



# CircRASSF2 promotes IGF1R and osteosarcoma metastasis via sponging miR-6838-5p

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**Background:** Osteosarcoma (OS) often occurs in children and adolescents and is highly malignant. Analyzing the pathogenesis of OS has great significance for prognosis and the discovery of new treatment strategies.

**Methods:** The effects and mechanism of circular RNA (circRNA) on OS were analyzed, as was the correlation between circRASSF2 and insulin-like growth factor 1 receptor (IGF1R) in data from The Cancer Genome Atlas (TCGA). The expression levels of microRNA (miR)-6838-5p and circRASSF2 in OS cells and osteoblasts were detected. The dual luciferase report was used to verify the targeting relationship. OS cells overexpressing circRASSF2, miR-6838-5p and/or IGF1R were constructed. The expression level of IGF1R and the biological behavior of the cells were detected. Eighty-two pairs of OS tissue and adjacent normal tissue samples were collected, and the levels of circRASSF2, miR-6838-5p, and IGF1R mRNA were detected by reverse transcription-quantitative PCR (RT-qPCR).

**Results:** Compared with osteoblasts, OS cells showed lower expression of miR-6838-5p and higher expression of circRASSF2. The dual luciferase report confirmed that miR-6838-5p targeted IGF1R. Overexpression of IGF1R significantly blocked the anticancer effects of miR-6838-5p. The dual luciferase report verified that circRASSF2 targeted miR-6838-5p, and promoted the expression of IGF1R. Overexpression of circRASSF2 not only promoted the malignant biological behavior of OS cells, but also blocked the anticancer effects of miR-6838-5p. In OS tissue, circRASSF2 and IGF1R were upregulated, and the two were positively correlated. MiR-6838-5p was downregulated, which negatively correlated with both circRASSF2 and IGF1R. High levels of circRASSF2 were associated with higher stage and metastasis of OS.

**Conclusions:** In conclusion, the promoting effects of IGF1R on OS are targeted by miR-6838-5p. CircRASSF2 restored the expression of IGF1R by sponging miR-6838-5p, thereby promoting the progression of OS.

**Keywords:** Osteosarcoma (OS); circRASSF2; microRNA-6838-5p (miR-6838-5p); insulin-like growth factor 1 receptor (IGF1R)

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## Introduction

Osteosarcoma (OS) often occurs in children and adolescents and is highly malignant. Amputation was the standard treatment in the 20th century, but the 5-year survival rate of patients was only 15–20% (1). Advances in medical technology have improved the survival rate, and the 5-year survival rate has increased to 70% (2). However, the survival rate of patients with metastatic OS is only ~20%, and metastasis is one of the risk factors for poor prognosis in OS patients (3,4). Analyzing the pathogenesis of OS has great significance for prognosis and the discovery of new treatment strategies.

Insulin-like growth factor 1 receptor (IGF1R) can be activated by IGF1, causing tyrosine phosphorylation of a variety of substrates [e.g., insulin receptor substrates (IRS1/2), Shc, etc.], thereby inducing signal transduction. Phosphorylated IRS1 activates PI3K, thereby promoting tumor transformation and metastasis (5,6). Studies confirm that IGF1R increases the proliferation and metastasis of OS cells by activating the PI3K/AKT pathway (7,8). In addition, expression of IGF1R is regulated at the post-transcriptional level; for example, the expression of IGF1R is targeted by microRNA (miR)-139-5p and miR-939-5p (9,10). MiR-6838-5p is a newly discovered miRNA that exerts anticancer effects in breast cancer (11) and gastric cancer (12), but its role in OS is still unclear.

The functions of miRNA are also targeted and regulated by non-coding RNAs (ncRNAs), long ncRNAs (lncRNAs) or circular RNAs (circRNAs) can absorb miRNA, thereby blocking the inhibition of target genes by the miRNAs (13,14). CircRNAs are ncRNAs with a closed circular structure that is usually formed by the reverse splicing of the exon transcription product RNA (13,14). CircRNAs do not have the complete structure of the end of mRNA and will not be hydrolyzed by exonuclease, so are structurally stable (15). CircRASSF2 can restore the expression level of target genes by “sponging” downstream miRNAs, thereby promoting the progression of laryngeal cancer (15) and thyroid cancer (16). However, the significance and role of circRASSF2 in OS is still unclear.

Through preliminary bioinformatics analysis and sequence prediction, it is found that circRASSF2 is positively correlated with IGF1R, and both of them have binding sites with miR-6838-5p. Therefore, in the present study, we mainly analyzed the mechanism by which circRASSF2 regulates the proliferation and metastasis of OS cells by sponging miR-6838-5p to promote the expression of IGF1R, providing new ideas for the diagnosis

and treatment of OS.

We present the following article in accordance with the MDAR reporting checklist (available at <https://dx.doi.org/10.21037/atm-21-6123>).

## Methods

### Bioinformatics methods

The correlation between RASSF2 and IGF1R in peripheral blood was tested by Pearson test, using data from The Cancer Genome Atlas (TCGA) database, and the analysis tool was GEPIA (<http://gepia.cancer-pku.cn/>).

### Dual luciferase report

The 3'-UTR sequence of wild-type (wt-) IGF1R mRNA was amplified to the downstream site of the pGL4 luciferase vector (Promega, Madison, WI, USA). A rapid site-directed mutagenesis kit (D0206, Beyotime Biotechnology, Shanghai, China) was used to generate the mutated (mut-) IGF1R mRNA 3'-UTR. The U2OS and HOS cells were seeded in 24-well plates at a density of  $3 \times 10^4$ /well. After 24 h, 1  $\mu$ g of wt-IGF1R mRNA 3'-UTR or mut-IGF1R mRNA 3'-UTR luciferase plasmid, 50 nM miR-6838-5p mimic or miR-6838-5p NC, 150 ng of Renilla luciferase plasmid (Beyotime) were transfected into cells via Lipofectamine<sup>TM</sup> 2000 (Invitrogen Corporation, Carlsbad, CA, USA) transfection reagent. The cells were then incubated at 37 °C for 36 h. According to the manufacturer's protocol, a dual luciferase reporter gene detection kit (Promega) was used to detect luciferase activity. All data were normalized to Renilla luciferase activity. For the verification of the targeted binding of circRASSF2 and miR-6838-5p, the method was similar to the description given above.

