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MicroRNA-98 Plays a Suppressive Role in Non-Small Cell Lung Cancer Through Inhibition of SALL4 Protein Expression

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MicroRNAs (miRs) have been demonstrated to be significantly associated with the development and progression of non-small cell lung cancer (NSCLC). However, the underlying mechanism of miR-98 in mediating the malignant phenotypes of NSCLC cells remains obscure. In this study, we found that miR-98 was significantly downregulated in NSCLC tissues compared to nontumor lung tissues. Downregulation of miR-98 was significantly associated with poor differentiation and advanced clinical stage. Restoration of miR-98 expression significantly decreased the proliferation, migration, and invasion of NSCLC A549 and H1229 cells. SALL4 was identified as a target gene of miR-98, and the protein expression of SALL4 was negatively regulated by miR-98 in NSCLC A549 and H1229 cells. Overexpression of SALL4 promoted A549 and H1229 cell proliferation, migration, and invasion and reversed the suppressive effects of miR-98 on the malignant phenotypes of A549 and H1229 cells. Moreover, SALL4 was found to be significantly upregulated in NSCLC tissues compared to the nontumor lung tissues. We then observed an inverse correlation between the miR-98 and SALL4 levels in NSCLC tissues. In vivo study revealed that miR-98 overexpression suppressed NSCLC growth. In summary, we demonstrate that miR-98 acts as a tumor suppressor in NSCLC cells by inhibiting the protein expression of its target gene SALL4. Therefore, our study highlights the importance of the miR-98/SALL4 axis in NSCLC.

Key words: MicroRNAs (miRs); Non-small cell lung cancer (NSCLC); Tumor suppressor; SALL4

INTRODUCTION

Non-small cell lung cancer (NSCLC) accounts for about 85% of all lung cancers, and the most common NSCLCs are adenocarcinoma, squamous cell carcinoma, large-cell carcinoma, and nonsquamous cell carcinoma^{1,2}. Although great improvements have been made in surgical resection, radiotherapy, and chemotherapy, the overall survival of patients with late-stage NSCLC remains unsatisfactory^{3,4}. Studies in recent years have identified some important oncogenes and tumor suppressors involved in NSCLC growth and metastasis, suggesting that they may become promising therapeutic targets^{5,6}. Understanding the molecular mechanisms underlying the development and progression of NSCLC should be beneficial in the development of effective therapeutic strategies for this disease.

MicroRNAs (miRs), a kind of small, noncoding RNA molecules of 20–25 nucleotides in length, can inhibit gene expression at the posttranscriptional level through binding to the 3'-untranslated region (UTR) of their target genes, resulting in mRNA degradation or translation

inhibition⁷. miRs have been found to participate in many biological processes such as cell proliferation, differentiation, survival, apoptosis, and motility^{8,9}. Moreover, deregulation of miRs has been observed in NSCLC, and many of them function as oncogenes or tumor suppressors, such as miR-9, miR-21, miR-145, miR-367, and so forth^{10–14}. These miRs may become promising therapeutic targets or candidates for the treatment of NSCLC.

miR-98, an important member of the let-7/miR-98 family, has been reported to be involved in many pathological processes such as Alzheimer's disease, schizophrenia, and tumorigenesis^{15–17}. Wang et al. found that miR-98 suppressed cell proliferation, migration, and invasion in hepatocellular carcinoma by targeting CTHRC1¹⁸. Du et al. found that miR-98 could inhibit the growth and metastasis of oral squamous cell carcinoma by suppressing the protein expression of IGF1R¹⁹. In addition, miR-98 can inhibit the metastasis of melanoma through a negative feedback loop with its target gene IL-6²⁰. Recently, miR-98 was found to inhibit the malignant phenotypes of NSCLC cells through directly targeting ITGB3 and

PAK1^{21,22}. As one miR has many target genes⁷, whether other targets of miR-98 exist in NSCLC still needs to be fully investigated.

Our study aimed to investigate the clinical significance of miR-98 expression in NSCLC, as well as the underlying mechanism of miR-98 in mediating the proliferation, migration, and invasion of NSCLC cells.

MATERIALS AND METHODS

Tissue Sample Collection

The study was approved by the ethics committee of Second Xiangya Hospital of Central South University, Changsha, P.R. China. NSCLC tissues ($n=88$) and non-tumor lung tissues ($n=15$) were collected at our hospital from January 2010 to March 2011. All written informed consents were obtained. The tissues were confirmed by pathologists at our hospital. NSCLC patients did not receive preoperative radiotherapy or chemotherapy. After surgical resection, all tissues were immediately snap frozen in liquid nitrogen and stored at -80°C . The clinicopathological information is summarized in Table 1.

Real-Time qPCR Assay

Total RNA was extracted using TRIzol reagent (Thermo Fisher Scientific, Waltham, MA, USA) according to the manufacturer's instructions. Reverse Transcription Kit (Thermo Fisher) was used to convert RNA into cDNA

according to the manufacturer's instructions. For miR-98 expression detection, MiRNA Q-PCR Detection Kit (GeneCopoeia, Rockville, MD, USA) was used to conduct real-time PCR on the ABI 7300 plus thermocycler. U6 gene was used as an internal reference. For mRNA detection, the Q-PCR Detection Kit (Thermo Fisher) was used to conduct real-time PCR according to the manufacturer's instructions. GAPDH was used as an internal reference. The PCR conditions were 95°C for 5 min, and 40 cycles of 95°C for 15 s and 60°C for 30 s. The relative expression of miR and mRNA was analyzed using the $2^{-\Delta\Delta\text{Ct}}$ method.

Cell Culture and Transfection

Normal lung epithelial cell line BEAS-2B and human NSCLC cell lines A549, HCC827, H1229, and SKMES-1 were purchased from the Cell Bank of Central South University (Hunan Sheng, P.R. China). Cells were cultured in Dulbecco's modified Eagle's medium (DMEM; Thermo Fisher Scientific) supplemented with 10% fetal bovine serum (FBS; Thermo Fisher Scientific). Cells were cultured at 37°C in a humidified atmosphere with 5% CO_2 . Cells were passaged every 3 days to maintain exponential growth. A549 and H1229 cells were transfected with miR-98 mimic, scramble miR mimic (miR-NC), miR-98 inhibitor, negative control (NC) inhibitor, pcDNA3.1-SALL4 expression plasmid, or blank

Table 1. Association Between miR-98 Expression and Clinicopathologic Features of Patients With Non-Small Cell Lung Cancer

Variables	No.	Low miR-98 ($n=45$)	High miR-98 ($n=43$)	p Value
Age (years)				0.64
<60	25	14	11	
≥ 60	63	31	32	
Sex				0.805
Male	67	35	32	
Female	21	10	11	
Hypotype				0.674
Adenocarcinoma	49	24	25	
Squamous and others	39	21	18	
Differentiation				0.017*
Well moderated	37	13	24	
Poor	51	32	19	
Tumor size (cm)				0.392
<3	40	18	22	
≥ 3	48	27	21	
TNM stage				0.033*
I/II	25	8	17	
III/IV	63	37	26	
Smoking status				0.276
Never	16	6	10	
Ever	72	39	33	

*The difference has statistical significance.

pcDNA3.1 vector using Lipofectime 2000 (Thermo Fisher Scientific) according to the manufacturer's instructions.

