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ORIGINAL RESEARCH

RETRACTED ARTICLE: Long-Noncoding RNA CASC9 Promotes Progression of Non-Small Cell Lung Cancer by Promoting the Expression of CDC6 Through Binding to HuR

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Objective: The long-noncoding RNAs (lncRNAs) have been identified as key players in diverse cellular processes in non-small cell lung cancer (NSCLC). However, the understanding of biological functions and detailed mechanisms of lncRNAs is still limited. Herein, the lncRNA cancer susceptibility candidate 9 (CASC9) on NSCLC progression is investigated.

Materials and Methods: Expressions of CASC9, HuR and cell division cycle 6 (CDC6) in NSCLC tissues were detected with quantitative real-time polymerase chain reaction (qRT-PCR). The cell counting kit-8, transwell assays, and flow cytometry were used to examine cell proliferation, migration, and the cell cycle. Tumor growth in vivo was evaluated by xenograft tumor experiments and immunohistochemistry. RNA-binding protein immunoprecipitation (RIP) was performed to identify the interaction between HuR and CDC6, and CASC9 and HuR.

Results: CASC9, CDC6 and HuR expression were found significantly upregulated in NSCLC tissues, which predicted poorer 5-year overall survival in NSCLC patients. Inhibition of CASC9 significantly reduced the malignancy of NSCLC cells, such as proliferation, migration and cell cycle. In vivo experiments further demonstrated that CASC9 knockdown reduced the tumor growth and the Ki-67 expression. Moreover, CASC9 knockdown inhibited the expression of CDC6 which was detected overexpressed in NSCLC tumor tissues. Then, up-regulation of CDC6 could partly reverse the negative effects of CASC9 on cell proliferation, migration and cell cycle. RIP assay and rescue experiment showed that CASC9 regulated CDC via binding to HuR.

Conclusion: Our results indicate that CASC9 conferred an aggressive phenotype in NSCLC and might be a pivotal target for this disease.

Keywords: lncRNA, non-small cell lung cancer, proliferation, migration, cell cycle

Introduction

Lung cancer has become the most commonly diagnosed respiratory cancer in recent years and the leading cause of cancer-related mortality worldwide. According to Global Cancer Statistics 2018, lung cancer is the most frequent cancer among males and the second common cancer among females, remaining the leading cause of cancer death among the overall populations.[1] Pathologically, non-small cell lung cancer (NSCLC) occupies 80–85% of lung cancer cases and its 5-year survival rate has

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been reported to be less than 20%.[2] Despite the improvements in treatments to lung cancer, most patients progress to advanced stages for lack of early detection, and thus missing the opportunity to receive surgery.[3] Radiotherapy, chemotherapy and targeted therapy are recommended for patients in advanced stages. However, resistance to these treatments, patient compliance and side effects can be an important issue.[4,5] Therefore, it is of great necessity to identify novel molecules and targets for early diagnosis, accurate prognostic prediction and targeted therapy in NSCLC.

Long non-coding RNAs (lncRNAs) are a special class of transcripts with length>200 bases and limited protein-coding capacity.[6,7] With the rapid development of genome sequence, more and more lncRNAs were investigated, and their indispensable functions in regulating gene expression during the transcription, post-transcription and translation processes have been identified in numerous cancer types.[8–10]

Long noncoding RNA cancer susceptibility candidate 9 (CASC9) is located at the human chromosome 8q21.13. It has been reported in recent studies that the over-expression of CASC9 can promote the malignant phenotype of cancer cells in colorectal cancer and breast cancer.[11,12] However, the role of CASC9 in NSCLC has not been reported yet.

Cell division cycle 6 (CDC6) was originally identified as one of the mutations that can arrest the budding yeast cell cycle. As for the human CDC6 gene, it is located at chromosome 17q21.3 and controlled by the E2F family of transcription factors that regulate S-phase-promoting genes. CDC6 serves as one of the key regulators in the initiation of DNA replication, with the evidence that the absence of CDC6 could lead to the G1 phase arrest.[13,14] Therefore, CDC6 has been identified as a novel target in numerous cancers.[15,16]

In the present study, we observed the over-expression of CASC9 in NSCLC tumor tissues and its function in promoting NSCLC cell proliferation, migration and cell cycle. Meanwhile, we discovered CASC9 could exert its roles via regulating CDC6, however, the underlying mechanism still needs to be addressed. Therefore, this study aimed to explore how CASC9 functioned in the procedure of NSCLC.

Materials and Methods

Cancer Tissue Collection

A total of 48 NSCLC tumor tissues and paired 48 adjacent normal tissues were obtained from the Xi'an Medical University between November 2017 and September 2019. All collected samples were snap-frozen in liquid nitrogen and stored at −80°C for subsequent analyses. This study was approved by the Ethics Committee of Xi'an Medical University (XAMU20171128) and obtained the written informed consent from each patient. The clinicopathological information of 48 NSCLC patients was shown in Table 1.

Cell Culture and Transfection

The human bronchial epithelioid cells (HBE) and NSCLC cell lines (H1650, H460, SPC-A1 and A549) were purchased from the Cell bank of Chinese academy of sciences (Shanghai, China). Cells were cultured in Roswell Park Memorial Institute (RPMI) 1640 medium (GIBCO-BRL; Thermo Fisher Scientific, USA) containing 10% fetal bovine serum (Hyclone, USA) at 37°C with 5% CO_2 and saturated humidity. Cells were transfected with sh-CASC9, sh-HuR and CASC9, CDC6, HuR overexpression plasmids and paired negative control which were provided by Genchem (Shanghai, China), followed by mixing with lipo2000 (Thermo Fisher Scientific, USA).

