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ORIGINAL RESEARCH

RETRACTED ARTICLE: *LEF1-AS1*, a long-noncoding RNA, promotes malignancy in glioblastoma

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Objectives: The long-noncoding RNAs (lncRNAs) are identified as new crucial regulators of diverse cellular processes in glioblastoma (GBM) tissue. However, the expression pattern and biological function of lncRNAs remain largely unknown. Here, for the first time, the effects of lncRNA lymphoid enhancer-binding factor 1 antisense RNA 1 (*LEF1-AS1*) on GBM progression both in vitro and in vivo are investigated.

Materials and methods: Expression profiles of *LEF1-AS1* in GBM specimens were investigated by bioinformatics analysis. *LEF1-AS1* expression in GBM tissues was detected using a quantitative polymerase chain reaction. *LEF1-AS1* expression was inhibited by transfecting the *LEF1-AS1*-specific small interfering RNAs (siRNAs) and stable cell lines established were inhibited by transfecting si-*LEF1-AS1* viruses. The Cell Counting Kit-8, ethynyl deoxyuridine, and colony formation assays were used to examine proliferation function. The flow cytometry detected cell-cycle change and apoptosis. Migration effects were detected by a Transwell assay. The tumor xenografts and immunohistochemistry were performed to evaluate tumor growth in vivo.

Results: In this study, *LEF1-AS1* expression was found significantly upregulated in GBM specimens compared with normal tissues. The 5-year overall survival in GBM patients from The Cancer Genome Atlas with high expression of *LEF1-AS1* was inferior to that with low expression. It was confirmed that expression of *LEF1-AS1* was higher in GBM tissues than normal ones. Knockdown of *LEF1-AS1* significantly inhibited the malignancy of GBM cells, including proliferation and invasion, and promoted cell apoptosis. The result of Western blot assays indicated that knockdown of *LEF1-AS1*-mediated tumor suppression in GBM cells may be via the reduction of ERK and Akt/mTOR signaling activities. Finally, the in vivo experiment also demonstrated that knockdown *LEF1-AS1* inhibited the growth-promoting effect of *LEF1-AS1* of U87 cells.

Conclusion: Our result indicated that lncRNA *LEF1-AS1* acts as an oncogene in GBM and may be a pivotal target for this disease.

Keywords: lncRNA, *LEF1-AS1*, glioblastoma, proliferation, invasion, apoptosis

Introduction

Glioblastoma (GBM) is the most common and aggressive tumor in the central nervous system,[1] with a median survival of patients of only 12–15 months.[2] Although some advances in the treatment of surgical, radiological, and chemotherapeutic interventions have greatly improved over the past 20 years, the prognosis of these patients still remains poor.[3] Therefore, understanding the molecular mechanisms associated with the GBM development is critical to develop new approaches to overcome this disease, where long noncoding RNAs (lncRNAs) are promising candidates.

lncRNAs are functionally defined as transcribed RNA molecules >200 nt in length, which have no protein-coding potential and are uniquely expressed in differentiated

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tissues or specific cancer types.[4] lncRNAs can modulate the downstream target genes by multiple means via cis- and trans-regulatory effects, in both transcriptional and post-transcriptional levels,[5,6] which is distinct from microRNAs (miRNAs) and other smaller noncoding RNAs. Increasing evidence supports that lncRNAs are linked with tumorigenicity of cancer, including proliferation, metastasis, and apoptosis in lung cancer, breast cancer, ovarian cancer, and so on.[7–9] Many lncRNAs have also been found to be involved in GBM progression. Examples include HOX transcript antisense intergenic RNA,[10] colorectal neoplasia differentially expressed (CRNDE),[11] maternally expressed gene 3,[12] cancer susceptibility candidate 2,[13] and ANRIL (CDKN2B-AS1).[14] However, although many lncRNAs have been demonstrated to exert crucial regulating activities in the biological process during GBM development and progression, the function of the vast majority of these transcripts remains to be identified.