Western Blot

Cells were lysed with RIPA buffer to extract proteins, which were separated with 12% SDS-PAGE, and then transferred onto a polyvinylidene difluoride (PVDF) membrane (Thermo Fisher Scientific). The membrane was incubated with PBS containing 5% milk at room temperature for 3 h. The PVDF membrane was incubated with primary antibodies including SALL4, E-cadherin, N-cadherin, fibronectin, vimentin, MMP2, MMP9, and GAPDH (all from Abcam, Cambridge, MA, USA) at room temperature for 3 h, and then with secondary antibody (Abcam) at room temperature for 1 h. SuperSignal West Pico Chemiluminescent Substrate Kit (Pierce, Rockford, IL, USA) was then used to detect signals according to the manufacturer's instructions. The relative protein expression was analyzed by Image-Pro Plus 6.0 software (Media Cybernetics, Rockville, MD, USA), represented as the density ratio versus GAPDH.

MTT Assay

Cells were plated at a density of 10,000 cells per well in 96-well plates. After being cultured for 0, 24, 48, and 72 h, cells were incubated with MTT (0.5 mg/ml) for 4 h at 37°C. Then 150 mM DMSO solution was added to dissolve the formazan crystals. The absorbance was read at 570 nm using a microplate reader.

Wound Healing Assay

Cells were cultured to full confluence, and wounds of approximately 1-mm width were created with a plastic scribe. Cells were washed with PBS and incubated in DMEM without FBS. After wounding for 24 h, cells were incubated in DMEM with 10% FBS. After being cultured for 48 h, cells were observed under a microscope.

Transwell Assay

Transwell chambers precoated with Matrigel (BD Biosciences, San Jose, CA, USA) were used to perform the Transwell assay. Cell suspension containing 5×10^5 cells/ml was prepared in DMEM, 300 µl of which was added into the upper chamber. Then 500 µl of DMEM with 10% FBS was added into the lower chamber. After cells were incubated at 37°C for 24 h, a cotton-tipped swab was used to wipe out the cells that did not pass through the pores. Cells were fixed in 90% alcohol, stained with crystal violet, and observed under a microscope.

Bioinformatics Analysis and Luciferase Reporter Assay

TargetScan, miRanda, and PicTar bioinformatics software was used to predict the putative target genes of miR-98 according to the manufacturer's instructions.

The wild type (WT) or mutant type (MT) of SALL4 3'-UTR was cloned into the downstream of the firefly luciferase coding region of pMIR-GLO™ luciferase vector (Promega, Madison, WI, USA). A549 and H1229 cells were cotransfected with 200 ng of WT- or MT-SALL4-3'UTR plasmid, and 100 ng of the miR-98 mimic or miR-NC and the pRL-TK plasmid (Promega) for internal normalization. After transfection for 36 h, the luciferase activity was examined using the Dual-Luciferase Reporter Assay System (Promega) according to the manufacturer's instructions.

Stable Transfection and Tumor Growth Analysis

Male BALB/C-nu/nu nude mice (8 weeks) were purchased and maintained under specific pathogen-free conditions at the Animal Center of Central South University (Hunan Sheng, P.R. China). The mature miR-98 or SALL4 was cloned into the pLP/VSVG lentiviral vector. A549 cells were stably transfected with the pLP/VSVG-miR-98 plasmid, pLP/VSVG-SALL4 plasmid, or blank vector. Nude mice were injected subcutaneously in the dorsal flank with 1×10^7 A549 cells of each group. Nude mice were sacrificed 90 days after tumor implantation. Tumor weight was determined. Tumor volume was calculated using the formula $V (\text{mm}^3) = 0.5 \times a \times b^2$ (a is the maximum length to diameter, and b is the maximum transverse diameter).

Statistical Analysis

Data are expressed as mean \pm SD from at least three separate experiments. Independent *t*-tests were used to compare the differences between two groups. Qualitative data were analyzed by the chi-square test. Correlation was determined by Pearson correlation analysis. SPSS 20.0 was used to perform statistical analysis. A value of $p < 0.05$ was considered statistically significant.

RESULTS

Downregulation of miR-98 Is Associated With Malignant Progression in NSCLC

In this study, we first used real-time RT-PCR to determine the miR-98 expression level in NSCLC tissues ($n=88$). Nontumor lung tissues ($n=15$) were used as controls. We found that miR-98 was significantly downregulated in NSCLC tissues compared to nontumor lung tissues (Fig. 1A). To further confirm these findings, we examined the miR-98 expression in normal lung epithelial cell line BEAS-2B and human NSCLC cell lines including A549, HCC827, H1229, and SKMES-1. Expression levels of miR-98 were also reduced in NSCLC cell lines compared to BEAS-2B cells (Fig. 1B). Therefore, miR-98 is downregulated in NSCLC. We then studied the clinical significance of miR-98 expression in NSCLC. Based on the mean value of the miR-98 expression as

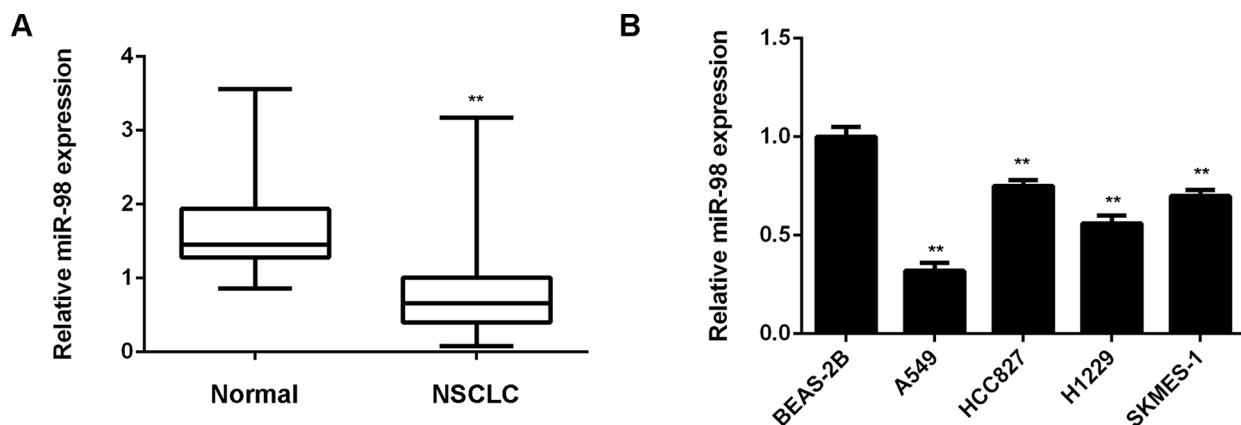


Figure 1. miR-98 is downregulated in NSCLC. (A) Real-time qPCR was conducted to determine the miR-98 levels in NSCLC tissues ($n=88$) and nontumor lung tissues ($n=15$). ** $p<0.01$ versus Normal. (B) Real-time qPCR was conducted to determine the miR-98 levels in normal lung epithelial BEAS-2B cells and human NSCLC cell lines A549, HCC827, H1229, and SKMES-1. ** $p<0.01$ versus BEAS-2B.

the cutoff point, NSCLC patients were divided into two groups: low miR-98 expression group and high miR-98 expression group. We found that low miR-98 expression was significantly associated with poor differentiation and advanced clinical stage, but not with age, sex, hypotype, tumor size, or smoking status (Table 1). Therefore, we suggest that decreased expression of miR-98 is associated with the malignant progression of NSCLC.

miR-98 Has Suppressive Effects on NSCLC Cell Growth and Metastasis In Vitro

A549 and H1229 were further used to study the regulatory role of miR-98 in NSCLC in vitro. As we had found that miR-98 was downregulated in NSCLC tissues and cell lines, A549 and H1229 cells were transfected with the miR-98 mimic to increase its expression. Transfection with miR-NC was used as the control group. Real-time PCR data indicated that miR-98 levels were significantly higher in the miR-98 group than in the miR-NC group (Fig. 2A and B). Further investigation showed that overexpression of miR-98 caused a significant reduction in cell proliferation (Fig. 2C and D). These findings suggest that miR-98 has a suppressive effect on NSCLC growth.

