

# Ribosome Binding Protein 1 Correlates with Prognosis and Cell Proliferation in Bladder Cancer

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**Introduction:** Ribosome binding protein 1 (RRBP1) is reported to be correlated with tumor formation and progression. However, the role of RRBP1 in bladder cancer is unclear. In this study, we aimed to investigate the expression of RRBP1 and its influence on cell proliferation in bladder cancer.

**Methods:** Quantification real-time polymerase chain reaction (qRT-PCR) and immunohistochemistry (IHC) were used to detect the expression levels of RRBP1 in 138 bladder cancer and matched adjacent normal bladder tissues. Then, the clinical significance of RRBP1 in bladder cancer was evaluated. The effect of RRBP1 on cell proliferation and its potential mechanism were further explored.

**Results:** Results show that the mRNA levels of RRBP1 in bladder cancer were significantly higher compared with those in normal tissues ( $P < 0.001$ ). IHC results show the high-expression rate of RRBP1 in bladder cancer was 68.8%, which was significantly greater than those in normal tissues (40.6%,  $P < 0.001$ ). RRBP1 high-expression was significantly associated with differentiation, T stage and lymph node metastasis in bladder cancer ( $P < 0.05$ ). The overall survival time of patients with RRBP1 high-expression was significantly reduced compared to those with RRBP1 low-expression. Moreover, RRBP1 overexpression significantly promoted cell proliferation, which was correlated with Smad1/Smad3/TGF- $\beta$ 1 signal pathway.

**Conclusion:** RRBP1 high-expression correlates with prognosis and promotes cell proliferation in bladder cancer, which could be a potential biomarker.

**Keywords:** RRBP1, prognosis, bladder cancer, survival, biomarker

## Introduction

Bladder cancer is one of the most common urological carcinomas in the world.<sup>1-3</sup> It is reported that the incidence of bladder cancer is still increasing.<sup>4,5</sup> Furthermore, bladder cancer presents a high recurrence rate and mortality rate because of the absence of typical symptoms at the early stage.<sup>6,7</sup> No reliable biomarkers are helpful for clinical therapy and survival estimation.<sup>8-10</sup> Therefore, identifying effective biomarkers for early diagnosis and prognosis assessment is needed for the clinical therapy of bladder cancer.

Ribosome binding protein 1 (RRBP1) is an endoplasmic reticulum membrane protein which plays a crucial role in the secretion and transportation of nascent proteins in mammalian cells.<sup>11-15</sup> In addition, RRBP1 is involved in the endoplasmic reticulum stress and unfolded protein response.<sup>16,17</sup> Nowadays, RRBP1 high-expression is reported in lung cancer,<sup>18</sup> breast cancer,<sup>19,20</sup> colorectal cancer,<sup>21,22</sup> esophageal carcinoma,<sup>23</sup> prostate cancer,<sup>24</sup> endometrial endometrioid adenocarcinoma<sup>25</sup> and

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ovarian cancer.<sup>26</sup> Moreover, RRBPI correlates with patients' survival in breast cancer,<sup>19</sup> colorectal cancer,<sup>22</sup> esophageal carcinoma,<sup>23</sup> prostate cancer,<sup>24</sup> endometrial endometrioid adenocarcinoma<sup>25</sup> and ovarian cancer.<sup>26</sup> However, the role of RRBPI in bladder cancer remains unknown.

In the present study, the expression of RRBPI and its clinical significance in bladder cancer were investigated. Moreover, the effect of RRBPI expression on cell proliferation and its potential mechanism were explored.

## Patients and Methods

### Patients and Samples

One hundred thirty-eight bladder cancer and matched adjacent normal tissues were obtained from the First Affiliated Hospital of Henan University of Science and Technology. All patients received surgical resection during 2010 to 2017. None of the patients were treated with chemotherapy or radiotherapy before surgery. Clinical-pathological characters including age, sex, history of smoking, lymph node metastasis, T stage and differentiation were obtained from hospital records. The follow-up period for patients was recorded from the day of surgery. The follow-up time was from 7 to 65 months. All patients agreed to participate in this study and provided written informed consent. All experiments were approved by the ethics committee of Henan University of Science and Technology, and performed in line with the Declaration of Helsinki and relevant laws and regulations. All animal experiments were performed in accordance with policies of the NIH Guide for the Care and Use of Laboratory Animals and the Institutional Animal Care and Use Committee (IACUC) of the First Affiliated Hospital of Henan University of Science and Technology.

