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ORIGINAL RESEARCH

RETRACTED ARTICLE: MicroRNA 628 suppresses migration and invasion of breast cancer stem cells through targeting SOS1

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Chenghui Lin[1,*]
Bin Gao[2,*]
Xuemao Yan[2]
Zixiong Lei[3]
Kebing Chen[3]
Yuquan Li[2]
Qing Zeng[2]
Zeqin Chen[2]
Haomiao Li[3]

[1]Department of Medical oncology, TangXia Hospital of DongGuan, DongGuan, P.R. China; [2]Department of Orthopedics, TangXia Hospital of DongGuan, DongGuan, P.R. China; [3]Department of Musculoskeletal Oncology, The Third Affiliated Hospital of Southern Medical University, Guangzhou, P.R. China

*These authors contributed equally to this work

Purpose: The purpose of this study is to evaluate the effect of miR-628 on migration and invasion of breast cancer stem cells (CSCs), which are essential for tumor recurrence and metastasis.

Materials and methods: Quantitative reverse transcription-polymerase chain reaction was used to determine the expression of microRNAs and mRNAs. A subpopulation of $CD44^+/CD24^-$ breast CSCs were sorted by flow cytometry. Transwell assays were used to evaluate cell migration and invasion. Luciferase reporter assays were performed to verify whether miR-628 targeted SOS Ras/Rac guanine nucleotide exchange factor 1 (SOS1). pcDNA3.1(+)-SOS1 was constructed for overexpressing SOS1 after transfection.

Results: Compared with primary breast cancer cells, bone metastatic breast cancer cells showed significant downregulation of *miR-628*. The $CD44^+/CD24^-$ breast CSC subpopulations in MDA-MB-231 and MCF-7 cell lines were analyzed and sorted. Transfection with an miR-628 mimic significantly suppressed the migration and invasion of these breast CSCs by targeting SOS1, which plays an essential role in epithelial-to-mesenchymal transition. Overexpression of SOS1 rescued miR-628-mediated migration and invasion by upregulating Snail and vimentin, and downregulating E-cadherin.

Conclusion: miR-628 suppressed migration and invasion of breast CSCs of MDA-MB-231 and MCF-7 cells by directly targeting SOS1. Enhancement of miR-628 expression might be an effective strategy for managing breast cancer metastasis.

Keywords: breast cancer stem cells, $CD44^+/CD24^-$, miR-628, SOS1, migration, invasion

Introduction

Cancer stem cells (CSCs) are highly self-renewing and tumorigenic cells that can give rise to new tumors in organs with high efficiency.[1] CSCs are more likely to show multiple genetic alternations. Therefore, it is important to identify genetic alternations and their role in regulation of CSC characteristics. Since CSCs constitute 0.001%–0.1% of an isolated tissue, CSC isolation for research purposes is challenging.[2] Flow-cytometric cell sorting using cell surface markers, specifically targeting CSCs is useful for CSC isolation. The most common markers of breast CSCs are CD24, CD44, and ALDH1.[3] Specifically, $CD44^+/CD24^-$ is normally used in identifying human breast CSCs.[4] MDA-MB-231 and MCF-7 are 2 subtypes of breast cancer cell lines that are highly aggressive and non-metastatic, respectively.[5] In present study, we sorted $CD44^+/CD24^-$ CSCs of MDA-MB-231 and MCF-7, and investigated the role of microRNA (miRNA)-628 in these cells.

miRNAs are small non-coding RNAs that hybridize to the 3′ untranslated region (3′-UTR) of target mRNA and facilitate mRNA degradation, thereby regulating cell function, including development, differentiation, proliferation, and apoptosis.[6] Deregulation

Correspondence: Haomiao Li
Department of Musculoskeletal Oncology, The Third Affiliated Hospital of Southern Medical University, No 183, Zhongshan Avenue West, Guangzhou 510642, Guangdong, P.R. China
Email lihaom@mail.sysu.edu.cn

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of miRNA expression is associated with breast cancer cell invasion and migration. Downregulation of *miR-200c* promotes breast cancer cell invasion and migration.[7] miR205 suppresses the expression of cyclin D1 and Myc, leading to inhibition of cell proliferation and colony formation in MDA-MB-231 cells.[8] Comparison of the miRNA profiles of MDA-MB-231 and MCF-7 spheroid-enriched CSCs revealed that miR-15b, miR-34a, miR-148a, miR-628, and miR-196b were involved in CSC-associated signaling pathways and maintenance of CSC properties.[9] miR-628 inhibits osteogenesis by targeting runt-related transcription factor 2.[10] Furthermore, miR-628 as a novel biomarker of cardiac allograft vasculopathy (CAV), was significantly increased in CAV.[11]

Epithelial-to-mesenchymal transition (EMT) plays a critical role in migration and invasion during the early metastatic phase.[12] During EMT, expression of the major epithelial marker, E-cadherin, is downregulated, whereas those of mesenchymal markers, including Snail and vimentin, are upregulated.[13] The SOS Ras/Rac guanine nucleotide exchange factor 1 (SOS1) functions as a Ras guanine nucleotide exchange factor and facilitates the conversion of inactive Ras-guanosine diphosphate to active Ras-guanosine triphosphate.[14] A connection has been established between the Ras-mediated MEK/ERK signaling pathway and activation of EMT, increased metastatic potential, and poor patient survival.[15] In addition, SOS1 is involved in EMT regulation.[16] Whether miRNA deregulation is associated with SOS1-mediated migration and invasion is unclear. In the present study, we investigated the possible effects of miR-628 on SOS1-mediated migration and invasion of breast CSCs.