We further studied the regulatory role of miR-98 in NSCLC metastasis in vitro by performing wound healing and Transwell assays. The migration and invasion capacities of A549 and H1229 cells were significantly decreased after overexpression of miR-98 when compared to the miR-NC group (Fig. 3A–D). MMP2 and MMP9 are two important matrix metalloproteinases, which play a key role in tumor cell migration and invasion. Therefore, we examined the protein expression in each group. Western blot data showed that the protein levels of MMP2 and

MMP9 were significantly lower in the miR-98 group when compared with those in the miR-NC group (Fig. 3E and F). Based on the above data, we demonstrated that miR-98 has a suppressive effect on NSCLC cell growth and metastasis in vitro.

SALL4 Is a Target Gene of miR-98 in NSCLC Cells

We then used several common bioinformatics software to predict the putative target genes of miR-98. We found that SALL4 was a potential target gene of miR-98, with perfect base pairing at the seed sequences of miR-98 (data not shown). To confirm these findings, the WT- and MT-SALL4-3'UTR luciferase reporter plasmids were generated (Fig. 4A). Luciferase reporter assay data indicated that cotransfection with the miR-98 mimic and WT-SALL4-3'UTR luciferase reporter plasmid led to a significant decrease in the luciferase activity in A549 and H1229 cells when compared to the control group, which was eliminated by cotransfection with the MT-SALL4-3'UTR luciferase reporter plasmid (Fig. 4B and C). Accordingly, SALL4 is a target gene of miR-98.

We further showed that overexpression of miR-98 significantly reduced the protein expression of SALL4 in NSCLC cells (Fig. 5A and B). To confirm these findings, A549 and H1229 cells were transfected with the miR-98 inhibitor to further downregulate its expression. After transfection, miR-98 levels were reduced in the miR-98 inhibitor group when compared with those in the NC inhibitor group (Fig. 5C and D). We then found that knockdown of miR-98 upregulated the protein expression of SALL4 in NSCLC cells (Fig. 5E and F). Therefore, miR-98 negatively regulates the protein expression of SALL4 in NSCLC cells.

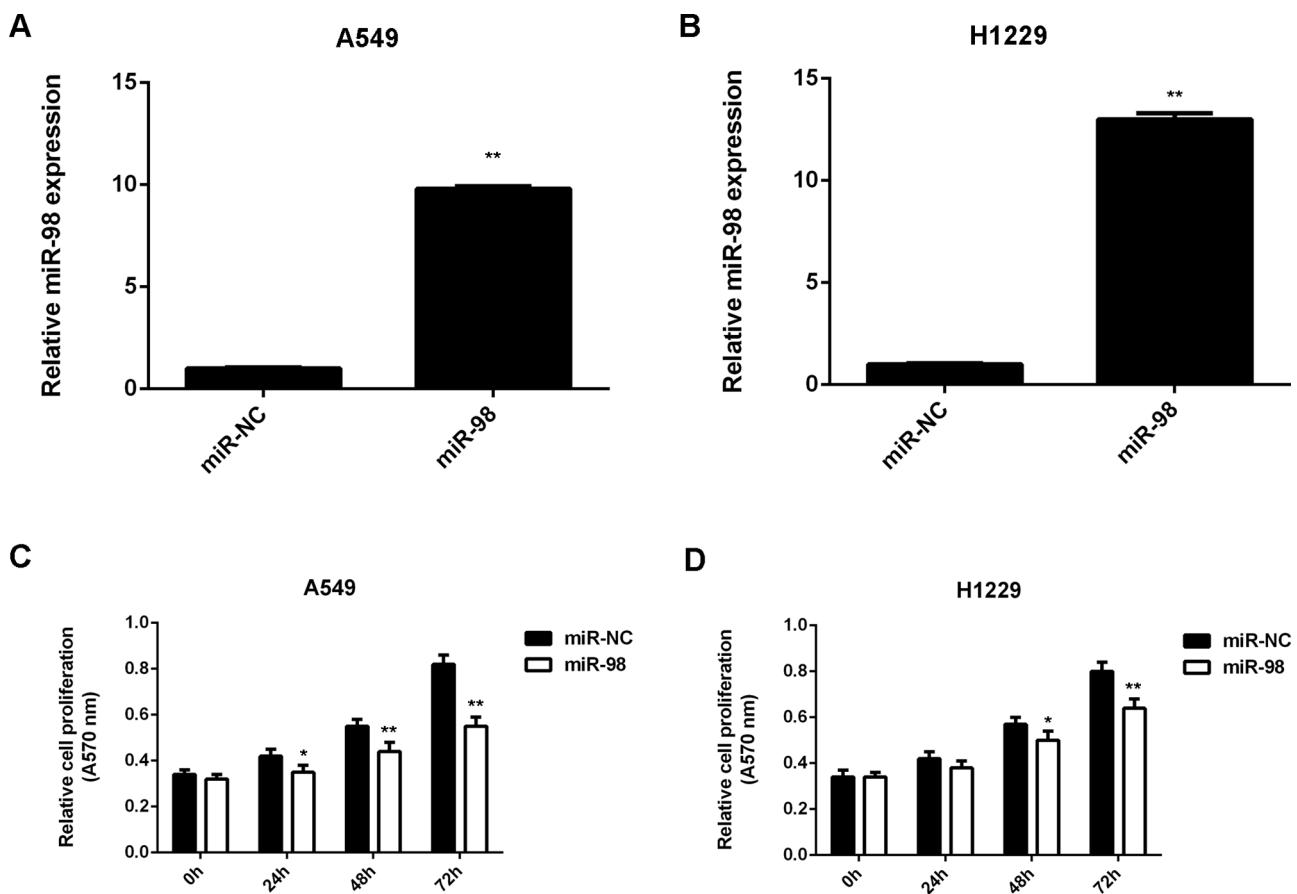


Figure 2. miR-98 inhibits the proliferation of NSCLC cells. A549 and H1229 cells transfected with the miR-98 mimic or scramble miR mimic (miR-NC). (A, B) Real-time RT-PCR was used to examine the miR-98 levels. (C, D) MTT assay was performed to examine cell proliferation. * $p<0.05$, ** $p<0.01$ versus miR-NC.

