OncoTargets and Therapy

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ORIGINAL RESEARCH

RETRACTED ARTICLE: Long noncoding RNA UCA1 targets miR-582-5p and contributes to the progression and drug resistance of bladder cancer cells through ATG7-mediated autophagy inhibition

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Background: Rently, the incidence of bl der ca has bee on the rise. Accumulating researches have been conducted to clari molecular ch isms and potential therapeutic targets of bladder cancer. The presen study a s to explore the regulatory mechanism of the urothelial carcinoma-associated 1 (UCA1)-miR- 2-5p-ATG7 axis in bladder cancer.

Methods: Quantitative real me polymerase chain eaction was used to detect mRNA level. Relative protein expressio was detected western blot. wound healing assay and transwell were used to determine mig tion and inv ion of cells. in addtion, luciferase reporter assay and immunohisto hemistry we erfor d.

Results: UCA1 xpre n was upregulated in bladder cancer tissues and cells, while the depletion of UCA1 y shR A1 ted in the suppression of cell proliferation, invasion, migration, a resista e. Further studies demonstrated that UCA1 could directly interact with mi 582-5p, nd that here was an inverse correlation between miR-582-5p and UCA1. In a ition, w d that ATG7 is a target of miR-582-5p and can be downregulated by either miR 5p overexpression or UCA1 knockdown. In particular, the autophagy is reduced when U 1 shRNA is introduced. Moreover, the in vivo experiment further demonstrated the contributio of UCA1 in bladder cancer including tumor growth, invasion, and migration, and A1 knockdown can inhibit the aforementioned activities.

Co lusion: These results provided evidence for a novel UCA1 interaction regulatory network in bladder cancer, that is, UCA1-miR-582-5p-ATG7-autophagy axis. Our study provides a new insight into the treatment of bladder cancer.

Keywords: lncRNA UCA1, miR-582-5p, bladder cancer, migration and invasion, resistance

Introduction

Bladder cancer ranks ninth among all cancers in the world, with an estimated 430,000 new cases in 2012.[1] More than 60% of all bladder cancer cases and half of all the 165,000 bladder cancer deaths occur in the less developed countries.[1,2] There exists an obvious male predominance, and the bladder cancer cases in men counts three-quarters.[3] Approximately 30% of primary bladder cancers are muscle invasive with high risk of death from distant metastases before they were diagnosed, and thus suggesting a poor prognosis; in addition, 70% of cancers are non-muscle invasive tumors with high recurrence after surgical excision.[4] Because the effective strategies for early detection of bladder cancer remain elusive, the recurrence and mortality rates are high even though the risk factors for bladder cancer have been identified.[4] Thus, it is practical to explore a

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new biomarker for detection and develop an understanding of the molecular mechanism of the target gene for bladder cancer.

One long noncoding RNA that has attracted significant attention is urothelial carcinoma-associated 1 (UCA1), which is highly expressed in tumor tissue, and therefore can be related to clinical parameters.[5] It may regulate tumor cell proliferation, invasion, apoptosis, and migration, so UCA1 can be applied in clinical prognosis and targeted therapy.[5] Moreover, UCA1 is significantly upregulated in most tumor cancer cells, including bladder cancer.[6] A previous study reported that UCA1 may have a diagnostic value in bladder cancer.[7] A lot of researches have revealed the tumorigenic role and the regulatory mechanism in bladder cancer. For example, UCA1 was reported to increase the chemoresistance of bladder cancer cells by regulating Wnt signaling.[6] In addition, UCA1 was reported to enhance the proliferation, invasion, migration, and reduce apoptosis of bladder cancer cells.[8,9] A previous study demonstrated that UCA1 can interact with variety of miRNAs to modulate cancer development, such as miR-204-5p,[10] miR-143,[11] miR-216b,[12] or miR-193a-3p.[13] Interestingly, miR-582-5p has been reported to inhibit tumor proliferation in bladder cancer.[14] Meanwhile, upregulation of miR-582-5p was reported to regulate cell proliferation and apoptosis by targeting AKT3 in human endometrial carcinoma,[15] among others. According to the articles, miR-582-5p may act as a suppressor in bladder cancer.

Autophagy is a constitutively active evolutionarily conserved physiologic catabolic process that is maintained at a basal rate by cells throughout the body. Accumulating studies showed that autophagy protects some cancers against anticancer treatments. The importance of autophagy has been reported in bladder cancer. Bladder cancer cell lines exhibited activated autophagic flux compared with SV-HUC-1 cells.[17] In addition, the anticancer role of autophagy inhibition in bladder cancer progression was demonstrated in known bladder cancer cell lines SV-HUC-1, RT-4, and 5637.[17] Autophagy inhibition with bafilomycin A1 or knockdown of autophagy related protein 7 (ATG7) resulted in cell death in those cell lines.[17] Moreover, inhibition of autophagy in hepatocellular carcinoma has been reported to be associated with poor prognosis and promote tumorigenesis.[18]

In the present study, we showed that UCA1 was overexpressed in bladder cancer and it may play an oncogenic role in promoting malignancy of bladder cancer cells, including proliferation, promotion, and autophagy activation. Importantly, our mechanistic analysis revealed that UCA1 might function as an endogenous sponge to upregulate the expression of ATG7 through directly interacting and inhibiting the expression of miR-582-5p. Our present results provide a novel UCA1-miR-582-5p-ATG7 axis in regulation of bladder cancer, shedding new light on the diagnosis and treatment of bladder cancer.

Materials and methods

Tissue samples

Bladder cancer tissues and adjacent normal specimens were collected after obtaining written informed consent from 40 patients undergoing excision at the Renmin Hospital of Wuhan University. The details of tissues from 40 patients are summarized in Table 1. The study was approved by the Research Ethics Committee of the Renmin Hospital of Wuhan University. Our study was in accordance with the Declaration of Helsinki.

Cell culture

The human bladder cancer cell lines (SV-HUC-1, HT-1376, T24, J82, 5637, EJ cells) were purchased from the American type culture collection (ATCC, Manassas, VA, USA). HT-1376, J82, and EJ cells were grown in Eagle's Minimum Essential Medium (Gibco, Carlsbad, CA, USA) complemented with 10% FBS (Life Technologies, Grand Island, NY, USA). SV-HUC-1, T24, and 5637 cells were grown separately in ATCC-formulated F-12K medium (Gibco), McCoy's 5a Medium Modified (Gibco), RPMI-1640 Medium (Gibco) complemented with 10% FBS (Gibco), and all cell lines were incubated at 37°C in a 5% CO_2 incubator.

Quantitative real-time polymerase chain reaction

Total RNA was extracted from cells or tissues using TRIzol reagent (Invitrogen, Carlsbad, CA, USA) according to the

Table 1 Details of tissues from patients

Variables	(N=40)
Gender	
Male	30
Female	10
Age (years)	
<50	28
≥50	12
Tumor size	
<5 cm	15
≥5 cm	25
Recurrence	
Absent	9
Present	31
Muscle invasive or not	
NMIBC	13
MIBC	27
Histological grade	
Well/moderately	18
Poorly/others	22

Abbreviations: MIBC, muscle-invasive bladder cancer; NMIBC, non-muscle-invasive bladder cancer.

