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ORIGINAL RESEARCH

RETRACTED ARTICLE: Long noncoding RNA SNHG15 serves as an oncogene and predicts poor prognosis in epithelial ovarian cancer

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Objective: This study aims to investigate the functional role of long noncoding RNA SNHG15 in epithelial ovarian cancer (EOC).

Materials and methods: The expression of SNHG15 was measured in EOC cells and tissues using qRT-PCR. The correlation of SNHG15 expression and the clinicopathological characters was statistically analyzed. The prognosis of patients with different clinical features in the high/low SNHG15 expression groups were calculated. Moreover, univariate and multivariate Cox regression analyses were performed to identify the risk factors for poor overall survival (OS) and progression-free survival (PFS). The effect of SNHG15 on the migration and invasion was evaluated using Transwell and Matrigel, respectively. The proliferation ability of EOC cells was tested using colony formation and MTT assay. The influence of SNHG15 on the cisplatin resistance was detected by measuring cell inhibition rate and cell viability.

Results: SNHG15 was upregulated in EOC cells and tissues. High SNHG15 expression was correlated with EOC progression and predicted poor OS and PFS in different subgroups of EOC patients. Moreover, multivariate Cox regression analysis defined high SNHG15 expression as an independent risk factor for poor OS and PFS. Furthermore, functional assays showed that the overexpression of SNHG15 promoted migration and invasion, while the loss of SNHG15 suppressed migration and invasion. Furthermore, the proliferation of EOC cells was improved after the ectopic expression of SNHG15, which was suppressed with SNHG15 deficiency. In addition, cisplatin-resistant EOC cells were established for detecting the effect of SNHG15 on EOC chemoresistance. The results showed that cisplatin-resistant EOC cells exhibited much higher levels of SNHG15 expression than controls, and SNHG15 contributed to the chemoresistance of EOC cells.

Conclusion: This study confirms that SNHG15 contributes to the migration, invasion, proliferation, and chemoresistance of EOC. SNHG15 may serve as a potential therapeutic target and prognostic biomarker of EOC patients.

Keywords: noncoding RNA, ovarian cancer, proliferation, metastasis, chemoresistance

Introduction

Ovarian cancer (OC) accounts for 5% malignancies in female patients and is the fifth leading cause of death due to cancer in women.[1] Among the diverse histological subtypes of OC, epithelial OC (EOC) accounts for ~85%–90% of all types of OC. Despite years of developing aggressive surgical techniques and novel adjuvant treatment strategies, EOC remains the one of the most lethal gynecologic malignancies. Current primary treatment strategies for EOC are mainly surgical resection and systemic platinum-based chemotherapy. Unfortunately, ~80% of patients will experience

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a recurrence within 24 months after completing primary therapy.[2,3] Furthermore, no reliable method or biomarker currently exists for the prediction of prognosis, which makes it rather difficult to administer individual treatment before recurrence. Not surprisingly, the prognosis for patients with recurrence is poor. Therefore, new methods for the prediction of prognosis and new therapeutic strategies are urgently needed.

The number of long noncoding RNAs (lncRNAs), transcripts longer than 200 nucleotides that do not harbor protein-coding signatures, has exploded in recent years.[4] Currently, it has been identified that lncRNAs have myriad molecular functions across many cellular pathways and processes, including oncogenic signaling and are likely to serve as the basis for many clinical applications in oncology.[5–7] When dysregulated, numerous lncRNAs are involved in EOC initiation, development, progression, and chemoresistance.[8] The involvement of lncRNAs in different EOC stages with various modes of action provides the opportunity to intervene at specific points in EOC development.[9] Therefore, lncRNAs are suggested to be potential prognostic biomarkers and therapeutic targets in EOC patients. LncRNA SNHG15, located on chromosome 7p13, has been reported as an oncogene in various types of cancer, such as gastric cancer,[10] glioma,[11] non-small-cell lung cancer,[12] osteosarcoma,[13] colorectal cancer,[14] and breast cancer.[15] However, the clinical significance and functional role of SNHG15 in EOC has not yet been identified.

This study aimed to investigate the role of SNHG15 in EOC. The expression of SNHG15 in EOC cell and tissues was detected, and the relationships between SNHG15 expression and the clinicopathological features of EOC patients were analyzed. The prognostic value of SNHG15 in different subgroups of EOC patients was defined. Furthermore, the effect of SNHG15 on the migration, invasion, proliferation, and chemoresistance of EOC cells was also explored.

Materials and methods

Cell culture

The human EOC cell lines (HO89110, OVCAR3, IGROV-1, OV90, A2780, and SKOV3) and normal human ovarian surface epithelial (HOSE) cell line were purchased from the Cell Bank of Type Culture Collection, Chinese Academy of Science (Shanghai, People's Republic of China). The cell lines were tested 1 month before the experiments for authentication via methods including morphologic analysis, growth curve analysis, and mycoplasma detection. HO89110 cells and OVCAR3 cells were maintained in DMEM (Invitrogen, Carlsbad, CA, USA), whereas the others were maintained in RPMI-1640 medium (Invitrogen) supplemented with 10% FBS (Invitrogen), 2 mM glutamine (Sigma-Aldrich, St. Louis, MO, USA), 100 mg/mL penicillin (Sigma-Aldrich), and 100 mg/mL streptomycin (Sigma-Aldrich), and incubated at 37°C in a humidified atmosphere with 5% CO_2. SNHG15 siRNAs (si-1, si-2, si-3, and si-4), ectopic expression plasmid (pcDNA3.1–SNHG15), nontargeting control siRNAs (siNC), and empty vector (pcDNA3.1–Vector) were all purchased from GenePharma Co. (Shanghai, People's Republic of China). Transfection was conducted using Lipofectamine 2000 transfection reagent (Invitrogen) according to the manufacturer's instructions.

