

# World Journal of *Gastroenterology*

*World J Gastroenterol* 2019 December 28; 25(48): 6876-6958



**EDITORIAL**

- 6876 Wrap choice during fundoplication  
*Bramhall SR, Mourad MM*

**OPINION REVIEW**

- 6880 Gastric electrical stimulation: An emerging therapy for children with intractable gastroparesis  
*Setya A, Nair P, Cheng SX*

**ORIGINAL ARTICLE****Basic Study**

- 6890 Comprehensive multi-omics analysis identified core molecular processes in esophageal cancer and revealed GNGT2 as a potential prognostic marker  
*Liu GM, Ji X, Lu TC, Duan LW, Jia WY, Liu Y, Sun ML, Luo YG*

**Case Control Study**

- 6902 Diagnostic and prognostic value of lncRNA cancer susceptibility candidate 9 in hepatocellular carcinoma  
*Zeng YL, Guo ZY, Su HZ, Zhong FD, Jiang KQ, Yuan GD*

**Retrospective Study**

- 6916 Operative complications and economic outcomes of cholecystectomy for acute cholecystitis  
*Rice CP, Vaishnavi KB, Chao C, Jupiter D, Schaeffer AB, Jenson WR, Griffin LW, Mileski WJ*

**Observational Study**

- 6928 Hepatitis C virus eradication with directly acting antivirals improves health-related quality of life and psychological symptoms  
*Nardelli S, Riggio O, Rosati D, Gioia S, Farcomeni A, Ridola L*

**Prospective Study**

- 6939 Significance of postoperative follow-up of patients with metastatic colorectal cancer using circulating tumor DNA  
*Benešová L, Hálková T, Ptáčková R, Semyakina A, Menclová K, Pudil J, Ryska M, Levý M, Šimša J, Pazdírek F, Hoch J, Blaha M, Minárik M*

**CASE REPORT**

- 6949 Pulmonary tumor thrombotic microangiopathy of hepatocellular carcinoma: A case report and review of literature  
*Morita S, Kamimura K, Abe H, Watanabe-Mori Y, Oda C, Kobayashi T, Arao Y, Tani Y, Ohashi R, Ajioka Y, Terai S*

**ABOUT COVER**

Editorial board member of *World Journal of Gastroenterology*, Fabio Grizzi, PhD, Assistant Professor, Department of Immunology and Inflammation, Humanitas Clinical and Research Hospital, Rozzano 20089, Italy

**AIMS AND SCOPE**

The primary aim of *World Journal of Gastroenterology* (*WJG*, *World J Gastroenterol*) is to provide scholars and readers from various fields of gastroenterology and hepatology with a platform to publish high-quality basic and clinical research articles and communicate their research findings online.

*WJG* mainly publishes articles reporting research results and findings obtained in the field of gastroenterology and hepatology and covering a wide range of topics including gastroenterology, hepatology, gastrointestinal endoscopy, gastrointestinal surgery, gastrointestinal oncology, and pediatric gastroenterology.

**INDEXING/ABSTRACTING**

The *WJG* is now indexed in Current Contents®/Clinical Medicine, Science Citation Index Expanded (also known as SciSearch®), Journal Citation Reports®, Index Medicus, MEDLINE, PubMed, PubMed Central, and Scopus. The 2019 edition of Journal Citation Report® cites the 2018 impact factor for *WJG* as 3.411 (5-year impact factor: 3.579), ranking *WJG* as 35<sup>th</sup> among 84 journals in gastroenterology and hepatology (quartile in category Q2). CiteScore (2018): 3.43.

**RESPONSIBLE EDITORS FOR THIS ISSUE**

Responsible Electronic Editor: *Yan-Liang Zhang*  
 Proofing Production Department Director: *Xiang Li*

**NAME OF JOURNAL**

*World Journal of Gastroenterology*

**ISSN**

ISSN 1007-9327 (print) ISSN 2219-2840 (online)

**LAUNCH DATE**

October 1, 1995

**FREQUENCY**

Weekly

**EDITORS-IN-CHIEF**

Subrata Ghosh, Andrzej S Tarnawski

**EDITORIAL BOARD MEMBERS**

<http://www.wjgnet.com/1007-9327/editorialboard.htm>

**EDITORIAL OFFICE**

Ze-Mao Gong, Director

**PUBLICATION DATE**

December 28, 2019

**COPYRIGHT**

© 2019 Baishideng Publishing Group Inc

**INSTRUCTIONS TO AUTHORS**

<https://www.wjgnet.com/bpg/gerinfo/204>

**GUIDELINES FOR ETHICS DOCUMENTS**

<https://www.wjgnet.com/bpg/GerInfo/287>

**GUIDELINES FOR NON-NATIVE SPEAKERS OF ENGLISH**

<https://www.wjgnet.com/bpg/gerinfo/240>

**PUBLICATION MISCONDUCT**

<https://www.wjgnet.com/bpg/gerinfo/208>

**ARTICLE PROCESSING CHARGE**

<https://www.wjgnet.com/bpg/gerinfo/242>

**STEPS FOR SUBMITTING MANUSCRIPTS**

<https://www.wjgnet.com/bpg/GerInfo/239>

**ONLINE SUBMISSION**

<https://www.f6publishing.com>

## Case Control Study

## Diagnostic and prognostic value of lncRNA cancer susceptibility candidate 9 in hepatocellular carcinoma

Yong-Lian Zeng, Zhen-Ya Guo, Hui-Zhao Su, Fu-Di Zhong, Ke-Qing Jiang, Guan-Dou Yuan

**ORCID number:** Yong-Lian Zeng (0000-0003-2483-6200); Zhen-Ya Guo (0000-0001-9646-2020); Hui-Zhao Su (0000-0002-6060-9382); Fu-Di Zhong (0000-0003-0882-439X); Ke-Qing Jiang (0000-0002-5953-9129); Guan-Dou Yuan (0000-0002-4598-351X).

**Author contributions:** Zeng YL and Yuan GD designed the research; Guo ZY, Zhong FD, Jiang KQ and Su HZ performed the research; Zeng YL, Guo ZY and Yuan GD analyzed the data; Zeng YL and Yuan GD wrote the paper.

**Institutional review board statement:** This study was reviewed and approved by the First Affiliated Hospital of Guangxi Medical University Ethics Committee.

**Informed consent statement:** All patients in our study provided informed consent.

**Conflict-of-interest statement:** The authors declare no conflict of interest.

**Data sharing statement:** No additional data are available.

**STROBE statement:** The authors have read the STROBE Statement-checklist of items, and the manuscript was prepared and revised according to the STROBE Statement-checklist of items.

**Open-Access:** This article is an open-access article which was selected by an in-house editor and fully peer-reviewed by external reviewers. It is distributed in accordance with the Creative

**Yong-Lian Zeng, Zhen-Ya Guo, Hui-Zhao Su, Fu-Di Zhong, Ke-Qing Jiang, Guan-Dou Yuan,** Department of Hepatobiliary Surgery, The First Affiliated Hospital of Guangxi Medical University, Nanning 530021, Guangxi, China

**Corresponding author:** Guan-Dou Yuan, M.D., Ph.D., Department of Hepatobiliary Surgery, The First Affiliated Hospital of Guangxi Medical University, No. 6, Shuangyong Road, Nanning 530021, Guangxi, China. [yuan25958282@163.com](mailto:yuan25958282@163.com)

## Abstract

## BACKGROUND

Hepatocellular carcinoma (HCC) is a common malignant gastrointestinal tumor. There are currently few clinical diagnostic and prognostic markers for HCC. lncRNA cancer susceptibility candidate 9 (CASC9) is a long-chain non-coding RNA discovered in recent years, and previous studies have found that lncRNA CASC9 participates in the occurrence and development of HCC, but its clinical value remains unclear.

## AIM

To determine the expression of lncRNA CASC9 in HCC and its diagnostic and prognostic value.

## METHODS

Data on CASC9 expression in patients with HCC were collected from the Cancer Genome Atlas (TCGA) database to analyze the relationship between CASC9 and patient survival. A total of 80 HCC patients treated in The First Affiliated Hospital of Guangxi Medical University from May 2012 to January 2014 were enrolled in the patient group, and 50 healthy subjects were enrolled in the control group during the same period. CASC9 expression in the two groups was determined using quantitative real-time polymerase chain reaction, and its diagnostic and prognostic value was analyzed based on the CASC9 data and pathological data in these HCC patients. The relationship between CASC9 and patient survival was assessed during the 5-year follow-up period.