In this study, by performing microarrays on a local computer for gene expressions of lncRNAs profiling from the database of The Cancer Genome Atlas (TCGA) and the Gene Expression Omnibus (GEO), it was found that a new lncRNA lymphoid enhancer-binding factor 1 antisense RNA 1 (*LEF1-AS1*), which is located in chromosome 4q25, was upregulated in GBM with a poor 5-year survival rate. In addition, *LEF1-AS1* was also found to be upregulated in GBM tissues that were collected from the First Affiliated Hospital of Nanjing Medical University. Silencing *LEF1-AS1* inhibited GBM proliferation and invasion and induced G1 phase arrest and apoptosis in the GBM cells. Our results suggested that *LEF1-AS1* could act as a GBM oncogene, and it provided a potential novel therapeutic target for the treatment of GBM.

Materials and methods
Patients and samples
A total of 10 GBM tissues and 3 normal brain tissues were obtained from the Department of Neurosurgery, the First Affiliated Hospital of Nanjing Medical University. The samples were collected between November 2015 and September 2016. The three normal brain tissues were obtained from surgeries of brain trauma (n=1) and epilepsy (n=2). GBM (grade IV) was classified on the basis of the World Health Organization criteria. All specimens were snap-frozen in liquid nitrogen and stored at −80°C for a subsequent analysis. The ethical committees of Jiangsu Province Hospital affiliated to Nanjing Medical University approved this study. All patients' written informed consent were received from each patient for this study.

Cell lines culture conditions and small interfering RNA (siRNA) transfection
Human 293FT cells and U251 and U87 glioma cells were purchased from Shanghai Institutes for Biological Sciences, Cell Resource Center. All the cells were cultured in Dulbecco's Modified Eagle's Medium (Gibco BRL, Grand Island, NY, USA)/high glucose-containing 10% fetal bovine serum (FBS) (Gibco BRL) and maintained at 37°C with 5% CO_2. The GBM cell lines were transfected with siRNA using Lipofectamine2000 (Invitrogen, Carlsbad, CA, USA) according to the manufacturer's recommendations. *LEF1-AS1* RNAi segments (the RNAi sequence: si-*LEF1-AS1* 1# is sense: 5′-CCUGGGUGGAUAUUGUAAUTT-3′ and antisense: 5′-AUUACCAUAUCCACCCAGGTT-3′; si-*LEF1-AS1*#2 is sense: 5′-GGAGAUUAAUGCAGAACAATT-3′ and antisense: 5′-UUGUUCUGCAUUAAUCUCCTT-3′) were synthesized by Genepharma (Shanghai, China).

Plasmid constructs and the generation of stable cell lines
Amplification of *LEF1-AS1* transcript complementary DNA (cDNA) by polymerase chain reaction (PCR) inserted into the pLenti6/V5-D-TOPO vector, following the ViraPower™ Lentiviral Expression Systems (Thermo Fisher Scientific) protocol. The plasmid was packaged into 293FT cells. The resultant lentivirus particles were infected into U87MG cells and the stable cell lines were selected in a medium containing blasticidin (Thermo Fisher Scientific).

Quantitative real-time PCR
The total RNA from cell lines was isolated using TRIzol reagent (Thermo Fisher Scientific) following the manufacturer's instructions. The RNA concentrations and quality were estimated by the 260/280 nm absorbance using a Nanodrop Spectrophotometer (IMPLEN GmbH, Munich, Germany). cDNA was synthesized from 1 µg of RNA in a final volume of 20 µL with random primers using the PrimeScript RT Reagent Kit (Takara, Otsu, Japan). The primers were obtained from GenePharma. The sequences were shown as follows: *LEF1-AS1*, forward 5′-AAGGACGAGAGAAAAGCAC-3′, reverse 5′-CACACAAAGGGGAAGACC-3′; glyceraldehyde-3-phosphate dehydrogenase (GAPDH), forward 5′-AGCAAGAGCACAAGAGGAAG-3′, reverse 5′-GGTTGAGCACAGGGTACTTT-3′. Quantitative reverse real-time PCR was conducted in 10 µL reactions containing 0.2 µM of each primer, 5 µL SYBR Green PCR master mix (2×) (Takara) and 0.2 µL cDNA on a 7900 Fast Real-Time PCR System (Thermo Fisher Scientific). The reaction

mixtures were performed at 95°C for 30 seconds and then were amplified for 40 cycles at 95°C for 5 seconds and 60°C for 31 seconds. The raw data from each target lncRNA were normalized with the corresponding GAPDH. Each sample was examined in triplicate.