Tissue collection

The current study included 182 primary EOC tissues and paired tumor adjacent tissues that were surgically resected between 2010 and 2014 at the China–Japan Union Hospital of Jilin University. The EOC tissues and paired tumor adjacent tissues were confirmed by pathological results. Collection and preservation of the tissues were strictly carried out. Immediately following surgical removal, the tissue samples were frozen in liquid nitrogen and stored at −80°C until use. Patients with two or more malignancies or accepted neoadjuvant therapies were excluded from the study. Clinical and pathological features of the patients are depicted in Table 1. Type I cancers were low grade with a serous, mucinous, endometrioid, or clear-cell histotype; Type II cancers were high grade with a serous, endometrioid,

Table 1 Correlation between SNHG15 expression and EOC clinicopathological features

Parameters	No of patients (n=182)	SNHG15 high/low (73/109)	*P*-value
Age			0.977
<60 years	85	34/51	
≥60 years	97	39/58	
CA125			0.081
<500 U/mL	104	36/68	
≥500 U/mL	78	37/41	
Cancer type			0.001
Type I	94	27/67	
Type II	88	46/42	
Ascites			0.043
<100 mL	111	38/73	
≥100 mL	71	35/36	
FIGO stage			0.049
I/II	41	11/30	
III/IV	141	62/79	

Abbreviations: EOC, epithelial ovarian cancer; FIGO, International Federation of Gynaecology and Obstetrics.

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or undifferentiated histotype.[16] International Federation of Gynaecology and Obstetrics (FIGO) OC staging system was used for clinical staging. All included patients gave written consent for tissue use in research. The ethics was conducted in accordance with the Declaration of Helsinki. This study was approved by the Ethics Committee of the China–Japan Union Hospital of Jilin University.

qRT-PCR assay

Total RNA was isolated from EOC cells and human tissues using TRIzol reagent (Invitrogen). Total RNA (1 mg) was reverse transcribed using a cDNA synthesis kit (Roche Diagnostics, Indianapolis, IN, USA) with anchored-oligo (dT) 18 primers. Quantitative PCR was performed under standard conditions using an Eppendorf real-time PCR machine and an SYBR Green I Master Kit (Roche Diagnostics). The reactions were performed at 95°C for 10 minutes to activate the polymerase, followed by 40 cycles at 95°C for 5 seconds, 55°C for 10 seconds, and 72°C for 20 seconds. GAPDH was used as endogenous controls. The relative expression level was calculated using the $2^{-\Delta\Delta Ct}$ method. The primer sequences used are as follows: SNHG15 (sense: 5′-CAACCATAGCGGTGCAACTGTGC-3′, antisense: 3′-GGCTGAACCAAGTTGCAAGTCATG-5′); GAPDH (sense: 5′-CAGTGCCAGCCTCGTCTAT-3′, antisense: 3′-AGGGGCCATCCACAGTCTTC-5′). The experiments were repeated three times in triplicate.

In vitro cell migration and invasion assay

The migration and invasion abilities of EOC cells with SNHG15 deficiency or ectopic expression were assessed by a Transwell assay and a Matrigel assay using Transwell chambers (pore size 8 μm; BD Biosciences). Cells (5×10^4) suspended in serum-free medium were seeded in the upper chamber (pre-coated with Matrigel in the Matrigel assay), while the lower chamber was filled with medium containing 20% FBS. After 24 hours of incubation, cells remaining on top of the membrane were removed using a cotton swab. Migrated/invaded cells on the lower surface of the membrane were stained with Giemsa, photographed with a light microscope (Olympus Corp., Tokyo, Japan), and counted. The experiments were repeated three times in triplicate.

Colony formation assay

The colony formation assay was performed to evaluate the proliferation ability of EOC cells. Briefly, EOC cells (500 cells per well) were incubated in 6-well plates, and the medium was changed every 3 days. Two weeks later, formed colonies were fixed with methanol for 15 minutes and stained with 0.1% crystal violet for another 15 minutes. Colonies with a diameter greater than 1 mm were counted under a light microscope (Olympus Corp.). The experiments were repeated three times in triplicate.

MTT assay

The MTT assay was conducted to assess the proliferation ability and cisplatin resistance. EOC cells (3,000 cells per well) were seeded in 96-well plates. After transfection, cells were incubated with 20 μL MTT (5 mg/mL) in each well at the indicated time points (0, 24, 48, 72 and 96 hours) for 4 hours. Then, dimethyl sulfoxide (Sigma) was added (150 μL/well) to each well to dissolve the formazan crystals followed by agitation of the plate for 10 minutes. OD was measured at 490 nm on a microplate reader (Molecular Devices, Sunnyvale, CA, USA). The experiments were repeated three times in triplicate.

To investigate the effect of cisplatin on cell proliferation, cisplatin (0.1 μM, 0–80 μM) was added to the culture medium, and cells were incubated for another 48 hours. Then the MTT assay was conducted to analyze the absorbance. The results of the OD values were calculated to obtain inhibition rates to suppress the effect of cisplatin. The experiments were repeated three times in triplicate.

Establishment of cisplatin resistant cells

EOC cells, A2780 and SKOV3, were treated with cisplatin (5 μM) for 3 hours and then allowed to recover for 2 weeks. Surviving cells were passaged and subjected to the next round of treatment. Sequentially increasing concentrations (5 μM) of cisplatin were used to select resistant cells and finally maintained at 35 μM. The obtained cisplatin-resistant A2780 cells and SKOV3 cells were named A2780-R and SKOV3-R, respectively.