### Cell Culture and Transfection

Human EJ, UM-UC-3 and T24 bladder cancer cell lines were obtained from the Cell Bank of Type Culture Collection of Chinese Academy of Sciences (Shanghai, China). Cells were cultured with RPMI-1640 (Gibco) with 10% heat-inactivated fetal bovine serum (Hyclone) at 37 °C in a humidified incubator with 5% CO<sub>2</sub>. Based on the manufacturer's instructions, cell transfection was successfully completed by Lipofectamine<sup>TM</sup> 2000 (Invitrogen, Thermo Fisher Scientific, Inc., USA). RRBPI downregulation was performed by transferring shRNA lentivirus vectors (Genepharma, Suzhou, China) and RRBPI overexpression was performed by transferring recombinant

lentivirus vectors (Genepharma, Suzhou, China). Non-target shRNA (Genepharma, Suzhou, China) lentivirus vectors were treated as the negative control.

### Quantification Real-Time Polymerase Chain Reaction (qRT-PCR)

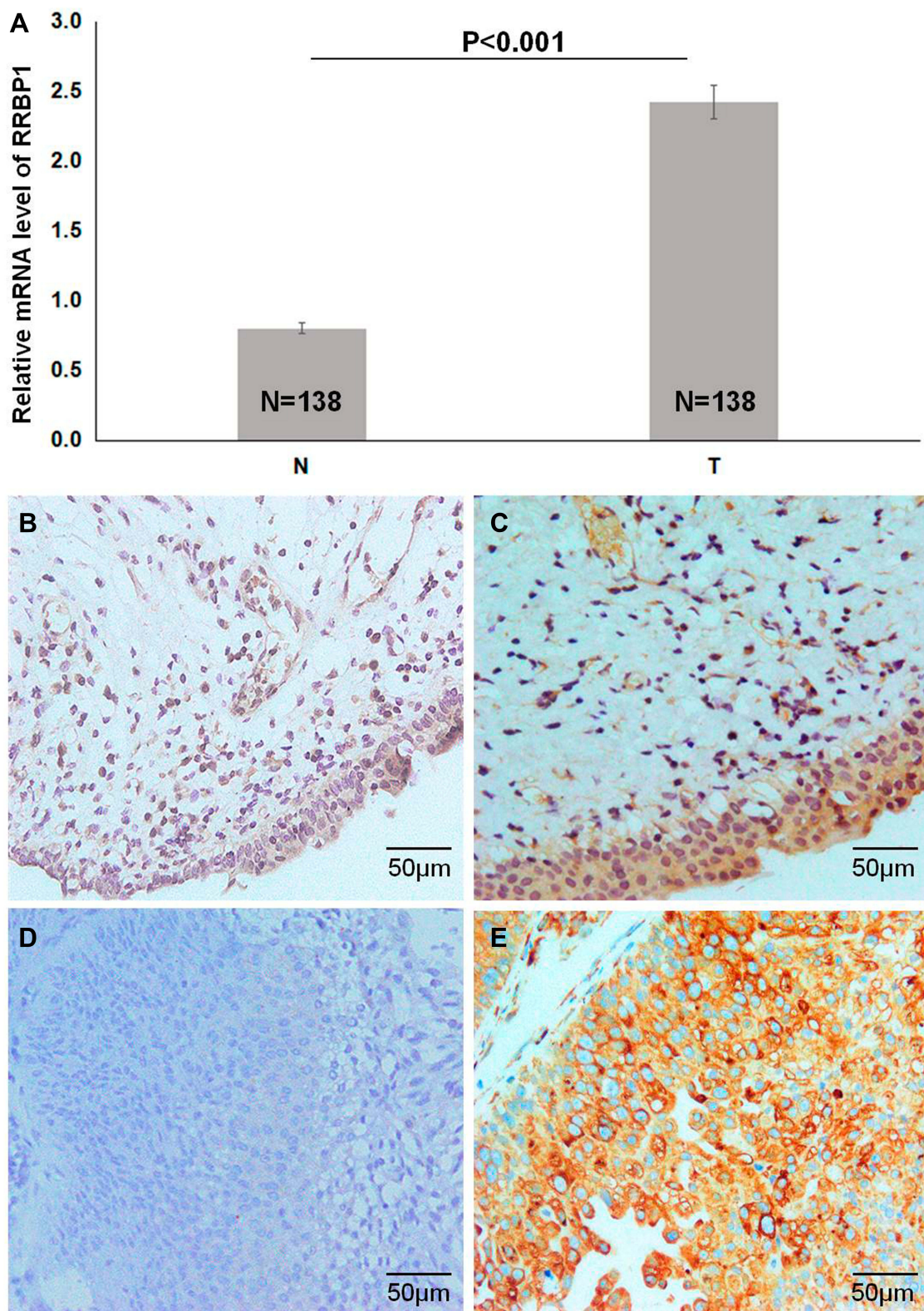
After surgery, all fresh tissues were collected and immediately stored in liquid nitrogen until RNA extraction. Total RNAs were obtained from fresh tissues and cells by using the manufacturer's protocol. The RNA was reversed into cDNA using a PrimeScript RT kit (Takara, Dalian, China). Real-time quantitative PCR was done by SYBR1 Premix Ex Taq. Primers for RRBPI were 5'-AACCTAATGGGAAGATACCTGA-3' (F) and 5'-CATGGCTGGAAGTGTGGC-3' (R). The primer sequence for GAPDH were 5'-CTGACGGGAAGCTCACTGG-3' (F) and 5'-TGAGGTCCACCACCTGTTG-3' (R). GAPDH was regarded as the internal control and each experiment was repeated three times. The relative expression level of RRBPI was compared using the  $2^{-\Delta\Delta Ct}$  method.