### Cell culture and treatment

Human osteoblast hFOB1.19 (ATCC<sup>®</sup> CRL-11372) and OS cell lines SAOS-2 (CL-0202, Procell Life Science&Technology Co., Ltd., Wuhan, China), U2OS (ATCC<sup>®</sup> HTB-96), HOS (ATCC<sup>®</sup> CRL-1543), and 293T (ATCC<sup>®</sup> ACS-4500) were maintained in DMEM complete medium containing 10% fetal bovine serum (FBS), 100 mg of streptomycin/mL, and 100 units of penicillin/mL (Solarbio, Beijing, China). The cells were cultured in a 5% CO<sub>2</sub> incubator at 37 °C and 95% humidity.

Adenovirus (Ad) encoding full-length human IGF1R and corresponding control AdGFP and AdshRNA were

purchased from GenePharma Co., Ltd. (Shanghai, China). The cells were transfected using Lipofectamine<sup>TM</sup> 2000 transfection reagent (Invitrogen), multiplicities of infection (MOI) =10. The miR-6838-5p mimic and corresponding negative control (NC) were purchased from GenePharma Co., Ltd. (Shanghai, China). The cells were transfected with 50 nM mimic (7 °C, 5% CO<sub>2</sub>, 48 h) using the Lipofectamine<sup>TM</sup> 2000 transfection reagent (Invitrogen).

In order to analyze the influence of circRASSF2 on the biological behavior of OS cells, circRASSF2 overexpression cells were constructed. The vector pLCDH-ciR (Ribobio, Guangzhou, China) carrying full-length circRASSF2 and corresponding NC were constructed (GenePharma). After the 293T (ATCC<sup>®</sup> ACS-4500) cells cultured in a 6-well plate reached 60%, Lipofectamine<sup>TM</sup> 2000 (5 µL, Invitrogen) was applied to transfect pLCDH-ciR into the cells, as well as psPAX2 and pMD2.G. After 6 h, the medium was replaced and incubation continued for 48 h. The supernatant was collected and passed through a 0.22-µm filter. Cells were infected using 8 µg/mL polybrene (Sigma) at approximately 70% confluence in complete supplemented medium; 0.5 µg/mL puromycin (Sigma) was used to select stably transfected cells.

#### **CCK-8 assay**

In this assay, 100 µL of cell suspension was added to the wells of 96-well plates with five replicate wells. After 48 h, 10 µL of CCK-8 solution was added to each well before incubating the cells for 2 h. At 450 nm wavelength, the optical density of each well was detected with a microplate reader (Biotek, Winooski, VT, USA).

#### **Scratch healing assay**

Cells were cultured in a 6-well plate according to the method described above to form a monolayer of cells, which was then scratched with a 200-µL plastic pipette. The scratch width at 0 h was recorded. The medium was poured off, and damaged cells were washed away. The cells were then cultured in serum-free medium for 24 h before microscopic analysis (Carl Zeiss, Germany) of the healing of the scratches.

#### **Transwell assay**

Transwell was divided into upper and lower chambers, Matrigel (1:8, Corning, USA) was added to the upper

chamber and incubated at 37 °C for 30 min. Next, 600 µL of complete medium (20% FBS) filled the lower chamber of the 24-well plate-Transwell device. The cells (5×10<sup>4</sup> cells/mL) were fed in serum-free medium at 37 °C for 24 h as a starvation treatment. After digestion, 100 µL of cell solution (5×10<sup>3</sup> cells/mL) was added to the hydrated Transwell. After 24 h, uninvaded cells were washed away. The cells that infiltrated the lower chamber were fixed with 95% ethanol, and stained with 0.1% crystal violet at room temperature for 20 min. The number of cells in five random fields in a ×400-fold field of view were counted.

#### **Reverse transcription-quantitative PCR (RT-qPCR)**

Briefly, total RNA in cells was extracted by Trizol Reagent (Thermo Fisher Scientific, Waltham, MA, USA). For circRNA and mRNA, using the Primescript RT Reagent kit (Takara, Shiga, Japan), each total RNA sample (1 µg) was subjected to reverse transcription reaction to obtain the cDNA template. When detecting circRNA, RNase-R was used to eliminate linear RNAs before reverse transcription. The qPCR amplification was executed with SYBR Green reagent (Takara, Tokyo, Japan) using the ABI 7500 fast real-time PCR System (Applied Biosystems, Foster City, CA, USA) under the following conditions: 95 °C for 10 s, followed by 40 cycles of 95 °C for 10 s, 50 °C for 30 s and 72 °C for 30 s. The expression of mRNA was normalized to GAPDH using the 2<sup>-ΔΔCt</sup> method. The sequences of primers were listed in *Table 1*.

For miRNA, total miRNA was extracted using the miRNeasy Mini kit (GE Healthcare, USA), and cDNA was formed by the TaqMan miRNA reverse transcription kit (DBI Bioscience, Germany). The TaqMan miRNA kit (DBI Bioscience) was applied to measure the expression level of miRNA, normalized to U6 using the 2<sup>-ΔΔCt</sup> method.

#### **Western blot**

Cells were incubated with RIPA lysis solution on ice for 30 min. Cell lysate samples were centrifuged for 20 min at 4 °C, 1,500 g to obtain the supernatant. The concentration of total proteins in the supernatant was determined using a BCA kit (Beyotime Biotechnology). In addition, proteins were separated using an Ambion PARISTM Kit (Invitrogen) strictly according to the instructions. SDS-PAGE was applied for the separation of proteins. After being transferred to a polyvinylidene fluoride membrane (EMD Millipore, USA), proteins were blocked with 5% skimmed

**Table 1** Sequences of primers

Gene	Sequences (5'-3')
F-circRASSF2	ATTCGCACCAATGCTTCA
R-circRASSF2	AGGGCGGGTTCCACTTC
F-miR-6838-5p	GCACTCCTGGATGCCAATCT
R-miR-6838-5p	CTCTACAGCTATATTGCCACGGAC
F-IGF1R	CTTTTCAAAGAGAGTGGCCCG
R-IGF1R	ACGGTGTACTTGCGCATCAG
R-GAPDH	GGTGAAGGTCGGAGTCAACG
F-GAPDH	CAAAGTTGTCATGGATGHACC
R-U6	CGCTTCGGCAGCACATAT
F-U6	AAATATGGAACGCTTCACGA

IGF1R, insulin-like growth factor 1 receptor.

milk for 2 h at room temperature. Rabbit anti-primary antibodies (1:1,000) were then added to the membrane to incubate proteins overnight at 4 °C. All primary antibodies used in this research were as follows: anti-IGF1R (ab182408, Abcam, Cambridge, MA, USA), anti-PI3K (ab32089), anti-p-PI3K (ab278733), anti-AKT (ab8805), anti-p-AKT (ab38449). Tris-buffered saline/0.1% Tween (TBST) solution was used to wash the membrane twice. Horseradish peroxidase-labeled goat anti-rabbit IgG secondary antibody (1:2,000, ab6721) was used to incubate the membrane for 2 h at 37 °C, which was then washed three times with TBST. The protein blots were visualized using enhanced chemiluminescence (Solarbio, China) and image analysis software IPP6.0 was used for the analysis of gray intensity. GAPDH served as the internal control.