Table 1 Correlation Between CASC9 Expression and Clinicopathological Characteristics in NSCLC Patients

Characteristics		CASC9 Expression Level	
	Low (n=23)	High (n=25)	*P*
Gender			
Male	12 (52.2%)	15 (60.0%)	0.5851
Female	11 (47.8%)	10 (40.0%)	
Age			
<60	10 (43.5%)	12 (48.0%)	0.7534
≥60	13 (56.5%)	13 (52.0%)	
Tumor size			
≤3cm	13 (56.5%)	9 (36.0%)	0.154
>3cm	10 (43.5%)	16 (64.0%)	
Tumor stage			
T1+T2	14 (60.9%)	15 (60.0%)	0.9509
T3+T4	9 (39.1%)	10 (40.0%)	
TNM stage			
I+II	17 (73.9%)	10 (40.0%)	0.018
III+IV	6 (26.1%)	15 (60.0%)	
Histological grade			
Well/moderate	12 (52.2%)	9 (36.0%)	0.2591
Poor/NS	11 (47.8%)	16 (64.0%)	
Lymph node metastasis			
M0	17 (73.9%)	11 (44.0%)	0.0357
M1	6 (26.1%)	14 (56.0%)	

Quantitative Real-Time PCR (RT-qPCR)

The TRIzol reagent (Thermo Fisher Scientific) was used to extract RNA samples from tissues and cultured cell lines. The RNA expression was quantified with a Nanodrop Spectrophotometer (IMPLEN GmbH, Munich, Germany) by measuring the absorbance at 260/280 nm. The PrimeScript RT Reagent Kit (Takara, Otsu, Japan) was utilized to synthesize complementary DNA (cDNA) from 1μg RNA. The final volume was 20μL containing random primers from GenePharma. Quantitative reverse real-time PCR was performed on a 7900 Fast Real-Time PCR System (Thermo Fisher Scientific). The amplification reaction volume was 10μL, which contained 0.2μM of each primer, 5μL of SYBR Green PCR master mix (2×) (Takara) and 0.2μL of cDNA. The reaction was performed at 95°C for 30 seconds, then at 95°C for 5 seconds for 40 cycles and 60°C for 31 seconds for the amplification. The examined lncRNA-CASC9 data were normalized according to their corresponding GAPDH. The relative expression of each sample was determined in technical triplicates. The sequences of primer pairs were shown below:

CASC9: forward 5′-AGA TGA AGC CGG TAC CTC AGAT-3′,

reverse 5′- TCA CTT TAA AGA GGG AG[illegible] AG-3′;

CDC6: forward 5′-AGAAGGGCCCCATC[illegible]TTGTG[illegible]

reverse 5′-TAGCTCTCCTGCAAAC[illegible]TCCA[illegible]-3′;

GAPDH: forward 5′-AGCAAG[illegible]CAC[illegible]CAGGA AG-3′,

reverse 5′-GGTTGAGCA[illegible]GGTACT[illegible]3′.

Cell Viability Assays

The Cell Counti[illegible] Kit-8 (CCK8; Beyotime, Jiangsu, China) was utilized to monitor the cell viability. An equal numb[illegible] of cells ([illegible]000 cells/well) were plated into 96-well plates w[illegible]ere cont[illegible]ned 100μL culture medium after tra[illegible]fecti[illegible]n and [illegible]μL CCK8 regent was then added to. The plat[illegible] were incubated at 37°C with 5% CO_2 for 2 hours, after wi[illegible]h the optical density at a wavelength of 450 nm was measured for each plate using a plate reader (Infinite M200; Tecan, Männedorf, Switzerland). Each group had five replicate wells and the experiments were run in triplicate.

Cell Cycle Assay

After being collected and washed twice with 1× PBS, cells were then fixed with 70% ethanol at −20°C for 24 h. After that, RNaseA (100μg/mL, Takara Bio, Inc., Otsu, Japan) and 1× PBS were added for 30 min at 37°C, followed by the cell staining with propidium iodide (50μg/mL, PI;BD Biosciences, San Jose, California) for 30 min at 20–25°C. Subsequently, fluorescence was acquired by flow cytometry on a Becton Dickinson FACSCalibur™ flow cytometer (BD Biosciences).

Transwell Assay

The transwell assay was performed to analyze cell migration in vitro. Two hundred μL cells cultured in serum-free medium were added into the upper chamber in a 24-well plate (Corning, New York), while 600μL medium supplemented with 20% fetal bovine serum (FBS) was added to the bottom wells of the chambers. After incubating, cells on the outer membrane were fixed with 4% paraformaldehyde, then stained with 0.1% crystal violet solution. Five randomly selected fields under a microscope were captured to observe migratory cells.

Western Blotting Analysis

[illegible]Lysis buffer (Cell Signaling Technology, Danfoss, MA, USA) containing phenylmethanesulfonyl fluoride (Beyotime) was used to lyse the stimulated cancer cell [illegible]s. Equal amounts of extracts were separated to 10% or 12.5% SDS PAGE gels (Abcam, Cambridge, UK), transferred onto polyvinylidene fluoride membranes (EMD Millipore), followed by incubation with primary antibodies at 4°C overnight. The primary antibodies were anti-CDC6 (ab109315, abcam), Ki-67 (ab245113, abcam), anti-PCNA (ab92552, abcam) and GAPDH (AF0009; Beyotime). HRP-conjugated secondary antibodies were used to incubate the membranes for 1 hour at room temperature, after which they were washed with TBST (PBS with 0.05% Tween20) 6 times. Finally, the visualization of the blot bands was achieved by Find-do ×6 Tanon (Tanon, Shanghai, China).

In vivo Experiments

Briefly, 4–5 weeks old BALB/c nude mice were obtained from the cancer institute at the Model Animal Research Center of Nanjing University (Nanjing, China) and randomly assigned into two groups. A549 cells stably transfected with sh-CASC9 or NC were utilized to investigate the effects of CASC9 on tumor growth. A total of 1×10^7 A549 cells were subcutaneously injected into the posterior flank of mice. Every 7 days, tumor volumes were measured using a caliper and calculated using the following equation: (short

diameter)2 × (long diameter)/2. After 28 days, all mice were sacrificed and the tumors were resected and fixed in formalin. The animals' experiments in this study were approved by the Institution of Animal Ethical and Welfare Committee of Xi'an Medical University (No.20171128) and in compliance with the guidelines of the National Animal Care and Use Committee.

Statistical Analysis

Results of at least three separate experiments were calculated as mean ± standard deviations (SD). Comparison within two groups was analyzed using the Student's *t*-test or one-way ANOVA with SPSS 16.0 software system (IBM Corp., Armonk, NY, USA). A P-value of <0.05 was considered statistically significant.

Results

CASC9 Was Overexpressed in NSCLC Tissues and Cells

Firstly, CACS9 was found overly expressed in NSCLC tumor tissues than adjacent normal ones (Figure 1A). Furthermore, CASC9 was more up-regulated in metastasis patients than in non-metastasis patients (Figure 1B). Meanwhile, in stage III-IV patients, we detected a higher expression level than that in stage I-II patients (Figure 1C). ROC curve analysis results showed CACS9 might be a biomarker for NSCLC with AUC=0.8034, Cutoff value=0.3663 (Figure 1D). The five-year overall survival analysis showed the up-regulation of CASC9 indicated poor prognosis compared to low expression group (Figure 1E). Furtherly, we found CASC9 was generally overexpressed in NSCLC cell lines (Figure 1F). Considering CASC9 was more up-regulated in SPC-A1 and A549 cells, we selected them for the further study.