### Western Blotting

Proteins were obtained by radioimmunoprecipitation assay lysis buffer (Abcam Corp, USA) and quantified by bicinchoninic acid. Protein, 50 µg per sample, was separated onto 10% SDS-PAGE gels and transferred onto a polyvinylidene difluoride (PVDF) filter membrane. Then, PVDF membranes were incubated with 5% non-fat dried milk, anti-RRBPI (Abcam Corp., USA), Smad-1 (Abcam Corp., USA), p-Smad-1 (Abcam Corp., USA), Smad-3 (Abcam Corp., USA), p-Smad-3 (Abcam Corp., USA), TGF-β1 (Abcam Corp., USA) and anti-GAPDH (Abcam Corp., USA), respectively. Finally, membranes were washed with phosphate-buffered saline (PBS) and incubated with secondary antibodies. Signals were developed using an enhanced chemiluminescence reaction kit (Applygen Technologies, Beijing, China).

### Immunohistochemistry (IHC)

All tissue sections were fixed with 0.4% formulation, rehydrated and embedded into paraffin. Tissue sections (3 µm thick) were deparaffinized with xylene and rehydrated with alcohol. Antigen retrieval was completed by sodium citrate buffer (pH 6.0) for 5 minutes at 100 °C. Then, sections were blocked into 0.3% hydrogen peroxide solution for 20 min and incubated with rabbit polyclonal RRBPI antibody (Abcam Corp., USA) overnight at 4 °C. Washing with PBS, sections were incubated with biotin-labeled secondary



**Figure 1** The expression levels of RRBPI were examined in bladder cancer. **(A)** The mRNA levels of RRBPI were tested by qRT-PCR (N: normal tissues; T: tumor tissues). **(B)** RRBPI low-expression in normal bladder tissues by IHC (N= 82). **(C)** RRBPI high-expression in normal bladder tissues by IHC (N= 56). **(D)** RRBPI low-expression in bladder cancer tissues by IHC (N= 43). **(E)** RRBPI high-expression in bladder cancer tissues by IHC (N= 95).