Table 2 Primers and shRNAs used in this study

Gene	Sequence (5′–3′)	Experimental use
UCA1	CTCTCCATTGGGTTCACCATTC GCGGCAGGTCTTAAGAGATGAG	qPCR
GAPDH	ACCACAGTCCATGCCATCAC TCCACCACCCTGTTGCTGTA	qPCR
ATG7	CTGCCAGCTCGCTTAACATTG CTTGTTGAGGAGTACAGGGTTTT	qPCR
UCA1 shRNA scramble	GatccTTCTCCGAACGTGTCACGTttcaagaga ACGTGACACGTTCGGAGAAttttttggaaa	RNA interference
UCA1 shRNA	GatccGTTAATCCAGGAGACAAAGAttcaagagaTCTTTGTCTCCTGGATTAACtttttggaaa	RNA interference

Abbreviations: qPCR, quantitative polymerase chain reaction; ATG7, autophagy-related 7.

manufacturer's protocol. Equal amounts of RNA were reversely transcribed to cDNA with SuperScript Reverse Transcriptase Kit (Vazyme, Nanjing, China). Then, mRNA level of miR-582, ATG7, and UCA1 was analyzed by SYBR Green PCR Master Mix (Vazyme) in a Fast Real-time PCR 7300 System (Applied Biosystems, Foster City, CA, USA). The original Ct values were adjusted to GAPDH. Data were analyzed according to the comparative Ct method also referred to as the $2^{-\Delta\Delta CT}$ method. The expression level of miR-582-5p was performed using miR-582-5p-specific primer. Primers were designed and are shown in Table 2. miR-582 was normalized to snRNA U6, ATG7 and UCA1 were normalized to GAPDH.

Cell transfection

UCA1 small hairpin (shRNA)/negative control shRNA plasmids were purchased from Genechem, Shanghai, China. The miR-582-5p inhibitors used in the experiment were designed and synthesized by Ribobio, Guangzhou, China. The T24 and 5637 cells were seeded in a six-well plate at a density of 1×10^4 cells/mL. After incubation for 24 hours, UCA1 shRNA, miR-582-5p mimic, and miR-582-5p inhibitor were transfected into two cell lines by using Lipofectamine®3000 (Invitrogen) according to the instructions.

Cell growth analysis

T24 and 5637 cells were divided into four groups: control, UCA1 shRNA, miR-582-5p inhibitor, and shRNA+inhibitor. Cell growth was detected by Cell Counting Kit-8 (CCK-8; Beyotime Institute of Biotechnology, Shanghai, China). Each group of cells (at a density of 2×10^3) was cultured on a 96-well plate in 200 µL medium for 24 hours. Then, the medium was replaced by fresh medium and incubation was continued for 24, 48, and 96 hours, respectively. Then, the medium of each well was replaced with 100 µL fresh media containing 10 µL CCK-8 reaction solution and incubated for 2 hours at 37°C, and then the absorbance were measured using a microplate reader (Thermo Fisher Scientific, Inc., Waltham, MA, USA) at 490 nm.

Western blot

Cells were lysed with RIPA Lysis Buffer (Beyotime Institute of Biotechnology). Equivalent amounts of protein sample were separated by 10% SDS-PAGE and transferred to PVDF membranes (Millipore, Billerica, MA, USA). After incubating with 5% skim milk in TBST, the membranes were incubated with rabbit primary antibodies (Abcam, Cambridge, MA, USA) against ATG7 (ab133528), LC3A/B (ab128025), P62 (ab155686), multidrug resistance protein 1 (MRP1, ab3368), lung resistance-related protein (LRP, ab92544), GST (ab19256), and Topoisomerase-II (TOPO-II, ab52934), respectively, at 4°C overnight. Then, they were incubated with HRP-conjugated secondary antibodies (ab6721) at room temperature for 1.5 hours. Finally, the blots were visualized by electrochemiluminescence (ECL) and detected using a ChemiDoc XRS imaging system. GAPDH was used as a loading control.

Migration and transwell invasion assay

T24 and 5637 cells were divided into four groups: control, UCA1 shRNA, miR-582-5p inhibitor, and shRNA+inhibitor. The confluent cell monolayer was scraped with a pipette tip in the middle of the well. After 24 hours incubation, the cell migration was captured with a DM2500 bright field microscope (LEICA, Wetzlar, Germany), and the migration distance was measured by the ImageJ software.

The invasion capacity of T24 and 5637 cells was performed using Transwell invasion assay. Briefly, cells transfected with miR-582 mimics were seeded in the upper chamber in DMEM supplemented with 0.1% FBS, and the lower chamber was filled with DMEM supplemented with 10% FBS. After 24 hours incubation, the bottom cells were fixed in 95% ethanol, stained with hematoxylin, and the number of invaded cells was counted by using a DM2500

bright field microscope at 400× magnification on 10 random fields in each well.

RNA overexpression and knockdown

For ATG7 overexpression, ATG7 mRNA sequence was synthesized and subcloned into the mammalian expression vector pcDNA3.1 (Invitrogen), and the empty pcDNA3.1 vector served as a negative control. shRNA against UCA1 (UCA1 shRNA) were obtained from Ribobio. miR-582-5p mimic, mimic mock, and miR-582-5p inhibitor were purchased from Ribobio. Plasmid, shRNA, or mimic transfection was performed by using Lipofectamine3000 reagent (Invitrogen) according to the manufacturer's protocol.

Luciferase reporter assay

The 3′-UTR of ATG7 or UCA1 mRNA containing predicted miR-582 binding sites or mutant binding sites was PCR-amplified and inserted into pMIR-control vectors. For luciferase reporter assays, wild-type or mutated versions of reporter plasmids, miR-582 mimics, and pcDNA3.1-ATG7 were transfected into HEK293 cells by Lipofectamine3000 reagent. At 48 hours after transfection, the luciferase activities were measured with a dual luciferase reporter assay system (Promega, Madison, WI, USA) according to the manufacturer's instructions.

Animal experimental protocols

Four-week-old BALB/c nude mice (male) were obtained from the Experimental Animal Center of Wuhan University (China). All animal experiments were conducted with approval from the National Institute of Health's Guidelines for the Care and Use of Laboratory Animals and the Animal Care and Research Committee of Wuhan University. Mice were housed under standard conditions (25°C±2°C, 70% humidity and 12-hour light–dark periods) and fed on regular sterile chow diet and water ad libitum. A total of 20 animals were equally divided into two groups. One group was injected subcutaneously with 5×10^6 T24 cells which have been transfected with UCA1 shRNA, and another group was injected with scrambled T24 cells. Tumor volumes were measured every 5 days for 30 days. After all mice were sacrificed, tumor volume was calculated by the formula length × width^2 ×0.5.

Immunohistochemistry

The paraffin-embedded tumor sections were stained for anti-Ki67, anti-PCNA, anti-MMP-9, and anti-VEGF (Abcam). Sections (2 μm) were deparaffinized and pretreated with citrate buffer using a heat-induced epitope retrieval protocol. Endogenous peroxidase was blocked with 20% hydrogen peroxide for 15 minutes at room temperature followed by incubation with anti-Ki67, anti-PCNA, anti-MMP-9, and anti-VEGF for 30 minutes, respectively. A biotinylated goat anti-mouse immunglobulin G secondary antibody (Dako, Glostrup, Denmark) was then applied to each slide for 30 minutes. After washing in Tris-hydrochloric acid buffer, the slides were incubated with peroxidase-conjugated streptavidin complex reagent (Dako) and developed with 3,3′-diaminobenzidine for 5 minutes. The slides were counterstained and dehydrated.

Bioinformatics dataset

Prediction of the interaction between miR-582 and ATG7 or UCA1 was performed using miRanda and TargetScan available online.

Statistical analysis

Data were analyzed by GraphPad Prism software, and the results were expressed as mean±SD. The statistical significance of the studies was analyzed using one-way ANOVA. The difference was considered significant at $P<0.05$ or $P<0.01$.