Cell viability assays

Cell viability was monitored using the Cell Counting Kit-8 (CCK8; Beyotime, Jiangsu, China). Cells (2,000 cells/well) in each group were plated into 96-well plates. The CCK8 regent (~10 µL) was added to each well containing 100 µL culture medium after transfection and then was incubated for 2 hours at 37°C with 5% CO_2. The plates were measured at a wavelength of 450 nm using a plate reader (Infinite M200; Tecan, Männedorf, Switzerland). Five replicate wells were designed in each group and experiments were repeated in triplicate.

Colony formation assay

Approximately 1×10^4 U87 and U251 cells were seeded in 6×6 cm plates with 10% FBS after transfecting with si-RNA or small interfering negative control (si-NC). After 2 weeks, the cells were fixed with methanol for 15 minutes and then stained with 1% crystal violet (Beyotime) for 30 minutes. Colonies with >50 cells/colony were counted under an inverted microscope (Olympus Corporation, Tokyo, Japan). All of the experiments were repeated in triplicate independently.

5-Ethynyl-2-deoxyuridine (EdU) assay

The U251 and U87 cells were cultured in 24-well plates pre-coated with 200 µL of 50 µM EdU labeling detection kit (Ribobio, Guangzhou, China) for 2 hours at 37°C after transfecting with si-RNA or si-NC. Then the cells were fixed with 4% paraformaldehyde (pH 7.4) for 30 minutes and incubated with 0.5% Triton X-100 (Sigma-Aldrich Co., St Louis, MO, USA) for 20 minutes at room temperature. After washing, the cells of each well were stained with Apollo fluorescent dye (Ribobio, Guangzhou, China) for 30 minutes. Subsequently, the DNA contents of cells in each well were stained with Hoechst 3334 (5 µg/mL) for 30 minutes and photographs of the cells were captured using a fluorescent microscope (Olympus).

Cell invasion assay

For cell invasion assay, serum-free media (100 µL) with the cell suspension (3×10^4 cells) were added into the top chamber of Transwell (8 µM pore, Millipore, Billerica, MA, USA) coated with 25 µL of Matrigel (BD Biosciences, San Jose,

CA, USA) and 75 µL of culture medium without FBS after transfecting with si-*LEF1-AS1* or si-NC for ~24 hours. The lower chambers were added the medium containing 10% FBS. After incubating for 48 hours at 37°C with 5% CO_2, the invading cells of the lower side membrane were fixed with methanol and stained with 0.1% crystal violet for 30 minutes. Six randomly chosen fields of each insert were counted using a digital microscope (Olympus).

Flow cytometric analysis

For cell-cycle analysis by flow cytometry, the U87 and U251 cells transfected for 72 hours were harvested and fixed in 70% ethanol overnight at 4°C after being washed three times by cold phosphate buffer solution (PBS). The cell nuclei were stained with 10 mg/mL ribonuclease and 1 mg/mL propidium iodide (PI) (Sigma-Aldrich Co.) at 37°C for 30 minutes in the dark. Finally, the DNA contents were analyzed on a FACSCalibur flow cytometer (Becton Dickinson, Franklin Lakes, NJ, USA). For cell apoptosis analysis, the cells were harvested and stained with annexin V-fluorescein isothiocyanate isomer (FITC) and PI using annexin V-FITC/PI double-staining kit (Beyotime) at 37°C for 30 minutes in the dark. The number of apoptotic cells was also quantified with the FACS Calibur flow cytometer.

