuated the Effects of FTX/Mir-144 Axis in GC Cells

In order to investigate the associations between ZFX and FTX/miR-144, we designed experiments targeting to reveal the roles of ZFX, FTX, miR-144, and ZFX+miR-144 in the cell viability, cell colony, cell proliferation, and cell apoptosis. Figure 7A shows the expression of ZFX mRNA level. We found that ZFX-pcDNA3 had the highest expression level, but shZFX had a quite low level. Figure 7B and C shows the MTT assay results. Figure 7B reveals that pcFTX had the highest cell viability, but pcFTX+siZFX lowered the effect. Figure 7C shows that miR-144+pcZFX lowered the cell viability that was promoted by pcZFX. Figure 7D and E displays the colony formation assays. The numbers of colonies were in consistent with the findings in cell viability. Figure 7F and G shows the results of transwell assays. The above results show that siZFX partially reversed the FTX-induced cell proliferation and
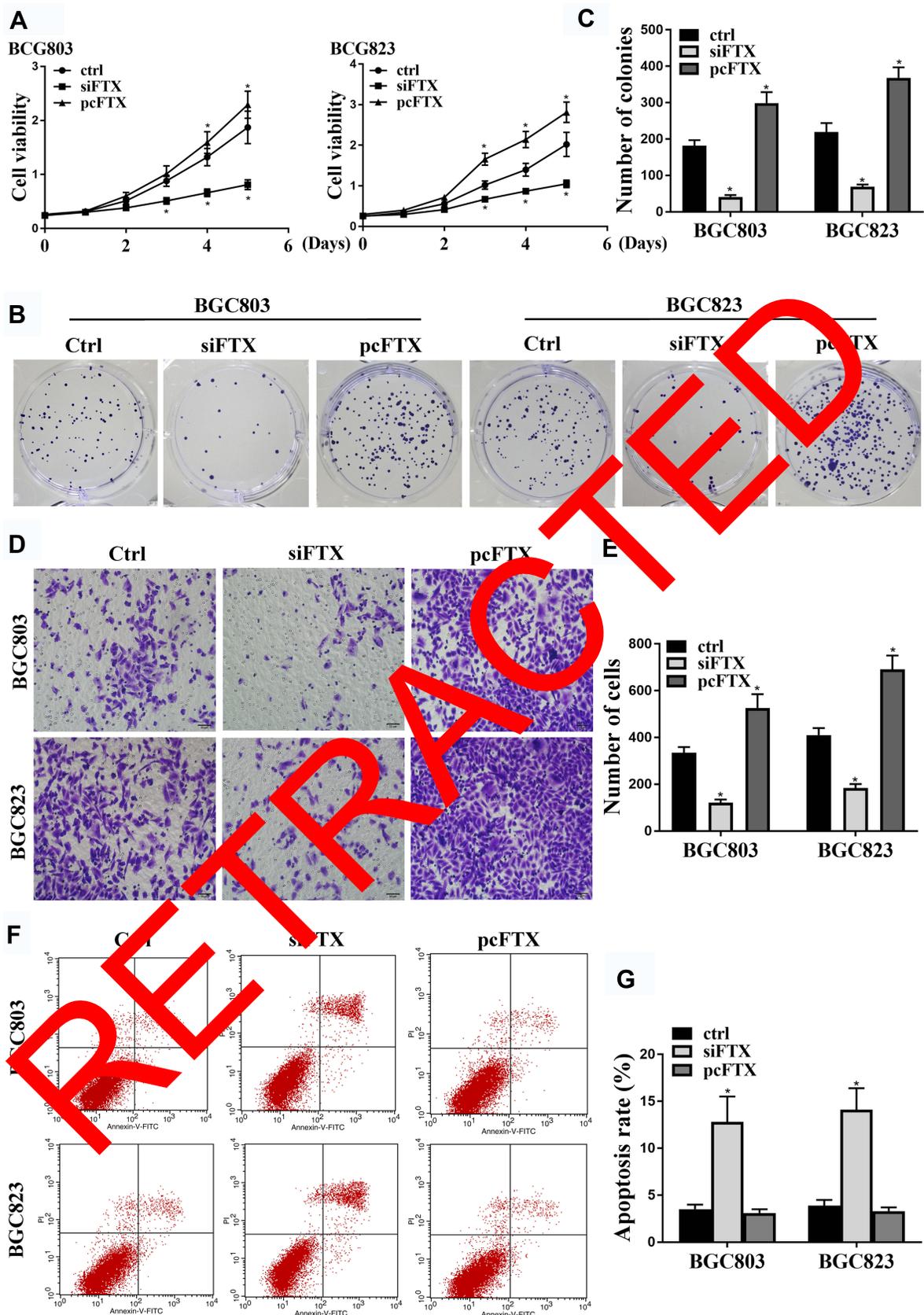
Figure 4 FTX promoted cell proliferation, migration, and invasion. (**A**) MTT assays for cell viability of si-FTX or pc-FTX–transfected GC cells. (**B** and **C**) Colony formation assays of si-FTX or pc-FTX–transfected cells. (**D** and **E**) Transwell assays of si-FTX or pc-FTX–transfected cells on GC cell migration. (**F** and **G**) Cell apoptosis rate for BGC803 cells and BGC823 cells transfected with control, siFTX or pcFTX. *p<0.05; n = 3.
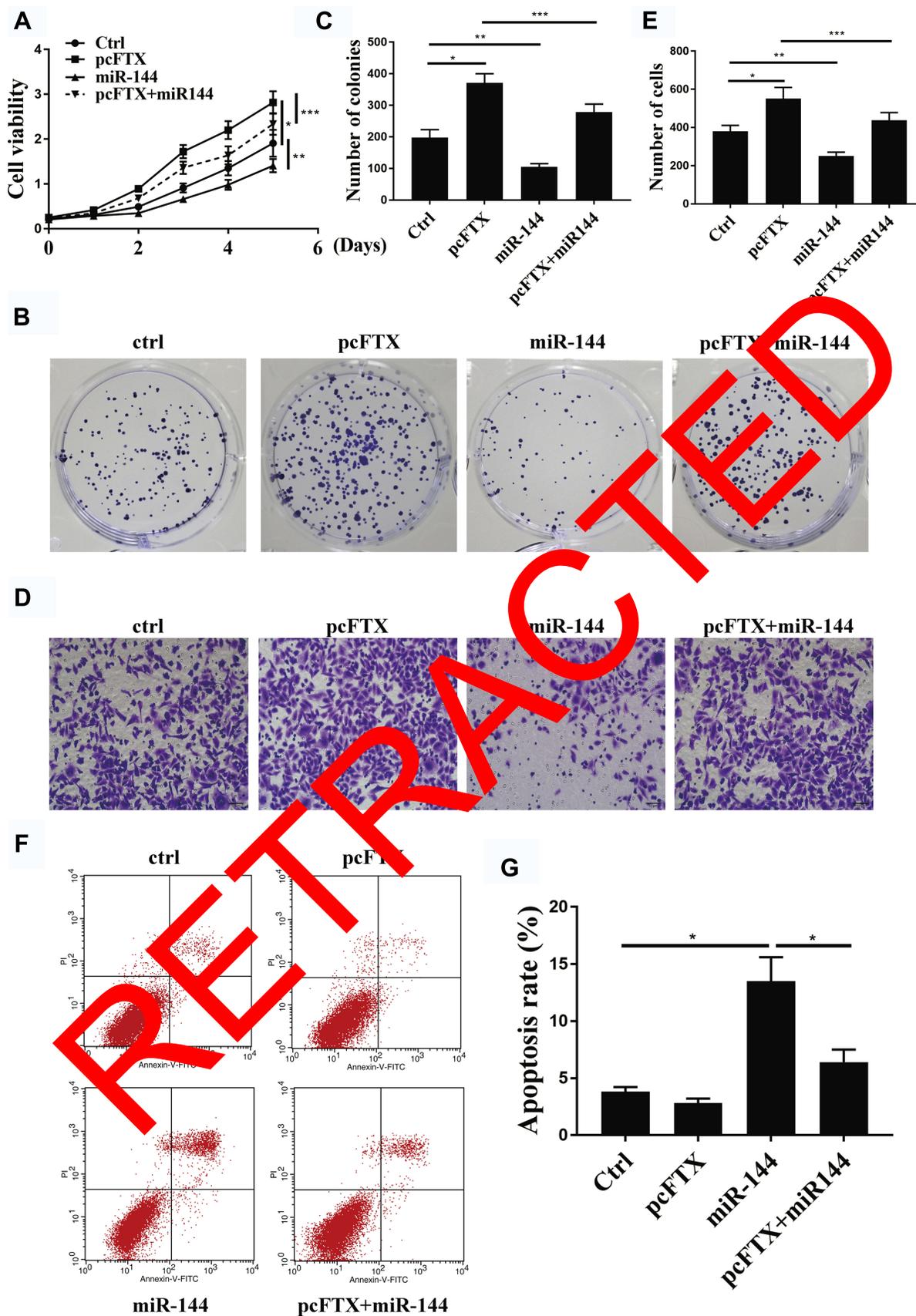
Figure 5 FTX promoted cell proliferation, migration, and invasion in GC cells that were attenuated by miR-144. (**A**) MTT assay. (**B** and **C**) Colony formation assays. (**D** and **E**) Transwell assays. (**F** and **G**) Cell apoptosis rate for cells transfected with control, pcFTX, miR-144 or pcFTX+miR144. *p<0.05, **p<0.05, ***p<0.05; n = 3.