Results

UCA1 and miR-582-5p are dysregulated in human bladder cancer and miR-582-5p may be a target of UCA1

To investigate the role of UCA1 and miR-582-5p in bladder cancer progression, we determined the expression level of UCA1 and miR-582-5p in bladder cancer tissue and adjacent healthy tissue. As a result, UCA1 was highly expressed in cancer tissue and miR-582-5p was lowly expressed compared with healthy tissue (Figure 1A and B). As shown in Figure 1C, UCA1 and miR-582-5p showed reversed expression in bladder cancer tissues. In addition, quantified expression of UCA1 and miR-582-5p was detected in human normal cell SV-HUC-1 and bladder cancer-derived cells HT-1376, T24, J82, 5637, and EJ by quantitative PCR (qPCR). We found that the expression level of UCA1 was significantly higher than that in normal SV-HUC-1 cells, including HT-1376 ($P<0.05$), J82 ($P<0.05$), and EJ ($P<0.05$), especially T24 and 5637 ($P<0.01$) cells (Figure 1D), while the expression level of miR-582-5p showed reversed result (Figure 1E). Since the inverse expression trend between UCA1 and miR-582-5p was observed in

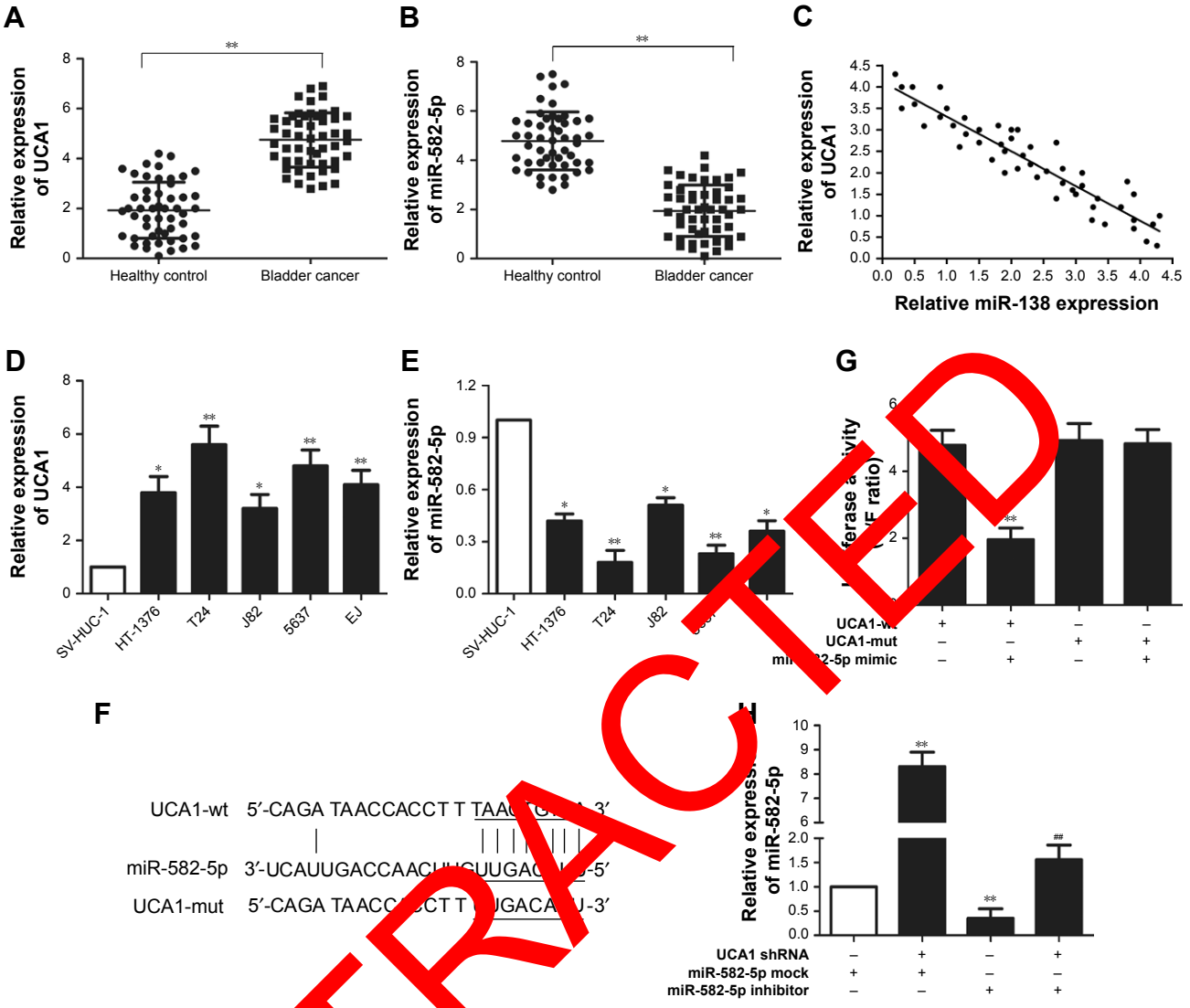

Figure 1 UCA1 and miR-582-5p are dysregulated in human bladder cancer and miR-582-5p may be a target of UCA1.

Notes: (**A**, **B**) qRT-PCR analysis of (**A**) UCA1 and (**B**) miR-582-5p expression levels in tumor tissues and adjacent normal tissues from bladder cancer patients. $^{**}P<0.01$ compared with healthy control. (**C**) Correlation between the UCA1 and miR-582-5p expression level. (**D**, **E**) qRT-PCR analysis of (**D**) UCA1 and (**E**) miR-582-5p levels in SV-HUC-1, HT-1376, T24, J82, 5637, and EJ cells. $^{**}P<0.01$ compared with SV-HUC-1, $^{*}P<0.05$ compared with SV-HUC-1. (**F**) Predicted target sites of miR-582-5p on UCA1. (**G**) Luciferase assay. HEK293T cells were co-transfected with either 50 nM miR-582-5p mimics or NC oligos and 200 ng of UCA1-wt or UCA1-mut using Lipofectamine® 3000. The relative firefly luciferase activity was measured 48 hours after transfection and was normalized with renilla luciferase activity. $^{**}P<0.01$ compared with UCA1-wt group. The data shown are the mean ± standard error of three individual experiments. (**H**) T24 cells were transfected with pcDNA3.1-UCA1 or pcDNA3.1-vector and treated with or without miR-582-5p inhibitor for 24 hours. The level of miR-582-5p in T24 cells with different treatment was examined by qPCR. $^{**}P<0.01$ compared with miR-582-5p mock, $^{\#\#}P<0.01$ compared with miR-582-5p inhibitor.

Abbreviations: mut, mutant; NC, negative control; qRT-PCR, quantitative polymerase chain reaction; wt, wild type.

bladder cancer cells and tissues (Figure 1A–E), we further studied whether there are direct interactions between them. Prediction of miR-582-5p target sites was performed by the online software miRnada Tools. As shown in Figure 1F, UCA1 contains many elements complementary to miR-582-5p regions. As shown in Figure 1G, miR-582-5p reduced luciferase activity in cells transfected with UCA1-wt ($P<0.01$), but had no effects in cells transfected with UCA1-mut. The expression levels of miR-582-5p were measured in UCA1 shRNA transfected T24 cells by quantitative real-time polymerase chain reaction (qRT-PCR). Expectedly, the expression levels of miR-582-5p were markedly elevated compared with the control group ($P<0.001$; Figure 1H). Bioinformatics and qRT-PCR results reveal that UCA1 interacts with miR-582-5p and downregulates its expression in T24 cells. To confirm this possibility, the wild-type sequence of UCA1 (UCA1-wt) or its mutant sequence (UCA1-mut) was subcloned into the pMIR luciferase reporter and then co-transfected with miR-582-5p mimics or controls into T24 cells. These results indicated that there are direct interactions between miR-582-5p and the miRNA recognition sites of UCA1.

UCA1 knockdown suppresses growth, migration, and invasion of T24 and 5637 cells via derepression of miR-582-5p

To further investigate the role of UCA1 and miR-582-5p in T24 and 5637, UCA1 shRNA and miR-582-5p inhibitor were performed in cell growth, invasion, and migration assay. CCK-8 results showed that UCA1 knockdown significantly inhibited the growth of T24 and 5637 cells (Figure 2A and B, $P<0.05$), while miR-582-5p inhibitor obviously promoted the growth of T24 and 5637 cells (Figure 2A and B, $P<0.05$).