### OS tissue collection

We collected 82 pairs of surgically resected OS tissue and adjacent normal tissue samples from patients diagnosed with OS, aged 12–29 years (43 males, 39 females) who had not received radiotherapy, chemotherapy or other anti-tumor treatments before surgery. The expression levels of circRASSF2, miR-6838-5p and IGF1R in each tissue were detected by RT-qPCR. Pearson correlation test was used to analyze the correlation between circRASSF2, miR-6838-5p and IGF1R. According to the median value of circRASSF2, the patients were divided into circRASSF2 high expression and low expression groups, and the relationships between

circRASSF2 and sex, age and clinicopathological characteristics were analyzed. All procedures performed in this study involving human participants were in accordance with the Declaration of Helsinki (as revised in 2013). All patients or their parents/guardians were informed and agreed to participate in the study. This study was approved by the Ethics Committee of the Affiliated Hospital of Guizhou Medical University (No. GZYD003-201753035).

### Statistical analysis

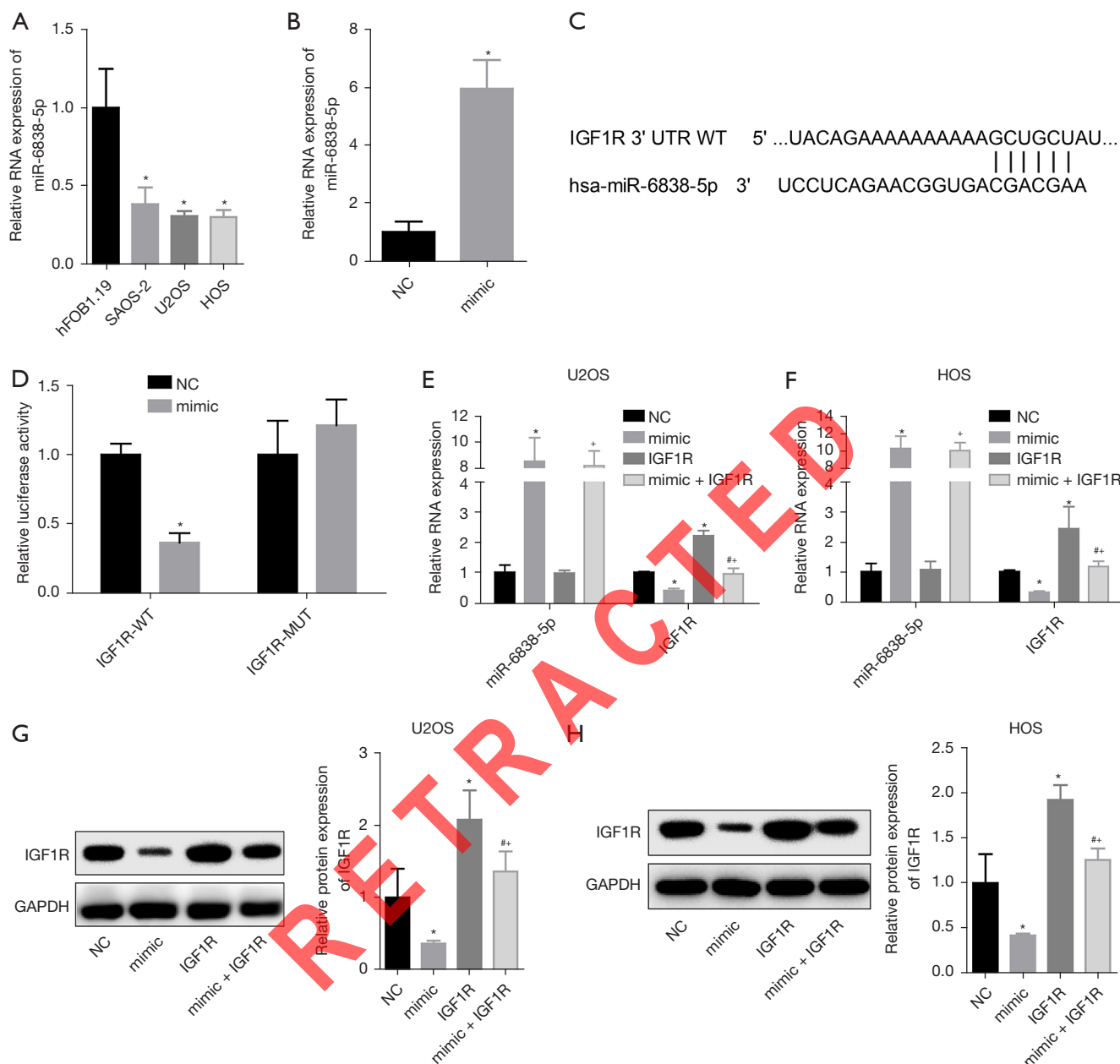
All experiments were performed independently three times. Data are presented as mean ± standard deviation (SD), and were processed by SPSS19.0 software (SPSS Inc., Chicago, IL, USA). Student's *t*-test was used for comparison between two groups, and for comparison among at least three groups, one-way analysis of variance (ANOVA) was applied. The relationships between circRASSF2 and sex, age and clinicopathological characteristics were tested by chi-square.  $P < 0.05$  indicated that the difference was statistically significant.