A

Position 62-91 of ZFX 3' UTR	5' ...AAUCAGUCUCAUUCACAUACAAUACUGUA...
	III III III I IIIIIIII
hsa-miR-144	3' GAUCA-UGUA---GUA-GAUAUGACAU

Figure 6 ZFX was a direct miR-144 target. (**A**) The putative target sequence for miR-144 on the 3′-UTR of ZFX. (**B**) RT-PCR detected the expression of miR-144 mRNA level. (**C**) The luciferase activity detection by luciferase reporter assay. (**D**) Western blot assay for the determination of the ZFX protein expression. (**E**) Western blot assay to determine the protein expressions of ZFX, cyto c, casp3, and GAPDH. *p<0.05; **p<0.05; n = 3.
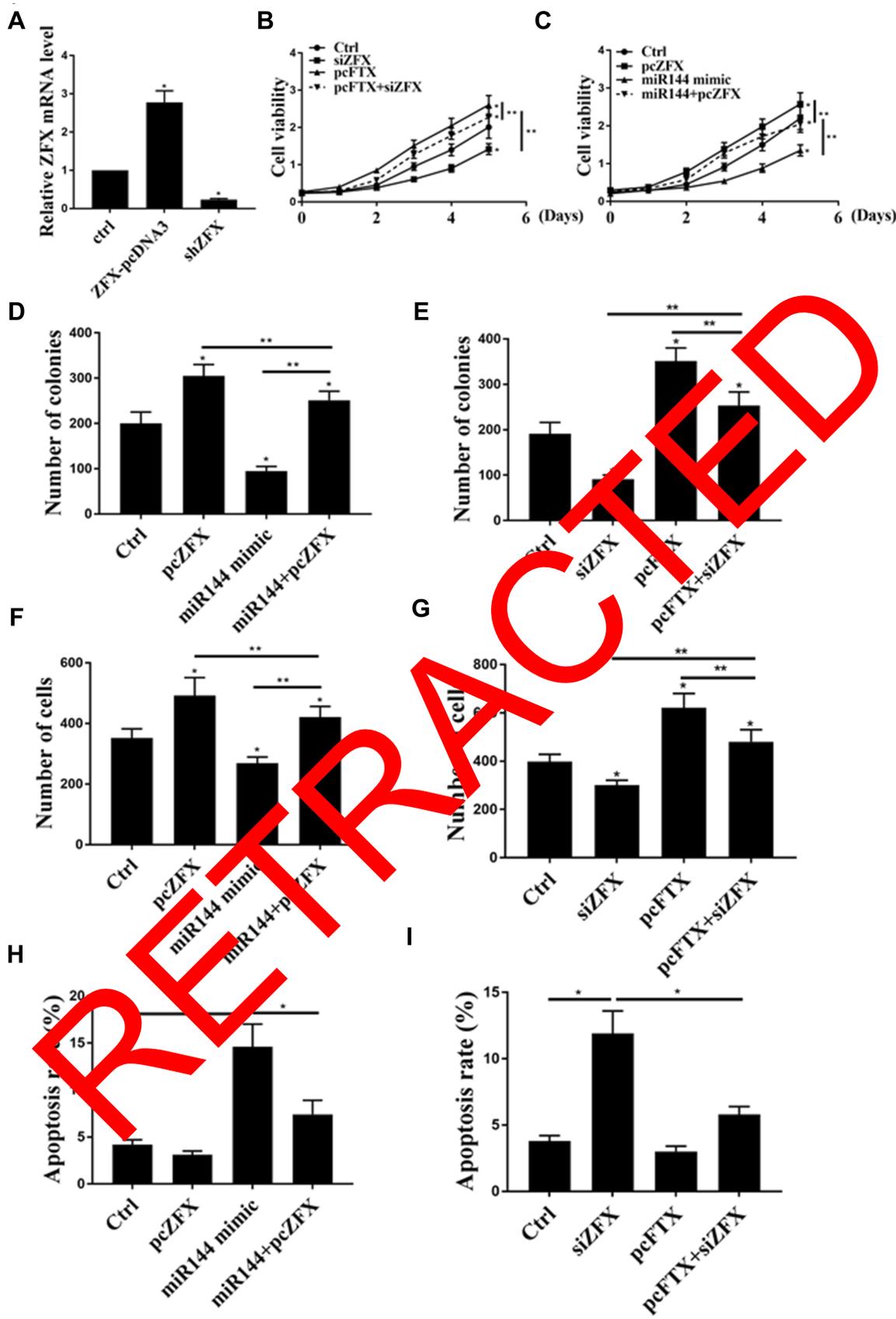
Figure 7 ZFX attenuated the effects of FTX/miR-144 axis in GC cells. (**A**) The expression of ZFX mRNA level. (**B** and **C**) MTT assay for the cell viability evaluation. (**D** and **E**) Colony formation assays. (**F** and **G**) Transwell assays. I. Apoptosis rate of cells transfected with control, siZFX, pcFTX, or cFTX+siZFX. *p<0.05, **p<0.05; n=3.