## RESULTS

Analysis of data from TCGA database revealed that control samples showed significantly lower CASC9 expression than carcinoma tissue samples ( $P < 0.001$ ); the low CASC9 expression group had a higher survival rate than the high CASC9 expression group ( $P = 0.011$ ), and the patient group showed significantly increased expression of serum CASC9, with the area under the curve (AUC) of 0.933. CASC9 expression was related to tumor size, combined hepatitis, tumor,

Commons Attribution Non Commercial (CC BY-NC 4.0) license, which permits others to distribute, remix, adapt, build upon this work non-commercially, and license their derivative works on different terms, provided the original work is properly cited and the use is non-commercial. See: <http://creativecommons.org/licenses/by-nc/4.0/>

**Manuscript source:** Unsolicited manuscript

**Received:** September 29, 2019

**Peer-review started:** September 29, 2019

**First decision:** November 10, 2019

**Revised:** November 27, 2019

**Accepted:** December 13, 2019

**Article in press:** December 13, 2019

**Published online:** December 28, 2019

**P-Reviewer:** Aykan NF, Hann HW

**S-Editor:** Wang J

**L-Editor:** Webster JR

**E-Editor:** Ma YJ



node, metastasis (TNM) staging, lymph node metastasis, differentiation and alpha fetoprotein, and the high CASC9 expression group showed lower 1-year, 3-year and 5-year survival rates than the low CASC9 expression group (all  $^aP < 0.05$ ). Multivariate Cox regression analysis revealed that TNM staging, lymph node metastasis, differentiation, alpha fetoprotein and CASC9 were independent factors affecting the prognosis of patients. Stage I+II patients with lymph node metastasis, low differentiation, and alpha fetoprotein  $> 200$  ng/mL had a poor 5-year survival rate.

### CONCLUSION

High CASC9 expression is beneficial in the prognosis of HCC patients. CASC9 is expected to be a potential diagnostic and prognostic indicator of HCC.

**Key words:** lncRNA cancer susceptibility candidate 9; Hepatocellular carcinoma; Prognosis; Kyoto Encyclopedia of Genes and Genomes; Gene Ontology; Competing endogenous RNA

©The Author(s) 2019. Published by Baishideng Publishing Group Inc. All rights reserved.

**Core tip:** Previous studies have found that lncRNA cancer susceptibility candidate 9 (CASC9) can promote the survival of hepatocellular carcinoma (HCC) cells through AKT ions, but it is not clear whether lncRNA CASC9 can be used as a clinical indicator of diagnosis and prognosis in patients with HCC. This study confirmed that lncRNA CASC9 can be used as a potential prognostic and diagnostic indicator in patients with HCC and it may be a potential therapeutic target for HCC.

**Citation:** Zeng YL, Guo ZY, Su HZ, Zhong FD, Jiang KQ, Yuan GD. Diagnostic and prognostic value of lncRNA cancer susceptibility candidate 9 in hepatocellular carcinoma. *World J Gastroenterol* 2019; 25(48): 6902-6915

**URL:** <https://www.wjgnet.com/1007-9327/full/v25/i48/6902.htm>

**DOI:** <https://dx.doi.org/10.3748/wjg.v25.i48.6902>

## INTRODUCTION

Liver cancer is a common digestive tract cancer<sup>[1]</sup>. An epidemiological investigation reported 800 thousand new and dead liver cancer patients in 2018, and liver cancer was ranked the sixth most common cancer worldwide and the second major cause of cancer death in humans<sup>[2]</sup>. Hepatocellular carcinoma (HCC), the most common liver cancer, is accompanied by insidious clinical manifestations in the early stage; thus, most HCC patients are already in middle or advanced stages when admitted to hospital, and are unsuitable for surgical treatment, which seriously affects patients' quality of life<sup>[3]</sup>. At present, there are no good diagnostic markers for early HCC, and alpha fetoprotein (AFP) is the most widely used serological marker for HCC diagnosis; however, 30% of patients with HCC do not show increased AFP, and can even be negative, which increases the diagnosis difficulty of HCC<sup>[4]</sup>. Therefore, it is particularly important to identify a biomarker of HCC with high specificity.

Due to its prominent use in various disciplines, lncRNA has been a hot research topic in recent years<sup>[5]</sup>. lncRNAs are non-coding RNAs with lengths exceeding 200 nucleotides. Initially, scholars considered that lncRNAs lacked prominent protein coding ability, but recent studies found that lncRNAs have regulatory functions in a variety of mechanisms, including epigenetic modification, transcriptional regulation and post-transcriptional modification<sup>[6-8]</sup>. A previous study demonstrated that lncRNA ZEB1-AS1 is a potential prognostic indicator of HCC due to its differential expression in this tumor<sup>[9]</sup>. Another study found that lncRNA MALAT1 promotes the proliferation, migration and invasion of HCC by antagonizing miR-142-3p<sup>[10]</sup>.

Cancer susceptibility candidate 9 (CASC9), located on human chromosome 8q21.13, is a member of the lncRNA family<sup>[11]</sup>. Previous studies revealed that CASC9 was differentially expressed in esophageal cancer and lung adenocarcinoma, and was closely related to biological functions such as proliferation, invasion and metastasis<sup>[12,13]</sup>. However, there are few studies on whether CASC9 is expressed in HCC and whether it has clinical diagnostic and prognostic value. Therefore, this

study analyzed CASC9 expression in HCC based on the Cancer Genome Atlas (TCGA) database and clinical verification, in order to provide a potential index for clinical diagnosis.

## MATERIALS AND METHODS

### **Acquisition and analysis of TCGA data**

Data on gene expression in HCC were downloaded for analysis by logging into TCGA, selecting Access TCGA Data and entering the database. The data were acquired from the core sample database of TCGA, and sequencing and analysis were performed on the acquired data based on a standardized processing scheme (<http://can-cergenome.nih.gov/cancerogenomics/tissuesamples>). The data included a total of 424 patients, involving 374 cancer samples and 50 control samples. Clinical data on HCC patients were acquired from <http://gdac.broadinstitute.org> for analysis, and excluded patients without detailed data and a survival time less than 30 d. Original data on CASC9 were processed through  $\log(X+1, 2)$  to analyze the differences between control samples and carcinoma tissues, and a survival curve for high and low expression groups was drawn according to the median value of CASC9.

### **Bioinformatic analysis of lncRNA**

Starbase 3.0 was adopted to predict lncRNA CASC9 targeted microRNA (miR), and miRDB, miRTarBase, and TargetScan were adopted to predict target genes of potential miR on-line. Cytoscape software was adopted to draw the competing endogenous (ce)RNA network, and David software to analyze target genes based on the Kyoto Encyclopedia of Genes and Genomes and Gene Ontology (GO) enrichment analysis.

### **Collection of patient samples**

A total of 80 HCC patients (50 males and 30 females with an average age of  $54.6 \pm 5.0$  years) treated in The First Affiliated Hospital of Guangxi Medical University from May 2012 to January 2014 were enrolled in the patient group, and 50 healthy subjects (29 males and 21 females with an average age of  $53.7 \pm 4.1$  years) were enrolled in the control group. This study was approved by the First Affiliated Hospital of Guangxi Medical University Ethics Committee. The patients meeting the following criteria were included: Patients diagnosed with HCC based on imaging and pathologic biopsy; patients meeting the TNM staging criteria for HCC by the American Joint Committee on Cancer in 2009<sup>[14]</sup>; patients who had not taken part in any previous targeted tumor research (surgery, radiotherapy and chemotherapy, *etc.*), understood the study and signed an informed consent form (including their families) and patients whose expected survival time was more than 3 mo. The following patients were excluded: Patients with other combined tumors, renal function diseases, infection before admission, and those unwilling to cooperate.