## Results

### miR-6838-5p targets and inhibits IGF1R expression in OS cells

In order to preliminarily analyze the expression characteristics of miR-6838-5p in OS, firstly its expression in human osteoblast (hFOB1.19) and OS cell lines (SAOS-2, U2OS, and HOS) was detected: miR-6838-5p was significantly downregulated in the OS cell lines, and U2OS and HOS cells were selected for follow-up expression analysis ( $P < 0.05$ ) (Figure 1A). Firstly, miR-6838-5p overexpression cell models were constructed, and it was verified by RT-qPCR that the expression of miR-6838-5p increased by almost 6-fold after transfection of miR-6838-5p mimic ( $P < 0.05$ ) (Figure 1B). The binding sites of miR-6838-5p and the 3'-UTR of IGF1R mRNA are shown in Figure 1C. The dual luciferase report study showed that when miR-6838-5p mimic and wt-IGF1R were transfected, the relative luciferase activity was significantly reduced ( $P < 0.05$ ), which verified the target binding relationship between miR-6838-5p and IGF1R (Figure 1D).

U2OS and HOS cells were divided into four groups: NC group, mimic group, IGF1R group and mimic + IGF1R group. By transfecting miR-6838-5p mimic and/or the



**Figure 1** MiR-6838-5p is downregulated and targets IGF1R in OS cell lines. (A) Expression levels of miR-6838-5p in human osteoblast (hFOB1.19) and OS cell lines (SAOS-2, U2OS, and HOS). (B) Expression levels of miR-6838-5p in cells after transfection of miR-6838-5p NC and miR-6838-5p mimic. (C) Binding site of miR-6838-5p and the 3'-UTR region of IGF1R mRNA. (D) Dual luciferase report verifying the targeting of miR-6838-5p and IGF1R. (E,F) Expression of miR-6838-5p and IGF1R mRNA in each group of cells. (G,H) IGF1R protein expression in each group of cells. \* $P < 0.05$  vs. NC group; # $P < 0.05$  vs. mimic group; \* $P < 0.05$  vs. IGF1R group. MiR, microRNA; IGF1R, insulin-like growth factor 1 receptor; OS, osteosarcoma; NC, negative control.

IGF1R overexpression plasmid, miR-6838-5p and/or the IGF1R were overexpressed. RT-qPCR and western blots confirmed that overexpression of miR-6838-5p reduced

the expression of IGF1R mRNA and protein ( $P < 0.05$ ). Overexpression of IGF1R blocked the inhibitory effect of miR-6838-5p on IGF1R protein expression (Figure 1E-1H).



### ***MiR-6838-5p inhibits proliferation, migration and invasion of OS cells by targeting IGF1R***

The experimental results for the biological behavior of OS cells showed that when the expression of IGF1R protein in the cells increased, the proliferation, migration and invasion abilities of U2OS and HOS cells also significantly increased ( $P < 0.05$ ) (Figure 2A-2F). The proliferation, migration and invasion of the cells in the mimic group were significantly less than in the NC group ( $P < 0.05$ ) (Figure 2A-2F). In addition, the above indicators in the mimic + IGF1R group cells were significantly higher than in the mimic group and less than in the IGF1R group ( $P < 0.05$ ) (Figure 2A-2F). This suggested that miR-6838-5p can inhibit the malignant biological behavior of OS cells, and these effects are inseparable from the activation of IGF1R.

In addition, the PI3K/AKT was a key signaling pathway downstream of IGF1R, and was involved in the proliferation and metastasis of OS cells. The results of this study showed that overexpression of IGF1R increased the phosphorylation levels of PI3K and AKT proteins, while overexpression of miR-6838-5p not only inhibited the expression of IGF1R protein, but also inhibited the activation of the PI3K/AKT pathway ( $P < 0.05$ ) (Figure 2G,2H). These results showed that overexpression of IGF1R blocked the inhibitory effect of miR-6838-5p, as well as PI3K/AKT pathway, on the proliferation and aggressiveness of OS cells. It preliminarily proved that miR-6838-5p played a tumor suppressor effect in OS by targeting the expression of IGF1R.

### ***CircRASSF2 restores the expression of IGF1R by targeting miR-6838-5p***

In order to find the circRNA upstream of miR-6838-5p/IGF1R, the circRNAs targeted by miR-6838-5p were predicted by sequence, and based on the principle of ceRNA, the circRNA positively related to IGF1R was selected. The results showed that circRASSF2 positively correlated with the level of IGF1R ( $P < 0.05$ ) (Figure 3A). The RT-qPCR results also showed that circRASSF2 was upregulated in OS cells, and circRASSF2 expression was the highest in the two cell lines U2OS and HOS ( $P < 0.05$ ) (Figure 3B). In OS cells, the targeted binding of circRASSF2 to miR-6838-5p was verified by the dual luciferase report assay ( $P < 0.05$ ) (Figure 3C-3E). This suggested that circRASSF2 might restore the expression of IGF1R by sponging miR-6838-5p.