Statistical analysis

The statistical calculations were performed with GraphPad Prism 6.0 for Windows (GraphPad Software, La Jolla, CA, USA). The results are shown as the mean ± SD. The statistical significance of the differences among different groups was calculated using a two-tailed Student's *t*-test or chi-squared test. Kaplan–Meier plots for overall survival (OS) and progression-free survival (PFS) were plotted, and analysis was done using the log-rank test. Univariate and multivariate Cox regression analyses were conducted to analyze the risk factors for poor prognosis. A *P*-value of less than 0.05 was considered to be statistically significant.

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Results

SNHG15 is upregulated in EOC and is associated with cancer progression

To examine the role of SNHG15 in EOC, the expression of SNHG15 was measured in HOSE and six EOC cell lines. Interestingly, qRT-PCR results found that SNHG15 was upregulated in six EOC cell lines relative to HOSE (Figure 1A). Further detection of the SNHG15 expression level was conducted in 182 EOC tissues and paired tumor adjacent tissues. As expected, EOC tissues displayed much higher level of SNHG15 than paired tumor adjacent tissues (Figure 1B). Furthermore, patients with Type II cancers showed higher SNHG15 levels than patients with Type I cancers (Figure 1C). For a better understanding of the clinical significance of SNHG15 in EOC, the involved patients were divided into two groups, the low SNHG15 expression group (n=109) and the high SNHG15 expression group (n=73), with the mean SNHG15 expression level serving as the cutoff value. As shown in Table 1, the differences in the clinicopathological features between the low SNHG15 expression group and the high SNHG15 expression group were statistically evaluated. High SNHG15 expression was revealed to correlate with cancer type (P=0.001), ascites (P=0.043), and FIGO stage (P=0.049) (Table 1). Therefore, the overexpression of SNHG15 is associated with the clinical progression of EOC.

SNHG15 predicts poor prognosis in different subgroups of EOC patients

OS and PFS are two fundamental parameters evaluating the prognosis of cancer patients. The predictive value of SNHG15 on OS and PFS was explored in different subgroups of EOC patients. The results showed that patients with low SNHG15 expression had a significantly improved OS rate (Figure 2A, left) and PFS rate (Figure 2A, right) than patients with high SNHG15 expression. For patients with Type I cancers, high SNHG15 expression reduced the OS rate compared with low SNHG15 expression, although no statistical

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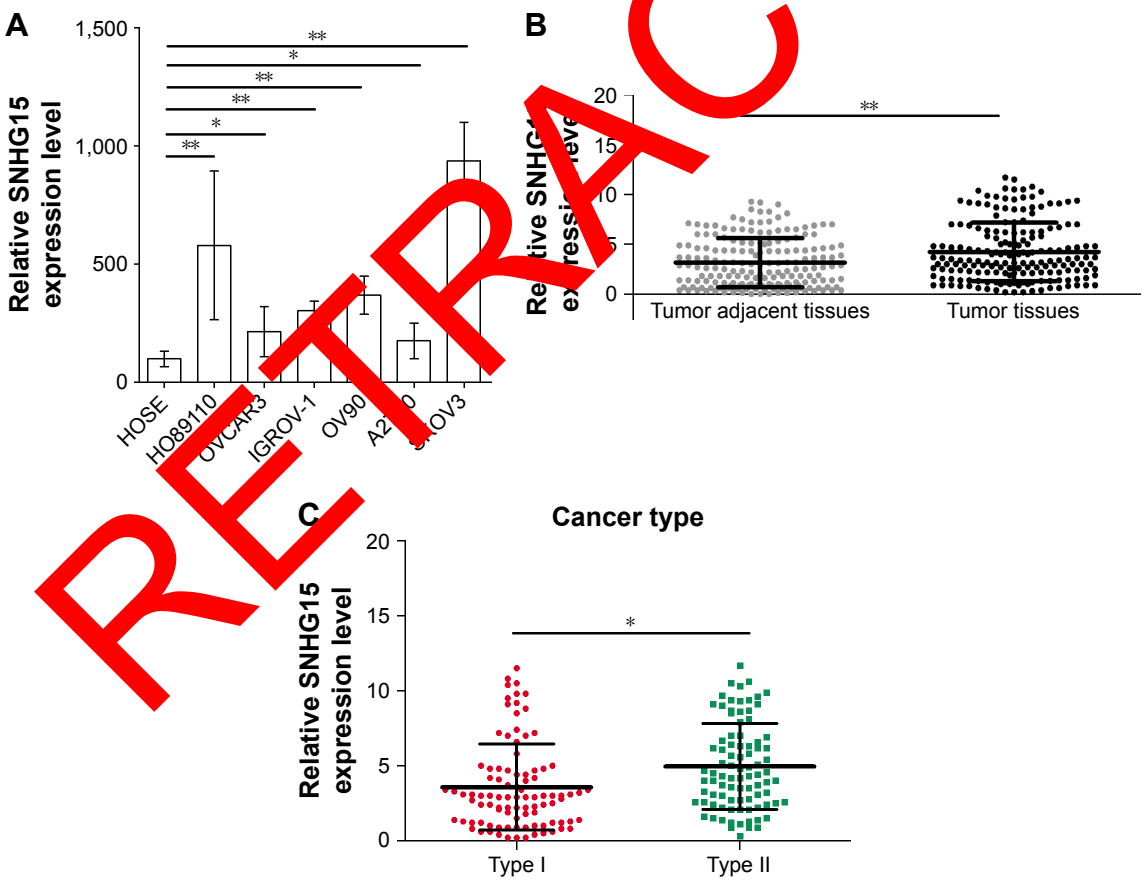

Figure 1 SNHG15 is upregulated in EOC.
Notes: (**A**) Expression of SNHG15 was measured in six EOC cell lines (HO89110, OVCAR3, IGROV-1, OV90, A2780, and SKOV3) and normal cell line human ovarian surface epithelial (HOSE) by qRT-PCR assay. (**B**) Expression of SNHG15 was detected in EOC tissues and paired tumor adjacent tissues (n=182) by a qRT-PCR assay. (**C**) Expression of SNHG15 in Type I and Type II disease was detected by a qRT-PCR assay. *P<0.05 and **P<0.01.
Abbreviation: EOC, epithelial ovarian cancer.