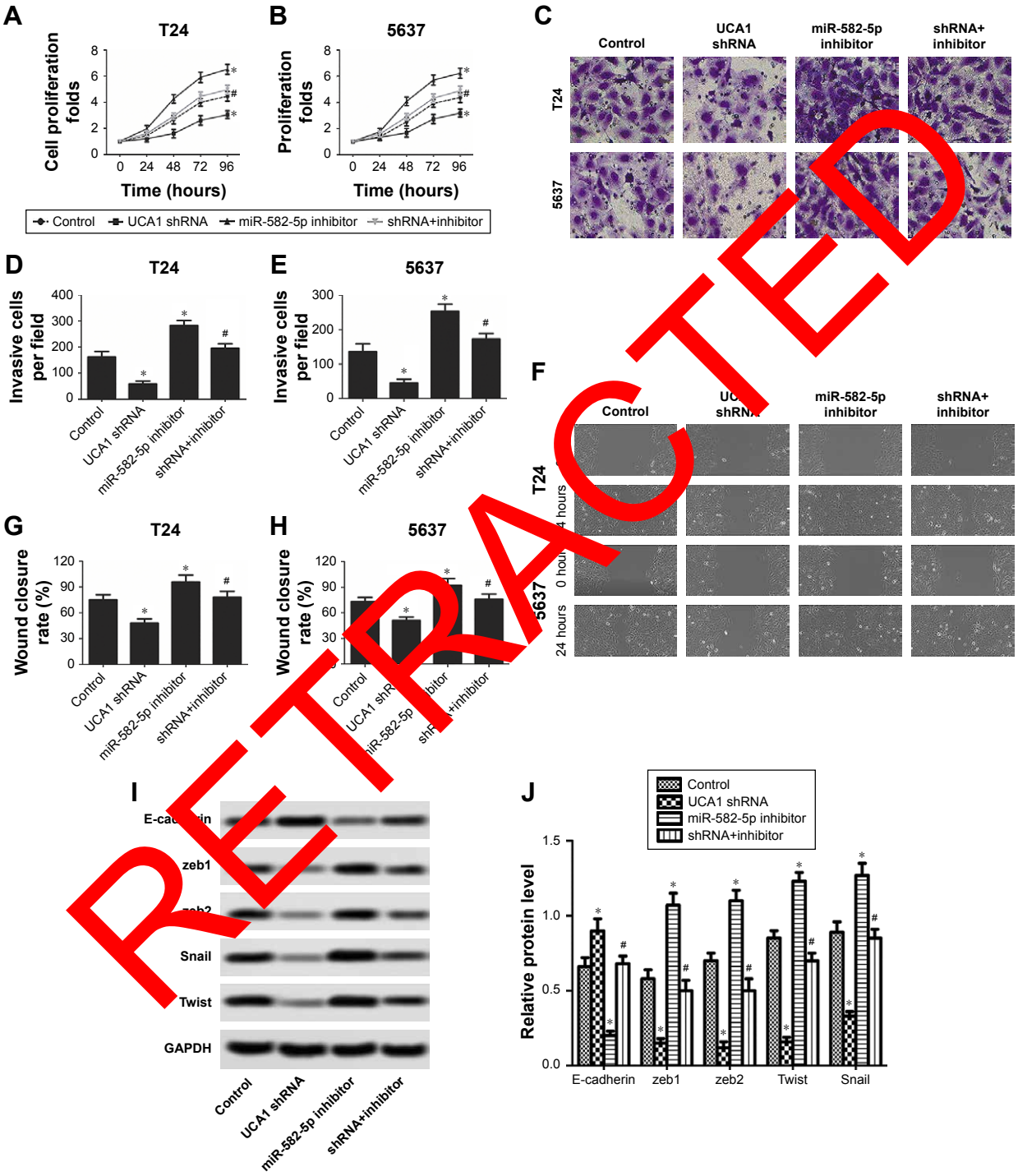

Figure 2 UCA1 knockdown suppresses growth, migration, and invasion of T24 and 5637 cells.
Notes: T24 and 5637 cells were divided into 4 groups: control, UCA1 shRNA, miR-582-5p inhibitor, and shRNA+inhibitor. (**A**) T24 and (**B**) 5637 cell proliferation was determined by CCK-8 assay. (**C**) Matrigel invasion assay (original magnification, 400×). (**D**, **E**) Quantification of invasion cells. (**F**) Cell migration assay (original magnification, 200×). (**G**, **H**) Quantification of Figure 2F. (**I**, **J**) Relative protein expression of EMT markers. *$P<0.05$ compared with control, #$P<0.05$ compared with miR-582-5p inhibitor.
Abbreviations: CCK-8, Cell Counting Kit-8; EMT, epithelial–mesenchymal transition.

Then, Transwell assay results showed that UCA1 knockdown significantly inhibited the invasion of T24 and 5637 cells (Figure 2C–E, $P<0.05$), while miR-582-5p inhibitor obviously promoted the invasion of T24 and 5637 cells (Figure 2C–E, $P<0.05$). Moreover, wound healing results showed that UCA1 knockdown significantly inhibited the migration of T24 and 5637 cells (Figure 2F–H, $P<0.05$), while miR-582-5p inhibitor obviously promoted the migration of T24 and 5637 cells (Figure 2F–H, $P<0.05$). As shown in Figure 2I and J, UCA1 knockdown significantly inhibited the expression of zeb1/2, snail, and twist, significantly increased E-cadherin ($P<0.05$); reversely, miR-582-5p inhibitor showed contrary result. Beside, combination of UCA1 shRNA and miR-582-5p inhibitor exhibited a subdued activity compared with miR-582-5p inhibitor alone, which suggested that UCA1 knockdown suppresses growth, migration, and invasion of T24 and 5637 cells via derepression of miR-582-5p.

UCA1 knockdown reduces the resistance of T24 and 5637 cells via derepression of miR-582-5p

The effects of UCA1 knockdown on resistance was determined by measuring multidrug resistance modulators including MRP1, LRP, GST, and TOPO-II. As shown in Figure 3A–D, compared with the control group, the protein expressions of MRP1, LRP, and GST were significantly decreased in UCA1 shRNA group. But for TOPO-II, it was demonstrated that UCA1 shRNA could enhance its expression, while miR-582-5p inhibitor showed opposite effects.