To further verify the effects of circRASSF2 on OS

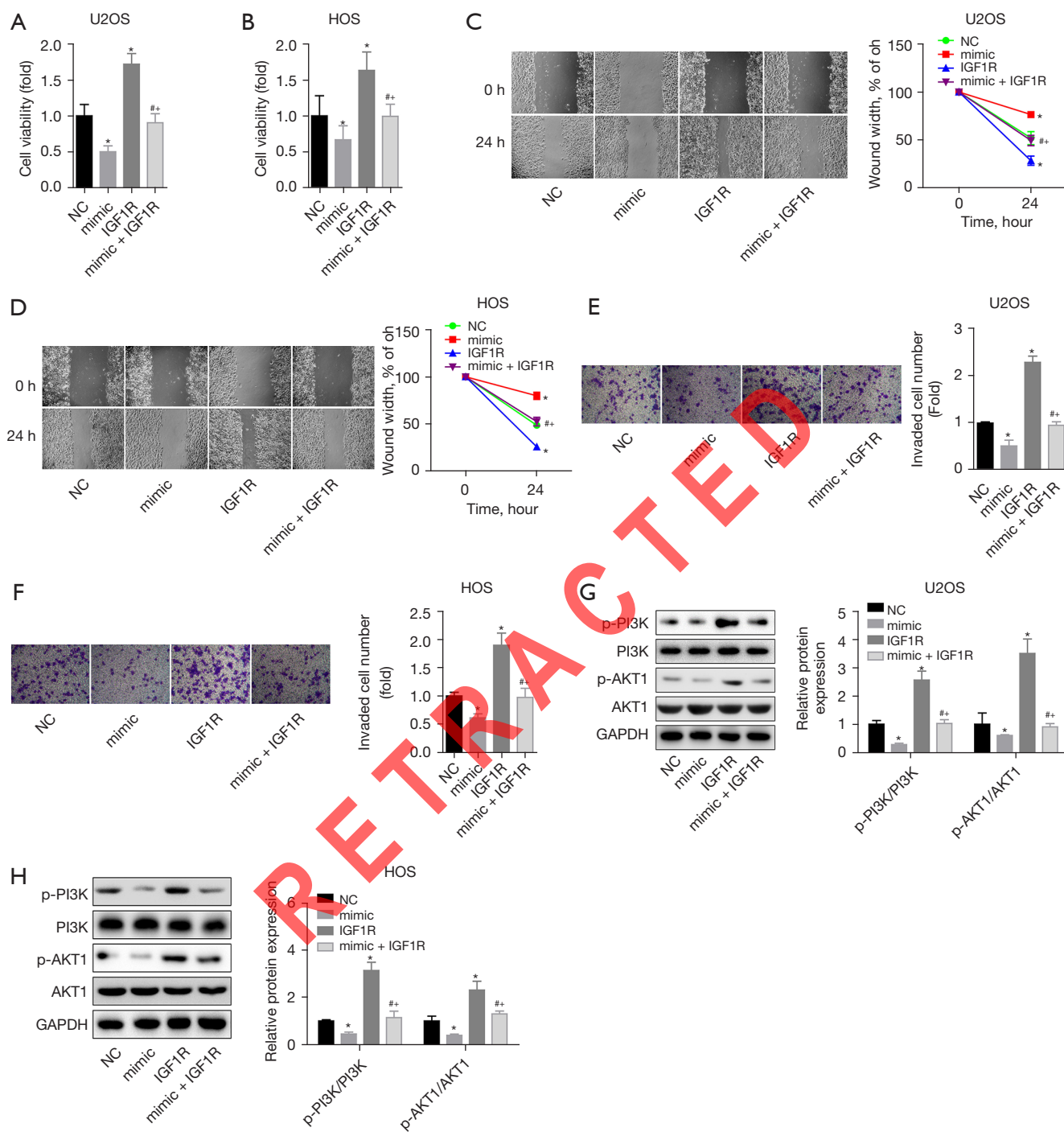
cells through regulation of miR-6838-5p/IGF1R, U2OS and HOS cells were divided into four groups: NC group, circRASSF2 group, mimic group, circRASSF2 + mimic group. By transfecting miR-6838-5p mimic and/or circRASSF2 overexpression plasmid, miR-6838-5p and/or IGF1R were overexpressed. Firstly, IGF1R mRNA and protein were detected by RT-qPCR and western blot, which showed that after overexpression of circRASSF2, the expression of IGF1R mRNA and protein in the cells was significantly increased, and the expression of IGF1R mRNA and protein in the circRASSF2 + mimic group was significantly higher than in the mimic group ( $P < 0.05$ ) (Figure 3F-3I). Overexpression of circRASSF2 reduced the inhibitory effect of miR-6838-5p on IGF1R, suggesting that circRASSF2 restored the expression of IGF1R by sponging miR-6838-5p.

### ***CircRASSF2 promotes the malignant biological behavior of OS cells by promoting PI3K/AKT***

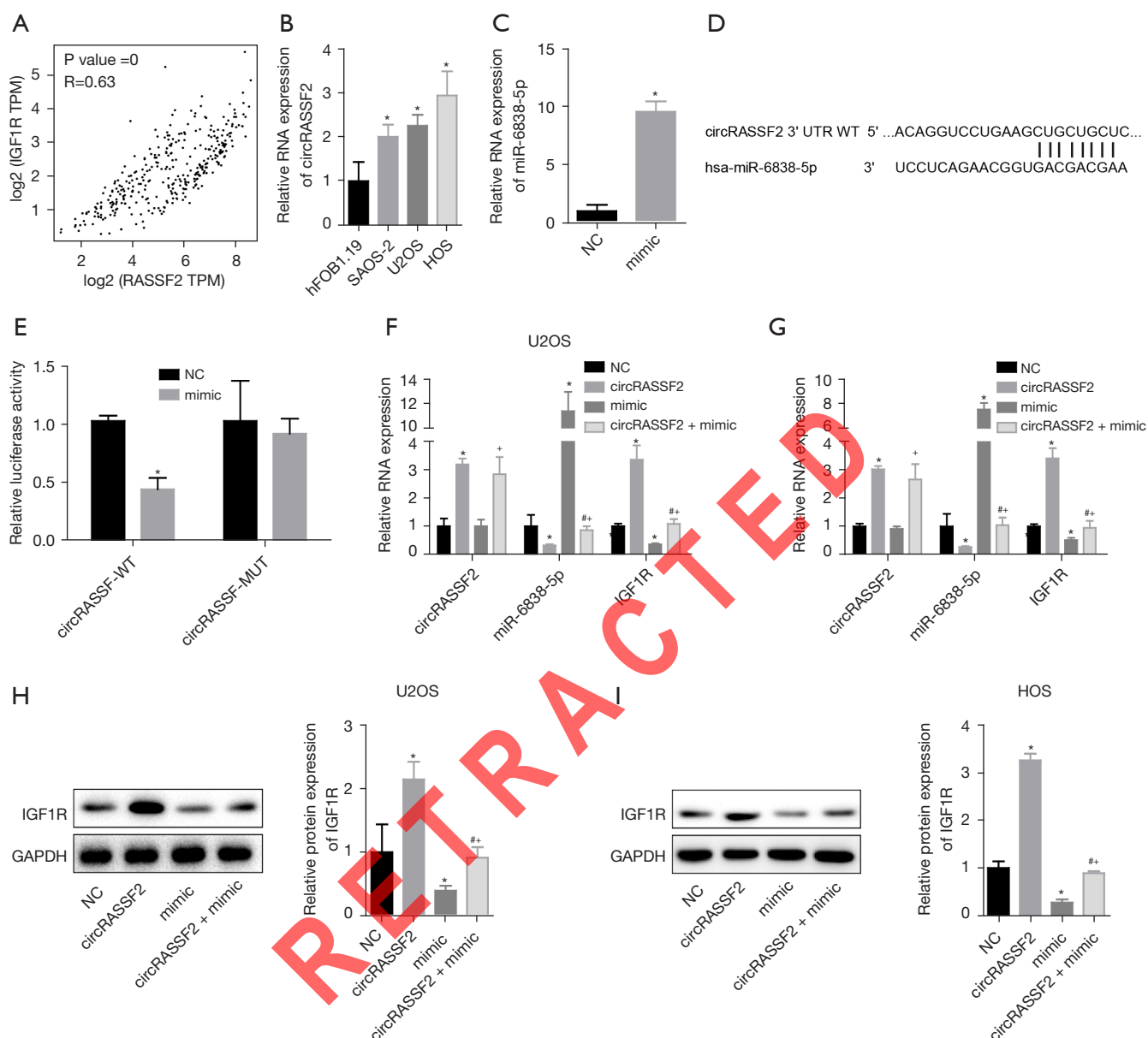
The results for the testing of the biological behaviors of the cells showed that the proliferative, migratory and invasive abilities of the cells in the circRASSF2 group were significantly higher than those in the NC group. In addition, the proliferative, migratory and invasive abilities of the cells in the circRASSF2 + mimic group were significantly higher than in the mimic group ( $P < 0.05$ ) (Figure 4A-4F). Regarding the PI3K/AKT pathway downstream of IGF1R, the results of this study also showed that overexpression of circRASSF2 not only promoted the expression of IGF1R protein, but also promoted the phosphorylation of PI3K and AKT. Overexpression of circRASSF2 could also reduce the inhibitory effect of miR-6838-5p on the PI3K/AKT pathway (Figure 4G,4H). Overexpression of circRASSF2 not only promoted the malignant biological behavior of OS cells, but also removed the inhibitory effects of miR-6838-5p on the cells.