CASC9 Inhibition Suppressed Cell Proliferation, Migration and Cell Cycle in vitro

The sh-CASC9 was employed to knock down the expression of CASC9 (Figure 2A). When transfected with sh-CASC9, the proliferation of A549 and SPC-A1 cells was inhibited (Figure 2B and C), as well as the cell migration (Figure 2D). Additionally, the cell cycle was also detected. As the result shown, down-regulated CASC9 induce G1 phase arrest in both cells (Figure 2E).

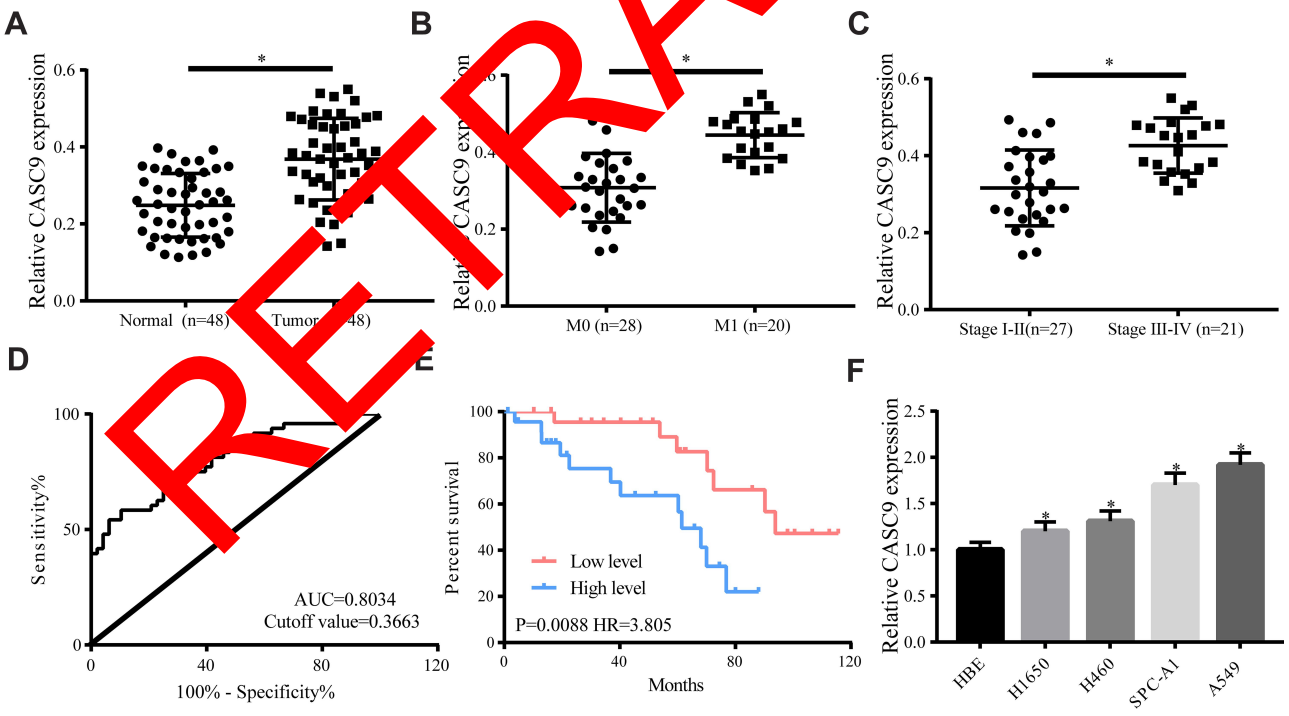

Figure 1 CASC9 was over-expressed in NSCLC tissues and cells. (**A**) The expression of CASC9 enriched significantly in tumor tissues than para-cancerous tissues. (**B**) The over-expression of CASC9 was significantly associated with metastasis in NSCLC patients. (**C**) Higher level of CASC9 expression was found in patients in the advanced stages (III–IV stage) than those in the I–II stage. (**D**) The ROC curve showed the potential of CASC9 as a biomarker for early diagnosis. The AUC was 0.8034, with the cutoff value of 0.3663. (**E**) Kaplan–Meier analysis showed that the overexpression of CASC9 predicted significantly poorer prognosis in NSCLC patients. (**F**) CASC9 was generally overexpressed in NSCLC cell lines than human normal bronchial epithelial (HBE) cells. *P<0.05.

CASC9 Deficiency Inhibited Tumor Growth in vivo

Whether sh-CASC9 can decrease tumorigenesis in vivo was assessed using mouse xenografts injected with A549 cells. The tumors in the sh-CASC9 group were substantially smaller than the control group (Figure 3A), as well as for the tumor volume and weight (Figure 3B and C). The qPCR results showed sh-CASC9-transfected cells presented a lower level of CASC9 expression in tumor tissues compared to the control cells (Figure 3D). In addition, IHC staining indicated that the Ki-67 and PCNA-positive cells from tumors in the sh-CASC9 group were obviously decreased compared to that in the control group (Figure 3E and F), indicating that CASC9 deficiency reduced tumor growth in vivo.

CASC9 Regulated the Expression of CDC6

When cells were transfected with sh-CASC9, a reduce in CDC6 expression was obviously observed at mRNA and protein level (Figure 4A and B). Additionally, when the expression of CASC9 was up-regulated, the mRNA and protein level of CDC6 was raised (Figure 4C and D). Furtherly, we found CDC6 was also up-regulated in NSCLC tumor tissues (Figure 4E and F). Therefore, CDC6 might be active in the procedure of NSCLC.

CASC9 Promoted Cell Proliferation, Migration and Cell Cycle via Regulating CDC6

We employed the CDC6 over-expression vector to raise the CDC6 expression in SPC-A1 and A549 cells (Figure 5A and B). When we down-regulated CASC9 and up-regulated CDC6 at the same time in both cells, we found the up-regulation of CDC6 could partly reverse the negative effects of shCASC9 on cell proliferation, migration, as well as cell cycle (Figure 5C–F). The above results confirmed that CASC9 exerted its roles via regulating CDC6.