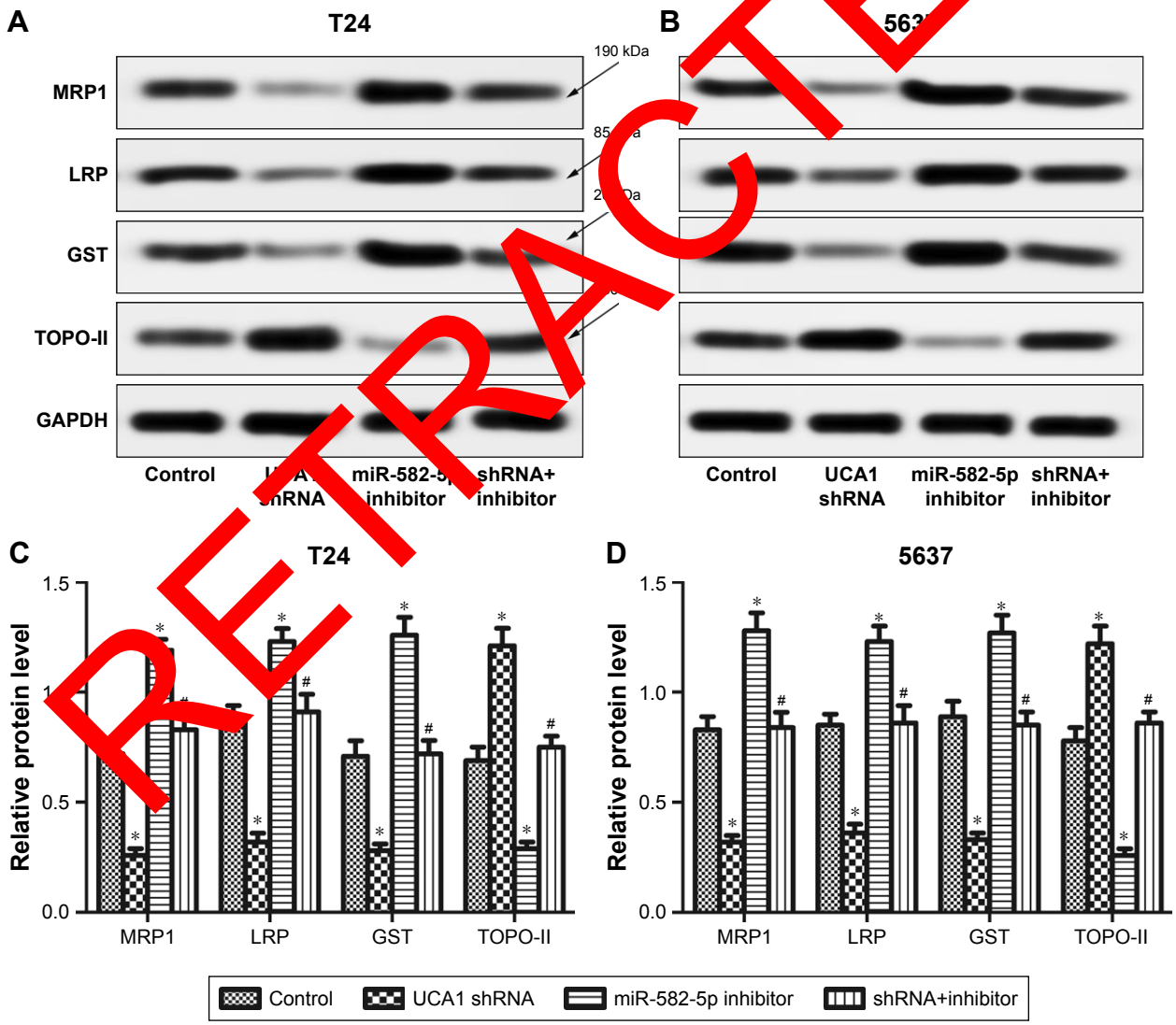

Figure 3 UCA1 knockdown reduces the resistance of T24 and 5637 cells.

Notes: T24 and 5637 cells were divided into four groups: control, UCA1 shRNA, miR-582-5p inhibitor, and shRNA+inhibitor. (**A**, **B**) The expressions of MRP1, LRP, GST, TOPO-II and GAPDH were measured by Western blot in (**A**) T24 and (**B**) 5637 cells. (**C**, **D**) Quantification of Figure 3A and B. All the experiments were repeated three times. *$P<0.05$ compared with control, #$P<0.05$ compared with miR-582-5p inhibitor.

These results indicated that UCA1 shRNA could downregulate the expressions of MRP1, LRP, GST, and upregulate the expression of TOPO-II.

UCA1 knockdown inhibits autophagy of T24 and 5637 cells via derepression of miR-582-5p, and miR-582-5p directly represses ATG7

The effect of UCA1 knockdown on autophagy inhibition was verified by measuring microtubule-associated protein 1 B/A1-light chain 3 (LC3-II/LC3-I) ratio (autophagy marker), autophagy substrate p62. As shown in Western blotting (Figure 4A and B), the UCA1 shRNA transfection decreased LC3-II levels, suggesting that the conversion of LC3-I to LC3-II was inhibited ($P<0.05$). The decreased LC3-II thus accounts for significant decrease of LC3-II/LC3-I ratio (Figure 4C and D). Since p62 is a substrate for autophagy degradation, increased p62 expression by UCA1 shRNA confirmed that UCA1 knockdown suppressed cellular autophagy ($P<0.05$, Figure 4C and D). ATG7 was downregulated by UCA1 shRNA and upregulated by miR-582-5p inhibitor ($P<0.05$, Figure 4C and D). These results validated that UCA1 knockdown inhibited tumor cell autophagy. The results indicated that UCA1 knockdown inhibits autophagy of T24 and 5637 cells via derepression of miR-582-5p. As shown in Figure 4E, ATG7 contains many elements complementary to miR-582-5p regions. As shown in Figure 4F, miR-582-5p reduced luciferase activity in cells transfected with ATG7-wt ($P<0.01$), but no effects in cells transfected with ATG-mut. These results indicated that miR-582-5p directly targets and represses ATG7. Considering the interaction between UCA1 and miR-582-5p, it is reasonable to speculate that UCA1 may upregulate ATG7. Expectedly, the mRNA expression level of ATG7 was significantly suppressed by miR-582-5p mimic in both T24 and 5637 cells compared with the control ($P<0.05$, Figure 4G). The result suggested that UCA1 knockdown can negatively regulate ATG7 translation. Collectively, the results indicated that UCA1 modulated bladder cancer via UCA1-miR-582-5p-ATG7-autophagy axis.

UCA1 knockdown inhibits cell growth and metastasis of T24 and 5637 cells via autophagy inhibition

To confirm the role of UCA1-miR-582-5p-ATG7-autophagy axis in bladder cancer, 10 nM rapamycin (CST, #9904) was introduced to perform the experiments. As shown in Figure 5A–D, UCA1 shRNA negatively regulated autophagy as evidenced by decreased LC3-II and increased P62 as well as LC3-II/LC3-I ratio, while rapamycin play the opposite role. Moreover, UCA1 shRNA reduced the resistance as evidenced by reduced expression of drug resistance-related proteins including MRP1, LRP, and GST; similarly, rapamycin exhibited reversed activity. Interestingly, UCA1 shRNA significantly reduced cell growth, cell invasion, and migration while rapamycin showed reversed effects in these activities ($P<0.05$, Figure 5E–J). These results confirmed that UCA1 modulated bladder cancer cells via inhibiting miR-582-5p–ATG7-autophagy axis.

UCA1 knockdown inhibits cell growth in vivo

Previous in vitro studies have shown that UCA1 knockdown suppressed bladder cancer cell growth and autophagy. We, therefore, studied the effects of UCA1 in T24 cell xenografted tumor mice in vivo. Consistent with the results in vitro, UCA1 knockdown markedly suppressed the tumor growth (volume) compared with the control (Figure 6A and B). Obviously, UCA1 knockdown downregulated the mRNA level of UCA1 and ATG7 but upregulated the mRNA level of miR-582-5p ($P<0.01$, Figure 6C–E). Moreover, immunohistochemistry results showed that UCA1 knockdown decreased the expressions of Ki67, PCNA, MMP-9, and VEGF in vivo ($P<0.01$, Figure 6F). The results supplemented the anticancer activity of miR-582-5p in vivo.

Discussion

A large number of researches reported that UCA1 might be a biomarker of bladder cancer[19] and contributed to cell proliferation, apoptosis inhibition,[9] and metastasis in bladder cancer.[8,20] In addition, the previous study demonstrated that UCA1 was upregulated in bladder cancer tissues[7] and cell lines.[8] In our study, we confirmed that UCA1 was upregulated in bladder cancer tissues and cell lines, including HT-1376, T24, J82, 5637, and EJ cells, especially in T24 and 5637 cells. Beside, UCA1 was upregulated in T24 cell xenografted tumor. As previous researches mentioned, UCA1 increased cell proliferation, invasion, and migration of bladder cancer.[8,20] In the present study, as expected, UCA1 acts as an oncogene was verified by knockdown experiments. Knockdown of UCA1 significantly decreased cell growth, invasion, and migration in T24 and 5637 cells. Interestingly, we first revealed that UCA1 activated cell autophagy in bladder cancer cells. Our findings reveal that UCA1 functions