### ***CircRASSF2 and IGF1R increases in OS tissue, while miR-6838-5p decreases***

The expression levels of circRASSF2, miR-6838-5p and IGF1R in OS tissues and adjacent normal tissues were preliminarily analyzed and the results revealed that compared with normal tissues, the expression levels of circRASSF2 and IGF1R mRNA in OS tissue were significantly increased, while miR-6838-5p was significantly

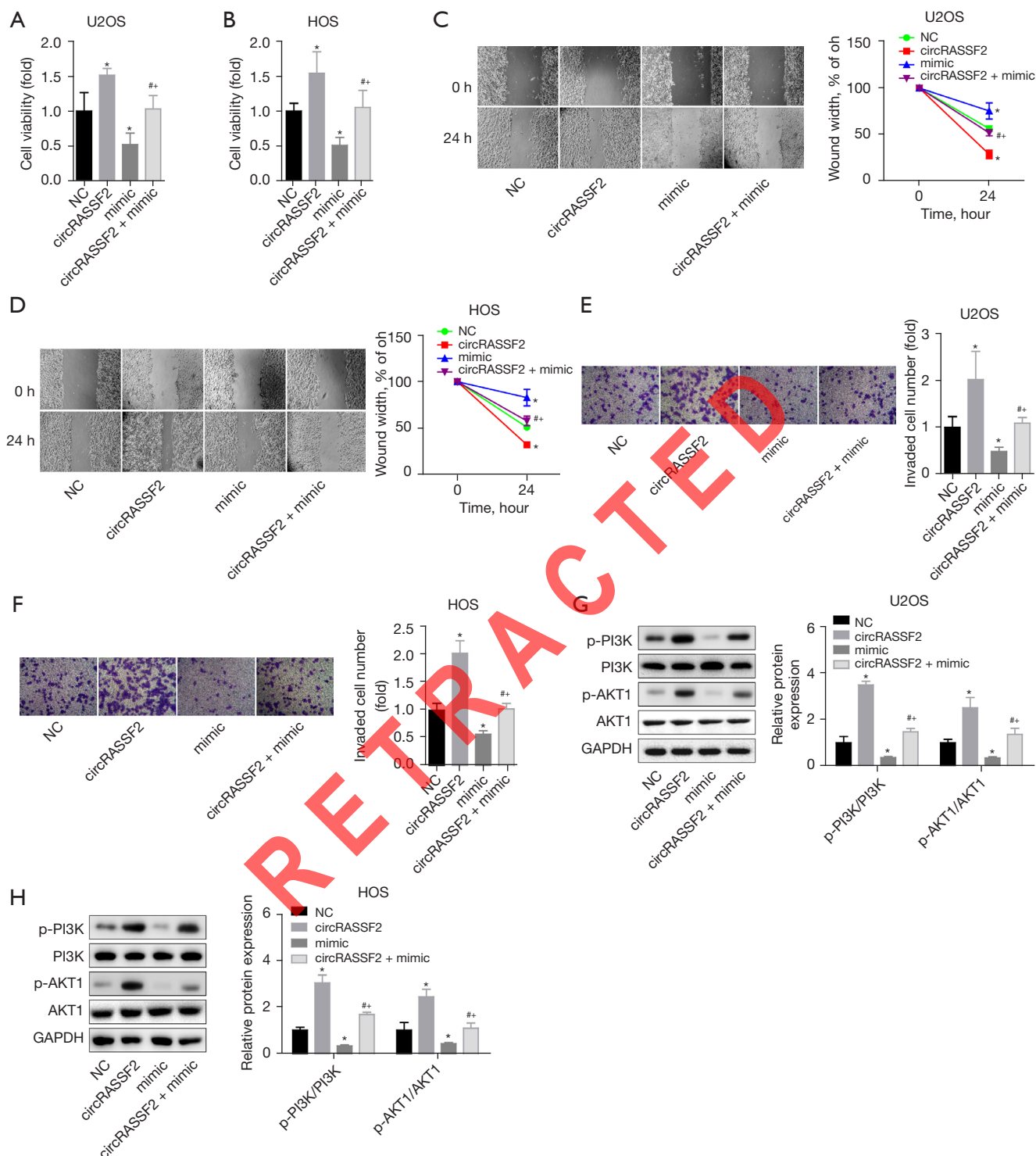


**Figure 2** MiR-6838-5p inhibits the proliferation, migration and invasion of OS cells by targeting IGF1R/PI3K/AKT. (A,B) Comparison of cell proliferative activity of each group. (C,D) Comparison of migratory ability of each group ( $\times 100$ ). (E,F) Comparison of invasive ability of each group (stained with 0.1% crystal violet,  $\times 400$ ). (G,H) Comparison of phosphorylation levels of PI3K and AKT proteins in each group. \* $P < 0.05$  vs. NC group; # $P < 0.05$  vs. mimic group; \* $P < 0.05$  vs. IGF1R group. MiR, microRNA; OS, osteosarcoma; IGF1R, insulin-like growth factor 1 receptor; NC, negative control.