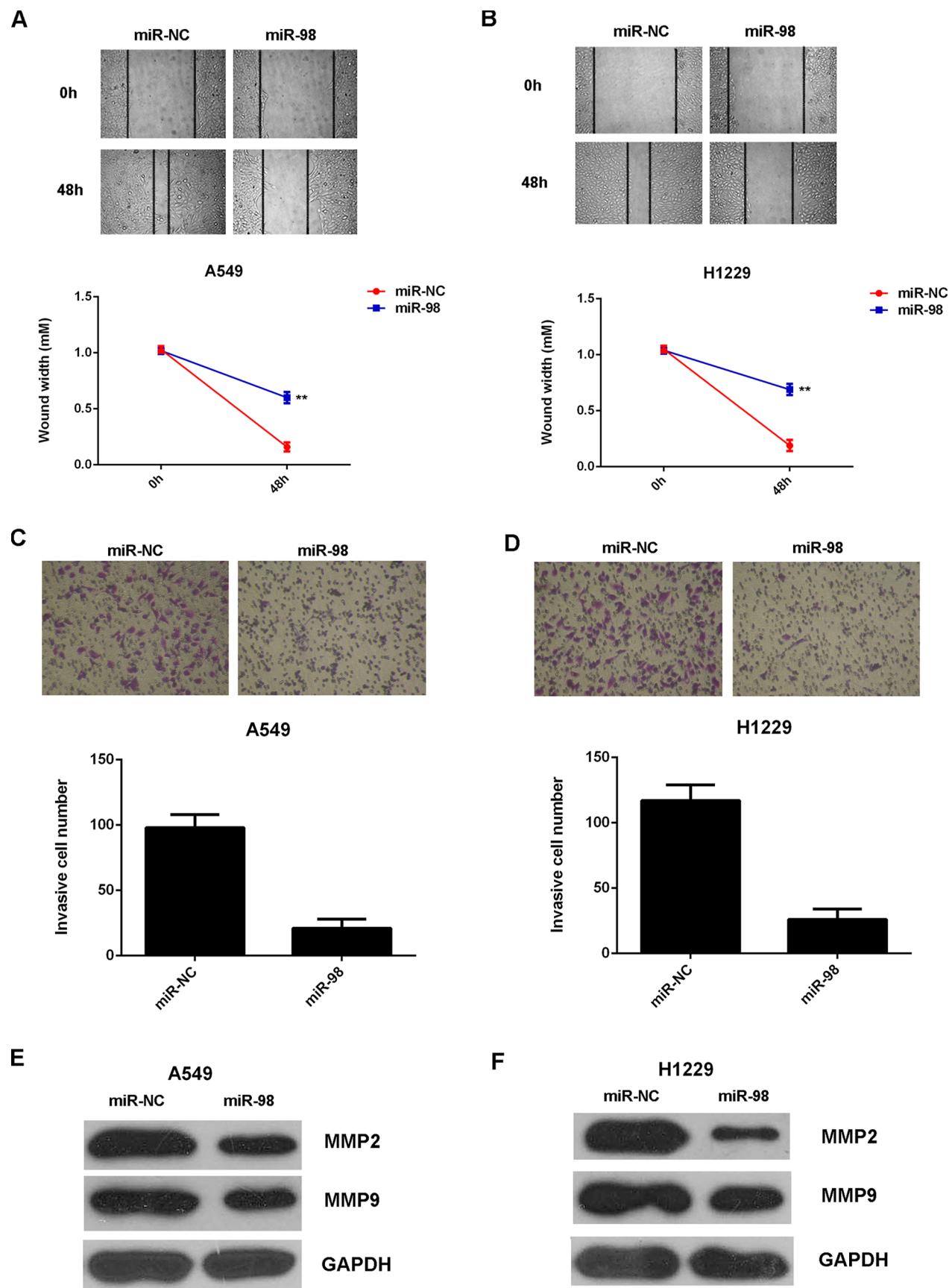
SALL4 Is Upregulated in NSCLC and Reverse Correlated With miR-98 Levels

The expression level of SALL4 was further determined in NSCLC. We found that the mRNA levels of SALL4 were significantly upregulated in NSCLC tissues compared to nontumor lung tissues (Fig. 6A). Moreover, an inverse correlation was observed between the miR-98 and SALL4 mRNA levels in NSCLC tissues (Fig. 6B), which suggests that upregulation of SALL4 may be caused by the decreased expression of miR-98 in NSCLC. In addition, we further examined the expression of SALL4 in NSCLC cell lines and normal lung epithelial BEAS-2B cells. We found that the protein levels of SALL4 were significantly increased in NSCLC cell lines compared to BEAS-2B cells (Fig. 6C).

SALL4 Is Involved in the miR-98-Mediated Growth and Metastasis of NSCLC Cells

As we found that SALL4, upregulated in NSCLC, was negatively mediated by miR-98, we then studied whether

SALL4 was involved in the miR-98-mediated growth and metastasis of NSCLC cells. miR-98-overexpressing A549 and H1229 cells were transfected with pcDNA3.1-SALL4 expression plasmid. The protein levels of SALL4 were significantly higher in the miR-98 + SALL4 group when compared with those in the miR-98 group (Fig. 7A and B). MTT assay data further indicated that cell proliferation capacity was increased in the miR-98 + SALL4 group compared to the miR-98 group (Fig. 7C and D), suggesting that the suppressive effect of miR-98 on NSCLC cell proliferation is through inhibition of SALL4. Afterward, we found that the migration and invasion of NSCLC cells were also significantly upregulated in the miR-98 + SALL4 group when compared to the miR-98 group (Fig. 8A–D). Taken together, overexpression of SALL4 eliminated the suppressive effects of miR-98 on the malignant phenotypes of A549 and H1229 cells. Therefore, SALL4 acts as a downstream effector in the miR-98-mediated growth and metastasis of NSCLC cells.