antibodies. Signals were developed by diaminobenzidine tetrahydrochloride. PBS substituted with primary antibody was used as negative controls. Prostate cancer tissues with positive expression of RRBPI were used as positive controls.<sup>24</sup> The scores were scored according to the number of positive cells and staining intensity. Percentage of cells was scored as follows: 1 (<25%), 2 (25%–50%), 3 (>51%). Staining intensity was divided into blank (0), weak (1), moderate (2) and strong (3). Total score ranged from 0 to 9. Using semiquantitative analysis, RRBPI expression was scored as low-expression (<4) and high-expression ( $\geq 4$ ).<sup>24</sup>

### Cell Counting Kit-8 (CCK-8) Analysis

Cell proliferation was assessed by CCK-8 assay. Cells were transferred and seeded in 96-well plates ( $1.5 \times 10^3$  cells/well) for 5 days. According to the manufacturer's instructions, cells were cultured with 10  $\mu$ L of CCK-8 for 3 h, and the optical density of each well was determined by a microplate reader at 450 nm. Each experiment was repeated in triplicate at the same condition.

### Colony Formation Analysis

Transfected cells were seeded into 6-well plates at a density of  $1 \times 10^3$  cells/well. After 2 weeks, cells were obtained and fixed with 100% methanol. Then, cells were incubated with 0.1% crystal violet and stained with hematoxylin for counting under an optical microscope. Each experiment was repeated in triplicate at the same condition.

### Tumor Xenograft in vivo

Balb/c nude mice (4–5 weeks old) were obtained from the Animal Center and kept on specific pathogen-free conditions. To evaluate the tumor growth between the shRNA group and negative control group,  $5 \times 10^6$  bladder cancer cells were subcutaneously injected into the flank regions of legs (4 mice per group). Tumor size was recorded every 3–5 days. Finally, tumor weight was measured and tumor volumes were calculated by the formula: volume = (length  $\times$  width<sup>2</sup>)/2.

### Statistical Analysis

Data were characterized as mean  $\pm$  standard deviation (SD), and performed by SPSS software (version 19.0; SPSS, Chicago, IL, USA). The expression levels of RRBPI between bladder cancer and matched adjacent normal tissues were compared by paired *t*-test. The association between RRBPI expression and clinical-pathological characters was analyzed by Chi-square test ( $\chi^2$ ). Survival analysis was compared by using the Kaplan–Meier method with Log rank test.

**Table 1** The Expression of RRBPI Was Examined in Bladder Cancer by IHC

Types	N	RRBPI		P value
		Low-Expression (%)	High-Expression (%)	
Bladder cancer tissue	138	43 (31.2)	95 (68.8)	<0.001
Normal bladder tissue	138	82 (59.4)	56 (40.6)	

Hazard ratio was estimated using Cox's proportional hazards model. Statistical significance was  $P < 0.05$ .

## Results

### RRBPI Expression and its Clinical Significance in Bladder Cancer

To evaluate the expression of RRBPI, the mRNA levels of RRBPI were detected in 138 cases of bladder cancer and normal bladder tissues by qRT-PCR. As shown in Figure 1A, the mRNA levels of RRBPI in bladder cancer was significantly higher compared with adjacent normal bladder tissues ( $P < 0.001$ ). Then, the protein expression levels of RRBPI were further investigated by IHC analysis. Results show that positive staining of RRBPI was mainly distributed in the cell