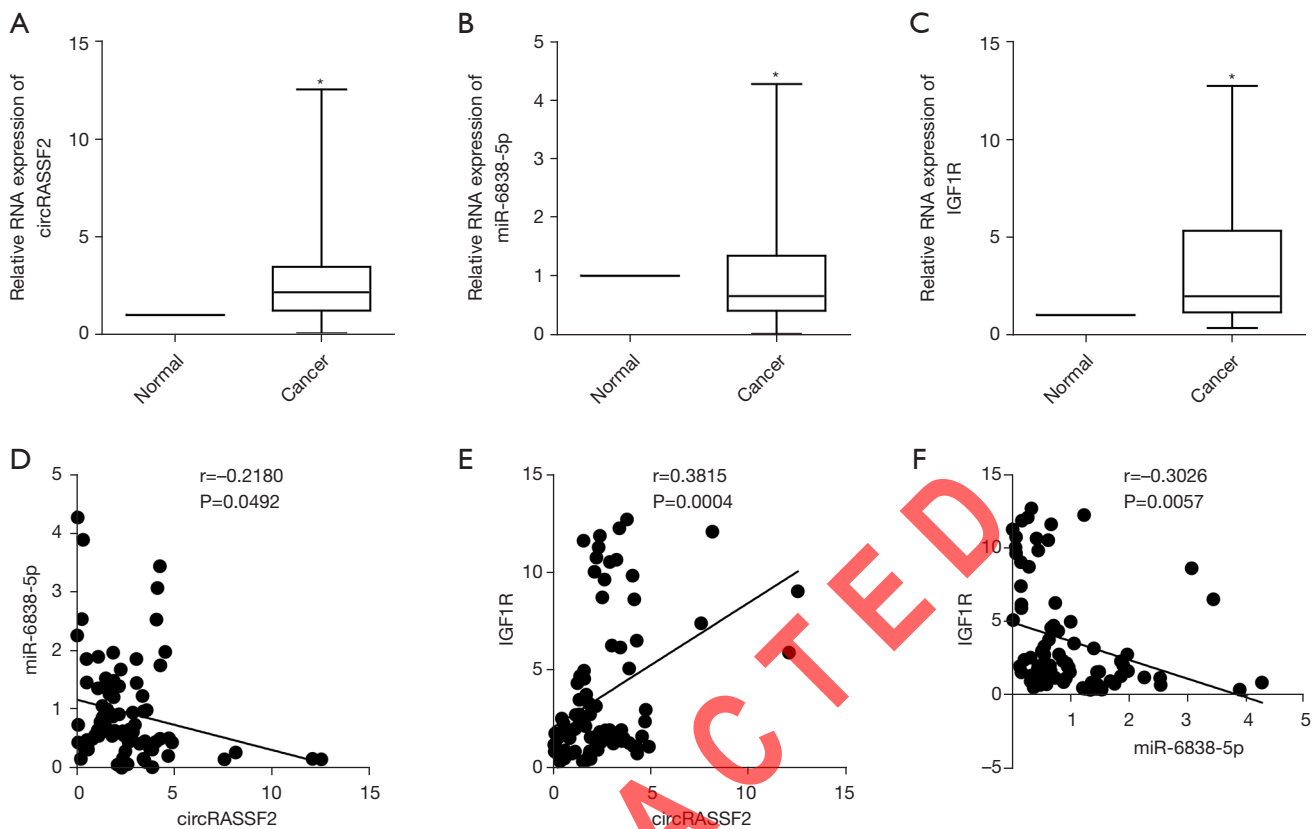


**Figure 3** CircRNA (circRASSF2) promotes the expression of IGF1R by targeting miR-6838-5p. (A) Correlation between circRASSF2 and IGF1R in OS tissues in the TCGA database. (B) Expression levels of circRASSF2 in human osteoblast (hFOB1.19) and OS (SAOS-2, U2OS, HOS) cell lines. (C) Expression levels of miR-6838-5p in cells after transfection of miR-6838-5p NC and miR-6838-5p mimic. (D) Binding site of miR-6838-5p and circRASSF2. (E) Dual luciferase report verifying the targeting of miR-6838-5p and circRASSF2. (F,G) Expression of circRASSF2, miR-6838-5p and IGF1R mRNA in each group of cells. (H,I) IGF1R protein expression in each group of cells. \* $P < 0.05$  vs. NC group; # $P < 0.05$  vs. circRASSF2 group; \* $P < 0.05$  vs. mimic group. CircRNA, circular RNA; IGF1R, insulin-like growth factor 1 receptor; OS, osteosarcoma; TCGA, The Cancer Genome Atlas; NC, negative control.





**Figure 4** CircRNA (circRASSF2) activates the PI3K/AKT pathway and promotes the proliferation and metastasis by sponging miR-6838-5p. (A,B) Comparison of cell proliferative activity of each group. (C,D) Comparison of migratory ability of each group ( $\times 100$ ). (E,F) Comparison of invasive ability of each group (stained with 0.1% crystal violet,  $\times 400$ ). (G,H) Comparison of phosphorylation levels of PI3K and AKT proteins in each group. \* $P < 0.05$  vs. NC group; # $P < 0.05$  vs. circRASSF2 group; + $P < 0.05$  vs. mimic group. CircRNA, circular RNA; NC, negative control; IGF1R, insulin-like growth factor 1 receptor; NC, negative control.