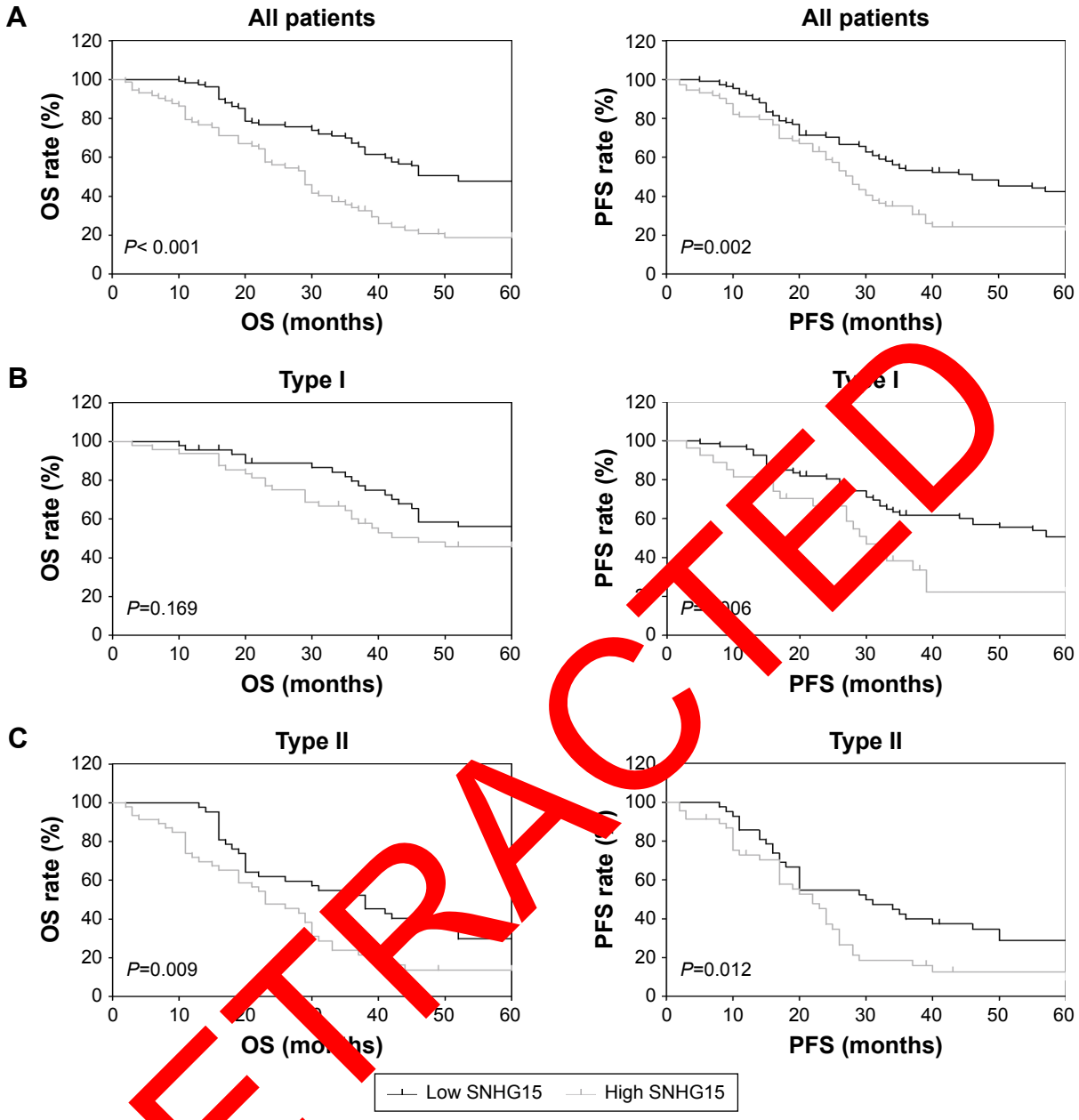

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Figure 2 SNHG15 predicts poor prognosis in different subgroups of EOC patients.
Notes: (**A**) The OS and PFS rate of EOC patients with low SNHG15 expression and high SNHG15 expression were calculated. (**B**) The OS rate and PFS rate of patients with Type I cancers in the low SNHG15 expression group and the high SNHG15 expression group were calculated. (**C**) The OS rate and PFS rate of patients with Type II cancers in the low SNHG15 expression group and the high SNHG15 expression group were calculated.
Abbreviations: EOC, epithelial ovarian cancer; OS, overall survival; PFS, progression-free survival.

significance was found (Figure 2B, left). However, the PFS rate was significantly elevated in the low SNHG15 expression group compared with the high SNHG15 expression group (Figure 2B, right). Moreover, in the subgroup of patients with Type II disease, high SNHG15 expression indicated poor OS (Figure 2C, left) and PFS (Figure 2C, right).