**Table 2** RRBPI Expression Correlated with Clinical-Pathological Characters in Bladder Cancer

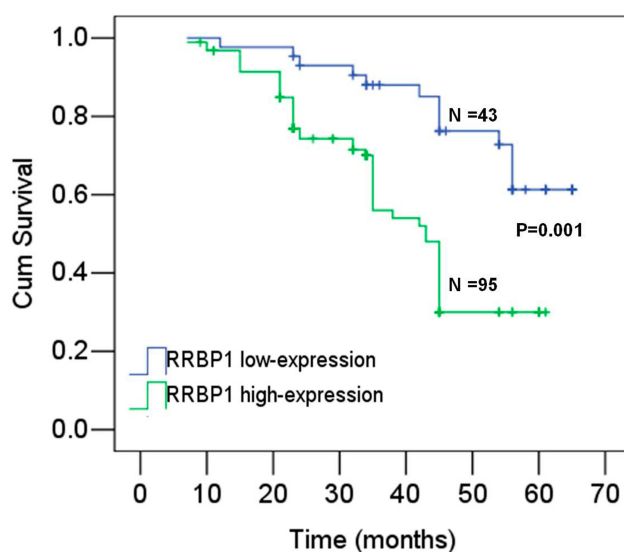
Clinical-Pathological Characters	N	RRBPI		P value
		Low-Expression	High-Expression	
Age (years)				0.265
≤60	60	22	38	
>60	78	21	57	
Gender				0.270
Male	69	25	44	
Female	69	18	51	
Smoking history				0.265
Negative	81	22	59	
Positive	57	21	36	
T stage				<0.001
Ta–T2a	65	30	35	
T2b–T4	73	13	60	
Lymph node metastasis				0.010
Negative	70	29	41	
Positive	68	14	54	
Differentiation				<0.001
High grade	34	22	12	
Moderate–low grade	104	21	83	

cytoplasm and stained as brown and yellow (Figure 1B–E). Semiquantitative analysis of IHC score show the high-expression rate of RRBPI in bladder cancer was 68.8%, which was significantly greater than those in normal tissues (40.6%,  $P < 0.001$ , Table 1).

Subsequently, the association between RRBPI expression and clinical-pathological characters was investigated based on the IHC scores. Results show RRBPI high-expression was significantly associated with differentiation, T stage and lymph node metastasis in bladder cancer ( $P < 0.05$ , Table 2), while not correlated with age, sex and smoking history ( $P > 0.05$ , Table 2). In addition, the prognostic value of RRBPI was further investigated in bladder cancer. Kaplan–Meier analysis revealed that the overall survival time of patients with RRBPI high-expression was significantly reduced compared to those with RRBPI low-expression (Figure 2,  $P = 0.001$ ). Furthermore, overall survival time was correlated with differentiation, T stage and lymph node metastasis ( $P < 0.05$ , Table 3). Multivariate Cox regression analysis showed that RRBPI expression, differentiation, T stage and lymph node metastasis were independent prognostic factors for overall survival in bladder cancer (Table 4,  $P < 0.05$ ). However, age, sex and smoking history were not significantly correlated with prognosis.

## RRBPI Promotes Cell Proliferation in Bladder Cancer

To investigate the biological role of RRBPI in bladder cancer, the effect of RRBPI expression on cell proliferation was



**Figure 2** Kaplan–Meier survival analysis shows patients with RRBPI overexpression had unfavorable survival.

**Table 3** Survival Analysis Performed by the Kaplan–Meier Method

Variables	N	Survival Time (Month, 95% CI)	P value
RRBPI			
Low-expression	43	56 (51–61)	0.001
High-expression	95	43 (39–47)	
Age (years)			0.916
≤60	60	48 (43–53)	
>60	78	47 (42–52)	
Gender			0.076
Male	69	51 (46–56)	
Female	69	45 (41–49)	
Smoking history			0.363
Negative	81	46 (42–50)	
Positive	57	49 (44–54)	
T stage			<0.001
T <sub>a</sub> –T <sub>2a</sub>	65	55 (51–59)	
T <sub>2b</sub> –T <sub>4</sub>	73	41 (37–45)	
Lymph node metastasis			<0.001
Negative	70	54 (50–58)	
Positive	68	41 (36–44)	
Differentiation			<0.001
High grade	34	60 (57–63)	
Moderate–low grade	104	41 (38–44)	