**Figure 5** Expression characteristics and correlation of circRNA (circRASSF2), miR-6838-5p and IGF1R in OS. Comparison of (A) circRASSF2, (B) miR-6838-5p and (C) IGF1R expressions in OS and adjacent normal tissues. Correlation between (D) miR-6838-5p and circRASSF2, (E) IGF1R and circRASSF2 and (F) IGF1R and miR-6838-5p in OS tissues. \* $P < 0.05$  vs. normal group. CircRNA, circular RNA; miR, microRNA; IGF1R, insulin-like growth factor 1 receptor; OS, osteosarcoma.

decreased (Figure 5A-5C). The level of miR-6838-5p negatively correlated with circRASSF2 (Figure 5D). The level of IGF1R mRNA positively correlated with circRASSF2 (Figure 5E). The level of IGF1R mRNA negatively correlated with miR-6838-5p (Figure 5F). Moreover, based on the median value of circRASSF2, the patients were divided into circRASSF2 high expression group and low expression group. The expression of circRASSF2 had no significant relationship with the patient's age, sex or tumor size. High levels of circRASSF2 were associated with higher clinical stage and distant metastasis (Table 2). These results matched with those of the cell experiments and suggested that circRASSF2 has a role in promoting progression in OS.

## Discussion

Migration and invasion are the keys to metastasis and

recurrence of OS, as well as being risk factors of a poor prognosis (17,18). IGF1R is the upstream activator of multiple signaling pathways, and a key factor in progression of OS (19,20). IGF1R is targeted and regulated by miRNA, and the significance and regulatory mechanism of ncRNA in OS is a research focus (21). miRNAs are a type of short (~22 nucleotides), conserved endogenous RNA. They efficiently bind to the 3'-UTR region of mRNA. This complementary base pairing can prevent translation or induce mRNA degradation (22,23). miR-6838-5p was newly discovered (Ensembl: ENSG00000283969; miRBase: MI0022684) in 2018 to be related to nerve pain in patients with spinal cord injury (24). miR-6838-5p can also prevent the nuclear translocation of  $\beta$ -catenin through targeted inhibition of GPRIN3, thereby inhibiting malignant behavior of gastric cancer cells (12). Similarly, in breast cancer, miR-6838-5p directly inhibits the expression of WNT3A to reduce cell proliferation (11). Although miR-6838-5p is upregulated

**Table 2** Correlation between circRASSF2 expression and clinicopathological features in patients with OS

Characteristics	Total number	CircRASSF2 expression		P value
		High (n=41)	Low (n=41)	
Age (years)				0.647
<18	52	25	27	
≥18	30	16	14	
Sex				0.269
Male	43	24	19	
Female	39	17	22	
Tumor size (cm)				0.641
<5	54	26	28	
≥5	28	15	13	
Clinical stage				0.038
I-IIA	53	22	31	
IIB/III	29	19	10	
Distant metastasis				0.007
Negative	59	24	35	
Positive	23	17	6	

OS, osteosarcoma.

in renal cell carcinoma and participates in its invasiveness by targeting the DMTF1/ARF-p53 pathway (25), we found that compared with osteoblasts, OS cells showed lower expression of miR-6838-5p. The dual luciferase report confirmed that miR-6838-5p targeted IGF1R, and increasing the expression of miR-6838-5p inhibited IGF1R protein expression. In addition, the results of biological behavior experiments showed that overexpression of miR-6838-5p inhibited the proliferation, migration and invasion of OS cells, while overexpression of IGF1R significantly blocked the anticancer effects of miR-6838-5p. These results showed that in OS cells, the tumor suppressor effect of miR-6838-5p is inseparable from targeted inhibition of IGF1R.

The miRNA can be adsorbed by ncRNAs, thereby inhibiting their function (26). The ncRNAs mainly include lncRNA and circRNA. Their ceRNA functions are similar, but due to the closed-loop structure of circRNA, the stability of circRNA is much higher than that of lncRNA (27,28). The way that circRNA regulate gene expression through miRNA has been revealed in OS (29-31). In order

to find the upstream circRNA that regulates miR-6838-5p/IGF1R, we carried out sequence prediction, based on the positive correlation between circRNA and IGF1R. The results showed that circRASSF2 (NM\_170774,) targets miR-6838-5p, and bioinformatics analysis showed that circRASSF2 positively correlated with IGF1R. The targeted binding relationship between circRASSF2 and miR-6838-5p was verified by the dual luciferase report. In addition, overexpression of circRASSF2 increased the expression of IGF1R protein, and blocked the inhibitory effect of miR-6838-5p on IGF1R. circRASSF2 was first clinically verified in 2019, and that study also showed that circRASSF2 was upregulated in the circulating exosomes in patients with laryngeal squamous cell carcinoma (LSCC), and silencing circRASSF2 inhibited both the growth of LSCC *in vivo* and the expression of IGF1R protein (15). circRASSF2 is also overexpressed in papillary thyroid carcinoma tissues (16). *In vitro* experiments have shown that circRASSF2 promotes the expression of TLR4 by targeting miR-1178 and participates in tumor progression (16). In the present study, our results showed that overexpression of circRASSF2 not only improved the proliferative, migratory and invasive abilities of OS cells, but also deleted the negative effect of miR-6838-5p on the malignant behavior of cells. Combining the above-mentioned literature and the results of this study, it is suggested that in OS cells, circRASSF2 blocks the targeting function of miR-6838-5p by adsorbing miR-6838-5p, thereby promoting the expression of IGF1R protein. This activates the PI3K/AKT pathway, which in turn promotes OS cell proliferation and movement, and promotes OS progression. In addition, clinical research results of this study also show that miR-6838-5p is downregulated in OS and negatively correlated with IGF1R, and circRASSF2 is upregulated and positively correlated with IGF1R. High levels of circRASSF2 are related to the clinical stage and metastasis of OS, which further suggests the role of circRASSF2 in the progression of OS, and may become a new target for diagnosis and treatment.

## Conclusions

In summary, the promoting effects of IGF1R on OS are targeted by miR-6838-5p. circRASSF2 restores the expression of IGF1R by sponging miR-6838-5p, thereby promoting the progression of OS. The clinical significance of circRASSF2 and miR-6838-5p in OS deserve further analysis, and the regulatory effect of circRASSF2/miR-

6838-5p on the expression of IGF1R and the progression of OS still needs to be studied *in vivo*.

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## Footnote

*Reporting Checklist:* The authors have completed the MDAR reporting checklist. Available at <https://dx.doi.org/10.21037/atm-21-6123>

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*Ethical Statement:* The authors are accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved. All procedures performed in this study involving human participants were in accordance with the Declaration of Helsinki (as revised in 2013). All patients or their parents/guardians were informed and agreed to participate in the study. This study was approved by the Ethics Committee of the Affiliated Hospital of Guizhou Medical University (No. GZYD003-201753035).

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