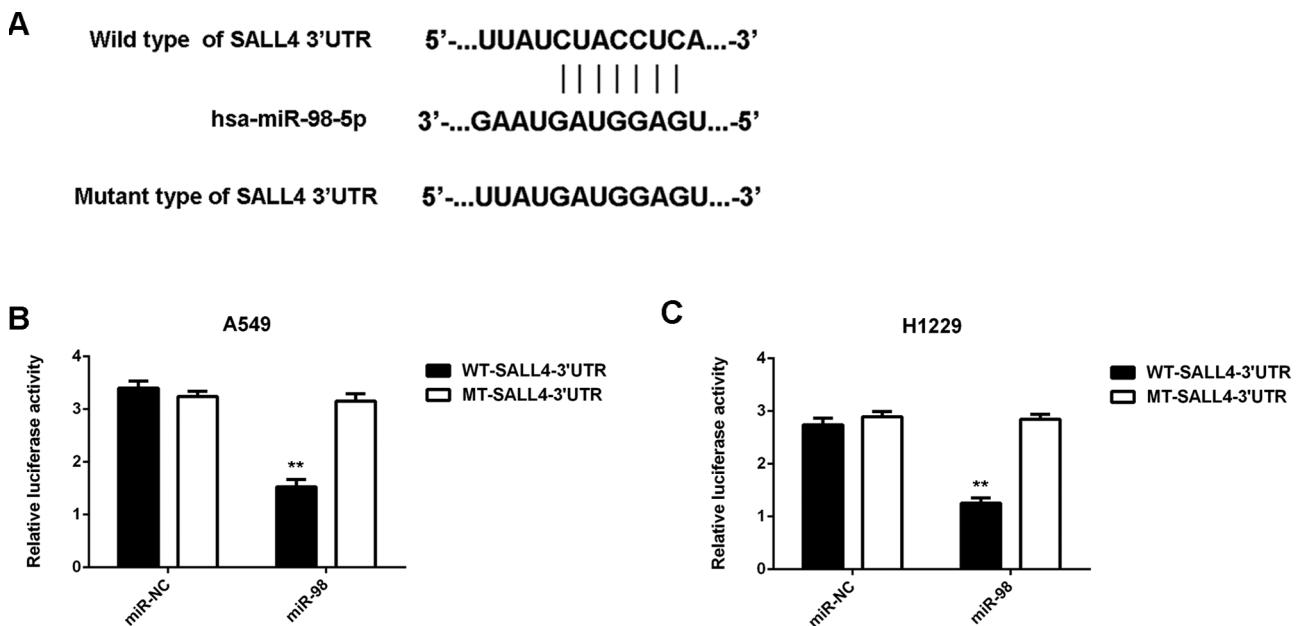


Figure 4. SALL4 is a target gene of miR-98 in NSCLC cells. (A) Representation of the vectors containing the wild-type (WT) or mutant-type (MT) 3'-UTR of SALL4 used in the luciferase assay. (B, C) The luciferase activity was notably decreased in A549 and H1229 cells cotransfected with miR-98 mimics and WT-SALL4-3'UTR reporter plasmid, but unaltered in A549 and H1229 cells cotransfected with miR-98 mimics and MT-SALL4-3'UTR plasmid. ** $p < 0.01$ versus miR-NC.

Effects of miR-98 and SALL4 on NSCLC Growth In Vivo

We then studied the effects of miR-98 and SALL4 on NSCLC growth in vivo. miR-98 or SALL4 was cloned into the pLP/VSVG lentiviral vector. The pLP/VSVG-miR-98 or pLP/VSVG-SALL4 plasmid was then stably transfected into A549 cells. After transfection, miR-98 and SALL4 expression was significantly increased when compared to the control group that was transfected with a blank vector (Fig. 9A and B). Afterward, nude mice were subcutaneously implanted with A549 cells of each group, and the tumor grew gradually after implantation. The mice were sacrificed on the 90th day after implantation. We found that SALL4 overexpression remarkably promoted tumor growth, while overexpression of miR-98 significantly suppressed tumor growth when compared to the control group (Fig. 9C). Tumor weight and volume were increased in the SALL4 group, but decreased in the miR-98 group when compared to the control group (Fig. 9D and E). These findings further suggest that miR-98 inhibits NSCLC growth in vivo, at least, via directly targeting SALL4.

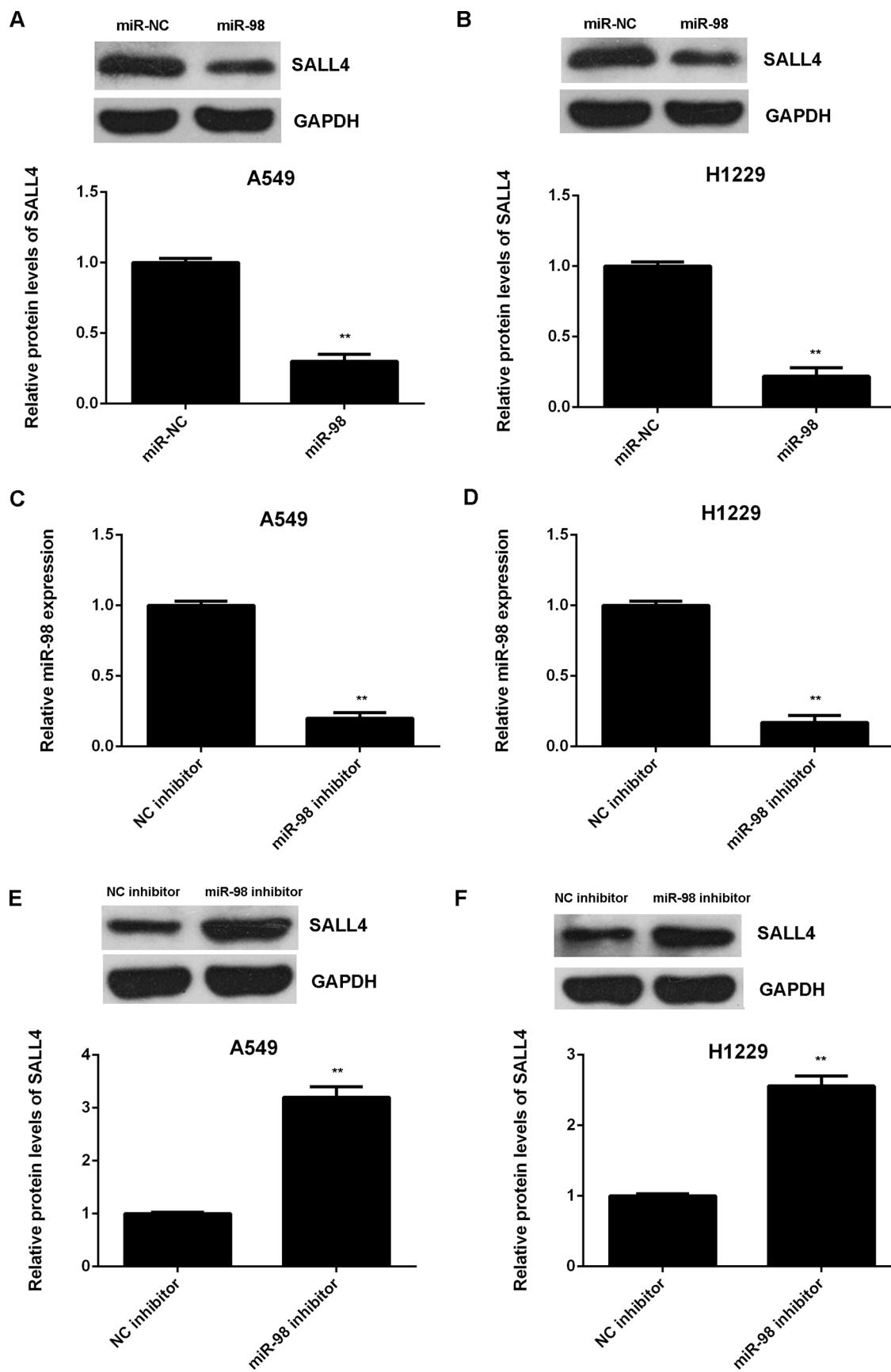
DISCUSSION

A variety of miRs have been demonstrated to participate in the development and malignant progression of NSCLC^{11,23}, but the underlying mechanism remains largely unclear. Here we reported that miR-98 was significantly downregulated in NSCLC, which was associated with disease progression. Further investigation revealed that miR-98 inhibited the proliferation, migration, and invasion of NSCLC cells in vitro, as well as tumor growth in vivo, at least partly, via directly targeting SALL4, an oncogene upregulated in NSCLC.

miR-98 has been demonstrated to act as a tumor suppressor or oncogene in different human cancers^{19,20,24}. It is downregulated and plays a suppressive role in glioma²⁴, oral squamous cell carcinoma¹⁹, and melanoma²⁰. On the contrary, it is upregulated and functions as an oncogene in gastric cancer²⁵, colon cancer²⁶, and small cell lung cancer²⁷. The dual roles of miR-98 are probably due to the fact that it functions through targeting different genes in different cancers. Recently, miR-98 was reported to be significantly downregulated in NSCLC and plays a

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Figure 3. miR-98 suppresses the migration and invasion of NSCLC cells. A549 and H1229 cells transfected with the miR-98 mimic or scramble miR mimic (miR-NC). Nontransfected A549 and H1229 cells were used as controls. (A, B) Wound healing assay and (C, D) Transwell assay were performed to determine cell migration and invasion. (E, F) Western blot was used to examine the protein levels of MMP2 and MMP9. ** $p < 0.01$ versus miR-NC.