Furthermore, the risk factors for poor OS and PFS were investigated with univariate and multivariate Cox regression analyses. The results discovered that Type II cancers (HR=2.430, 95% CI=1.656–3.565, $P<0.001$), advanced FIGO stage (HR=2.223, 95% CI=1.354–2.651, $P=0.002$), and high SNHG15 expression (HR=1.151, 95% CI=1.086–1.220, $P<0.001$) were risk factors for poor OS (Table 2). Further analysis of these factors with multivariate Cox regression analysis revealed that Type II cancers (HR=1.960, 95% CI=1.319–2.915, $P=0.001$), advanced FIGO stage (HR=1.424, 95% CI=1.108–3.071, $P=0.019$), and high SNHG15 expression (HR=1.136, 95% CI=1.069–1.208,

Table 2 Univariate and multivariate analysis of clinicopathological features for overall survival of EOC patients

Parameters	Univariate analysis			Multivariate analysis		
	HR	95% CI	*P*-value	HR	95% CI	*P*-value
Age: ≥60 years vs <60 years	0.810	0.558–1.176	0.268			
CA125: <500 U/mL vs ≥500 U/mL	1.194	0.819–1.741	0.356			
Cancer type: Type I vs Type II	2.430	1.656–3.565	<0.001	1.960	1.319–2.915	0.001
Ascites: <100 mL vs ≥100 mL	1.322	0.901–1.938	0.153			
FIGO stage: III/IV vs I/II	2.223	1.354–2.651	0.002	1.424	1.108–[illegible]	0.019
SNHG15: high vs low	1.151	1.086–1.220	<0.001	1.136	[illegible]069–[illegible]08	[illegible].001

Abbreviations: EOC, epithelial ovarian cancer; FIGO, International Federation of Gynaecology and Obstetrics.

P<0.001) are independent risk factors for poor OS (Table 2). Furthermore, a similar analysis was performed to identify the risk factors of poor PFS, and high SNHG15 expression (HR=1.120, 95% CI=1.056–1.189, *P*<0.001) was revealed as an independent risk factor for poor PFS (Table 3). Collectively, SNHG15 may be a promising prognostic biomarker for EOC patients with different histological types.

SNHG15 promotes the migration, invasion, and proliferation of EOC cells

To further verify the function of SNHG15 in EOC, SNHG15 was silenced with four siRNAs and overexpressed with pcDNA3.1–SNHG15 in SKOV3 cells and A2780 cells, respectively. The expression of SNHG15 in EOC cells after transfection was measured by a qRT-PCR assay (Figure 3A). siRNAs with relatively high efficacies (si-2 and si-4) were selected for further experiments. The Transwell and Matrigel assays were applied to investigate the effect of SNHG15 on the migration and invasion of EOC cells, respectively. Intriguingly, the overexpression of SNHG15 in A2780 cells markedly promoted the migration (Figure 3B) and invasion (Figure 3C) of EOC cells. Accordingly, interference with SNHG15 in SKOV3 cells notably suppressed the migration (Figure 3D) and invasion (Figure 3E) of EOC cells. Taken together, SNHG15 upregulation promotes the migration and invasion of EOC cells.

The proliferation of EOC cells after transfection was determined by a colony formation assay and a MTT assay. It was shown that the ectopic expression of SNHG15 increased the colony number (Figure 4A) and OD value (Figure 4B) of A2780 cells. The loss of SNHG15 decreased the proliferation of SKOV3 cells (Figure 4C and D).

Table 3 Univariate and multivariate analysis of clinicopathological features for progression-free survival of EOC patients

Parameters	Univariate analysis			Multivariate analysis		
	HR	95% CI	*P*-value	HR	95% CI	*P*-value
Age: ≥60 years vs [illegible] years	0.759	0.527–1.094	0.140			
CA125: <500 U/mL vs ≥[illegible]00 U/mL	1.103	0.762–1.597	0.603			
Cancer type: Type I vs Type II	2.054	1.418–2.974	<0.001	1.721	1.175–2.520	0.005
Ascites: <100 mL vs ≥100 mL	1.371	0.944–1.990	0.097			
FIGO stage: III/IV vs I/II	1.911	1.199–3.046	0.006	1.659	1.031–2.670	0.037
SNHG15: high vs low	1.134	1.072–1.200	<0.001	1.120	1.056–1.189	<0.001

Abbreviations: EOC, epithelial ovarian cancer; FIGO, International Federation of Gynaecology and Obstetrics.