CASC9 Directly Bound to HuR and Regulated CDC6

As RIP experiment results showed, HuR could bind to CDC6 in SPC-A1 and A549 cells (Figure 6A and B). When we reduced and raised HuR expression, the CDC6 expression was down-regulated and up-regulated, respectively (Figure 6C). The mRNA and protein level of HuR in NSCLC tumor tissues was up-regulated than normal ones (Figure 6D and E). Further, CASC9 and HuR expression has a positive correlation in NSCLC patients (Figure 6F). Meanwhile, we also demonstrated that CASC9 could bind to HuR via RIP experiment (Figure 6G and H). When CASC9 expression increased and decreased, the expression of HuR was raised and reduced, respectively (Figure 6I). Further, when cells transfected with sh-CASC9 and HuR over-expression vector simultaneously, the down-regulation of CDC6 caused by sh-CASC9 could be partly reversed by the up-regulation of HuR, which demonstrated that CASC9 might regulate CDC6 by binding to HuR (Figure 6J and K).

Discussion

With a further understanding of the pathogenesis of NSCLC in recent decades, the development of predicted biomarkers greatly provided a new insight into the treatment for NSCLC patients.[17] However, the established mechanisms cannot fully clarify the pathogenesis of NSCLC and a more thorough understanding are still needed. Hence, further investigations in the mechanisms and developments for the novel targeted therapies are of great importance for the treatment and prognosis in NSCLC patients.

As novel therapeutic targets, lncRNAs have been studied a lot and their roles of modulation in lung cancers have been found in previous studies.[18,19] In the present study, lncRNA CASC9 was notably up-regulated in NSCLC tissues, indicating CASC9 might have a significant contribution to malignant behaviors of NSCLC. To verify this hypothesis, CASC9 was down-regulated via sh-CASC9 in A549 and SPC-A1 cells, and the cell proliferation and migration were observed to be attenuated obviously. In in vivo experiment, the down-regulation of CASC9 inhibited tumor growth and the proliferation-related protein Ki-67 and PCNA were also down-regulated.

DNA replication in the cell cycle has a close relationship to the cell proliferation, quiescence, differentiation, senescence and apoptosis, within which CDC6 is the key protein for the initiation of the process. In this study, we found CASC9 caused G1 phase arrest of cell cycle, so we aimed to elucidate whether CASC9 regulated cell proliferation and cell cycle via CDC6. As expected, the protein level of CDC6 was reduced when CASC9 was down-regulated; however, CDC6 was over-expressed when CASC9 was knocked down. Furthermore, the level of CDC6 expression was significantly raised in NSCLC

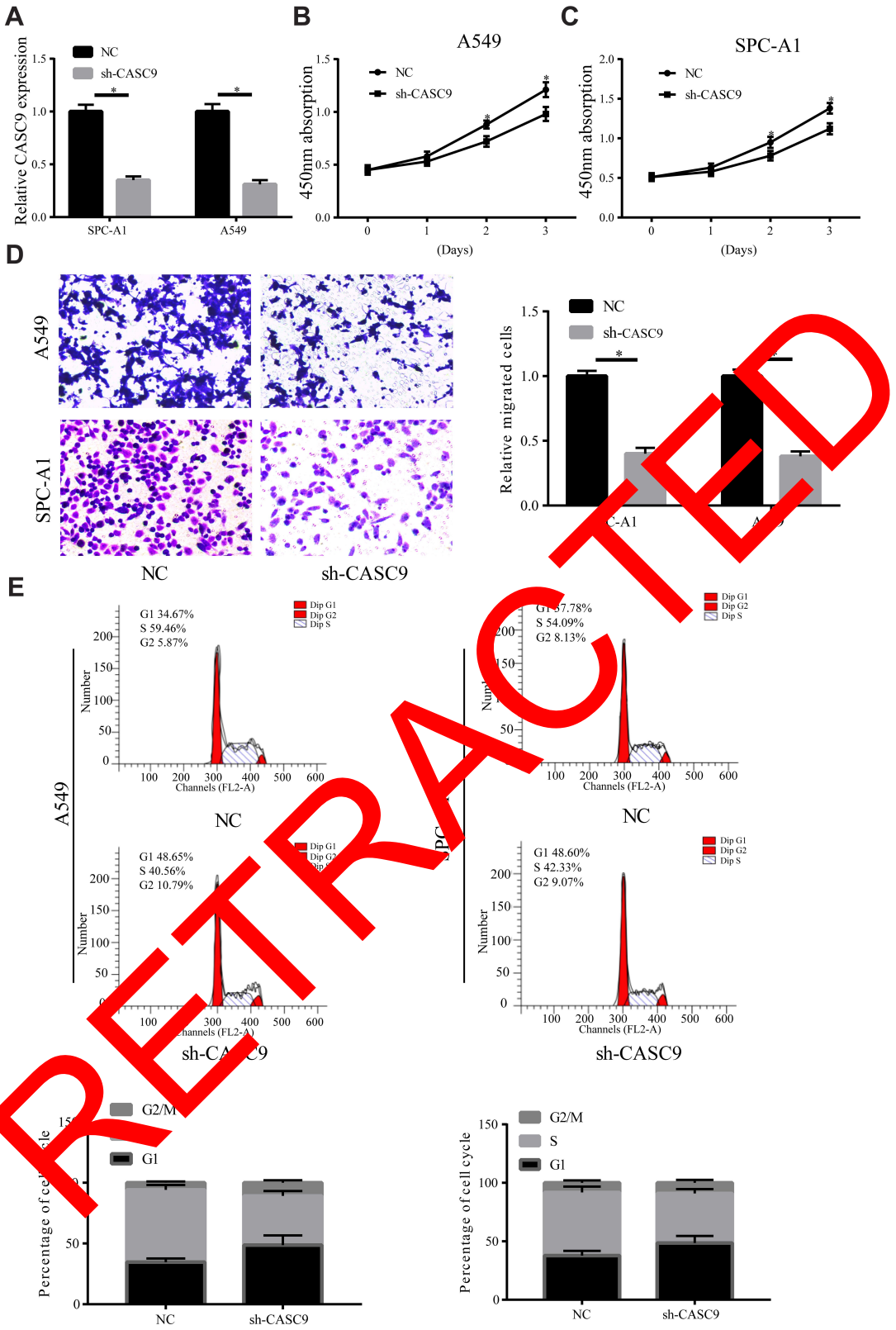

Figure 2 CASC9 inhibition suppressed cell proliferation, migration and cell cycle in vitro. (**A**) The level of CASC9 expression was significantly lower in A549 and SPC-A1 cells transfected with sh-CASC9, which led to the remarkable inhibition of cancer cell proliferation (**B** and **C**) and cell migration (**D**). (**E**) Down-regulated CASC9 in A1 and A549 cells inhibited the cell cycle transition from G1 to S phase. *P<0.05.