Materials and methods

Sample collection

Primary breast tumors and bone metastatic breast tumors were obtained from female breast cancer patients at the Department of Medical Oncology, TangXia Hospital of DongGuan. Written informed consent for the use of resected tissues and participation in this study was obtained from all patients before surgery. The research protocols were approved by the ethics committee of the Third Affiliated Hospital of Southern Medical University. Tumors were minced, followed by collagenase III (Sigma-Aldrich, St Louis, MO, USA) addition for digestion of tumor and normal tissues for 1 hour at 37°C with rotation. A filter (70 µM) (Falcon®, catalog number: 352350; BD Biosciences, San Jose, CA, USA) was used to remove undigested tissue. Red blood cells were lysed using ACK lysing buffer (Gibco, Grand Island, NY, USA) containing 0.15 M NH_4Cl, 10 mM $KHCO_3$, and 0.1 mM disodium salt of ethylenediaminetetraacetic acid and then collected. The remaining cells were washed with PBS and prepared for further analysis.

Cell culture

The MCF-7 and MDA-MB-231 cell lines, purchased from American Type Culture Collection (Manassas, VA, USA), were cultured as a monolayer in Roswell Park Memorial Institute (RPMI) 1640 medium (Life Technologies, Carlsbad, CA, USA) supplemented with 10% fetal bovine serum (FBS), 100 U/mL penicillin, and 100 µg/mL streptomycin (Life Technologies) at 37°C in a 5% humidified CO_2 atmosphere. When the cell culture was 80% confluent, the cells were trypsinized with 0.25% trypsin (Sigma-Aldrich) and harvested.

Flow cytometry and fluorescence-activated cell sorting (FACS) analysis

According to the experimental procedure described by Nami (2016),[17] MCF-7 and MDA-MB-231 cells were trypsinized, washed with Hank's balanced salt solution (HBSS), and pelleted by centrifugation. The cells (1×10^6) were then resuspended in 100 µL 2% FBS/HBSS. Fluorescein isothiocyanate (FITC)-conjugated mouse anti-human CD44 monoclonal antibody (20 µL; Biolegend, San Diego, CA, USA) and phycoerythrin (PE)-conjugated mouse anti-human CD24 monoclonal antibody (20 µL; Biolegend) were added to the cells and then incubated at 4°C for 1 hour in the dark with mild agitation. The cells were rinsed thrice with 2% FBS/HBSS, followed by addition of 400 µL 1 µg/mL 4′,6-diamidino-2-phenylindole solution (dissolved in 2% FBS/HBSS). CD44 and CD24 levels were determined using BD FACSAria™ III cell sorter (BD Biosciences). Cells stained with FITC- and PE-conjugated isotype control antibodies (Biolegend) were used as positive control and unstained cells as negative control.

Quantitative reverse transcription-polymerase chain reaction (qRT-PCR)

TRIzol reagent (Invitrogen, Carlsbad, CA, USA) was used to extract total RNA following the manufacturer's instructions. First-strand cDNA was reverse transcribed from 2 µg total RNA for each sample using oloney Murine Leukemia Virus Reverse Transcriptase (M-MLV) reverse transcriptase (Promega, Madison, WI, USA). qRT-PCR was employed to determine the expression levels of *miR-410*, *miR-211*, *miR-628*, and *SOS1* using the SYBR Green qPCR SuperMix (Invitrogen). Primer sets used were as follows: miR-410 forward, 5′-ACACTCCAG CTGGGAATATAACACAGATGGCC-3′ and reverse,

5′-CTCAACTGGTGTCGTG GA-3′; miR-211 forward, 5′-ACACTCCAGCTGGGTTCCCTTTGTCATCCTTC-3′ and reverse, 5′-CTC AACTGGTGTCGTGGA-3′; miR-628 forward, 5′-ACACTCCAGCTGGGTCTAGTAAGAGTGG CA GT-3′ and reverse, 5′-CTCAACTGGTGTCGTGGA-3′; U6 forward, 5′-CTCGCTTCGGCAGCACA-3′ and reverse, 5′-AACGCTTCACGAATTTGCGT-3′; SOS1 forward, 5′-TCCACGAAGACGACCAGAAT-3′ and reverse, 5′-GGG GACTGTCCAAATGCTTA-3′; 18S rRNA forward, 5′-CCT GGATACCGCAGCTAGGA-3′ and reverse, 5′-GCGGC GCAATACGAATGCCCC-3′. PCR amplification conditions were 50°C for 2 minutes and 94°C for 2 minutes, followed by 40 cycles of 94°C for 15 seconds and 60°C for 32 seconds. PCR was performed using the ABI PRISM® 7,500 sequence detection system (Applied Biosystems; Foster City, CA, USA). U6 and 18S rRNAs were used as internal standard controls. All reactions were performed in triplicate. For each target, experimental protocols were designed and optimized for efficiency near one using the $2^{-\Delta\Delta CT}$ method.

Western blotting

Total protein was extracted using appropriate volumes of the radioimmunoprecipitation assay buffer (Sigma-Aldrich). A bicinchoninic acid protein assay kit (Pierce Biotechnology, Rockford, IL, USA) was used to determine protein concentration with bovine serum albumin as the standard. Gel loading buffer (250 mM Tris-HCl pH 6.8, 50% v/v glycerol, 10% w/v sodium dodecyl sulfate [SDS], and 0.5% w/v bromophenol blue) was then added to protein samples before denaturing at 95°C for 5 minutes. The samples were subjected to 10% SDS polyacrylamide gel electrophoresis for separating protein bands corresponding to Snail, E-cadherin, vimentin, and SOS1. Then, the proteins were transferred to polyvinylidene difluoride membranes (Millipore, Billerica, MA, USA). The membranes were blocked with 5% non-fat milk in Tris-buffered saline with 0.1% Tween-20 for 1 hour and agitated at 50 rpm, followed by incubation with primary antibodies Snail (1:1,000; (Abcam, Cambridge, MA, USA), E-cadherin (1:1,000; Cell Signaling Technology, Beverly, MA, USA), vimentin (1:1,000; Cell Signaling Technology), and SOS1 (1:1,000; Cell Signaling Technology) at 4°C overnight, and with secondary antibodies for 2 hours at room temperature. Finally, the membranes were incubated with the Immun-Star™ WesternC™ Chemiluminescent (Bio-Rad, Berkeley, CA, USA) substrate solution and exposed to X-ray films. Densitometric analysis was performed on Western blot images from 3 independent experiments using the Image Pro-Plus 6.0 software (Media Cybernetics, Silver Spring, MD, USA). The results of densitometric analysis were expressed as relative ratio of the target protein to the reference protein. The relative ratio of target protein in the control group was set as 1.