**Abbreviation:** CI, confidence interval.

investigated. As shown in Figure 3A, RRBPI was highly expressed in EJ cells, but was relatively low in UM-UC-3 and T24 cells. Therefore, RRBPI expression was downregulated in EJ cells and upregulated in T24 cells. As shown in Figure 3B, Western blot analysis shows RRBPI downregulation and upregulation were successfully performed. Then, the proliferation and clone formation of bladder cancer cells were evaluated in vitro. Results showed that RRBPI knockdown significantly inhibited proliferation in EJ cells (Figure 3C), while RRBPI overexpression significantly promoted proliferation in T24 cells. Meanwhile, the colony number in cells with RRBPI downregulation was significantly decreased, while it was significantly increased in cells with RRBPI overexpression (Figure 4A). To further investigate the effects of RRBPI expression on cell proliferation, xenografts in vivo were performed. The results showed that RRBPI knockdown significantly suppressed the growth of bladder cancer xenografts (Figure 4B).

To further explore the potential mechanism of RRBPI in bladder, the TGF- $\beta$ 1/Smad pathway was investigated. As shown in Figure 4C, the expression of TGF- $\beta$ 1 was significantly decreased with the knockdown of RRBPI. The protein

**Table 4** Prognostic Factors Evaluated by Multivariate Cox Regression Analysis

Variables	Hazard Rate	95% CI	P value
RRBP1 (High-expression vs Low-expression)	2.556	1.307–5.000	0.006
Age ( $\leq 60$ years vs $>60$ years)	1.439	0.782–2.635	0.238
Gender (Male vs Female)	0.709	0.394–1.274	0.250
Smoking history (Positive vs Negative)	0.571	0.449–1.426	0.450
T stage (T2b–T4 vs Ta–T2a)	4.148	1.027–3.998	0.042
Differentiation (Moderate–low grade vs High grade)	5.418	1.181–6.947	0.020
Lymph node metastasis (Positive vs Negative)	2.693	1.557–4.66	$<0.001$

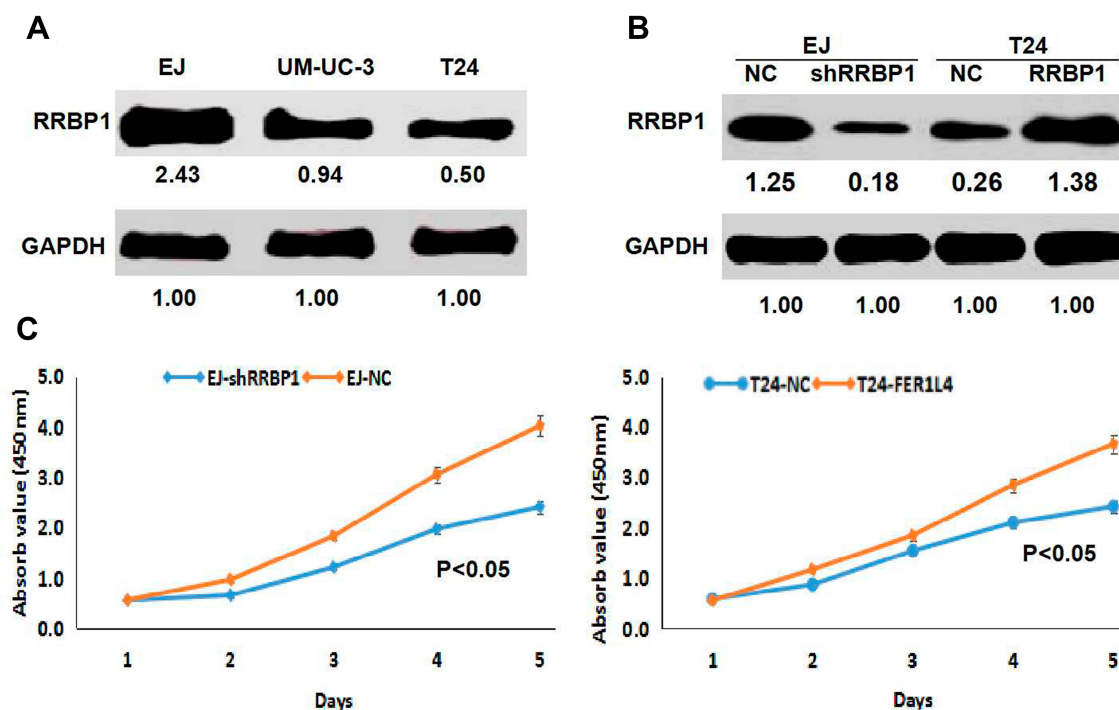
**Abbreviations:** vs, Versus; CI, confidence interval.

expression levels of Smad1 and Smad3 were unchanged regardless of the RRBPI expression interference, while RRBPI downregulation resulted in the decrease of p-Smad1/3.