### **Sample collection and detection**

Peripheral venous blood (5 mL) was obtained from the patients, centrifuged at 3000 rpm for 10 min after 30 min and the supernatant collected. Total RNA in the collected supernatant was extracted with TRIzol reagent (Carlsbad Invitrogen Company, California, United States), and the purity, concentration and integrity of the total RNA were determined using ultraviolet spectrophotometry and agarose gel electrophoresis. Reverse transcription was performed using TransScript<sup>®</sup> miRNA RT Enzyme Mix and 2×TS miRNA Reaction Mix in the TransScript Green Two-Step quantitative real-time polymerase chain reaction SuperMix kit (Beijing TransGen Biotech Co., Ltd., China) in strict accordance with the original kit instructions. The amplification system of CASC9 consisted of 1  $\mu$ L of cDNA, 0.4  $\mu$ L of upstream and downstream primers, respectively, 10  $\mu$ L of 2X TransScript<sup>®</sup> Tip Green qPCR SuperMix, Passive Reference Dye (50X), and Nuclease-free water (added to 20  $\mu$ L in total). The amplification conditions were as follows: Pre-denaturation at 94°C for 30 s, denaturation at 94°C for 5 s and annealing extension at 60°C for 30 s, with 40 cycles in total. Triplicate wells were prepared for each sample, and the experiment was repeated three times. Glyceraldehyde-3-phosphate dehydrogenase was used as an internal reference, and 2<sup>- $\Delta$ ct</sup> was used to analyze the data. Experiments were carried out using a 7500 PCR instrument (ABI, United States).

### **Follow-up of patients**

The patients were followed-up for 5 years by telephone interview and clinic reexamination. During the 1<sup>st</sup> year, the patients were followed-up at the 3<sup>rd</sup>, 6<sup>th</sup>, 9<sup>th</sup> and 12<sup>th</sup> month, respectively, and during the remaining 4 years, they were followed-up

once every 4 mo.

### **Statistical analysis**

In this study, the acquired data were statistically analyzed using the SPSS20.0 software package, and figures were drawn using the GraphPad 7 software package. The distribution of measurement data was analyzed using the *K-S* test, and the data in normal distribution were expressed as mean  $\pm$  SD. Comparisons between groups were performed using independent-samples *T* test. Comparisons within groups were analyzed by paired *t* test, and expressed as *t*. Ranked data were analyzed using the rank sum test, and expressed as *Z*. Enumeration data were analyzed using the chi-square test. ROC curves of CASC9 to evaluate its diagnostic value in HCC were drawn, and a K-M curve for 5-year survival of patients was also drawn. The log-rank test was adopted for analysis. Multivariate Cox regression analysis was adopted to analyze independent risk factors for patients.  $P < 0.05$  indicated a significant difference.

## **RESULTS**

### **CASC9 expression in TCGA**

Analysis of data from TCGA database on CASC9 expression in HCC patients showed that control samples had significantly lower CASC9 expression than carcinoma tissue samples ( $P < 0.001$ ), and the grouping of patients according to median CASC9 expression revealed that the low CASC9 expression group had a higher survival rate than the high CASC9 expression group ( $P = 0.011$ , [Figure 1](#)).

### **Comparison of baseline data**

Comparisons between the patient group and control group showed that there were no significant differences between the groups in terms of gender, age, body mass index (BMI), past medical history, smoking history, history of alcoholism and place of residence, while a difference in AFP expression was observed between the two groups ( $P < 0.001$ , [Table 1](#)).

### **CASC9 expression in patients and its clinical value**

The expression of serum CASC9 in the patient group was significantly higher than that in the control group, and the ROC curve showed that the AUC was 0.933. Further analysis of the relationship between CASC9 and clinical pathological data showed that tumor size, combined hepatitis, TNM staging, lymph node metastasis, differentiation and AFP were closely related to CASC9 expression. In addition, the analysis of ROC curves showed that CASC9 was associated with tumor size, TNM staging, lymph node metastasis, differentiation and AFP ([Figure 2](#) and [Tables 2](#) and [3](#)).

### **Relationship between CASC9 and patients' survival**

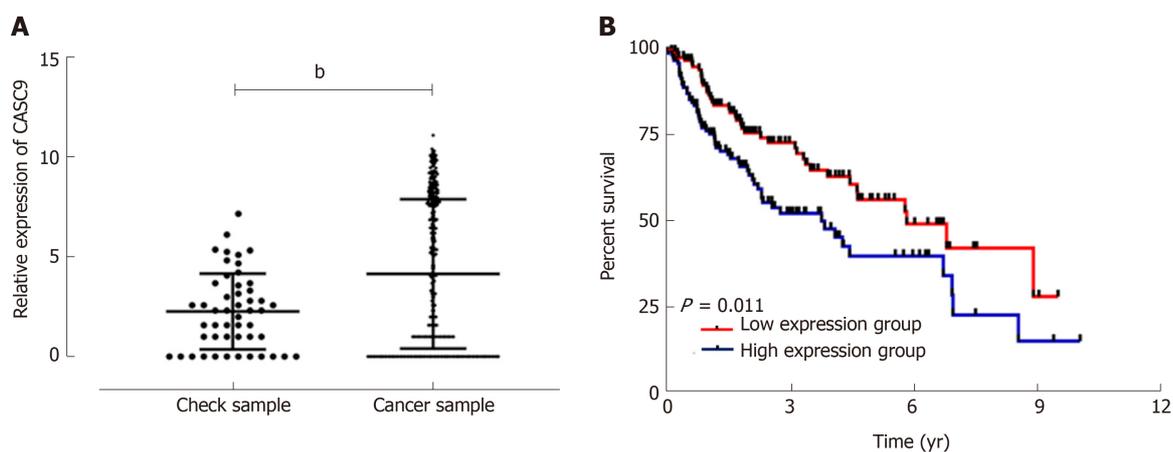
All the patients were successfully followed-up for 5 years in terms of survival. The patient group showed a 5-year survival rate of 17.50% with 14 patients surviving. The patients were grouped into the high CASC9 expression group and the low CASC9 expression group according to the median CASC9 expression (3.305), and survival was compared. The high CASC9 expression group showed significantly lower 1-year, 3-year and 5-year survival rates than the low CASC9 expression group (all  $P < 0.05$ , [Figure 3](#)).

### **Independent factors affecting prognosis of patients**

Univariate Cox regression analysis of the pathological data showed that TNM staging, lymph node metastasis, differentiation, AFP and CASC9 were factors which affected the prognosis of patients, and multivariate Cox regression analysis of these factors showed that TNM staging, lymph node metastasis, differentiation, AFP, and CASC9 were independent factors affecting the prognosis of patients ([Table 4](#)). In addition, the survival curves in terms of TNM staging, lymph node metastasis, differentiation, AFP and patients' 5-year survival indicated that stage I+II patients with lymph node metastasis, low differentiation, and AFP  $> 200$  ng/mL showed poor 5-year survival ([Figure 4](#)).

### **Bioinformatic analysis**

Seventeen CASC9 potential targeted miRs were identified by Starbase 3.0, and 89 mRNAs were found by predicting the downstream mRNA of the 17 targeted miRs with miRDB, miRTarBase, and TargetScan. We used Cytoscape software to construct the interaction map between 1ncRNA-miRNA-mRNAs, and GO enrichment and



**Figure 1** Cancer susceptibility candidate 9 expression and survival from TCGA database. A: Cancer susceptibility candidate 9 (CASC9) was highly expressed in cancer patients; B: The survival rate of the high CASC9 expression group was lower than that of the low CASC9 expression group ( $P = 0.011$ ). <sup>b</sup> $P < 0.01$ . CASC9: Cancer susceptibility candidate 9.

Kyoto Encyclopedia of Genes and Genomes pathway enrichment analysis were performed on the 89 mRNAs in the ceRNA network using DAVID and KOBAS, and 18 GO functions with  $P < 0.05$  and 8 signal transduction pathways with  $P < 0.05$  were found (Tables 5 and 6).

## DISCUSSION

HCC, a digestive system neoplasm with high incidence and mortality, is a common disease in male patients, and morbidity in men compared to women is 2.81:1<sup>[15]</sup>. A Chinese tumor epidemiology survey reported that more than 400 thousand new and dead patients with HCC were observed in 2015; however, there is no effective diagnosis and treatment plan for this disease<sup>[16]</sup>. At present, AFP is the main clinical serodiagnostic index for HCC, but relevant studies have found that AFP expression increases in liver diseases such as hepatitis; thus, its specificity is low<sup>[17]</sup>. Therefore, the key to resolving the problem is to identify biological indices with high sensitivity and specificity.