miRNA, plasmid construction, transfection, and luciferase assays

The miR-628 mimic and negative control were obtained from RiboBio (Guangzhou, China). Cells (1×10^5/well) were cultured in 6-well plates and transfected with 100 pmol/well miR-628 mimic using the Hilymax transfection agent (Dojindo Laboratories, Kumamoto, Japan) according to the manufacturer's instructions. The negative control consisted of a random sequence (5′-GUGGAUUUUGUUCCAUCA-3′) that does not affect human cells. The 3′-UTR of human SOS1 mRNA was cloned into the *Xho*I/*Not*I sites of the psiCHECK™-2 vector (Promega) using the In-Fusion Advantage PCR cloning kit (Clontech, Mountain View, CA, USA). Luciferase assays were conducted as follows. Cells were cultured in 6-well plates for 24 hours at 37°C, followed by transfection with 4 µg/well of psiCHECK-SOS1 3′-UTR reporter vector or a negative control. SOS1 mutants with mutations in specific sites of the 3′-UTR reporter were also transfected and incubated for 6 hours at 37°C. After transfection at 37°C for 48 hours, firefly and Renilla luciferase activities were determined using the dual-luciferase reporter assay kit (Promega). Luciferase assays were repeated thrice.

The full length *SOS1* open reading frame was cloned into vector pcDNA3.1(+) and named as pcDNA3.1(+)-SOS1. Cells were transfected with vector pcDNA3.1(+)-SOS1 using Lipofectamine 2000 (Lipo; Thermo Fisher Scientific, Waltham, MA, USA) according to the manufacturer's instructions. After 8 hours of transfection, RPMI 1640 medium containing 10% FBS was used to culture the cells for another 48 hours.

Cell invasion and migration assays

Cells (1×10^5) suspended in 200 µL RPMI 1640 medium without FBS were added to the Matrigel (Corning, New York, NY, USA)-coated (50 µL of 1 mg/mL) upper wells of Transwell inserts (Corning). The bottom wells contained RPMI 1640 medium with 10% FBS. After 24 hours, the non-invading cells remaining in the upper wells were discarded. Cells that invaded the bottom wells through the insert membrane were gently rinsed with PBS, immediately fixed in pre-cooled methanol (−20°C), and stained with crystal violet solution. The stained cells were imaged using an inverted microscope (Leica DMI-4000B; Leica Microsystems Wetzlar GmbH, Wetzlar,

Germany) equipped with a camera (Leica). Five independent fields per well were imaged. Each assay was performed in triplicate. The stained cells were counted using Image Pro-Plus 6.0 software (Media Cybernetics). For migration assays, the procedure was similar to that of the invasion assay, except that the inserts were not pre-coated with Matrigel.

Statistical analysis

All data are expressed as the mean ± SD. The results were analyzed using student's *t*-test for 2 groups. The results were analyzed using one-way analysis of variance followed by post hoc least significant difference test for >2 groups. *P*-value <0.05 was considered statistically significant ($P<0.05$; $P<0.01$).

Ethics approval and informed consent

The study was performed after obtaining consent from the local ethics committee and the patients.

Results

Comparison of miR-211, miR-410, and miR-628 expression between primary breast cancer cells and bone metastatic breast cancer cells

To determine the effects of miRNAs on bone metastasis of breast cancer cells, the difference in expression levels of miR-211, miR-410, and miR-628 were compared between primary breast cancer cells and bone metastatic breast cancer cells. As seen in Figure 1, *miR-211* (2.03±0.22, $P<0.05$) and *miR-410* (2.97±0.14, $P<0.05$) were significantly upregulated in bone metastatic breast cancer cells compared with primary breast cancer cells. In contrast, *miR-628* (0.36±0.22, $P<0.05$) was significantly downregulated in bone metastatic breast cancer cells. Hence, we focused on studying the possible role of miR-628 in regulating metastasis of breast cancer cells.

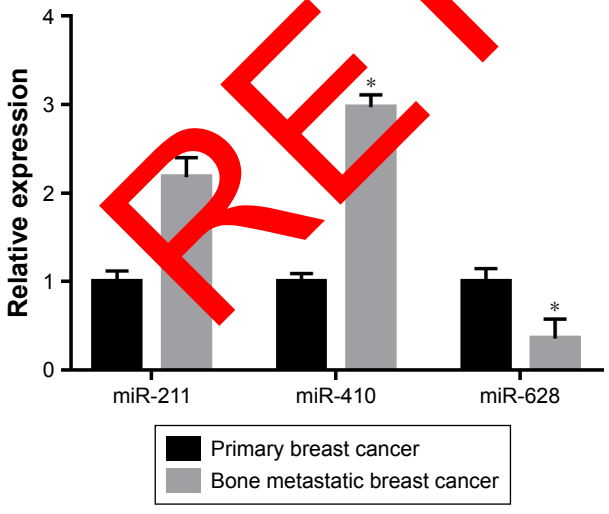

Figure 1 Expression levels of miR-211, miR-410, and miR-628 in primary breast cancer cells and bone metastatic breast cancer cells.
Note: Results show mean ± SD of miRNA levels in 3 independent experiments (*$P<0.05$).