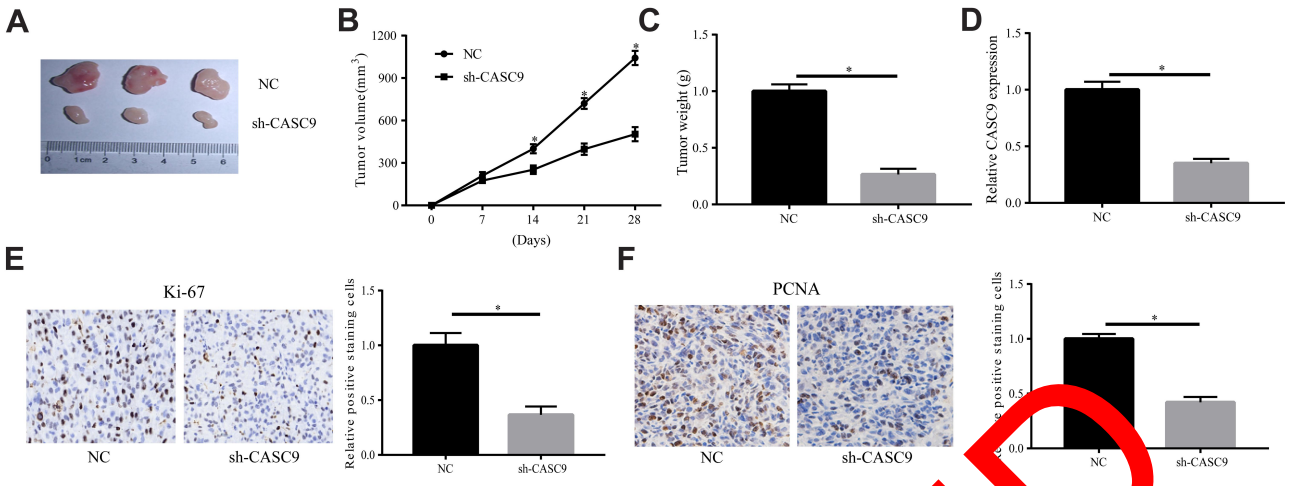

Figure 3 CASC9 deficiency inhibited tumor growth in vivo. (**A**) All nude mice inoculated were sacrificed at the 28th days of injection. (**B**) After injection of A549 cells transfected with sh-CASC9 or empty vector, the tumor size was monitored every 7 days. (**C**) Tumor weights of mouse xenografts were measured. (**D**) qRT-PCR detected CASC9 expression in tumor tissues. (**E** and **F**) IHC showed Ki-67 and PCNA expression in mouse xenografts. *P<0.05.