LncRNA is a long-chain non-coding RNA. A previous study demonstrated that lncRNAs participate in the occurrence and development of various cancers<sup>[18]</sup>. A study by Ma *et al.*<sup>[19]</sup> found that the biological function of HCC was inhibited by regulating the expression of miR-122-5p in HCC based on lncRNA ANRIL knockout. CASC9 is a newly discovered tumor susceptibility gene. A study by Luo *et al.*<sup>[20]</sup> found that CASC9 and CPSF3 could cooperatively regulate TGF- $\beta$  signaling pathway conduction in colorectal cancer, and a study by Liang *et al.*<sup>[21]</sup> reported that CASC9 promoted metastasis of esophageal squamous cell carcinoma by up regulating LAMC2 expression through an interaction with CREB binding protein. However, there are few reports on CASC9 in HCC at present. A study by Noh *et al.*<sup>[22]</sup> showed that CASC9-mediated AKT ions promoted the survival of HCC cells, and there are no other relevant studies on whether CASC9 can be used as a diagnostic and prognostic indicator of HCC. Therefore, this study confirmed the expression and prognostic value of CASC9 in HCC based on the TCGA database, in order to provide a new potential clinical index.

TCGA database, one of the largest Cancer Genome Projects, contains a variety of tumor gene data<sup>[23]</sup>. In this study, we first extracted data on CASC9 expression in the tissues of HCC patients from TCGA database, analyzed these tissues, and found that CASC9 expression in carcinoma tissue samples was significantly higher than that in adjacent control tissue samples. The patients were divided into the high CASC9 expression group and the low CASC9 expression group according to the median CASC9 expression to determine survival of the patients. It was found that the low CASC9 expression group had a higher survival rate than the high CASC9 expression group. The above results indicated that CASC9 may be a potential diagnostic and prognostic indicator of HCC. Further clinical research demonstrated that the expression of serum CASC9 in HCC patients was consistent with the data from TCGA database. In addition, we found that the AUC of CASC9 expression ( $> 0.9$ ) had very high diagnostic value based on ROC curves. We further analyzed the relationship between CASC9 and 1-year, 3-year and 5-year survival rates in HCC patients, and

Table 1 Baseline analysis, *n* (%)

Factors		Patient group ( <i>n</i> = 80)	Control group ( <i>n</i> = 50)	$\chi^2 / t$	<i>P</i> value
Gender				0.264	0.609
	Male	50 (62.50)	29(58.00)		
	Female	30 (37.50)	21 (42.00)		
Age (yr)		54.6 ± 5.0	53.7 ± 4.1	1.068	0.288
BMI (kg/m <sup>2</sup> )		22.86 ± 1.93	23.17 ± 2.07	0.866	0.388
Past medical history					
	Hypertension	25 (31.25)	10 (20.00)	1.979	0.160
	Hyperlipidemia	13 (16.25)	6 (12.00)	0.445	0.505
	Diabetes	20 (25.00)	10 (20.00)	0.433	0.510
Smoking history				0.081	0.776
	Yes	50 (62.50)	30 (60.00)		
	No	30 (37.50)	20 (40.00)		
History of alcoholism				0.494	0.482
	Yes	15 (18.75)	7 (14.00)		
	No	65 (81.25)	43 (86.00)		
Place of residence				0.177	0.674
	Urban area	45 (56.25)	30 (60.00)		
	Rural area	35 (43.75)	20 (40.00)		
Tumor size					
	≥ 5 cm	45 (56.25)			
	< 5 cm	35 (43.75)			
Combined hepatitis					
	Yes	70 (87.50)			
	No	10 (12.50)			
TNM staging					
	Stage I+II	33 (41.25)			
	Stage III+IV	47 (58.75)			
Lymph node metastasis					
	Yes	42 (52.50)			
	No	38 (47.50)			
Differentiation					
	Low differentiation	27 (33.75)			
	Moderate + high differentiation	53 (66.25)			
AFP (ng/mL)				59.583	< 0.001
	≤ 200	25 (31.25)	50 (100.00)		
	>200	55 (68.75)	0 (0.00)		

BMI: Body mass index; AFP: Alpha fetoprotein; TNM: Tumor, node, metastasis.

differences between the low CASC9 expression group and high CASC9 expression group in 1-year, 3-year and 5-year survival rates were found, which indicated that CASC9 could be adopted as an index for determining the short-term and long-term survival rates of HCC patients. We also analyzed the relationship between CASC9 and pathological data, and found that CASC9 was closely related to tumor size, TNM staging, lymph node metastasis, differentiation, and AFP, which indicated that CASC9 was closely related to the occurrence and development of HCC. In addition, CASC9 had certain diagnostic value in determining tumor size, TNM staging, lymph node metastasis, differentiation and AFP. A study by Gao *et al*<sup>[24]</sup> revealed that CASC9 was also highly expressed in esophageal carcinoma, and had relatively high diagnostic value (AUC: 0.814). However, the AUC of CASC9 in our study group was 0.933. This indicated that CASC9 may have higher diagnostic value for HCC than for esophageal carcinoma, but whether it is a diagnostic index still requires further investigation.

Pathological data on HCC patients were obtained to further analyze independent factors affecting the prognosis of patients, and TNM staging, lymph node metastasis,

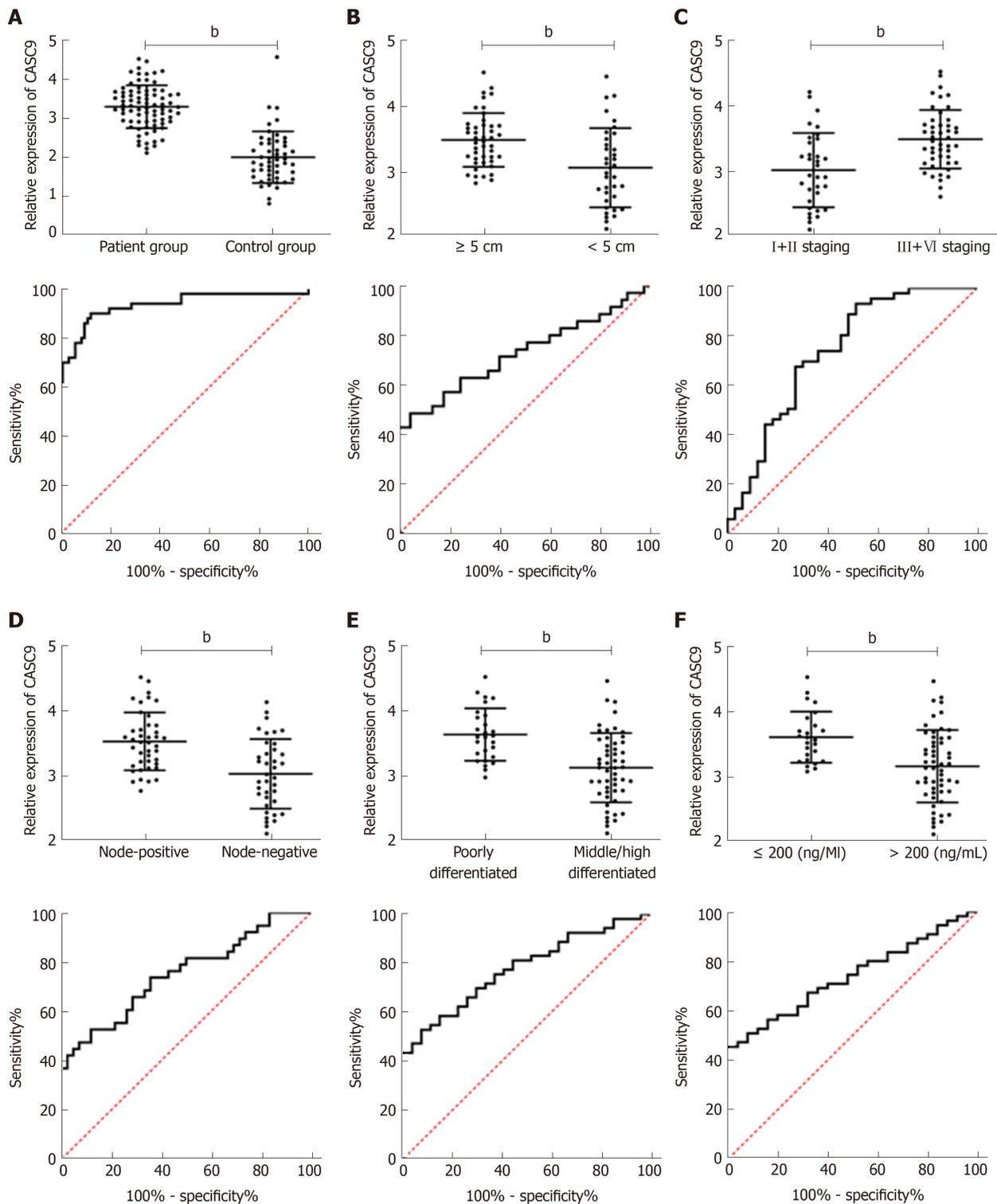
**Table 2 Relationship between cancer susceptibility candidate 9 and pathological data**