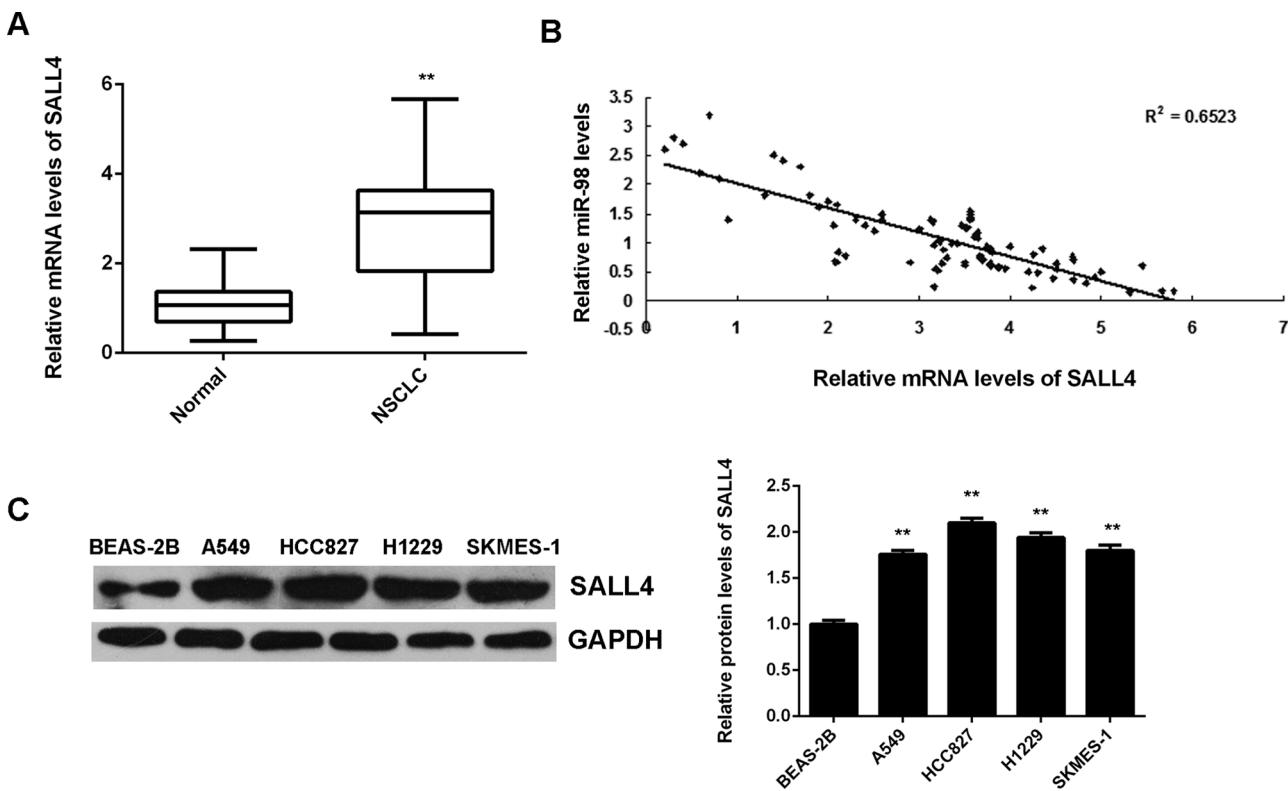


Figure 6. SALL4 is upregulated in NSCLC, inversely correlated to miR-98 levels. (A) Real-time qPCR was conducted to determine the mRNA levels of SALL4 in NSCLC tissues ($n=88$) and nontumor lung tissues ($n=15$). ** $p<0.01$ versus Normal. (B) An inverse correlation was observed between the miR-98 and SALL4 mRNA levels in NSCLC tissues. (C) Western blot was used to examine the protein levels of SALL4 in normal lung epithelial BEAS-2B cells and human NSCLC cell lines A549, HCC827, H1229, and SKMES-1. ** $p<0.01$ versus BEAS-2B.

suppressive role^{21,22}. Ni et al. found that miR-98 targeted ITGB3 to inhibit proliferation, migration, and invasion of NSCLC cells²¹. Yang et al. showed that miR-98 inhibited cell proliferation and invasion of non-small cell carcinoma lung cancer by targeting PAK1²². Moreover, overexpression of miR-98 could increase A549 cell spontaneous apoptosis and sensitize cells to cisplatin, at least partly, by upregulation of HMGA2²⁸. In addition, upregulation of miR-98 in the serum of NSCLC patients is associated with better outcomes of radiotherapy²⁹. Our study showed that miR-98 was significantly downregulated in NSCLC tissues and cell lines when compared with that in nontumor lung tissues or normal lung epithelial cells. We further showed that low expression of miR-98 was significantly associated with poor differentiation and advanced clinical stage in NSCLC, suggesting that downregulation

of miR-98 may contribute to the malignant progression of NSCLC. NSCLC A549 and H1229 cell lines were further used to investigate the regulatory mechanism of miR-98 in NSCLC growth and metastasis. We found that overexpression of miR-98 significantly suppressed the proliferation, migration, and invasion of A549 and H1229 cells, which suggests that miR-98 has an inhibitory effect on NSCLC growth and metastasis.

SALL4, a zinc finger transcription factor, is an important stem cell marker participating in the maintenance of self-renewal of embryonic stem cells³⁰. Recently, SALL4 has been identified as an oncogene in some common cancer types^{31,32}. Yong et al. reported that SALL4 was reexpressed in a subgroup of patients who have hepatocellular carcinoma and an unfavorable prognosis³³. Yue et al. showed that high expression of SALL4 predicted a

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Figure 5. SALL4 was negatively regulated by miR-98 in NSCLC cells. (A, B) Western blot was conducted to examine the protein expression of SALL4 in A549 and H1229 cells transfected with the miR-98 mimic or scramble miR mimic (miR-NC). ** $p<0.01$ versus miR-NC. Afterward, A549 and H1229 cells were transfected with the miR-98 inhibitor or negative control (NC) inhibitor. (C, D) Real-time qPCR was conducted to determine the miR-98 levels. (E, F) Western blot was conducted to examine the protein expression of SALL4. ** $p<0.01$ versus NC inhibitor (C–F).

malignant phenotype and poor prognosis of breast invasive ductal carcinoma³⁴. In addition, SALL4 was found to be an oncogene in glioma³⁵, endometrial cancer³⁶, intrahepatic cholangiocarcinoma³⁷, colon cancer³⁸, ALK⁺ anaplastic large cell lymphoma³⁹, and esophageal squamous cell carcinoma⁴⁰. Recently, Rodriguez et al. reported that a high expression of SALL4 was correlated with low differentiation of NSCLC⁴¹. Kobayashi et al. found that SALL4 was upregulated in lung cancer and played a promoting role in cell proliferation⁴². Moreover, SALL4 was identified as a drug-resistant factor in lung cancer, and high expression of SALL4 is associated with shorter

period until recurrence⁴³. Therefore, SALL4 may become a potential therapeutic target for NSCLC.