Western blotting analysis

The stimulated cancer cell lines were lysed with radioimmunoprecipitation assay lysis buffer (Cell Signaling Technology, Danfoss, MA, USA) containing phenylmethanesulfonyl fluoride (Beyotime). Equal amounts of protein lysate were separated on 10% or 12.5% SDS PAGE gels (Abcam, Cambridge, UK) and then transferred to polyvinylidene fluoride membranes (EMD Millipore). The membranes were incubated with the primary antibodies at 4°C overnight. The following primary antibodies were used: anti-human matrix metallopeptidase 2 (MMP2) (#4022; Cell Signaling Technology), MMP9 (#13667; Cell Signaling Technology), p-ERK (4370P; Cell Signaling Technology), extracellular signal-regulated kinase 1/2 (ERK1/2) (4695P; Cell Signaling Technology), Akt (#4691; Cell Signaling Technology), p-Akt (#4060; Cell Signaling Technology), Bcl-2 (#4223; Cell Signaling Technology), Bax (#2772; Cell Signaling Technology), p27 (#2552; Cell Signaling Technology), p-mTOR (#2971; Cell Signaling Technology), mTOR (2983P; Cell Signaling Technology), cyclinD1 (#2978; Cell Signaling Technology), and GAPDH (AF0009; Beyotime). After incubation, the membranes were incubated with an horseradish peroxidase-conjugated secondary antibody for 1 hour at room temperature. Then, the membranes were washed six times

with TBST (PBS with 0.05% Tween20). The blot bands were visualized by Find-do ×6 Tanon (Tanon, Shanghai, China).

In vivo experiments

BALB/c nude mice at 4–5 weeks of age purchased from the animal center at the cancer institute at the Model Animal Research Center of Nanjing University (Nanjing, China) were maintained under pathogen-free conditions and manipulated according to the protocols. The animals from this study were approved by the Institution of Animal Ethical and Welfare Committee of Nanjing Medical University and the guidelines of National Animal Care and Use Committee were used. The effects of *LEF1-AS1* on tumor growth were explored using U87 cells stably transfected with si-*LEF1-AS1* or si-NC. The mice were randomly assigned into two groups and subcutaneously injected with 1×10^7 U87 cells into a single side of posterior flank of each mouse. To examine tumor growth, tumor volumes were measured using a caliper for every 3 days. The tumor volume was calculated by using the following formula: (short diameter)^2 × (long diameter)/2. The mice were sacrificed after 24 days. The tumors were resected and fixed in formalin.

## Statistical analysis

The data were expressed as mean ± standard deviations of at least three separate experiments and analyzed using the Student's *t*-test or one-way analysis of variance by using an SPSS 16.0 software system (IBM Corp., Armonk, NY, USA). A *P*-value of <0.05 was considered statistically significant.