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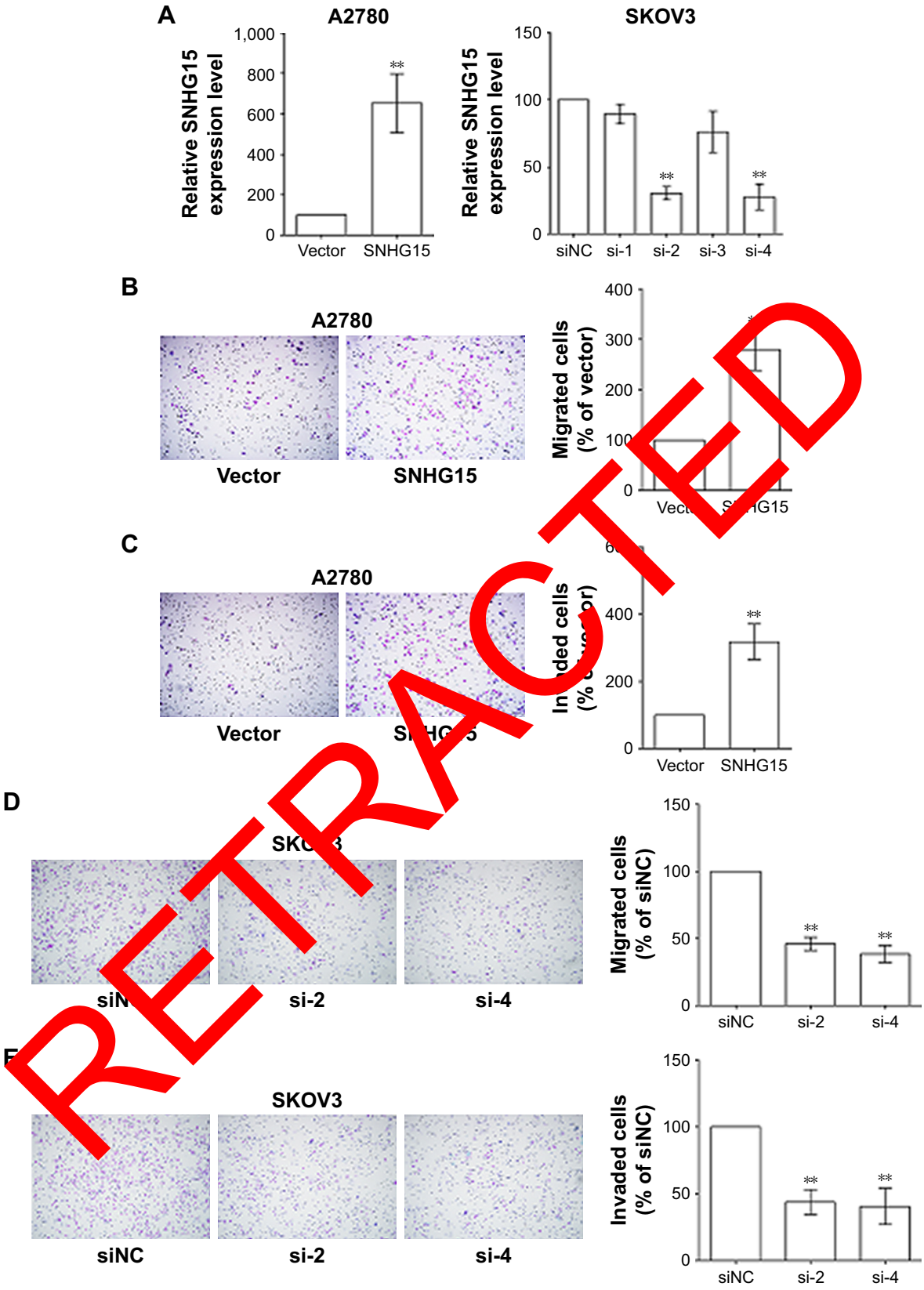

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Figure 3 SNHG15 promotes the migration and invasion of EOC cells.

Notes: (**A**) Expression of SNHG15 in A2780 cells with SNHG overexpression and SKOV3 cells with SNHG15 deficiency was detected by a qRT-PCR assay. (**B**) Migration ability of A2780 cells with SNHG15 overexpression was evaluated by a Transwell assay. (**C**) Invasion ability of A2780 cells with SNHG15 overexpression was evaluated by a Matrigel assay. (**D**) Migration ability of SKOV3 cells with SNHG15 deficiency was evaluated by a Transwell assay. (**E**) Invasion ability of SKOV3 cells with SNHG15 deficiency was evaluated by a Matrigel assay. $^{**}P<0.01$.

Abbreviations: EOC, epithelial ovarian cancer; siNC, nontargeting control siRNAs.