Factors	Patient group (n = 80)	T	P value
Gender		0.308	0.759
	Male (n = 50)	3.287 ± 0.553	
	Female (n = 30)	3.326 ± 0.553	
Age (yr)		0.751	0.455
	< 55 (n = 35)	3.354 ± 0.504	
	≥ 55 (n = 45)	3.261 ± 0.585	
Tumor size		4.357	< 0.001
	≥ 5 cm (n = 45)	3.489 ± 0.414	
	< 5 cm (n = 35)	3.06 ± 0.611	
Combined hepatitis		0.575	0.567
	Yes (n = 70)	3.315 ± 0.540	
	No (n = 10)	3.208 ± 0.634	
TNM stage		4.157	< 0.001
	Stage I+II (n = 33)	3.496 ± 0.448	
	Stage III+IV (n = 47)	3.024 ± 0.567	
Lymph node metastasis		4.557	< 0.001
	Yes (n = 42)	3.54 ± 0.445	
	No (n = 38)	3.038 ± 0.538	
Differentiation		4.387	< 0.001
	Low differentiation (n = 27)	3.642 ± 0.405	
	Moderate + high differentiation (n = 53)	3.128 ± 0.535	
AFP (ng/mL)		3.617	0.001
	≤ 200 (n = 25)	3.609 ± 0.393	
	> 200 (n = 55)	3.162 ± 0.557	

AFP: Alpha fetoprotein; TNM: Tumor, node, metastasis.

differentiation, AFP and CASC9 were found to be independent prognostic factors for HCC patients based on multivariate analysis. A study by Tan and Huang confirmed that TNM staging, lymph node metastasis, differentiation, and AFP were closely related to the prognosis of patients, which was consistent with the findings in our study<sup>[25,26]</sup>. However, we found that tumor size was not related to prognosis in this study, which was inconsistent with the previous study findings. We speculated that this may be related to the collected samples. The tumor size data in this study were relatively intensively distributed with an average size of  $4.8 \pm 0.8$  cm, which may be the reason for this difference. Our study confirmed, for the first time, that CASC9 was an independent prognostic factor for HCC patients, indicating that CASC9 may be a prognostic and diagnostic index for HCC.

A co-expression network of lncRNA-miR-mRNA was constructed and 17 CASC9 targeted miRs, and 89 targeted mRNAs were observed. The top 10 functions in GO enrichment analysis were negative regulation of transcription from the RNA polymerase II promoter, positive regulation of transcription regulatory region DNA binding, cytoplasm, positive regulation of transcription, DNA-templated, osteoblast differentiation, neuron projection morphogenesis, transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific, negative regulation of sequence-specific DNA binding transcription factor activity, and neuron projection, respectively, and the 8 different signal transduction pathways in the Kyoto Encyclopedia of Genes and Genomes analysis were microRNAs in cancer, pathways in cancer, p53 signaling pathway, Chagas disease (American trypanosomiasis), proteoglycans in cancer, cell cycle, PI3K-Akt signaling pathway, and Hippo signaling pathway, respectively. According to the above research, CASC9 can participate in various biological pathways by regulating the miR/mRNA axis, and it is noteworthy that signal pathways such as microRNAs in cancer, pathways in cancer, p53 signaling pathway, PI3K-Akt signaling pathway, and Hippo signaling pathway are important cancer-related signal transduction pathways<sup>[27-29]</sup>. CASC9 can also participate in the occurrence of these pathways by regulating the miR/mRNA axis, which provides an important cornerstone for our subsequent research.



**Figure 2** Cancer susceptibility candidate 9 expression in patients, its relationship with tumor size, Tumor, Node, Metastasis staging, lymph node metastasis, differentiation, and alpha fetoprotein expression, and its diagnostic value. A: Cancer susceptibility candidate 9 (CASC9) was highly expressed in the patient group, and the AUC was 0.933; B: Relationship between CASC9 expression and tumor size. The AUC was 0.726; C: Relationship between CASC9 expression and TNM staging. The AUC was 0.743; D: Relationship between CASC9 expression and lymph node metastasis. The AUC was 0.752; E: Relationship between CASC9 expression and differentiation. The AUC was 0.777; F: Relationship between CASC9 expression and AFP. The AUC was 0.738. <sup>b</sup> $P < 0.01$ . CASC9: Cancer susceptibility candidate 9; AUC: area under the curve.

Although this study confirmed the value of CASC9 in HCC, it still has some limitations. Firstly, we only analyzed patients with HCC and healthy subjects, but did not determine CASC9 expression in patients with hepatitis; thus, whether CASC9 can distinguish HCC from hepatitis still requires further research in healthy subjects. Secondly, how CASC9 participates in the occurrence and development of HCC is unclear. Lastly, this study only focused on Chinese patients, and whether CASC9

**Table 3** Receiver operating characteristic parameters

Factors	HCC diagnosis	Tumor size	TNM stage	Lymph node metastasis	Differentiation	AFP
AUC	0.933	0.726	0.743	0.752	0.777	0.738
SD	0.026	0.060	0.059	0.055	0.051	0.054
95%CI	0.882-0.983	0.608-0.845	0.628-0.858	0.645-0.859	0.678-0.876	0.632-0.844
<i>P</i> value	< 0.001	0.001	< 0.001	< 0.001	< 0.001	0.001
Specificity	87.50%	95.56%	48.48%	88.10%	92.59%	100.00%
Sensitivity	90.00%	48.57%	93.62%	52.63%	52.83%	45.45%
Youden index	77.50%	44.13%	42.10%	40.73%	45.42%	45.45%
Cut-off	< 2.672	< 2.916	> 2.919	< 3.057	< 3.148	< 3.057

AUC: Area under curve; HCC: Hepatocellular carcinoma; AFP: Alpha fetoprotein.

expression is increased in HCC patients of different races is unclear. Therefore, we hope to carry out bioinformatics and a basic study in the future to further analyze the way that CASC9 affects the occurrence and development of HCC, and obtain different pathological specimens for CASC9 detection in difference races, in order to address the shortcomings in this study. In conclusion, high CASC9 expression is beneficial for the prognosis of HCC patients, and CASC9 is expected to be a potential diagnostic and prognostic indicator of HCC.

**Table 4 Multivariate Cox regression analysis**

Factors	Univariate Cox			Multivariate Cox		
	P value	HR	95%CI	P value	HR	95%CI
Gender (male <i>vs</i> female)	0.272	1.320	1.320-0.804			
Age (< 55 yr <i>vs</i> ≥ 55 yr)	0.438	0.825	0.825-0.508			
Tumor size (≥ 5 cm <i>vs</i> < 5 cm)	0.952	1.015	1.015-0.624			
Combined hepatitis (yes <i>vs</i> no)	0.636	1.185	1.185-0.586			
TNM staging (stage I+II <i>vs</i> stage III+IV)	0.000	4.271	4.271-2.391	0.006	2.501	1.308-4.781
Lymph node metastasis (yes <i>vs</i> no)	0.001	0.428	0.428-0.259	0.025	0.535	0.309-0.924
Differentiation (low <i>vs</i> medium + high)	0.000	0.242	0.242-0.144	0.000	0.326	0.186-0.569
AFP (≤ 200 <i>vs</i> > 200 ng/mL)	0.025	1.914	1.914-1.086	0.042	1.935	1.023-3.662
CASC9 (< 3.305 <i>vs</i> ≥ 3.305)	0.005	2.023	2.023-1.235	0.021	2.024	1.112-3.682

AFP: Alpha fetoprotein; TNM: Tumor, node, metastasis; CASC9: Cancer susceptibility candidate 9.