Results

LEF1-AS1 expression was upregulated in GBM

To analyze lncRNA expression levels in GBM tissues compared with normal tissues, microarray data were downloaded first from TCGA and GEO data sets. A significant upregulation of *LEF1-AS1* expression levels was observed in GSE7696, GSE16011, GSE50161, and TCGA data set (Figure 1A). Next, the GBM gene expression data of TCGA were employed to analyze the association between *LEF1-AS1* expression and GBM patient prognosis. The Kaplan–Meier analysis and the log-rank test indicated that the 5-year overall survival in GBM patients with high expression of *LEF1-AS1* was notably shorter than that with low expression
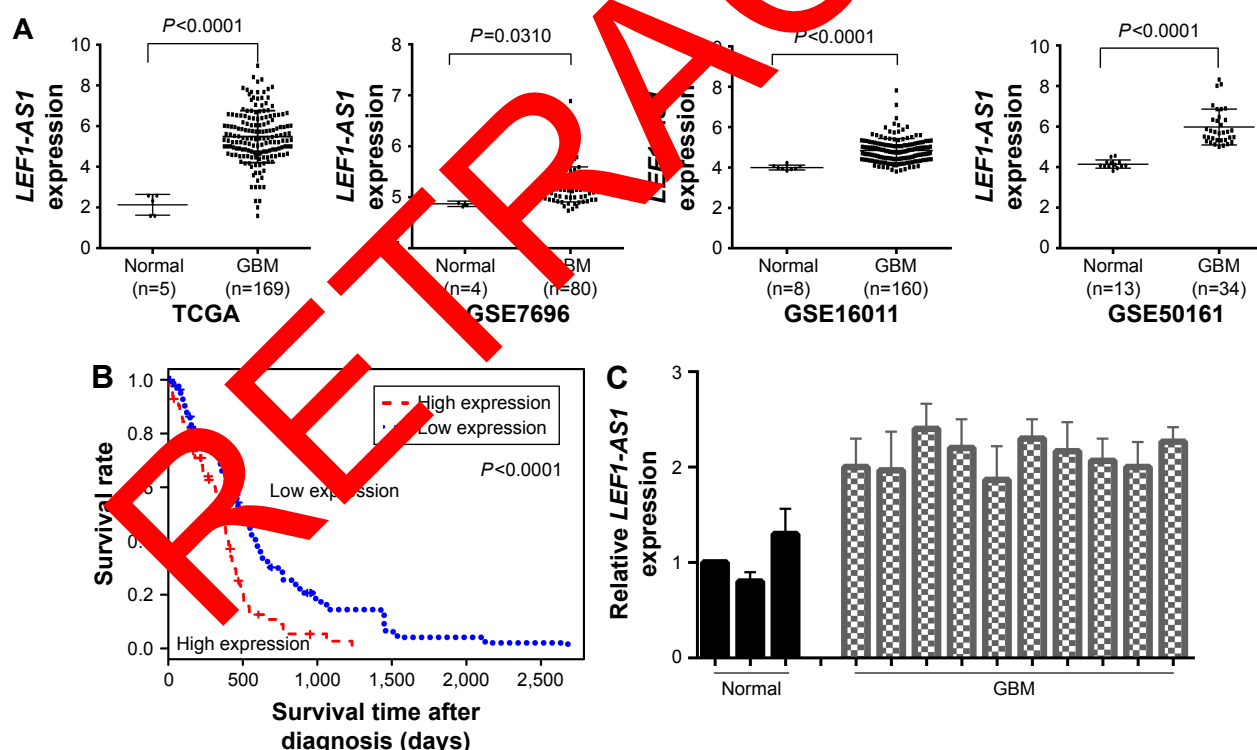
Figure 1 Upregulation of *LEF1-AS1* in GBM and its clinical significance.
Notes: (**A**) Relative expression of *LEF1-AS1* in GBM tissues compared to normal tissues was expressed at higher levels in TCGA and Gene Expression Omnibus data sets GSE7696, GSE16011, and GSE50161. (**B**) Kaplan–Meier analyses of the correlation between high and low *LEF1-AS1* expression levels in TCGA database and 5-year overall survival. (**C**) Relative expression of *LEF1-AS1* in GBM tissues (n=10) compared with corresponding normal tissues (n=3) was detected by qRT-PCR and normalized to GAPDH expression.
Abbreviations: *LEF1-AS1*, lymphoid enhancer-binding factor 1 antisense RNA 1; GBM, glioblastoma; TCGA, The Cancer Genome Atlas; GSE, gene expression omnibus data set; qRT-PCR, quantitative real-time polymerase chain reaction.

(P<0.0001) (Figure 1B). The real-time reverse transcription (RT)-PCR was performed to measure the expression levels of *LEF1-AS1* in 10 GBM tumors and 3 normal tissues. The results showed that the *LEF1-AS1* expression levels were significantly upregulated in GBM tissues compared with normal tissues (Figure 1C).

Knockdown of *LEF1-AS1* arrested cell proliferation in GBM cells

To evaluate the biological function of *LEF1-AS1* in GBM cells, a quantitative polymerase chain reaction (qPCR) was performed first to detect the knockdown efficiency of the *LEF1-AS1*-specific siRNAs in GBM cells. The silencing efficiency of si-*LEF1-AS1* was higher than that of the negative control siRNA in U87 and U251 cells (Figure 2A). The impact of *LEF1-AS1* knockdown on cell proliferation was assessed next. As shown in Figure 2B, the result of CCK8 indicated si-*LEF1-AS1* resulted in a significantly decreased proliferation of the U87 and U251 cells compared to the

respective NC group. The result of EdU-positive cell numbers also indicated that si-*LEF1-AS1* could inhibit the GBM cell proliferation (Figure 2C). Similarly, the result of colony formation assays showed that clonogenic survival was strikingly decreased following the inhibition of *LEF1-AS1* in two GBM cell lines (Figure 2D). The flow cytometric analysis revealed that si-*LEF1-AS1* induced GBM-cell G1 phase arrest in the U87 and U251 cells (Figure 3A).