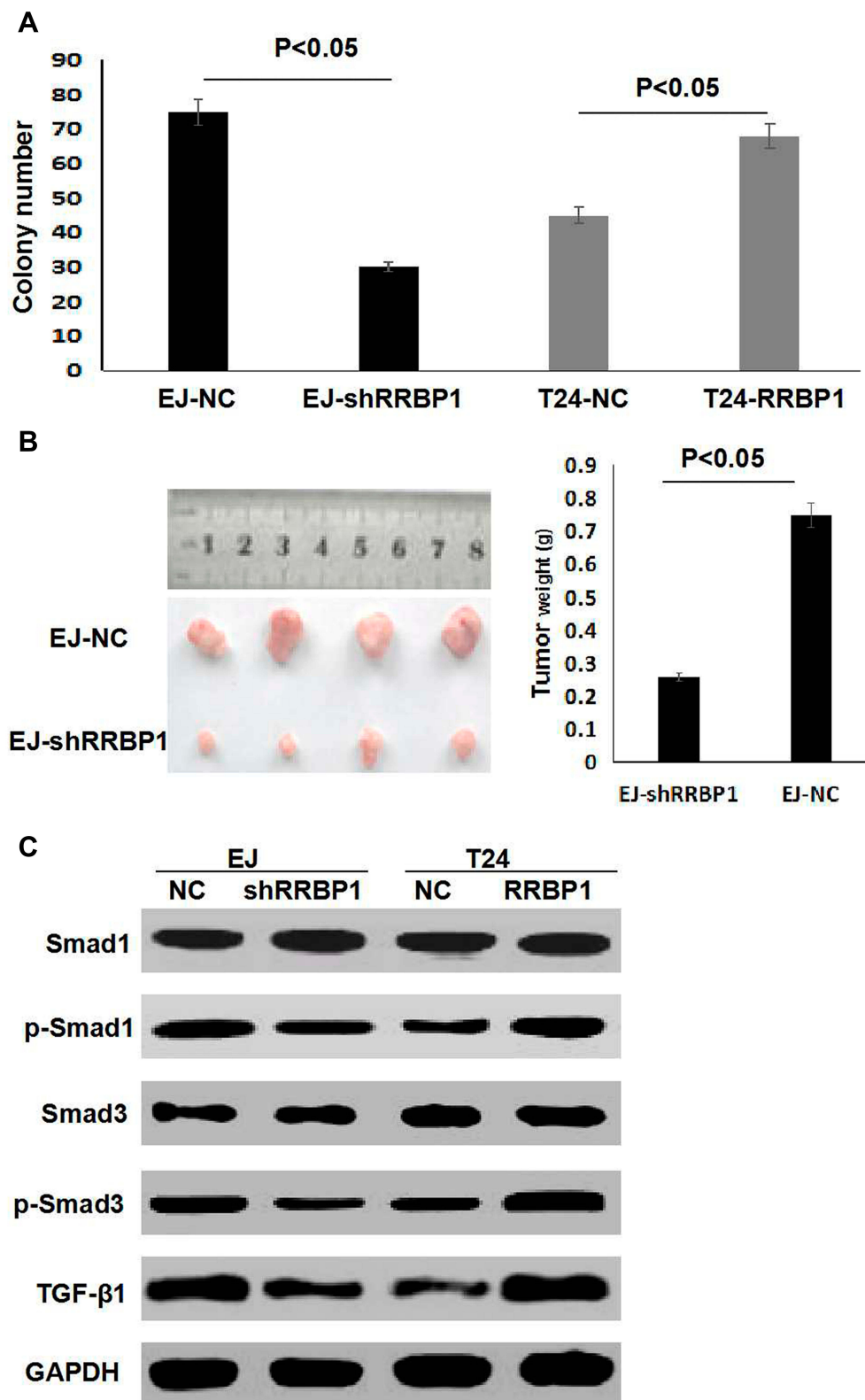
## Discussion

Recently, RRBPI overexpression has been reported in several types of tumor,<sup>16–26</sup> and could be regarded as a potential prognostic marker.<sup>19–24</sup> However, the role of RRBPI in bladder cancer remains unknown. In this study, the expression and clinical significance of RRBPI was investigated in bladder cancer. Results show that the mRNA levels of RRBPI in bladder cancer were significantly greater than those in normal

bladder tissues. Meanwhile, IHC results show that RRBPI was positively expressed in bladder cancer and located in the cell cytoplasm. The high-expression rate of RRBPI in bladder cancer was 68.8%, which was significantly higher than those in normal tissues (40.6%,  $P < 0.001$ ). These observations indicated that RRBPI overexpression was associated with the formation of bladder cancer, which was consistent with current reports.<sup>16–25</sup> Abnormal high-expression of RRBPI in bladder cancer might be helpful for the diagnosis of bladder cancer. In addition, RRBPI overexpression was significantly associated with differentiation, T stage and lymph node metastasis, which was in line with the reports in breast cancer,<sup>19</sup> colorectal cancer,<sup>22</sup> esophageal carcinoma<sup>23</sup> and prostate



**Figure 3** RRBPI overexpression promoted cell proliferation in vitro. (A) The protein expression levels of RRBPI were detected in bladder cancer cell lines by Western blot assay. (B) Western blot analysis revealed that RRBPI downregulation and upregulation were successfully performed. (C) CCK-8 assay shows RRBPI downregulation inhibited cell proliferation, while RRBPI overexpression promoted cell proliferation.



**Figure 4** RRBPI overexpression promoted cell proliferation in vivo. **(A)** RRBPI overexpression promoted colony formation. **(B)** RRBPI knockdown inhibited the growth of bladder cancer xenografts in vivo. **(C)** RRBPI overexpression activated the TGF- $\beta$ /Smad pathway.