miR-628 suppressed migration and invasion of the breast CSC subpopulation

To explore the effects of miR-628 on migration and invasion of the breast CSC subpopulation, the subpopulation of $CD44^+/CD24^-$ CSCs was sorted using flow cytometry. Results showed that the mean percentage of this subpopulation in MCF7 and MDA-MB-231 were 1.2±0.15 and 1.79±0.87, respectively (Figure 2A and B). Next, the miR-628 mimic was transfected in the CSC of MCF-7 and MDA-MB-231 cells and qRT-PCR was used to verify the success of the miR-628 mimic transfection. As shown in Figure 3A, the miR-628 mimic significantly upregulated the expression of miR-628 (94.71±1.7, $P<0.05$), compared with the negative control transfected group. The Transwell assays showed that miR-628 overexpression ameliorated migration (Figure 3B and C) and invasion (Figure 3D and E) of breast CSCs in MCF-7 and MDA-MB-231 cells. To investigate the underlying molecular mechanisms, we determined the protein levels of vimentin, Snail, and E-cadherin. Overexpression of miR-628 significantly downregulated vimentin and Snail expression and upregulated E-cadherin expression in MCF-7 and MDA-MB-231 cells (Figure 3F and G). This suggests that overexpression of miR-628 can effectively attenuate migration and invasion of breast CSCs in MCF-7 and MDA-MB-231 cell lines. miR-628 directly targets SOS1.

To examine if SOS1 is a direct target of miR-628, the 3′-UTR of *SOS1* was cloned in the luciferase construct psi-CHECK2 (Figure 4A), which was then subsequently transfected in the breast CSC subpopulations of MDA-MB-231 and MCF-7 cells. Results showed that miR-628 transfection significantly ameliorated the activity of the luciferase reporter gene fused to the *SOS1* 3′-UTR compared with the miR-NC (negative control) transfection. Moreover, miR-628 did not reduce the luciferase activity of the mutant construct, which contained mutations within the miR-628 binding site (Figure 4B and C). Next, we examined the mRNA expression levels of *SOS1* in miR-628 mimic- and miR-628 inhibitor-transfected groups. SOS1 mRNA levels did not significantly change in both MDA-MB-231 (Figure 5A) and MCF-7 (Figure 5B) cells; however, transfection of the miR-628 mimic significantly reduced SOS1 protein levels,

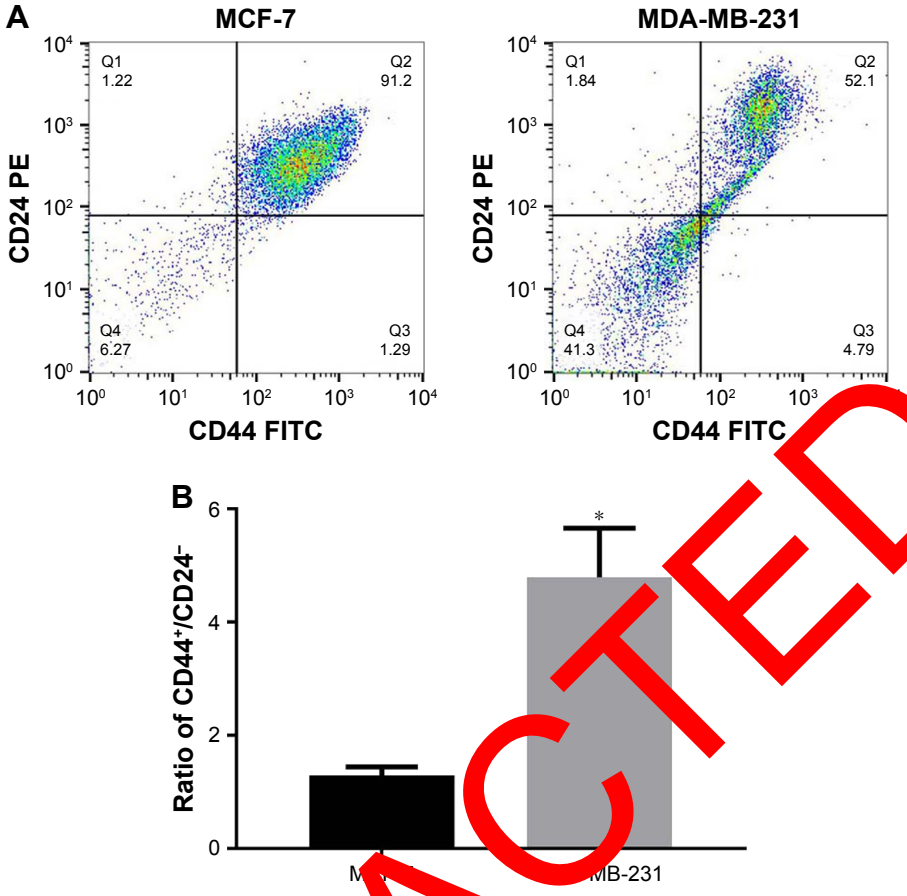

Figure 2 Subpopulations of CD44⁺/CD24⁻ cancer stem cells of breast cancer cell lines MCF-7 and MDA-MB-231 were sorted using a flow cytometer.
Notes: (**A**) Graphs showing CD44⁺/CD24⁻ breast CSC sorting by flow cytometry. Cells in Q3 are referred to as CD44⁺/CD24⁻ cells. (**B**) Percentage of CD44⁺/CD24⁻ breast CSC subpopulations in MCF-7 and MDA-MB-231 cells. Results represent the mean ± SD of 3 independent experiments (*$P<0.05$).
Abbreviations: CSC, cancer stem cell; FITC, fluorescein isothiocyanate.

whereas the miR-628 inhibitor increased SOS1 protein expression (Figure 5C). This suggests that SOS1 is a direct target of miR-628.