migration, and pcZFX partially reversed the effects of miR144 on cell proliferation and migration. Figure 7H and I illustrates that siZFX could promote the cell apoptosis, but FTX attenuated this effect.

Discussion

In recent years, there have been advancement and development in the diagnostics and treatment of gastric cancer.[17–19] However, the poor prognosis for gastric cancer still makes it rank as one of the most common death-leading diseases. It is critical to develop novel therapy strategies to enable more possibilities for GC patients. Accumulative evidences suggest that non-coding RNAs (lncRNAs) and microRNAs (miRNAs) could work together and increase the genetic functions in tumor biology.[4–6]

Previous reports have investigated many types of lncRNAs and found that each type is specific for different kinds of cancers.[20] Recent findings have revealed that lncRNA FTX could probably act as useful prognostic markers for multiple cancers.[21,22] Among all miRNAs, the role and relationship of miR-144 in the tumorigenesis has attracted lots of attention. In their results, miR-144 was working as a tumor suppressor.[23,24] However, the involvement of lncRNA-FTX and miR-144 has been remained to be blank in gastric cancer. Herein, we aim to identify their inner associations in the proliferation and invasion in GC developments.

Firstly, we aim to unveil the expression of these two RNAs, lncRNA-FTX and miR-144, in gastric cancer cells. Previous studies have discussed that the expression of FTX was usually up-regulated, while the expression of miR-144 was down-regulated during the growth and proliferation of cancer cells.[1] In 2016,Liu et al have found that FTX's up-regulation could promote the cell proliferation in hepatocellular carcinoma.[21] Although this study was analyzing the sponging effect between FTX with miR-545, it gives a clue about the possibility of some other microRNAs in the gastric cancer study, such as miR-144. MiR-144 was found to have down-regulation in gastric cancer..Liu has reported that this microRNA is closely related to gastric cancer, and could inhibit the metastasis through the targeting of MET expressions.[12] Our results further confirmed these phenomena. The qRT-PCR detection of lncRNA-FTX mRNA expressions shows that LncRNA-FTX expression in HS746T, BSG823, MKN28, 9811, BGC803, MGC803, BGC823 cell lines were all up-regulated, while miR-144 were all down-regulated. The above analysis and results unveiled the controversial relationship between FTX and miR-144.