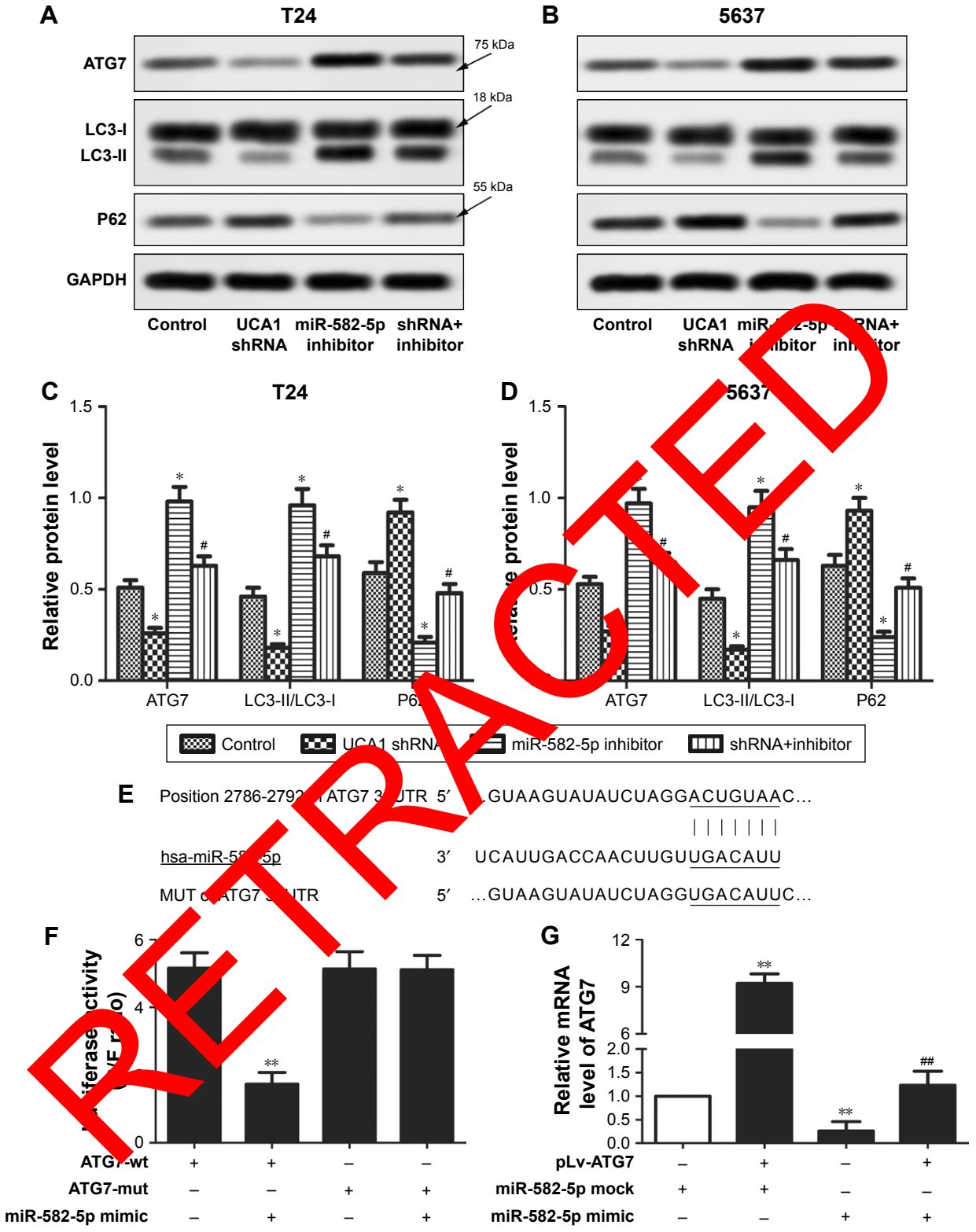

Figure 4 UCA1 knockdown inhibits autophagy of T24 and 5637 cells and ATG7 is a target of miR-582-5p.

Notes: T24 and 5637 cells were divided into four groups: control, UCA1 shRNA, miR-582-5p inhibitor, and shRNA+inhibitor. (**A**, **B**) The expressions of ATG7, LC3I/II, and P62 were measured by Western blot in (**A**) T24 and (**B**) 5637 cells. (**C**, **D**) Quantification of Figure 4A, B. $^{*}P<0.05$ compared with control, $^{\#}P<0.05$ compared with miR-582-5p inhibitor. (**E**) Predicted target sites of miR-582-5p on ATG7 and the mutant sequence are shown. (**F**) Luciferase assay. T24 cells were co-transfected with either 50 nM miR-582-5p mimics or NC oligos and 200 ng of ATG7-wt or ATG7-mut using Lipofectamine®3000. The relative firefly luciferase activity was measured 24 hours after transfection and was normalized with renilla luciferase activity. $^{**}P<0.01$ compared with ATG7-wt group. The data shown are the mean±standard error of three individual experiments. (**G**) T24 cells were transfected with pcDNA3.1-ATG7 or pcDNA3.1-vector and miR-582-5p mimic or mock for 24 hours. The mRNA level of ATG7 was examined by qPCR. All the experiments were repeated three times. $^{**}P<0.01$ compared with miR-582-5p mock. $^{\#\#}P<0.01$ compared with miR-582-5p mimic.

Abbreviations: mut, mutant; qPCR, quantitative PCR; wt, wild type.

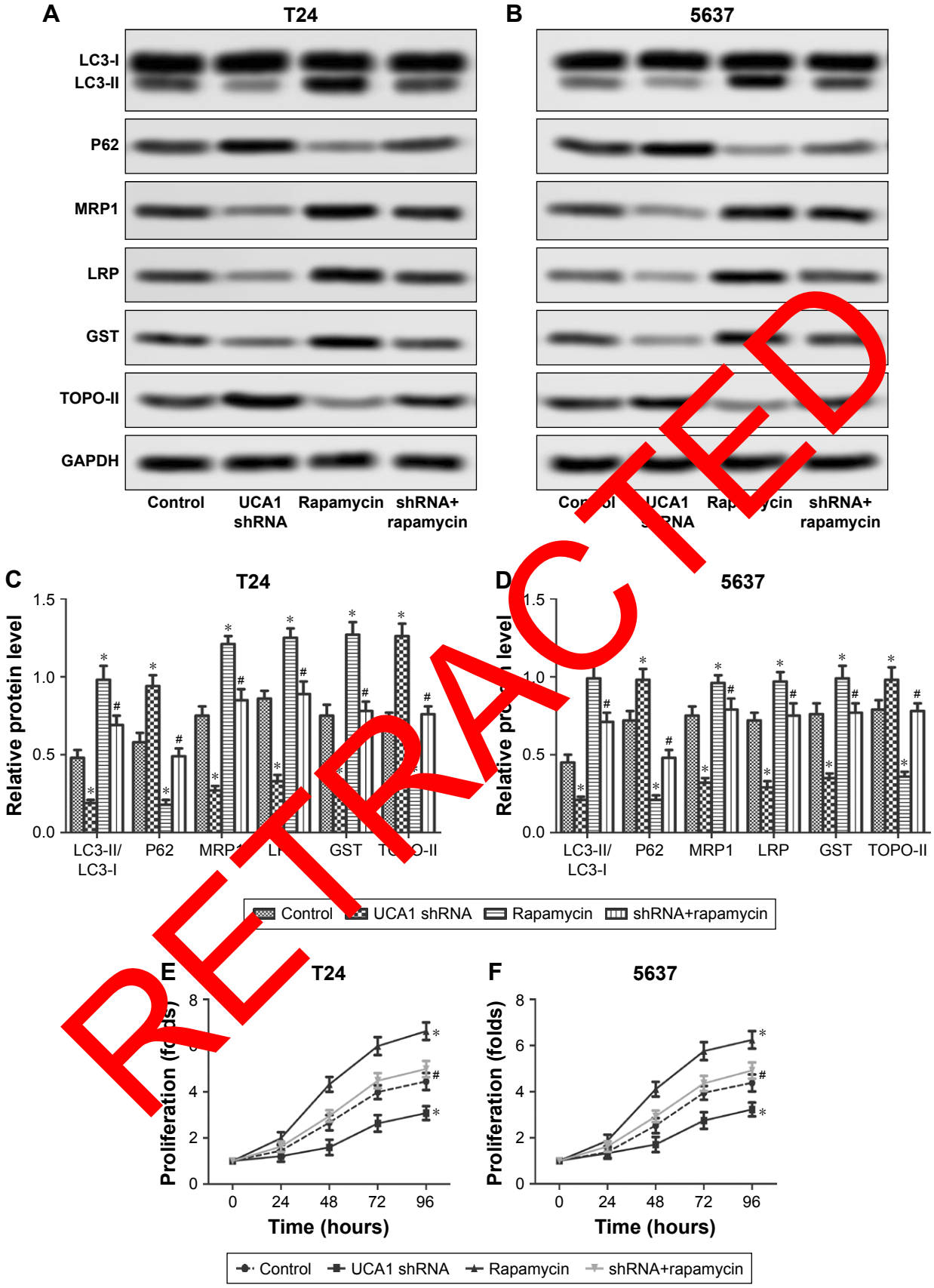

Figure 5 (*Continued*)