SOS1 overexpression reversed the effects of miR-628 on migration and invasion of breast CSCs

To further identify the association between miR-628 and SOS1, migration and invasion were re-evaluated in breast CSCs of MDA-MB-231 and MCF-7 cells transfected with pcDNA3.1(+)-SOS1 and the miR-628 mimic. *SOS1* transfection was able to reverse the effects of miR-628 on migration and invasion, as was evident from the increase in cell counts in the bottom wells of the assay plates (Figure 6A–D), upregulation of vimentin and Snail expression, and downregulation of E-cadherin expression (Figure 6E and F). These results indicated that miR-628 can potentially suppress migration and invasion of breast CSCs of MDA-MB-231 and MCF-7 cells by targeting SOS1.

Discussion

A substantial body of evidence indicates that miRNAs play key roles in oncogenesis, progression, and metastasis of breast cancer. To study the association of miRNA with breast cancer metastasis, we first surveyed the change in expression levels of miR-211, miR-410, and miR-628 between primary breast cancer cells and bone metastatic breast cancer cells. Of the miRNAs tested, miR-628 was presumed to be involved in breast cancer metastasis; however, the molecular mechanism was unclear.

Despite considerable advances in conventional chemotherapy for breast cancer treatment, chemotherapy resistance is attributed to the presence of CSCs that show increased expression of CD44 and ALDH1 surface markers and low expression of CD24.[18] CSCs derived from epithelial cells subsequently undergo EMT , which is responsible for tumor recurrence.[19] Several studies suggest that microenvironment stimuli can induce malignant transformation of differentiated cells into breast CSCs.[20] Cellular heterogeneity is a distinct

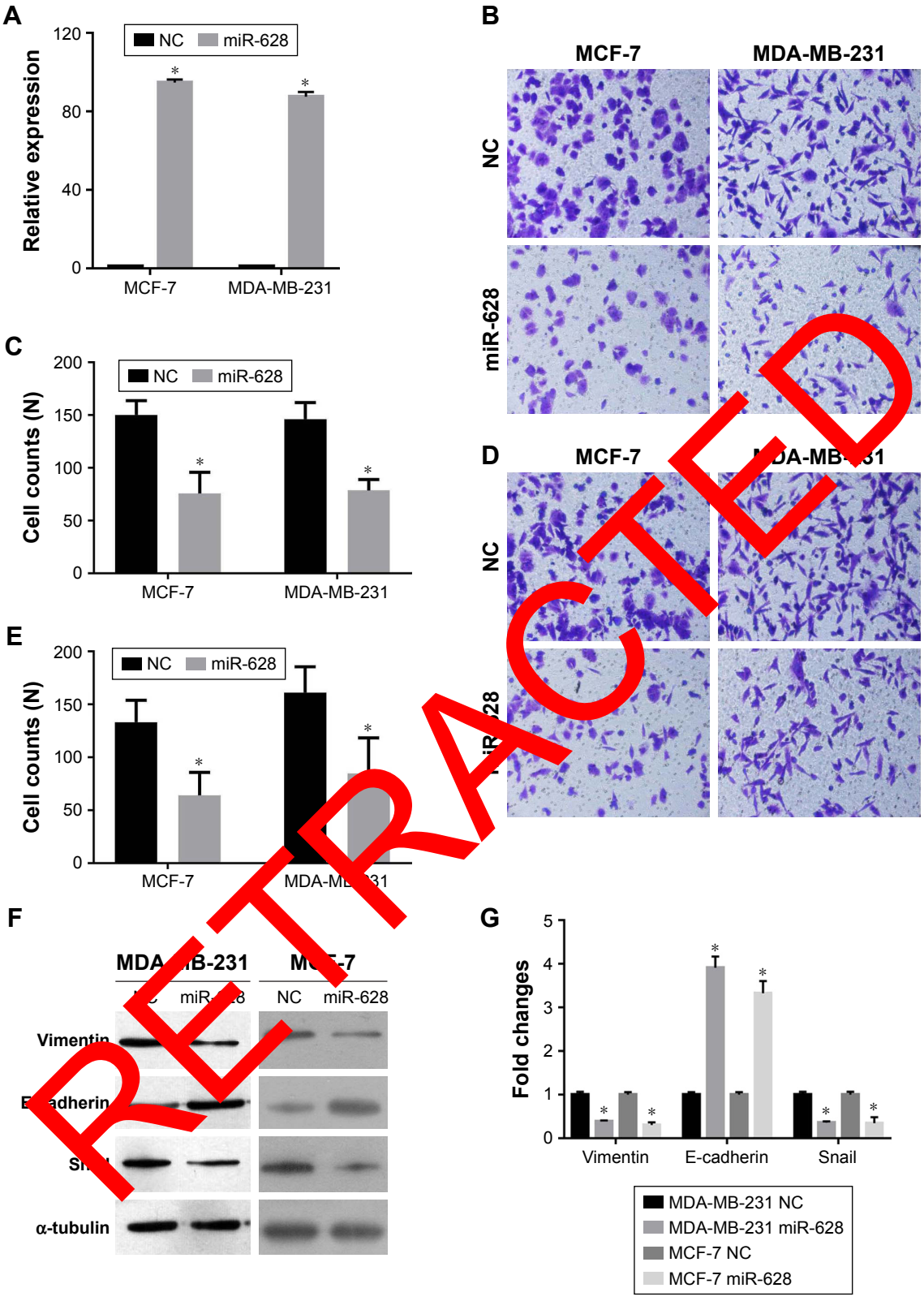

Figure 3 Effect of *miR-628* overexpression on migration and invasion of the breast CSC subpopulation in MCF-7 and MDA-MB-231 cell lines.
Notes: (**A**) miR-628 expression after miR-628 mimic was transfected into CSCs of MCF-7 and MDA-MB-231 cells was determined by qRT-PCR. (**B**–**D**) Effects of *miR-628* overexpression on migration (**B**, **C**) and invasion (**D**, **E**) of MCF-7 and MDA-MB-231 CSCs. (**F**) Cells were transfected with the miR-628 mimic. The effect of miR-628 mimic transfection on the protein levels of vimentin, Snail, and E-cadherin was analyzed by Western blotting. (**G**) Protein expression levels were statistically analyzed by quantitating the intensity of the protein bands relative to that of the internal loading control (α-tubulin). *Values indicate mean ± SD; $P<0.05$, magnification ×200.
Abbreviations: CSCs, cancer stem cells; NC, negative control; qRT-PCR, quantitative reverse transcription-polymerase chain reaction.