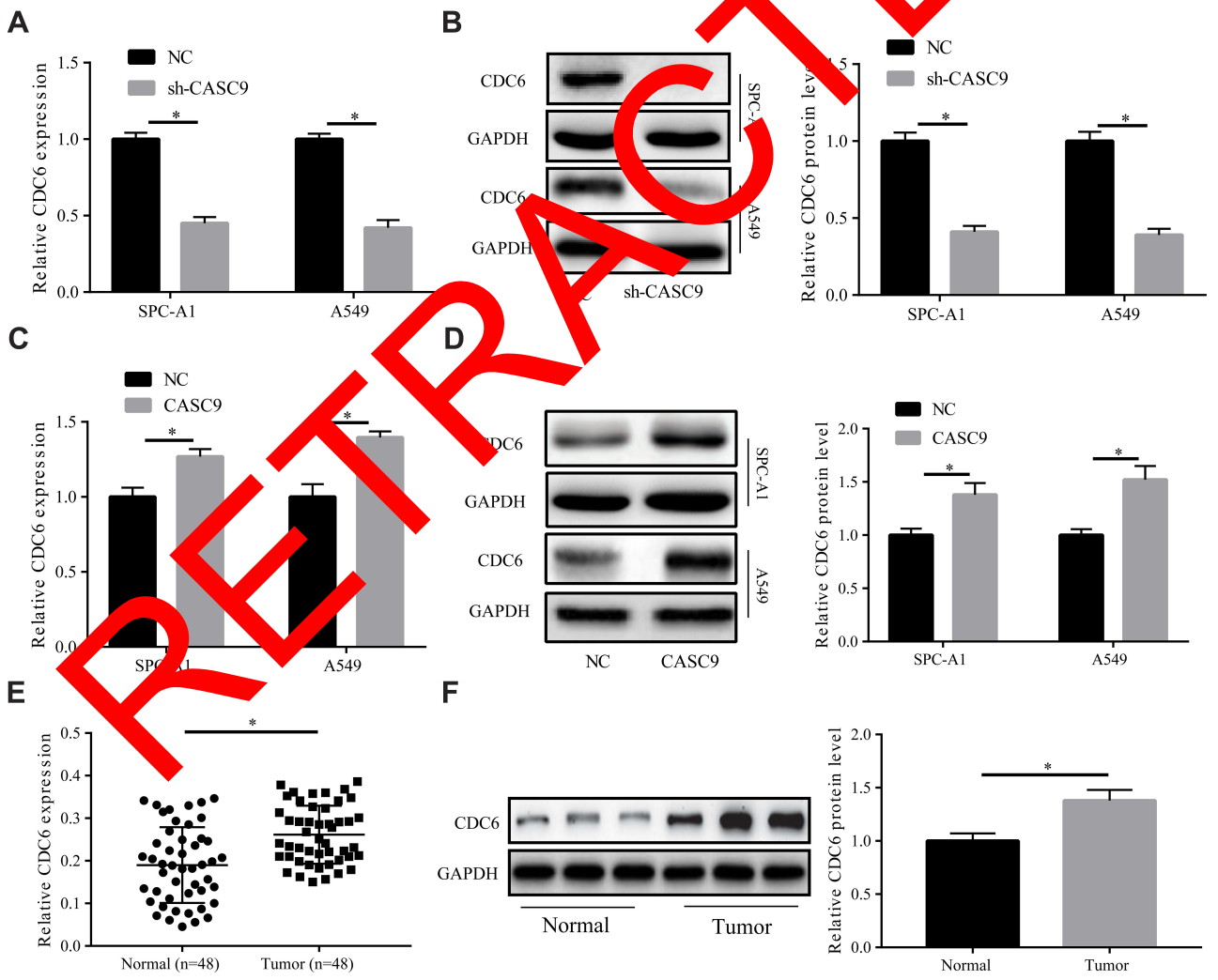

Figure 4 CASC9 regulated the expression of CDC6. (**A** and **B**) Knockdown of CASC9 in A1 and A549 cells down-regulated the CDC6 expression at both the mRNA and protein level, and vice versa (**C** and **D**). (**E** and **F**) The CDC6 was significantly over-expressed at both mRNA and protein level in tumor tissues when compared to para-cancerous ones. *P<0.05.

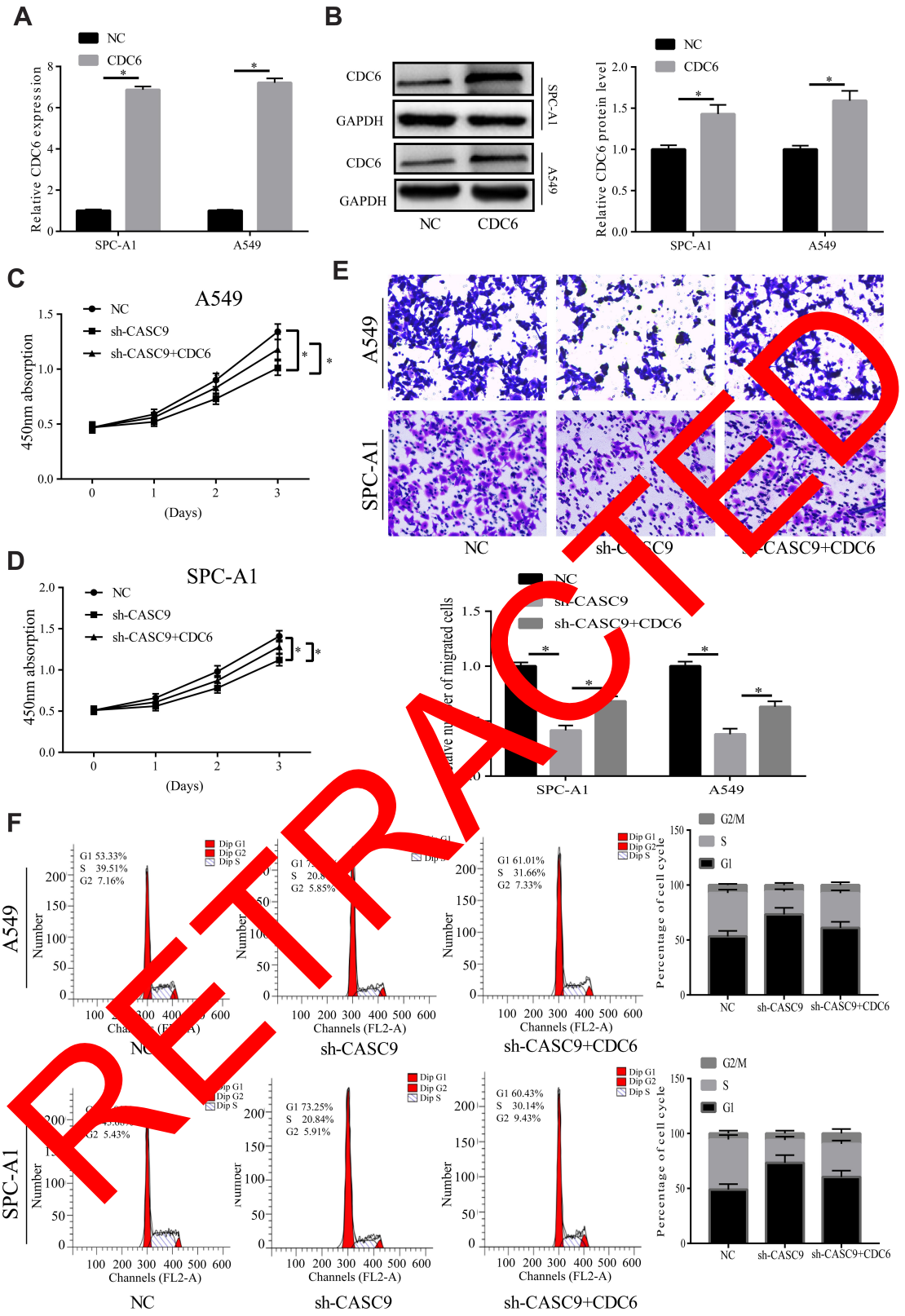

Figure 5 CASC9 promoted cell proliferation, migration and cell cycle via regulating CDC6. (**A** and **B**) CDC6 was over-expressed in SPC-A1 and A549 cells when transfected with CDC6 over-expression vector. When cells co-transfected with sh-CASC9 and CDC6 over-expression vector, CDC6 over-expression rescued the function on cell proliferation (**C** and **D**), migration (**E**) and cell cycle regulation (**F**) after CASC9 knockdown. *P<0.05.