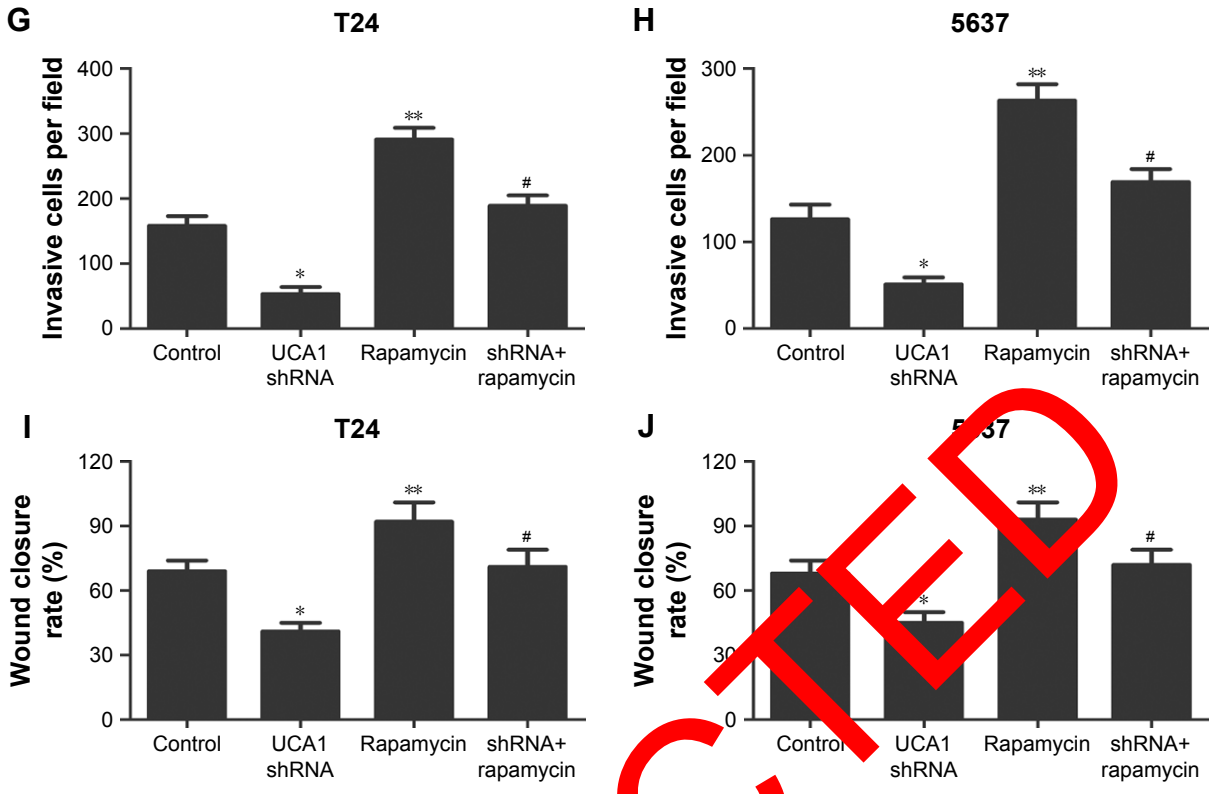

Figure 5 UCA1 knockdown inhibits cell growth and metastasis of T24 and 5637 cells v utophagy inhibit .
Notes: UCA1 was knockdown by shRNA in T24 and 5637 cells and treated with or wit t rapamycin (nM). (**A**, **B**) The expression of, LC3I/II, P62, MRP1, LRP, GST TOPO-II and GAPDH of (**A**) T24 and (**B**) 5637 cells by Western blot. (D) Quantificat f Figu A, B. (**E**, **F**) Cell growth was measured by CCK-8. (**G**, **H**) Cell invasion was determined by transwell assay. (**I**, **J**) Cell migration was deter ed ound healing assay. All the experiments were repeated three times. $^{*}P<0.05$, $^{**}P<0.01$ compared with control. $^{\#}P<0.05$ compared with rapamycin treated alone.
Abbreviation: CCK-8, Cell Counting Kit-8.

as an oncogene and promotes bladder c cer ma t pro gression. Furthermore, UCA1 mod ated b er cancer cell growth, invasion, and migrati a regulati utophagy.

In contrast with UCA1, previo studies showed that miR-582-5p was a nov tumor suppre or in some human cancers. For exam , miR-582-5p functions as a tumor suppressor by inhib g pr iferation through suppression of CDK1 expres n in h tocellu carcinoma.[21] Similarly, miR-582- p acts a the tum ppressor by targeting Rab27a in hum colo l carcinoma.[22] Recently, miR-582-5p was repor o inhibit invasion and migration of salivary adenoid cyst carcinoma cells by targeting FOXC1.[23] In cervical squamous cell carcinoma, mir-582 was reported to be reduced.[24] Expectedly, our findings suggested that there was an inverse correlation between UCA1 expression and miR-582-5p expression in bladder cancer tissues and cell lines. Mounting evidences have identified that the UCA1 can contribute to various cancers by interacting with microRNAs, thus inhibiting their expression.[10,13] According to the previous study results, it is reasonable to speculate that UCA1 might interact with miR-582-5p, serving as a potent natural miRNA sponge. As expected, a direct binding ability of the miR-582-5p response elements on the full-length UCA1 RNA was confirmed by luciferase assays. The regulatory mechanism between UCA1 and miR-582-5p is similar to the aforementioned studies.

Chemotherapy and cystectomy combination is a standard therapeutic strategy in patients with invasive and advanced bladder cancer. However, bladder cancer cells often develop drug resistance to chemotherapy via increasing autophagy, and about 50% of patients with advanced bladder cancer fail to respond to chemotherapy. Recently, UCA1 has been reported to increase chemoresistance in bladder cancer. One study investigated the role of the UCA1 in cisplatin resistance during chemotherapy for bladder cancer and clarified that UCA1 increases chemoresistance of bladder cancer cells by regulating Wnt signaling.[6] And another study showed that knockdown of UCA1 decreased chemoresistance to cisplatin/gemcitabine by suppressing cell proliferation and inducing apoptosis, while overexpression of UCA1 increased drug