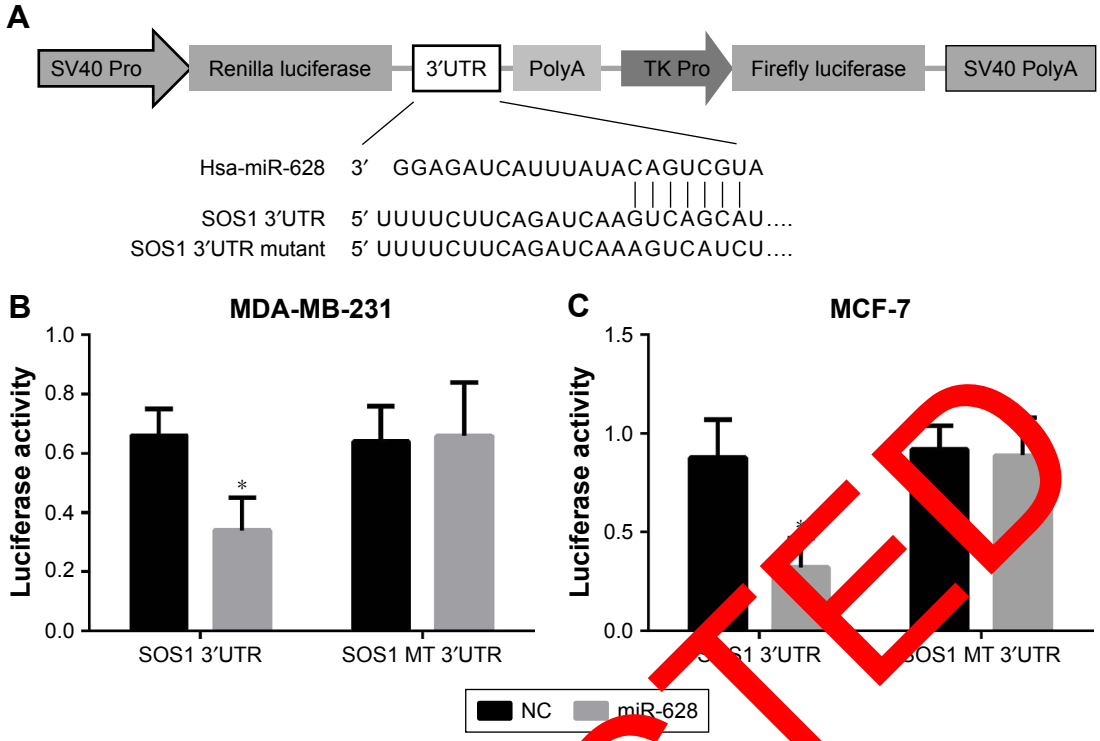

Figure 4 miR-628 directly targets SOS1.
Notes: (**A**) Schematic diagram of human SOS1 3′-UTR luciferase constructs with wild type and mutant (MT) (SOS1-3′-UTR) miR-628 target sequences. The breast CSCs of MDA-MB-231 (**B**) and MCF-7 (**C**) cells were transfected with luciferase constructs and the miR-628 mimic. Firefly luciferase activity was normalized to Renilla luciferase activity. *$P<0.05$.
Abbreviations: 3′-UTR, 3′ untranslated region; CSC, cancer stem cells; NC, negative control; SOS1, son of sevenless homolog 1; Ras/Rac guanine nucleotide exchange factor.

characteristic of tumors; therefore, we sorted CD44+/CD24− breast CSC subpopulations of MDA-MB-231 and MCF-7 cells for obtaining accurate information on breast CSCs. MCF-7 cells with estrogen receptors constitute a well-established model for drug evaluation in vitro. In contrast, MDA-MB-231 cells are estrogen-independent.[21] In this study, we used the breast CSCs of MDA-MB-231 and MCF-7 cell as cell models for studying the effects of miR-628 on migration and invasion.

As a biomarker, circulatory miR-628 is downregulated in prostate cancer.[22] In epithelial ovarian cancer cells, miR-628 can significantly reduce the percentage of cancer stem-like cells by inducing apoptosis. Fibroblast growth factor receptor 2 (FGFR2) in ovarian cancer is negatively associated with prognosis, whereas miR-628 ameliorates FGFR2-induced tumorigenicity of epithelial ovarian cancer.[23] In primary refractory patients with clear-cell metastatic renal cell carcinoma (MRCC), miR-628 was involved in significantly mediating prolonged survival.[24] In contrast, Prior et al (2014) suggested that upregulation of *miR-628* is significantly correlated with decreased overall survival and time to progression in patients with MRCC.[25] In our study, we showed that miR-628 was downregulated in bone metastatic breast cancer cells. Accordingly, we hypothesized that miR-628 suppresses migration and invasion of breast CSCs. As expected, the miR-628 mimic transfection significantly attenuated migration and invasion of the breast CSCs of MDA-MB-231 and MCF-7 cells.