**Table 5 The top 10 Gene Ontology enrichment functions**

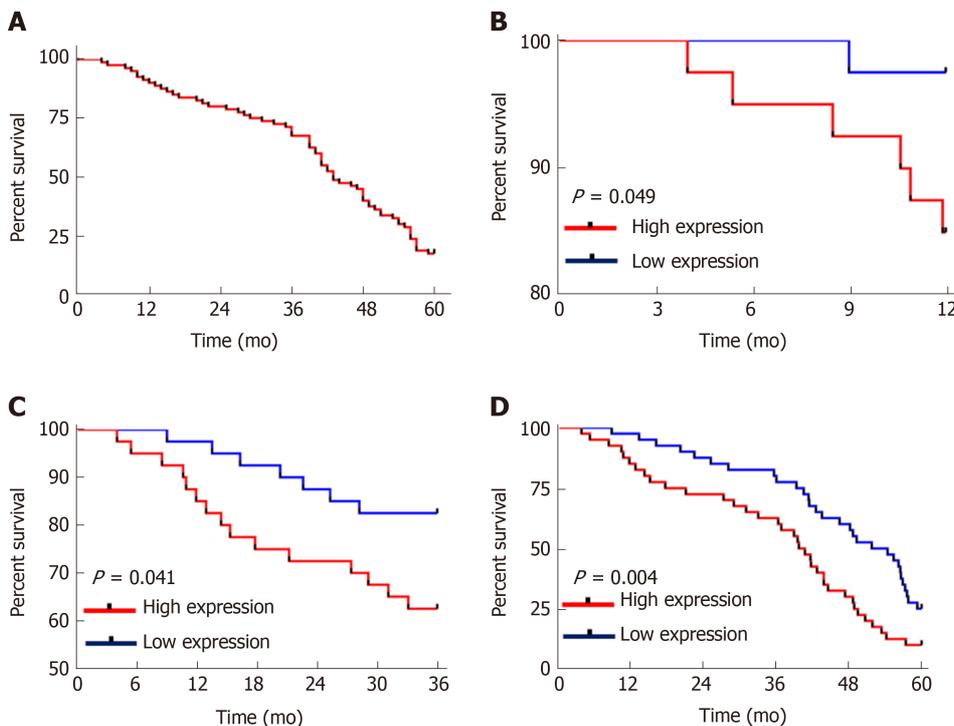
Term	Count	P value	Genes
Negative regulation of transcription from the RNA polymerase II promoter	9	0.001	<i>PHF19, SQSTM1, CPEB3, E2F7, ESR1, CBX2, SOX6, HMGA2, TWIST1</i>
Positive regulation of transcription regulatory region DNA binding	3	0.002	<i>WNT3A, HMGA2, TWIST1</i>
Cytoplasm	27	0.003	<i>CLSPN, CPEB3, TPM2, BDNF, RNF165, MAPT, STRIP2, HOXA10, FASN, PLCB1, CDC37L1, ARL2, IRAK1, SGK1, MAP2K1, KIF5A, DDX39B, PIM1, SOCS6, ESR1, SNAI2, WEE1, CDC25A, ADM, CA8, PSAT1, DUSP6</i>
Positive regulation of transcription, DNA-templated	6	0.009	<i>RET, MAP2K1, FOXK1, MYRF, ESR1, PLCB1</i>
Osteoblast differentiation	4	0.010	<i>WNT3A, FASN, SNAI2, TWIST1</i>
Neuron projection morphogenesis	3	0.011	<i>BDNF, SGK1, WEE1</i>
Transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific	5	0.019	<i>PLAG1, HOXA10, ESR1, HMGA2, MYBL2</i>
Negative regulation of sequence-specific DNA binding transcription factor activity	3	0.021	<i>PIM1, ESR1, TWIST1</i>
Neuron projection	4	0.027	<i>CPEB3, KIF5A, MAPT, SLC6A4</i>

PHF19: PHD finger protein 19; SQSTM1: Sequestosome 1; CPEB3: Cytoplasmic polyadenylation element binding protein 3; E2F7: E2F transcription factor 7; ESR1: Estrogen receptor 1; CBX2: Chromobox 2; SOX6: SRY-box transcription factor 6; HMGA2: High mobility group AT-hook 2; TWIST1: Twist family bHLH transcription factor 1; WNT3A: Wnt family member 3A; CLSPN: Claspin; TPM2: Tropomyosin 2; BDNF: Brain derived neurotrophic factor; RNF165: Ring finger protein 165; MAPT: Microtubule associated protein tau; STRIP2: Striatin interacting protein 2; HOXA10: Homeobox A10; FASN: Fatty acid synthase; PLCB1: Phospholipase C beta 1; CDC37L1: Cell division cycle 37 like 1; ARL2: ADP ribosylation factor like GTPase 2; IRAK1: Interleukin 1 receptor associated kinase 1; SGK1: Serum/glucocorticoid regulated kinase 1; MAP2K1: Mitogen-activated protein kinase kinase 1; KIF5A: Kinesin family member 5A; DDX39B: DEXD-box helicase 39B; PIM1: Pim-1 proto-oncogene, serine/threonine kinase; SOCS6: Suppressor of cytokine signaling 6; SNAI2: Snail family transcriptional repressor 2; WEE1: WEE1 G2 checkpoint kinase; CDC25A: Cell division cycle 25A; ADM: Adrenomedullin; CA8: Carbonic anhydrase 8; PSAT1: Phosphoserine aminotransferase 1; DUSP6: Dual specificity phosphatase 6; RET: Ret proto-oncogene; FOXK1: Forkhead box K1; MYRF: Myelin regulatory factor; PLAG1: PLAG1 zinc finger; MYBL2: MYB proto-oncogene like 2; SLC6A4: Solute carrier family 6 member 4.

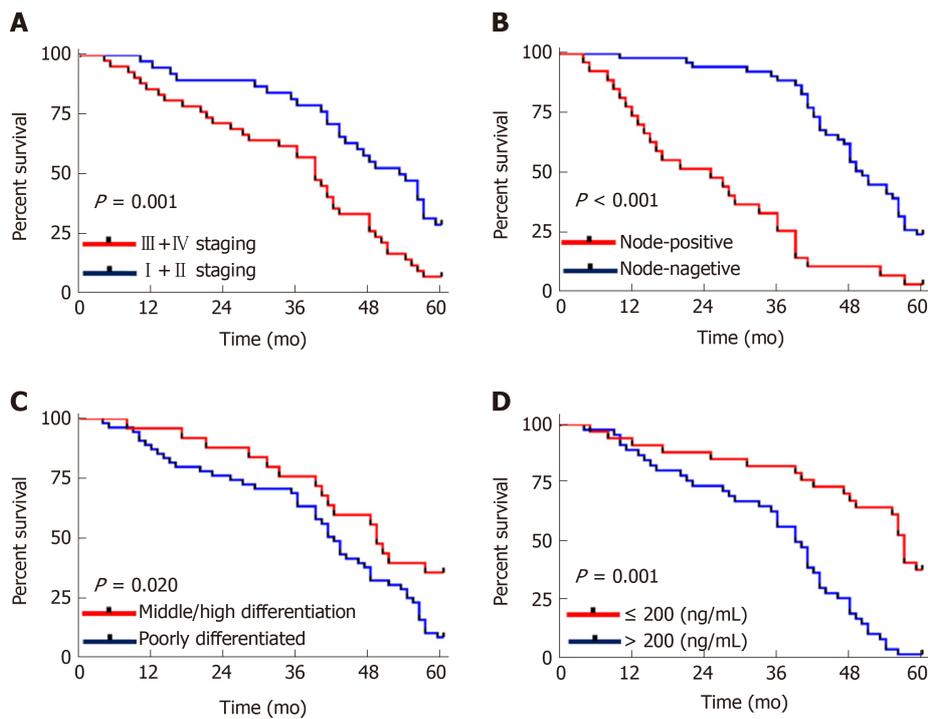
**Table 6** The top10 Kyoto Encyclopedia of Genes and Genomes signal pathways