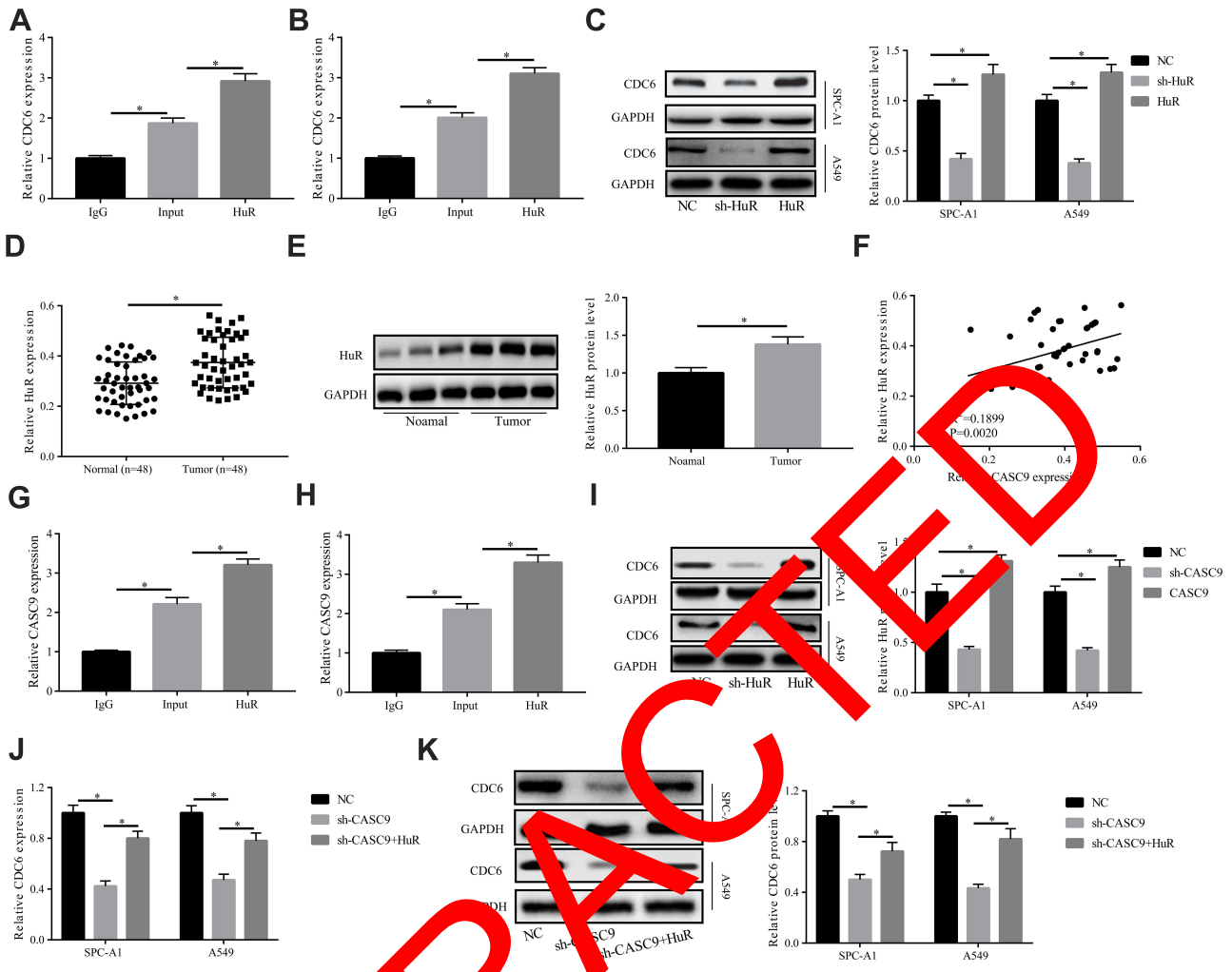

Figure 6 CASC9 directly bound to HuR and regulated CDC6, and **B**) RIP immunoprecipitation (RIP) assays demonstrated a direct association of HuR and CDC6. (**C**) The CDC6 levels were depressed when HuR was down-regulated in SPC-A1 and A549 cells, and vice versa. (**D** and **E**) HuR was significantly over-expressed in tumor tissues. (**F**) Significant association between CASC9 and HuR expression was found in NSCLC patients. R^2=0.1899, P=0.0020. (**G** and **H**) RIP assays demonstrated a direct association of CASC9 and HuR. (**I**) The HuR levels were depressed when CASC9 was down-regulated in SPC-A1 and A549 cells, and vice versa. (**J** and **K**) HuR over-expression rescued the inhibitory effects on CDC6 after CASC9 knockdown. *P<0.05.

tumor tissues, indicating CDC6 might also be involved in the malignancy of NSCLC. As the rescue experiment showed, the up-regulation of CDC6 could partly rescue the outcomes of CASC9 down-regulation on cell proliferation, migration and cell cycle. Combined with the above results, we confirmed that CASC9 played an important role in NSCLC by regulating CDC6. However, how CASC9 regulated CDC6 remained unclear.

As reported before, HuR could regulate CDC6 via binding to its 3′UTR regions.[20] HuR was identified as a member of the embryonic lethal abnormal vision (ELAV) family of RNA-binding proteins (RBPs) and was able to selectively bind to AU-rich elements (ARE) in the 3′ untranslated regions (3′-UTR) of target mRNAs to antagonize ARE-mediated mRNA degradation, leading to prolonged mRNA half-lives and increased translation.[21,22] Genes upregulated by HuR include cancer-trait proteins that promote cell proliferation and survival, local angiogenesis, as well as those that facilitate cancer cell invasion, metastasis, and evasion of immune recognition.[23] In this study, we conducted RIP experiment to verify the combination between HuR and CDC6. As results had shown, we found HuR could bind to CDC6 and CDC6 was also regulated by HuR in NSCLC cell lines. Meanwhile, the HuR was over-expressed in NSCLC tumor tissues, indicating HuR was also correlated with the progression of NSCLC.

Functions of LncRNAs on regulating gene activity and protein function rely on a variety of molecular mechanisms. Some lncRNAs are involved in interfering transcription, splicing RNA and quenching miRNA, while others

work via direct interaction with transcriptional factors, hormone receptors and other RNA-binding proteins.[24] As reported before, RPSAP52 lncRNA could inhibit p21Waf1/CIP axis by interacting with the HuR.[25] LncRNA RMST could interact with HuR and thus enhancing DNMT3 expression.[26] In view of this, we aimed to explore whether CASC9 could bind to HuR. Through RIP experiment, we confirmed the relationship between CASC9 and HuR, and HuR was regulated by CASC9 directly. Furtherly, the up-regulation of HuR could partly reverse the effects of sh-CASC9 on CDC6. Combined with the above results, CASC9 might regulate CDC6 via binding and regulating HuR.

Conclusion

In conclusion, we detected an increase of CASC9, CDC6 and HuR expression in NSCLC tissues. Down-regulation of CASC9 suppressed NSCLC cell proliferation and migration in vitro, tumor growth in vivo, and induced cell cycle arrest. Our data also provided strong evidence that HuR binds to CDC6 to upregulate CDC6 expression and CASC9 binds to HuR to upregulate HuR expression in NSCLC cells. Taken together, our findings revealed that CASC9 exerted its oncogenic roles by regulating CDC6 and CASC9 regulate CDC6 by combining and regulating HuR.