In addition, several miRs directly target SALL4 and function as tumor suppressors in different cancers. Cheng et al. found that miR-219 inhibited the proliferation, migration, and invasion of colon cancer cells by targeting SALL4³⁸. Lin et al. reported that miR-33b suppressed breast cancer metastasis through inhibition of HMGA2, SALL4, and Twist1 expression⁴⁴. However, the miR-related regulatory mechanism of SALL4 expression in NSCLC has never previously been studied. In the present study, we showed that SALL4, significantly upregulated in NSCLC,

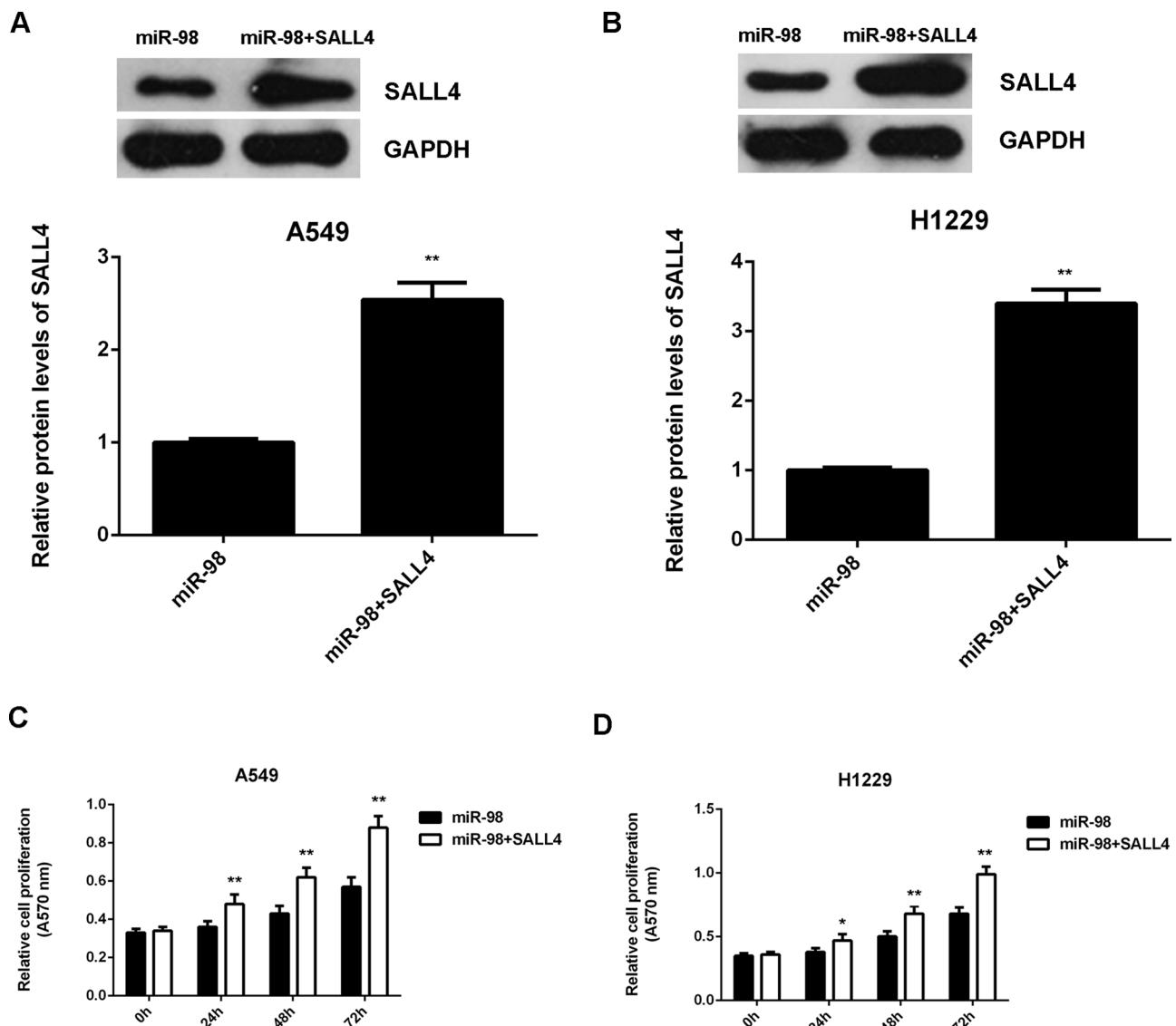


Figure 7. Overexpression of SALL4 eliminates the suppressive effects of miR-98 on NSCLC cell proliferation. A549 and H1229 cells were transfected with the miR-98 mimic or co-transfected with the miR-98 mimic and pcDNA3.1-SALL4 expression plasmid. (A, B) Western blot was conducted to examine the protein expression of SALL4. (C, D) MTT assay was performed to examine cell proliferation. * $p<0.05$, ** $p<0.01$ versus miR-98.