Term	Count	P value	Genes
MicroRNAs in cancer	7	0.002	<i>KIF23, CCNE1, MAP2K1, WNT3A, PIM1, HMGA2, CDC25A</i>
Pathways in cancer	8	0.005	<i>CCNE1, RET, MAP2K1, WNT3A, ITGA2, LAMC1, AXIN2, PLCB1</i>
p53 signaling pathway	4	0.007	<i>STEAP3, CCNE1, SERPINE1, CHEK1</i>
Chagas disease (American trypanosomiasis)	4	0.024	<i>GNAL, IRAK1, SERPINE1, PLCB1</i>
Proteoglycans in cancer	5	0.024	<i>MAP2K1, WNT3A, ESR1, ITGA2, TWIST1</i>
Cell cycle	4	0.030	<i>CCNE1, CHEK1, WEE1, CDC25A</i>
PI3K-Akt signaling pathway	6	0.038	<i>CCNE1, SGK1, MAP2K1, ITGA2, LAMC1, ANGPT2</i>
Hippo signaling pathway	4	0.048	<i>WNT3A, SERPINE1, AXIN2, SNAI2</i>
Small cell lung cancer	3	0.081	<i>CCNE1, ITGA2, LAMC1</i>
Progesterone-mediated oocyte maturation	3	0.082	<i>MAP2K1, CPEB3, CDC25A</i>

KIF23: Kinesin family member 23; CCNE1: Cyclin E1; MAP2K1: Mitogen-activated protein kinase kinase 1; WNT3A: Wnt family member 3A; PIM1: Pim-1 proto-oncogene, serine/threonine kinase; HMGA2: High mobility group AT-hook 2; CDC25A: Cell division cycle 25A; RET: Ret proto-oncogene; ITGA2: Integrin subunit alpha 2; LAMC1: Laminin subunit gamma 1; AXIN2: Axin 2; PLCB1: Phospholipase C beta 1; STEAP3: STEAP3 metalloredutase; SERPINE1: Serpin family E member 1; CHEK1: Checkpoint kinase 1; CPEB3: Cytoplasmic polyadenylation element binding protein 3; SGK1: Serum/glucocorticoid regulated kinase 1; ANGPT2: Angiopoietin 2; WEE1: WEE1 G2 checkpoint kinase; ESR1: Estrogen receptor 1; TWIST1: Twist family bHLH transcription factor 1; GNAL: G protein subunit alpha L; IRAK1: Interleukin 1 receptor associated kinase 1; SNAI2: Snail family transcriptional repressor 2.



**Figure 3** Relationship between cancer susceptibility candidate 9 and patients' survival. A: The overall survival of patients; B: The 1-year survival of patients in the high and low Cancer susceptibility candidate 9 (CASC9) expression groups ( $P = 0.049$ ); C: The 3-year survival of patients in the high and low CASC9 expression groups ( $P = 0.041$ ); D: The 5-year survival of patients in the high and low CASC9 expression groups ( $P = 0.004$ ). CASC9: Cancer susceptibility candidate 9.



**Figure 4 Relationship between tumor, node, metastasis staging, lymph node metastasis, differentiation, alpha fetoprotein and 5-year survival of patients.** A: The 5-year survival rate of stage I+II patients was higher than that of stage III+IV patients ( $P = 0.001$ ); B: The 5-year survival rate of patients without lymph node metastasis was higher than that of patients with lymph node metastasis ( $P < 0.001$ ); C: The 5-year survival rate of patients with moderate/high differentiation was higher than that of patients with low differentiation ( $P = 0.020$ ); D: The 5-year survival rate of patients with AFP  $\leq 200$  was higher than that of patients with AFP  $> 200$  ( $P = 0.001$ ).

## ARTICLE HIGHLIGHTS

### Research background

Liver cancer, the sixth most common cancer worldwide, is the second leading cause of cancer mortality. A lncRNA is a non-coding RNA with a length exceeding 200 nucleotides. Previous studies have found that lncRNAs are involved in the development and progression of hepatocellular carcinoma (HCC), but whether they can be used as potential diagnostic and prognostic indicators is unclear.

### Research motivation

lncRNA is a newly discovered non-coding RNA. Some studies have revealed that lncRNAs are differentially expressed in HCC and are expected to be measures of potential outcome. In this study, we found that lncRNA CASC9 was highly expressed in HCC patients based on the Cancer Genome Atlas (TCGA) database analysis and patients with high expression of CASC9 had a poor prognosis, which indicated that lncRNA CASC9 may be a potential diagnostic and prognostic indicator of HCC.

### Research objectives

This study aimed to identify the expression of lncRNA CASC9 in HCC, its diagnostic and prognostic value and to construct ceRNA network maps to further explore its underlying mechanism.

### Research methods

Data on the expression of lncRNA CASC9 in TCGA were extracted, clinical samples were collected to further determine the expression of lncRNA CASC9 in HCC, and the correlation between lncRNA CASC9 and pathological data and survival of HCC patients were analyzed. Potential microRNA and target genes of lncRNA CASC9 were analyzed using on-line prediction websites, and ceRNA maps were drawn. In addition, Kyoto Encyclopedia of Genes and Genomes and GO enrichment analysis were employed to analyze the potential mechanisms of lncRNA CASC9 in biological processes.

### Research results

Analysis revealed that lncRNA CASC9 was highly expressed in the tissues and serum of HCC patients and high expression of CASC9 was related to tumor size, TNM staging, lymph node metastasis, differentiation, and AFP. Further analysis showed that lncRNA CASC9 could be used as a diagnostic indicator of the above indices. Prognostic analysis revealed that the survival rate of patients with high expression of lncRNA CASC9 decreased, and Cox regression analysis

showed that lncRNA CASC9 could be used as an independent prognostic indicator in HCC patients. The bioinformatics analysis revealed that lncRNA CASC9 potentially targeted 17 miRNAs. A total of 89 mRNAs were found in mRNA prediction. GO enrichment and Kyoto Encyclopedia of Genes and Genomes pathway enrichment analysis revealed that lncRNA CASC9 participated in 18 GO functions and 8 signal transduction pathways.

### Research conclusion

lncRNA CASC9 is highly expressed in HCC patients, and may be a potential diagnostic and prognostic indicator of HCC.

### Research perspectives

It is necessary to further explore the value of lncRNA CASC9 in HCC, and prospective experiments and multi-center clinical studies are required to obtain more robust conclusions. In addition, we hope to further verify the relevant mechanisms of lncRNA CASC9 in HCC by carrying out relevant basic experiments, in order to address the deficiencies in this study.