Data Sharing Statement

The data used to support the findings of this study are available from the corresponding author (Raj Kumar Jha; email: ilku142@163.com) upon request.

Ethical Statement

The present study was approved by Xi'an Medical University. All patients provided written informed consent, and that this study was conducted in accordance with the Declaration of Helsinki.

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Disclosure

The authors declare that they have no conflicts of interest to disclose for this work.

References

1. Bray F, Ferlay J, Soerjomataram I, Siegel RL, Torre LA, Jemal A. Global cancer statistics 2018: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries. *CA Cancer J Clin*. 2018;68(6):394–424.
2. Tseng KY, Wang HC, Chang LL, Cheng KI. Advances in experimental medicine and biology: intrafascicular local anesthetic injection damages peripheral nerve-induced neuropathic pain. *Adv Exp Med Biol*. 2018;1099:65–76.
3. Brody H. Lung cancer. *Nature*. 2014;513(7517):S1. doi:10.1038/513S1a
4. Lemjabbar-Alaoui H, Hassan OU, Yang YW, Buchanan P. Lung cancer: biology and treatment options. *Biochim Biophys Acta*. 2015;1856(2):189–210.
5. Kruglyak KM, Lin E, Grossman FS. Next-generation sequencing and applications to the diagnosis and treatment of lung cancer. *Adv Exp Med Biol*. 2016;893:23–1
6. Guttman M, Russell P, Ingolia NT, Weissman JS, Lander ES. Ribosome profiling provides evidence that large noncoding RNAs do not encode proteins. *Cell*. 2013;154(1):240–251. doi:10.1016/j.cell.2013.06.009
7. Cech TR, Steitz JA. The noncoding RNA revolution-trashing old rules to forge new ones. *Cell*. 2014;157(1):77–94.
8. Thade VS, Pallo D, Kanduri C. Long noncoding RNA: genome organization and mechanism of action. *Adv Exp Med Biol*. 2017;1008:47–7
9. Yang Li P, Zhang G, Lu C, Wang H, Zhao G. Long non-coding RNA XLOC_008466 functions as an oncogene in human non-small cell lung cancer by targeting miR-874. *Cell Physiol Biochem*. 2017;42(1):126–136. doi:10.1159/000477121
10. Song X, Luo X, Gao Q, Wang Y, Gao Q, Long W. Dysregulation of LncRNAs in placenta and pathogenesis of preeclampsia. *Curr Drug Targets*. 2017;18(10):1165–1170. doi:10.2174/1389450118666170404160000
11. Luo K, Geng J, Zhang Q, et al. LncRNA CASC9 interacts with CPSF3 to regulate TGF-beta signaling in colorectal cancer. *J Exp Clin Cancer Res*. 2019;38(1):249. doi:10.1186/s13046-019-1263-3
12. Shao G, Wang M, Fan X, et al. lncRNA CASC9 positively regulates CHK1 to promote breast cancer cell proliferation and survival through sponging the miR195/497 cluster. *Int J Oncol*. 2019;54(5):1665–1675.
13. Borlado LR, Mendez J. CDC6: from DNA replication to cell cycle checkpoints and oncogenesis. *Carcinogenesis*. 2008;29(2):237–243.
14. Faghihloo E, Sadeghizadeh M, Shahmahmoodi S, Mokhtari-Azad T. Cdc6 expression is induced by HPV16 E6 and E7 oncogenes and represses E-cadherin expression. *Cancer Gene Ther*. 2016. doi:10.1038/cgt.2016.51
15. Lim N, Townsend PA. Cdc6 as a novel target in cancer: oncogenic potential, senescence and subcellular localisation. *Int J Cancer*. 2020;147(6):1528–1534. doi:10.1002/ijc.32900
16. An C, Liu G, Cheng S, et al. A pilot study of cdc6 as a biomarker for circulating tumor cells in patients with lung cancer. *J Clin Lab Anal*. 2020;e23245.
17. Camidge DR, Doebele RC, Kerr KM. Comparing and contrasting predictive biomarkers for immunotherapy and targeted therapy of NSCLC. *Nat Rev Clin Oncol*. 2019;16(6):341–355. doi:10.1038/s41571-019-0173-9
18. Li S, Mei Z, Hu HB, Zhang X. The lncRNA MALAT1 contributes to non-small cell lung cancer development via modulating miR-124/STAT3 axis. *J Cell Physiol*. 2018;233(9):6679–6688. doi:10.1002/jcp.26325

19. Yadav S, Agrawal S, Divya Ravali SS, Pandey A. Lung cancer: analysis of biomarkers and methods of diagnostic and prognostic value. *Cell Mol Biol (Noisy-Le-Grand)*. 2017;63(6):88–92. doi:10.14715/cmb/2017.63.6.18
20. Cai J, Wang H, Jiao X, et al. The RNA-binding protein HuR confers oxaliplatin resistance of colorectal cancer by upregulating CDC6. *Mol Cancer Ther*. 2019;18(7):1243–1254. doi:10.1158/1535-7163.MCT-18-0945
21. Ma WJ, Cheng S, Campbell C, Wright A, Furneaux H. Cloning and characterization of HuR, a ubiquitously expressed Elav-like protein. *J Biol Chem*. 1996;271(14):8144–8151. doi:10.1074/jbc.271.14.8144
22. Zhuang R, Rao JN, Zou T, et al. miR-195 competes with HuR to modulate stim1 mRNA stability and regulate cell migration. *Nucleic Acids Res*. 2013;41(16):7905–7919. doi:10.1093/nar/gkt565
23. Abdelmohsen K, Gorospe M. Posttranscriptional regulation of cancer traits by HuR. *Wiley Interdiscip Rev RNA*. 2010;1(2):214–229. doi:10.1002/wrna.4
24. Wapinski O, Chang HY. Long noncoding RNAs and human disease. *Trends Cell Biol*. 2011;21(6):354–361. doi:10.1016/j.tcb.2011.04.001
25. D'Angelo D, Arra C, Fusco A. RPSAP52 lncRNA Inhibits p21Waf1/CIP expression by interacting with the RNA binding protein HuR. *Oncol Res*. 2020;28(2):191–201. doi:10.3727/096504019X15761465603129
26. Peng WX, Koirala P, Zhang W, et al. lncRNA RMST enhances DNMT3 expression through Interaction with HuR. *Mol Ther*. 2020;28(1):9–18. doi:10.1016/j.ymthe.2019.09.024