cancer.<sup>24</sup> Moreover, survival analysis revealed that patients with RRBPI high-expression had unfavorable survival. RRBPI as well as differentiation, T stage and lymph node metastasis were independent prognostic factors in bladder cancer. These data indicated that RRBPI expression correlated with the progression of bladder and prognosis, which was consistent with the reports in esophageal carcinoma<sup>23</sup> and prostate cancer.<sup>24</sup>

Subsequently, the influence of RRBPI expression on cell proliferation and its potential mechanism were explored. Results show RRBPI downregulation significantly inhibited cell proliferation, while RRBPI overexpression significantly promoted cell proliferation in vitro. Moreover, RRBPI knockdown significantly suppressed the growth of bladder cancer xenografts in vivo. To investigate the potential mechanism of RRBPI, the TGF- $\beta$ /Smad pathway was evaluated. TGF- $\beta$ , as an oncogene, is widely involved in cell proliferation, migration and invasion.<sup>27–29</sup> TGF- $\beta$ /Smad signaling plays a key role in the epithelial–mesenchymal transition pathway and carcinogenesis in many cancer types.<sup>30–32</sup> Results show TGF- $\beta$ /Smad signaling was activated by RRBPI overexpression. Therefore, these data indicated that RRBPI overexpression promoted cell proliferation, which was connected with the TGF- $\beta$ /Smad pathway.

In conclusion, these data indicate that RRBPI is highly expressed in bladder cancer and correlates with clinical-pathological characters and prognosis. Moreover, RRBPI overexpression promotes cell proliferation, which is connected with the TGF- $\beta$ /Smad pathway.

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## Author Contributions

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

## Disclosure

All authors declare they have no financial disclosure and conflicts of interest.

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