## REFERENCES

- Ryerson AB, Ehemann CR, Altekruse SF, Ward JW, Jemal A, Sherman RL, Henley SJ, Holtzman D, Lake A, Noone AM, Anderson RN, Ma J, Ly KN, Cronin KA, Penberthy L, Kohler BA. Annual Report to the Nation on the Status of Cancer, 1975-2012, featuring the increasing incidence of liver cancer. *Cancer* 2016; **122**: 1312-1337 [PMID: 26959385 DOI: 10.1002/ncr.29936]
- 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**: 394-424 [PMID: 30207593 DOI: 10.3322/caac.21492]
- Zhao X, Chen Q, Liu W, Li Y, Tang H, Liu X, Yang X. Codelivery of doxorubicin and curcumin with lipid nanoparticles results in improved efficacy of chemotherapy in liver cancer. *Int J Nanomedicine* 2015; **10**: 257-270 [PMID: 25565818 DOI: 10.2147/IJN.S73322]
- Sauzay C, Petit A, Bourgeois AM, Barbare JC, Chauffert B, Galmiche A, Houesson A. Alpha-fetoprotein (AFP): A multi-purpose marker in hepatocellular carcinoma. *Clin Chim Acta* 2016; **463**: 39-44 [PMID: 27732875 DOI: 10.1016/j.cca.2016.10.006]
- Palazzo AF, Lee ES. Non-coding RNA: what is functional and what is junk? *Front Genet* 2015; **6**: 2 [PMID: 25674102 DOI: 10.3389/fgene.2015.00002]
- Chen X, Sun Y, Cai R, Wang G, Shu X, Pang W. Long noncoding RNA: multiple players in gene expression. *BMB Rep* 2018; **51**: 280-289 [PMID: 29636120 DOI: 10.5483/bmbrep.2018.51.6.025]
- Chiu HS, Somvanshi S, Patel E, Chen TW, Singh VP, Zorman B, Patil SL, Pan Y, Chatterjee SS; Cancer Genome Atlas Research Network, Sood AK, Gunaratne PH, Sumazin P. Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. *Cell Rep* 2018; **23**: 297-312.e12 [PMID: 29617668 DOI: 10.1016/j.celrep.2018.03.064]
- Klingenberg M, Matsuda A, Diederichs S, Patel T. Non-coding RNA in hepatocellular carcinoma: Mechanisms, biomarkers and therapeutic targets. *J Hepatol* 2017; **67**: 603-618 [PMID: 28438689 DOI: 10.1016/j.jhep.2017.04.009]
- Li T, Xie J, Shen C, Cheng D, Shi Y, Wu Z, Deng X, Chen H, Shen B, Peng C, Li H, Zhan Q, Zhu Z. Upregulation of long noncoding RNA ZEB1-AS1 promotes tumor metastasis and predicts poor prognosis in hepatocellular carcinoma. *Oncogene* 2016; **35**: 1575-1584 [PMID: 26073087 DOI: 10.1038/ncr.2015.223]
- Yu Q, Xiang L, Chen Z, Liu X, Ou H, Zhou J, Yang D. MALAT1 functions as a competing endogenous RNA to regulate SMAD5 expression by acting as a sponge for miR-142-3p in hepatocellular carcinoma. *Cell Biosci* 2019; **9**: 39 [PMID: 31168355 DOI: 10.1186/s13578-019-0299-6]
- Shang C, Sun L, Zhang J, Zhao B, Chen X, Xu H, Huang B. Silence of cancer susceptibility candidate 9 inhibits gastric cancer and reverses chemoresistance. *Oncotarget* 2017; **8**: 15393-15398 [PMID: 28146436 DOI: 10.18632/oncotarget.14871]
- Pan Z, Mao W, Bao Y, Zhang M, Su X, Xu X. The long noncoding RNA CASC9 regulates migration and invasion in esophageal cancer. *Cancer Med* 2016; **5**: 2442-2447 [PMID: 27431358 DOI: 10.1002/cam4.770]
- Zhou J, Xiao H, Yang X, Tian H, Xu Z, Zhong Y, Ma L, Zhang W, Qiao G, Liang J. Long noncoding RNA CASC9.5 promotes the proliferation and metastasis of lung adenocarcinoma. *Sci Rep* 2018; **8**: 37 [PMID: 29311567 DOI: 10.1038/s41598-017-18280-3]
- Kee KM, Wang JH, Lin CY, Wang CC, Cheng YF, Lu SN. Validation of the 7th edition TNM staging system for hepatocellular carcinoma: an analysis of 8,828 patients in a single medical center. *Dig Dis Sci* 2013; **58**: 2721-2728 [PMID: 23703450 DOI: 10.1007/s10620-013-2716-8]
- Siegel RL, Miller KD, Jemal A. Cancer statistics, 2016. *CA Cancer J Clin* 2016; **66**: 7-30 [PMID: 26742998 DOI: 10.3322/caac.21332]
- Chen W, Zheng R, Baade PD, Zhang S, Zeng H, Bray F, Jemal A, Yu XQ, He J. Cancer statistics in China, 2015. *CA Cancer J Clin* 2016; **66**: 115-132 [PMID: 26808342 DOI: 10.3322/caac.21338]
- Shu H, Li W, Shang S, Qin X, Zhang S, Liu Y. Diagnosis of AFP-negative early-stage hepatocellular carcinoma using Fuc-PON1. *Discov Med* 2017; **23**: 163-168 [PMID: 28472609]
- Schmitt AM, Chang HY. Long Noncoding RNAs in Cancer Pathways. *Cancer Cell* 2016; **29**: 452-463 [PMID: 27070700 DOI: 10.1016/j.ccell.2016.03.010]
- Ma J, Li T, Han X, Yuan H. Knockdown of lncRNA ANRIL suppresses cell proliferation, metastasis, and invasion via regulating miR-122-5p expression in hepatocellular carcinoma. *J Cancer Res Clin Oncol* 2018; **144**: 205-214 [PMID: 29127494 DOI: 10.1007/s00432-017-2543-y]
- Luo K, Geng J, Zhang Q, Xu Y, Zhou X, Huang Z, Shi KQ, Pan C, Wu J. lncRNA CASC9 interacts with CPSF3 to regulate TGF- $\beta$  signaling in colorectal cancer. *J Exp Clin Cancer Res* 2019; **38**: 249 [PMID: 31186036 DOI: 10.1186/s13046-019-1263-3]
- Liang Y, Chen X, Wu Y, Li J, Zhang S, Wang K, Guan X, Yang K, Bai Y. lncRNA CASC9 promotes esophageal squamous cell carcinoma metastasis through upregulating LAMC2 expression by interacting with the CREB-binding protein. *Cell Death Differ* 2018; **25**: 1980-1995 [PMID: 29511340 DOI: 10.1038/s41418-018-0488-4]

- 10.1038/s41418-018-0084-9]
- 22 **Noh JH**, Gorospe M. AKTions by Cytoplasmic lncRNA CASC9 Promote Hepatocellular Carcinoma Survival. *Hepatology* 2018; **68**: 1675-1677 [PMID: 30014487 DOI: 10.1002/hep.30165]
  - 23 **Anaya J**. OncoLnc: linking TCGA survival data to mRNAs, miRNAs, and lncRNAs. *PeerJ Computer Science* 2016; **2**: e67 [DOI: 10.7717/peerj-cs.67]
  - 24 **Gao GD**, Liu XY, Lin Y, Liu HF, Zhang GJ. lncRNA CASC9 promotes tumorigenesis by affecting EMT and predicts poor prognosis in esophageal squamous cell cancer. *Eur Rev Med Pharmacol Sci* 2018; **22**: 422-429 [PMID: 29424900 DOI: 10.26355/eurrev\_201801\_14191]
  - 25 **Tan YL**, Bai ZG, Zou WL, Ma XM, Wang TT, Guo W, Liu J, Li JS, Jie-Yin, Zang YJ, Zhang ZT. miR-744 is a potential prognostic marker in patients with hepatocellular carcinoma. *Clin Res Hepatol Gastroenterol* 2015; **39**: 359-365 [PMID: 25543521 DOI: 10.1016/j.clinre.2014.09.010]
  - 26 **Huang CS**, Yu W, Cui H, Wang YJ, Zhang L, Han F, Huang T. Increased expression of miR-21 predicts poor prognosis in patients with hepatocellular carcinoma. *Int J Clin Exp Pathol* 2015; **8**: 7234-7238 [PMID: 26261620]
  - 27 **Garzon R**, Calin GA, Croce CM. MicroRNAs in Cancer. *Annu Rev Med* 2009; **60**: 167-179 [PMID: 19630570 DOI: 10.1146/annurev.med.59.053006.104707]
  - 28 **Mello SS**, Attardi LD. Deciphering p53 signaling in tumor suppression. *Curr Opin Cell Biol* 2018; **51**: 65-72 [PMID: 29195118 DOI: 10.1016/j.ccb.2017.11.005]
  - 29 **Li X**, Wu C, Chen N, Gu H, Yen A, Cao L, Wang E, Wang L. PI3K/Akt/mTOR signaling pathway and targeted therapy for glioblastoma. *Oncotarget* 2016; **7**: 33440-33450 [PMID: 26967052 DOI: 10.18632/oncotarget.7961]



Published By Baishideng Publishing Group Inc  
7041 Koll Center Parkway, Suite 160, Pleasanton, CA 94566, USA  
Telephone: +1-925-2238242  
E-mail: [bpgoffice@wjgnet.com](mailto:bpgoffice@wjgnet.com)  
Help Desk: <http://www.f6publishing.com/helpdesk>  
<http://www.wjgnet.com>