EMT is a significant developmental process associated with cancer invasion and metastasis, which is mediated by the EMT markers Snail, E-cadherin, and vimentin. In clinical cases, upregulation of EMT markers in patients with breast cancer has been associated with poor clinical outcomes.[26] In our study, we observed that miR-628 mimic transfection significantly downregulated the expression of Snail and vimentin and upregulated E-cadherin expression. This indicates that suppression of EMT is involved in the mechanism of miR-628-mediated inhibition of invasion and migration of breast CSCs of MDA-MB-231 and MCF-7 cells.

SOS1 has been implicated in mediating EMT, whereas kindlin-2 was reported to promote EMT by activating Ras signaling via SOS1 recruitment.[16] *SOS1* knockdown reduces vimentin expression and increases E-cadherin expression.[27] In agreement with these observations, our study showed that

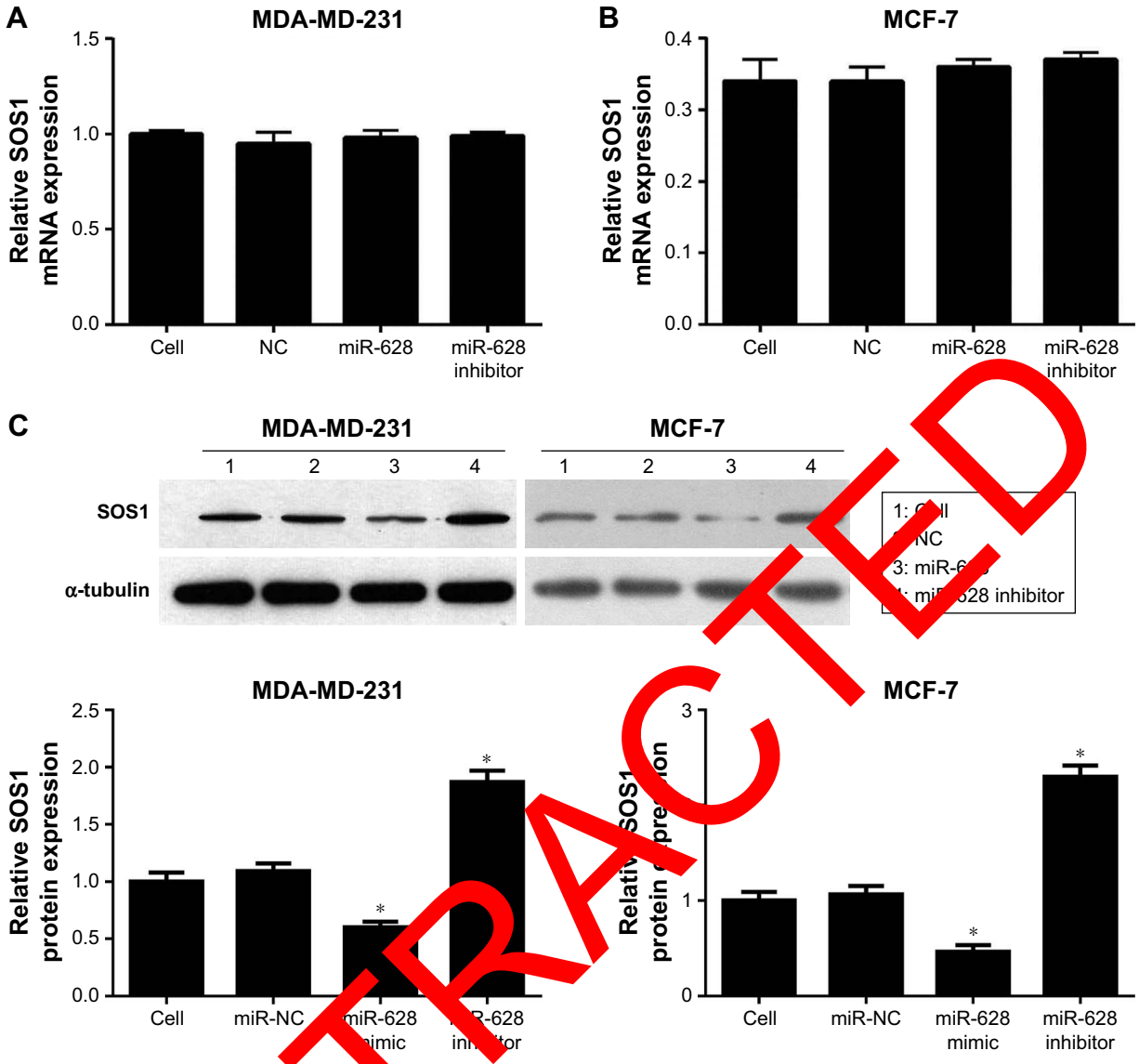

Figure 5 miR-628 suppressed the mRNA and protein expression of *SOS1*.
Notes: The breast CSCs of MDA-MB-231 (**A**) and MCF-7 (**B**) cells were transfected with the miR-628 mimic and miR-628 inhibitor, and SOS1 mRNA level was determined by qRT-PCR. (**C**) The breast CSCs of MDA-MB-231 and MCF-7 cells were transfected with miR-628 mimic and miR-628 inhibitor, and SOS1 protein level was analyzed by Western blotting. The protein expression levels were statistically analyzed by quantitating the intensity of the protein bands relative to that of the internal loading control (α-tubulin). Values indicate mean ± SD; *P < 0.05.
Abbreviations: CSCs, cancer stem cells; NC, negative control; SOS1, SOS Ras/Rac guanine nucleotide exchange factor; qRT-PCR, quantitative reverse transcription-polymerase chain reaction.