Previous studies have shown that miR-144 could negatively regulate some specific lncRNA. For example, lncRNA TUG1 has been widely reported tumorigenesis, which regulated the tumors by targeting miR-144, reported by Cai in 2015,[25] Ji in 2016,[26] and Lv in 2018.[27] In addition, lncRNA FTX could be regulated by some specific microRNAs, such as miR-545, reported by Zhao in 2014.[8] Our studies have determined whether miR-144 negatively and reciprocally regulates FTX. We found the significant suppression of FTX expression by miR-144 mimic. Conversely, pcFTX reduced miR-144 expression. The prediction of sequence targeting from online database and confirmed that there was a direct interaction between FTX and miR-144.

FTX has been found to promote many types of cancer cell tumor growth in vivo. For example, in 2016, Liu has found that FTX could promote the cancer cell growth in hepatocellular carcinoma.[21] In 2018, Yang found that lncRNA FTX could sponge miR-215, and thus promote the colorectal cancer progression.[28] However, the function of FTC in gastric cancers has remained largely unknown. Our study bridges this gap. We monitored the tumor growth from FTX stable knockdown cells. The tumors are smaller than tumors grown from control cells. Moreover, the tumor tissues collected from the FTX knockdown group had fewer Ki67-positive cells, whereas the FTX overexpression group had more Ki67-positive cells than the control group. The above results confirmed that the knockdown of FTX inhibited gastric cancer cell tumor growth in vivo.

As far as we know, we are the first to identify that FTX-promoted cell proliferation, migration, and invasion in gastric cancer cells. Our MTT and colony formation assays have confirmed the cell viability in various days. This finding together with the previous reported could further prove the functions of lncRNA FTX in various types of cancers.

In 2017, Ye has reported that miR-144 could attenuate long non-coding RNA bladder cancer association transcript 1, and thus promoted the proliferation, migration, and invasion of non-small cell lung cancer.[29] This is an evidence that the sponging effect between FTX and miR-144 could also contribute to other cancer cells. The MTT and colony formation assays found that FTX overexpression promoted cell proliferation in vitro, and miR-144 mimic-reduced cell proliferation. However, co-transfection miR-144 with pcFTX could reduce cell proliferation that was induced with FTX

overexpression. These results could support our suspect that sponging effect through FTX and miR-144 could work as promotion factors in gastric cancer development.

Our results further identify that ZFX is a direct miR-144 target. It was reported that ZFX is a direct target of miR-144, and regulation is achieved through a single miR-144 binding sequence in its 3′UTR.[14,30,31] In 2012, Akiyoshi has found the role of miR-144-ZFX axis in the dissemination of tumor cells.[30] In 2013, Zha has revealed the importance of miR-144-ZFX pathway in the non-small cell lung cancer regulation.[14] The MTT assay results had revealed that pcFTX had the highest cell viability, but pcFTX+siZFX lowered the effect. MiR-144+pcZFX lowered the cell viability that was promoted by pcZFX. The numbers of colonies were in consistent with the findings in cell viability. The above results confirmed that siZFX partially reverse the FTX–induced cell proliferation and migration, and pcZFX partially reversed the effects of miR144 on cell proliferation and migration. As a sum-up, ZFX attenuated the effects of FTX/miR-144 axis in GC cells.

ZFX has a group of isoforms, and some of them were reported to participate in the progression of cancer cells. For instance, Rahmati reported the expression profiles of ZFX isoform3/variant 5 in gastric cancer tissues and its association with tumor size.[32] Here in this paper, we did not investigate the details in the isoforms of ZFX. In the future, we are planning to study the effects of different ZFX isoforms in the development of gastric cancer.

Conclusion

In summary, the above results support a model in which the FTX/miR-144/ZFX cross-talk serves as critical effectors in gastric cancer tumorigenesis and progression, suggesting new therapeutic directions in gastric cancer.

Ethics Approval and Consent to Participate

The present study was approved by the Ethics Committee of The First Affiliated Hospital of Henan University of Science and Technology. The research has been carried out in accordance with the 1964 Helsinki Declaration and its later amendments or comparable ethical standards. All applicable institutional guidelines for the care and use of animals were followed.

Informed Consent

All patients and healthy volunteers provided written informed consent prior to their inclusion within the study.

Disclosure

The authors report no conflicts of interest in this work.

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