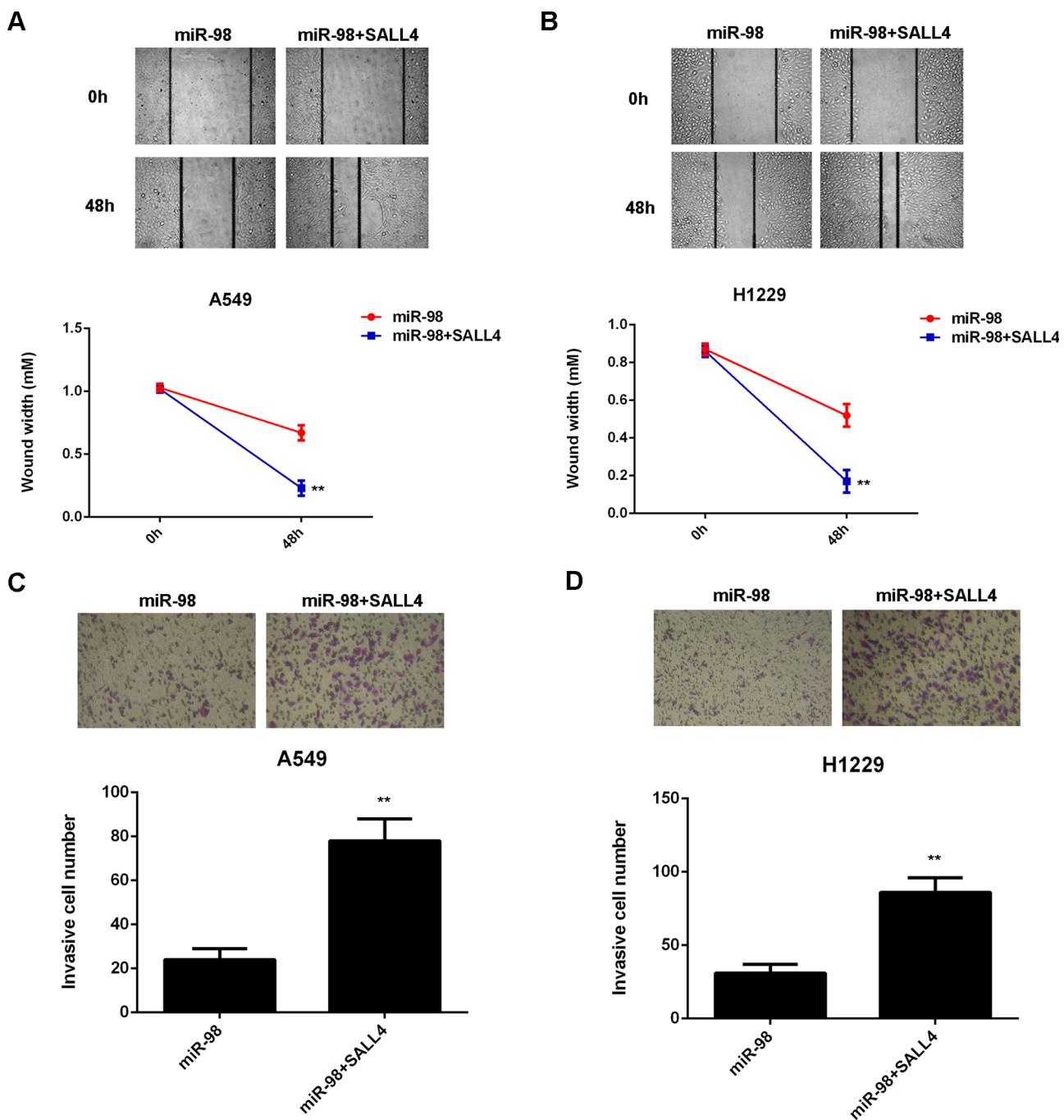


Figure 8. Overexpression of SALL4 eliminates the suppressive effects of miR-98 on NSCLC cell migration and invasion. A549 and H1229 cells were transfected with the miR-98 mimic or cotransfected with the miR-98 mimic and pcDNA3.1-SALL4 expression plasmid. (A, B) Wound healing and (C, D) Transwell assays were performed to determine cell migration and invasion. ** $p < 0.01$ versus miR-98.

was a novel target of miR-98, and the protein expression of SALL4 was negatively regulated by miR-98 in NSCLC cells. Moreover, overexpression of SALL4 eliminated the suppressive effects of miR-98 on the growth and metastasis of NSCLC cells in vitro. These findings

suggest that the suppressive role of miR-98 in NSCLC is through directly targeting SALL4. In vivo study further supports our conclusion that overexpression of miR-98 reduced the tumor growth of A549 cells, while upregulation of SALL4 promoted NSCLC growth in nude mice.

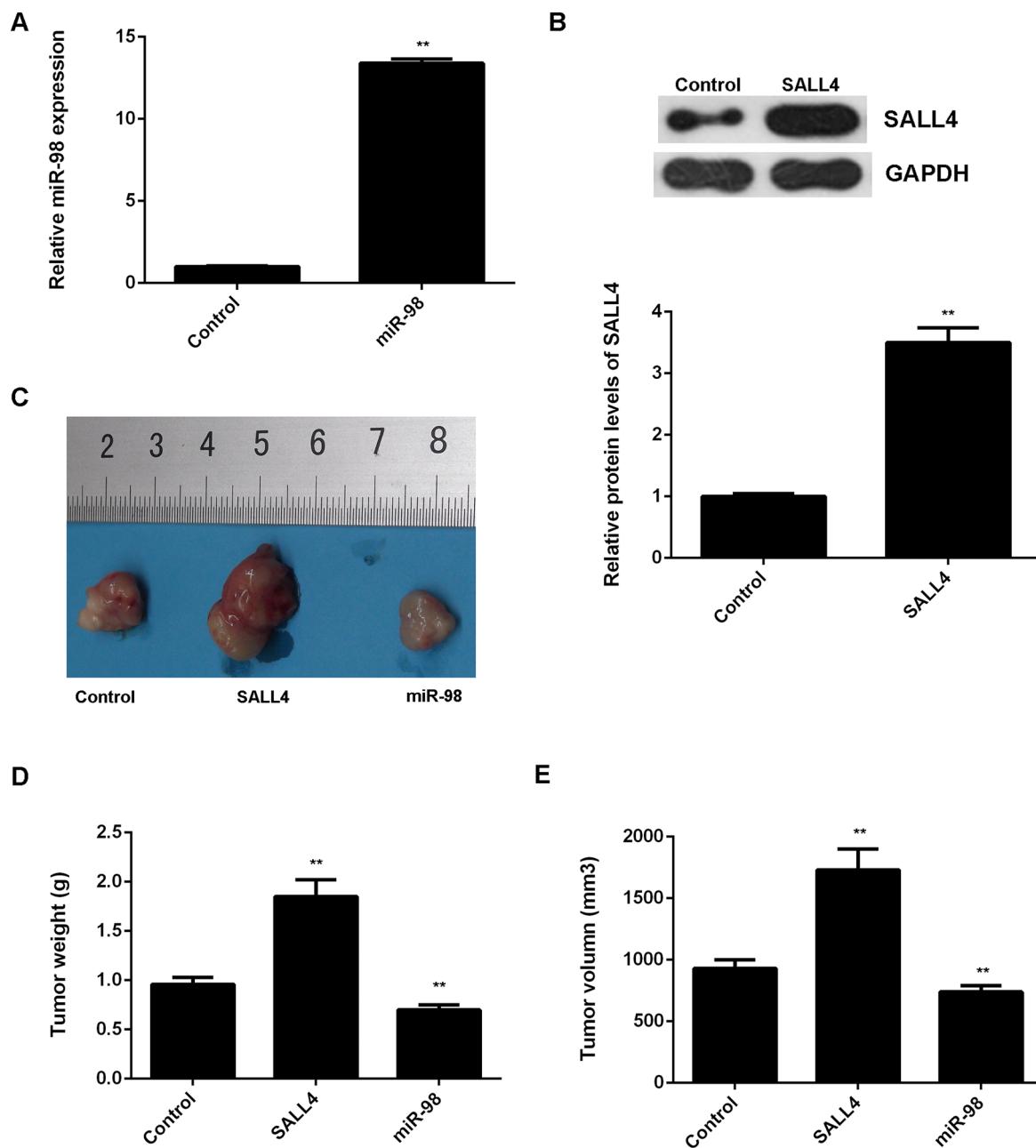


Figure 9. Effects of miR-98 and SALL4 on NSCLC growth in vivo. A549 cells were stably transfected with the blank pLP/VSVG vector as control, pLP/VSVG-miR-98 lentiviral plasmid, or pLP/VSVG-SALL4 lentiviral plasmid. (A) Real-time qPCR was conducted to examine the miR-98 levels. (B) Western blot was used to examine the protein levels of SALL4. Nude mice were subcutaneously implanted with the above cells. (C) On 90 days after implantation, the nude mice in each group were sacrificed, and the xenograft was obtained. (D) Tumor weight and (E) tumor volume were calculated. ** $p < 0.01$ versus Control.

To our knowledge, the present study showed that miR-98 acts as a tumor suppressor in NSCLC through directly targeting SALL4 for the first time. Therefore, we suggest that miR-98 and SALL4 may be promising therapeutic candidates and targets for NSCLC.

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