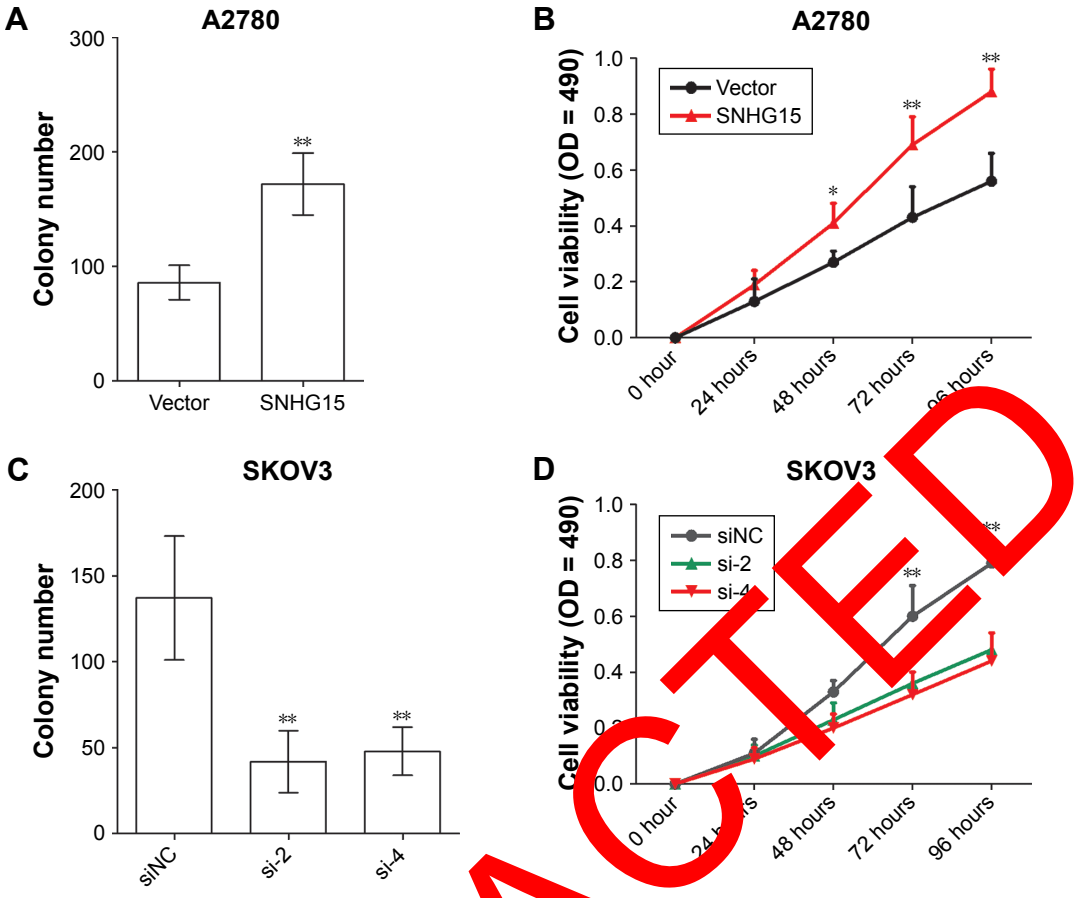

Figure 4 SNHG15 promotes the proliferation of EOC cells.
Notes: (**A**) The colony formation assay was used to determine the proliferation abi A2780 cells with SNHG15 overexpression. (**B**) The MTT assay was performed to investigate the proliferation ability of A2780 cells with SNHG15 ov xpre n. (**C**) T colony formation assay was adopted to determine the proliferation ability of SKOV3 cells with SNHG15 deficiency. (**D**) The MTT assay was perfor to inves ate the pr feration ability of SKOV3 cells with SNHG15 deficiency. *$P<0.05$ and **$P<0.01$.
Abbreviations: EOC, epithelial ovarian cancer; siNC, non eting cont siRNAs.

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These results indicate that SNHG celerates t proliferation of EOC cells.

SNHG15 contrib tes to the chemoresistance f EOC cells

Chemoresistanc rima contri ting factor leading to the final relap of EO patients. lluminate the function of SNHG15 on hemo f EOC cells, cisplatin-resistant cells (A2780-R d SKOV3-R) were established. The inhibition rates of cisp in on A2780-R cells (Figure 5A) and SKOV3-R (Figure 5B) cells were greatly reduced compared with A2780 cells and SKOV3 cells, respectively. Noticeably, A2780-R cells and SKOV3-R cells had much higher SNHG15 levels than A2780 cells and SKOV3 cells, respectively (Figure 5C and D), which implicated the function of SNHG15 on cisplatin resistance of EOC cells. In addition, the inhibition rate of cisplatin on A2780 cells with SNHG15 overexpression was decreased (Figure 5E), and SNHG15 deficiency in SKOV3 cells increased the inhibition rate of cisplatin significantly (Figure 5F). Therefore, SNHG15 contributes to the chemoresistance of EOC cells.

Discussion

lncRNAs are considered important factors in several histological types of OC.[9] Different variants of lncRNAs have been revealed to be correlated with the risk and functionality of EOC.[17,18] For example, the genotyping analyses of lncRNA HOX transcript antisense intergenic RNA (HOTAIR) indicated that rs4759314 and rs7958904 were significantly associated with epithelial EOC susceptibility, which suggested that HOTAIR variants could be a useful biomarker for the predisposition to epithelial EOC and for the early diagnosis of the disease.[17] Another study by Qiu et al[18] reported that HOTAIR rs920778 polymorphism influenced EOC susceptibility and prognosis. The involvement of lncRNAs in EOC has been widely reported, and current evidence demonstrates that lncRNAs could modulate EOC initiation, development, progression, and chemoresistance.