SOS1 overexpression significantly upregulated the expression of EMT biomarkers Snail and vimentin, and downregulated E-cadherin expression. Bioinformatic analysis predicted that SOS1 is a direct target of miR-628. Luciferase reporter assays, qRT-PCR, and Western blot analysis were used to support this prediction. In addition, conserved sequences for miR-628 binding in the 3′-UTR of the SOS1 mRNA were also identified by site-mutagenesis. This was verified by the rescue of EMT by *SOS1* overexpression, which was previously suppressed by miR-628 mimic transfection. These results suggest that miR-628 suppresses migration and invasion of breast CSCs of MDA-MB-231 and MCF-7 cells by directly targeting SOS1, which is involved in EMT.

Conclusion

Our study strongly suggests that miR-628 suppresses migration and invasion of the breast CSC subpopulations of MDA-MB-231 and MCF-7 cell lines by directly targeting SOS1 and subsequently attenuating the activity of Snail and vimentin while simultaneously enhancing E-cadherin activity. Elevation of *miR-628* expression might be an effective strategy for breast cancer metastasis management.

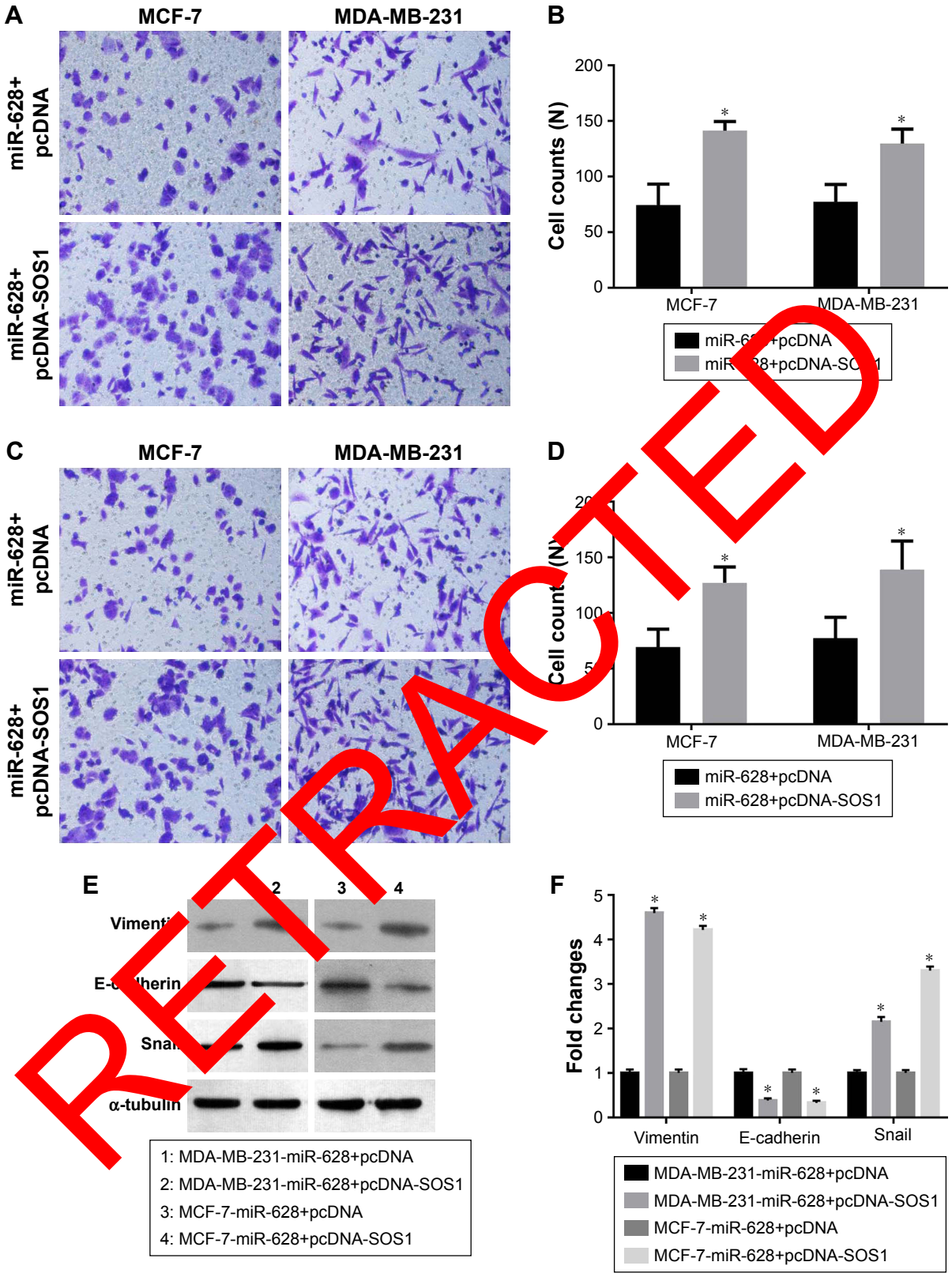

Figure 6 Effect of *miR-628* overexpression in the breast CSCs of MDA-MB-231 and MCF-7 cells was reversed after *SOS1* transfection.

Notes: The breast CSCs of MDA-MB-231 and MCF-7 cells transfected with pcDNA3.1(+)-SOS1 and miR-628 mimic were used in the Transwell migration (**A**, **B**) and invasion (**C**, **D**) assays; the plates were imaged by inverted microscopy and cells were counted. (**E**) The breast CSCs of MDA-MB-231 and MCF-7 cells were transfected with miR-628 mimic and pcDNA3.1(+)-SOS1, and the protein levels of vimentin, Snail, and E-cadherin were analyzed by Western blotting. (**F**) The protein levels were statistically analyzed by quantitating the intensity of the protein bands relative to that of the internal loading control (α-tubulin). Values indicate mean ± SD; $^*P<0.05$, magnification ×200.

Abbreviations: CSCs, cancer stem cells; NC, negative control; SOS1, SOS Ras/Rac guanine nucleotide exchange factor.

Acknowledgments

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Disclosure

The authors report no conflicts of interest in this work.

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