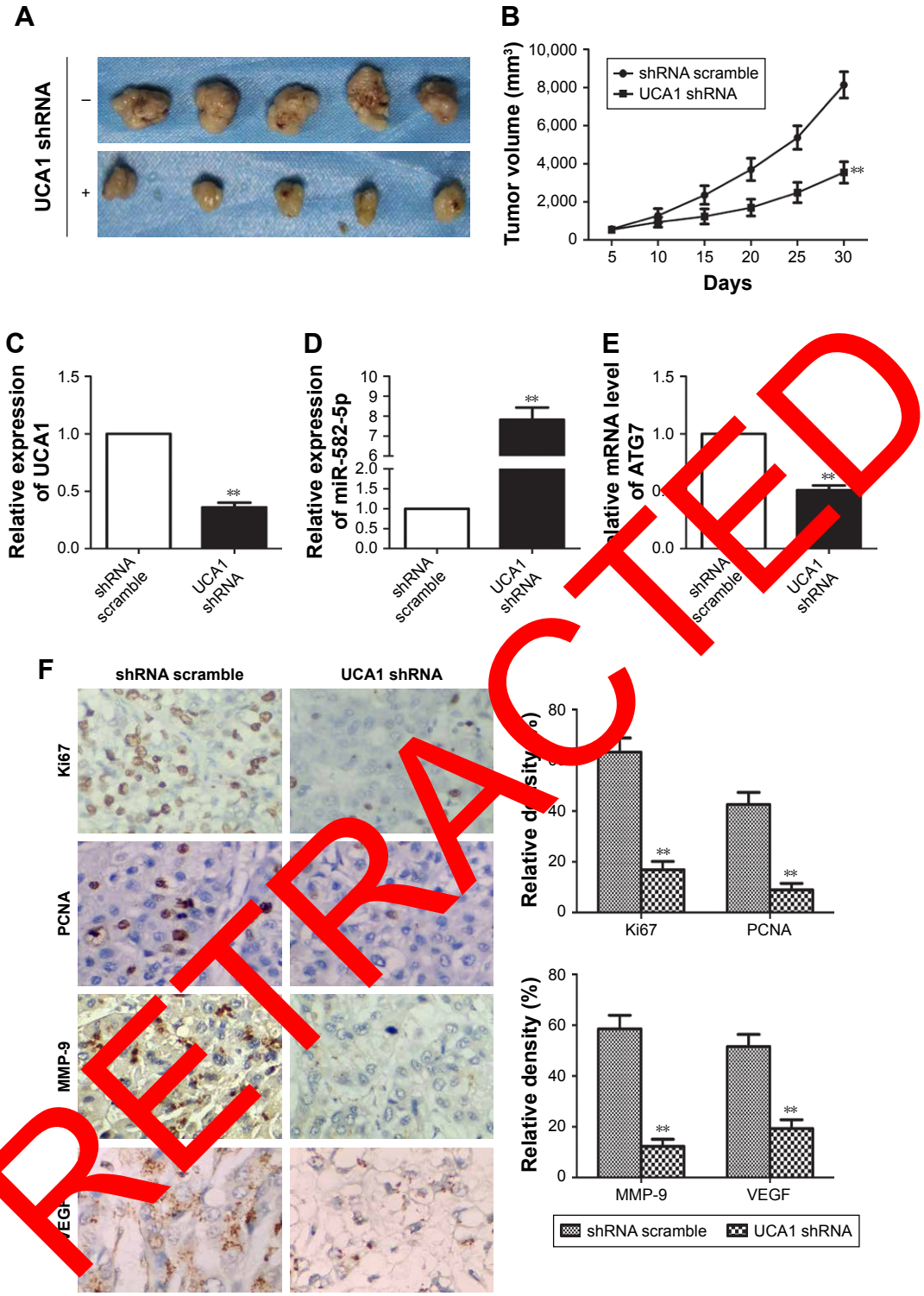

Figure 6 UCA1 knockdown inhibits cell growth and metastasis in vivo.
Notes: (**A**) Tumor images (n=5). (**B**) UCA1 shRNA decreased tumor volume. (**C–E**) The relative expressions of UCA1, miR-582-5p, and ATG7 were detected by qPCR. (**F**) The expressions of Ki67, PCNA, MMP-9, and VEGF were detected by immunohistochemistry. All the experiments were repeated three times. Magnification: 400×. $^{**}P<0.01$ compared with control.

resistance in bladder cancer cells.[25] MRP1, GST, LRP, and TOPO-II are the most prominent proteins in the development of drug resistance.[26] MRP1, GST, and LRP are positively related with drug resistance, while TOPO-II is negatively related with drug resistance.[27] The overexpression of MRP1 and LRP can increase the drug resistance by decreasing intracellular concentration and cellular cytotoxicity of anticancer drug.[27] The overexpression of GST could increase the drug

resistance by decreasing the concentrations of anticancer drugs through the GSH-conjugate export pump.[28] TOPO-II is the main target for many anticarcinogens. The downregulation or mutation of TOPO-II increases the drug resistance.[29] In the present study, UCA1 shRNA significantly downregulated the expressions of MRP1, GST, LRP and upregulated the expression of TOPO-II, which suggested that UCA1 knockdown reduced the drug resistance. Conversely, drug resistance was increased when rapamycin was introduced. These results demonstrated that UCA1 regulated drug resistance through autophagy modulation.

Autophagy is a mechanism that recycles cellular components through lysosomal degradation. Autophagy is highly activated in the hypoxic, nutrient-poor regions of tumor, because cancer cells utilize autophagy to tolerate environmental stress.[30] Thus, autophagy inhibition seems to be a therapeutic strategy though the controversial role in cancer. Autophagy has been shown to play a vital role in bladder cancer development, and its manipulation is emerging as a new therapeutic target. Autophagy is reported to be upregulated in various treatment modalities for bladder cancer.[31] The expressions of P62 and LC3II/LC3I may represent the autophagy level. The expression of LC3 was negatively correlated with P62 in cancer tissues.[32] In the present study, UCA1 shRNA significantly downregulated the expression of LC3II, but upregulated P62. The results indicated that UCA1 was positively correlated with autophagy and survival in T4 cells and 5637 cells as well as in xenografted tumors. Meanwhile, autophagy was activated when treated with miR-582-5p inhibitor. Expectedly, UCA1 shRNA could counteract the autophagy activation induced by miR-582-5p inhibitor, which may help in cancer cell survival.

ATG7 is an E1-like activating enzyme involved in the two ubiquitin-like systems required for autophagy.[33] A previous study showed that the level of ATG7 and its mediated autophagy were much higher in human bladder cancer cell lines.[34] Moreover, ATG7 has been reported to promote human bladder cancer tumorigenic growth in vitro and in vivo.[34] The deletion of ATG7 results in growth suppression and tumorigenesis inhibition of lung cancer.[35] In our study, through the transfection of miR-582-5p mimics and inhibitor, we demonstrated that miR-582-5p was able to modulate autophagy via interfering ATG7 expression levels, and this effect was mediated via a miR-582-5p consensus sequence contained in the 3′-UTR of the ATG7 gene. The role of miR-582-5p in the regulation of ATG7 expression was evidenced by luciferase assays. In addition, our experiments showed that transfection of T24 bladder cancer cells with the miR-582-5p mimic resulted in a decrease of ATG7 mRNA expression. Consequently, we observed that miR-582-5p-mediated decrease of ATG7 had an inhibitory effect on autophagy, showing lower level of LC3-II expression and, conversely, miR-582-5p inhibition (inhibitor) lead to the activation of the autophagy process, as evidenced by higher level of the LC3-II expression. This effect was further confirmed with the introduction of rapamycin (mTOR inhibitor), a well-studied autophagy inducer. We conducted the migration and invasion experiments in transfection UCA1 shRNA with or without rapamycin. The results indicated that UCA1-miR-582-5p-ATG7 axis regulated bladder cancer via autophagy pathway. The in vivo studies show consistent results with those in vitro, that is, UCA1 shRNA suppresses the human bladder cancer malignant progression, including growth suppression, invasion, and migration inhibition, as evidenced by reduced tumor volumes and low expressions of Ki67, PCNA, MMP-9, and VEGF.

Conclusion

Our present work highlights that UCA1 acts as an oncogene by promoting human bladder cancer malignant progression, including invasion, migration, growth, and drug resistance. Notably, mechanistic analysis reveals a novel UCA1-miR-582-5p-ATG7-autophagy signaling pathway regulatory network in bladder cancer.

Disclosure

The authors report no conflicts of interest in this work.

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