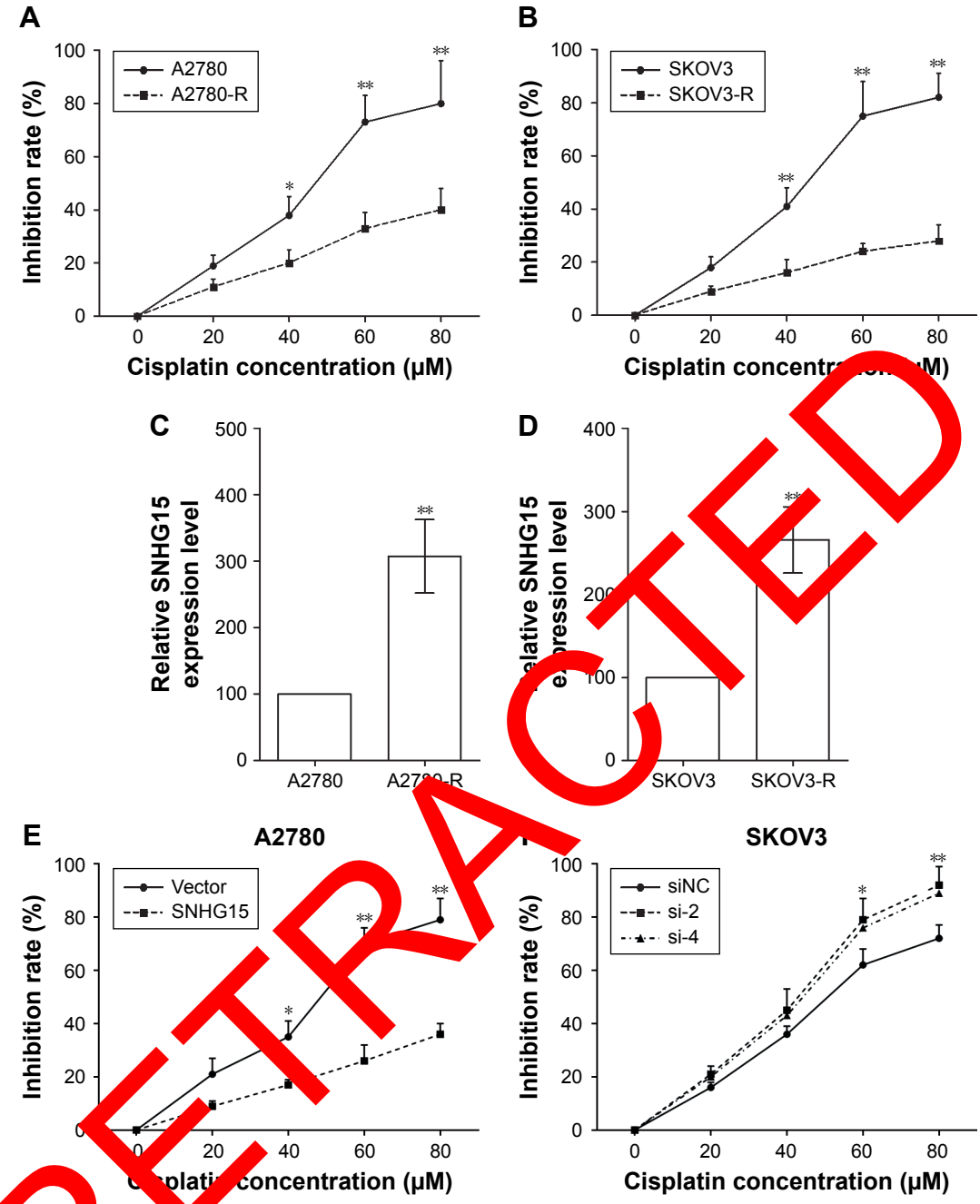

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Figure 5 SNHG15 contributes to the chemoresistance of EOC cells.

Notes: (**A**) The inhibition rate of cisplatin on A2780 cells and A2780-R cells were detected by MTT assay. (**B**) The inhibition rate of cisplatin on SKOV3 cells and SKOV3-R cells were detected by MTT assay. (**C**) Expression of SNHG15 in A2780 cells and A2780-R cells was detected by qRT-PCR assay. (**D**) Expression of SNHG15 in SKOV3 cells and SKOV3-R cells was detected by qRT-PCR assay. (**E**) Inhibition rates of cisplatin on A2780 cells transfected with SNHG15 overexpression plasmid and empty vector after cisplatin treatment were measured by MTT assay. (**F**) Inhibition rates of cisplatin on SKOV3 cells transfected with SNHG15 siRNAs and siNC after cisplatin treatment were measured by MTT assay. *$P<0.05$ and **$P<0.01$.

Abbreviations: A2780-R, cisplatin-resistant A2780 cells; EOC, epithelial ovarian cancer; SKOV3-R, cisplatin-resistant SKOV3 cells; siNC, nontargeting control siRNAs.

Metastasis-associated lung adenocarcinoma transcript 1 (MALAT1) is one of the major focuses in EOC, and in vivo studies have confirmed that MALAT1 could promote the growth and metastasis of EOC cells.[19–22] Some other lncRNAs, such as brain cytoplasmic RNA 200,[23] growth arrest-specific 5,[24] colon cancer associated transcript 2 (CCAT2),[25] and taurine upregulated gene 1[26] have also been revealed to mediate the biology of EOC cells. Furthermore, lncRNAs are considered as potentially novel clinical tools for patient management because they are often tissue-specific and exhibit poor sequence conservation across species.[27] Several lncRNAs have been identified as

potential diagnostic and prognostic prediction biomarkers in different EOC histological types, such as MALAT1,[19] C17orf91,[28] and CCAT2.[25] LncRNA-based diagnosis, prognostic prediction, and treatment may shed light on the management of EOC patients.

In 2013, Tani et al[29] discovered that SNHG15 was upregulated in HeLa Tet-off cells when exposed to cycloheximide, and the expression of SNHG15 increased in response to increasing concentrations of cycloheximide. Two years later, the same team found that the overexpression of SNHG15 caused a decrease in the cell viability of HEK293 cells, whereas it had no effect on cell proliferation.[30] Currently, SNHG15 has been reported to be overexpressed and serves as an oncogene in hepatocellular carcinoma,[31] pancreatic cancer,[32] glioma,[11] gastric cancer,[10] non-small-cell lung cancer,[12] colon cancer,[14] breast cancer,[15] and osteosarcoma.[13] Functionally, SNHG15 was involved in the proliferation, invasion, migration, chemoresistance, and autophagy of different cancers.[12,13,15,33] Mechanistically, SNHG15 could exert its functional by sponging miRNAs, such as miR-141,[13] miR-211-3p,[15] miR-153,[11] and miR-486.[12] Additionally, the RNA immunoprecipitation assay showed that SNHG15 could epigenetically repress the P15 and Kruppel-like factor 2 (KLF2) expression via binding to enhancer of zeste homologue 2 (EZH2) in pancreatic cancer cells.[32] Chen et al[10] reported that SNHG15 could regulate the expression of MMP2 and MMP9, which promoted cell proliferation and invasion. SNHG15 is involved in almost every aspect of cancer biology; it may be a promising biomarker and therapeutic target in cancer management.

The present study revealed that SNHG15 was overexpressed in EOC cell lines and tissues compared to HOSE cells and paired tumor adjacent tissues, respectively. Further statistical analysis found that high SNHG15 expression was correlated with EOC progression, which indicated its oncogenic role in EOC. Further investigations found that patients with high SNHG15 expression showed poor OS and PFS in different subgroups of EOC patients, and high SNHG15 expression was identified as an independent risk factor for poor OS and PFS. The results suggested the prediction value of SNHG15 for the prognosis of EOC patients. Moreover, the function of SNHG15 was verified in EOC cells, and SNHG15 was demonstrated to promote the migration, invasion, proliferation, and chemoresistance of EOC cells. However, the detailed mechanisms by which SNHG15 exerts its function were not investigated in the present study, and these mechanisms deserve further exploration.

Conclusion

Our findings present that SNHG15 may be a novel biomarker for prognostic prediction and a potential therapeutic target in EOC.

Disclosure

The authors report no conflicts of interest in this work.

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