Knockdown of *LEF1-AS1* promoted apoptosis and inhibited invasion in GBM cells

The flow cytometric analysis was performed to detect the function of si-*LEF1-AS1* on the apoptosis of GBM cells. The results are shown in Figure 3B. It suggested that the low *LEF1-AS1* expression promoted the apoptosis of GBM cells. The invasiveness effects of *LEF1-AS1* on GBM cells were checked by a Matrigel invasion assay. As is shown in Figure 3C, the numbers of U87 and U251 cells in the
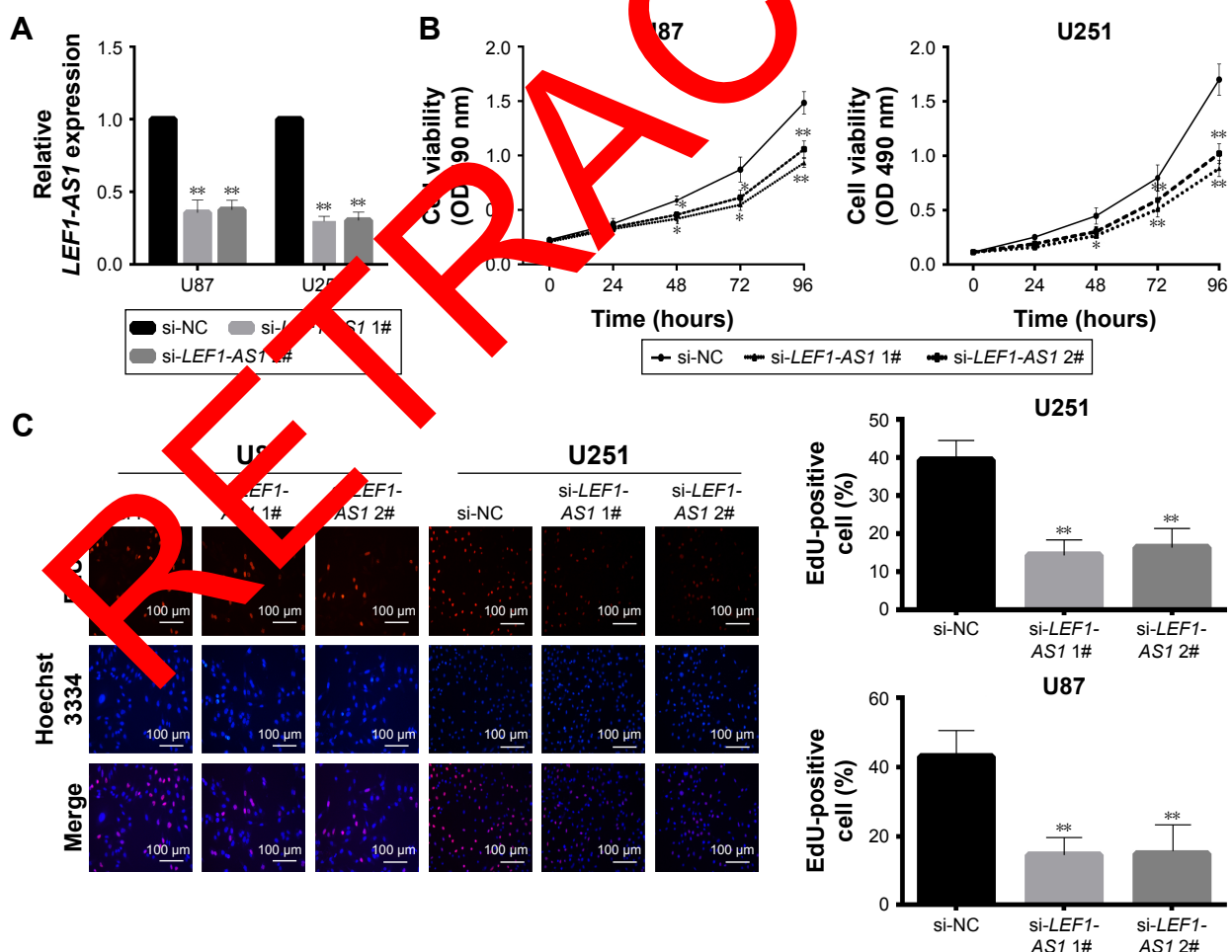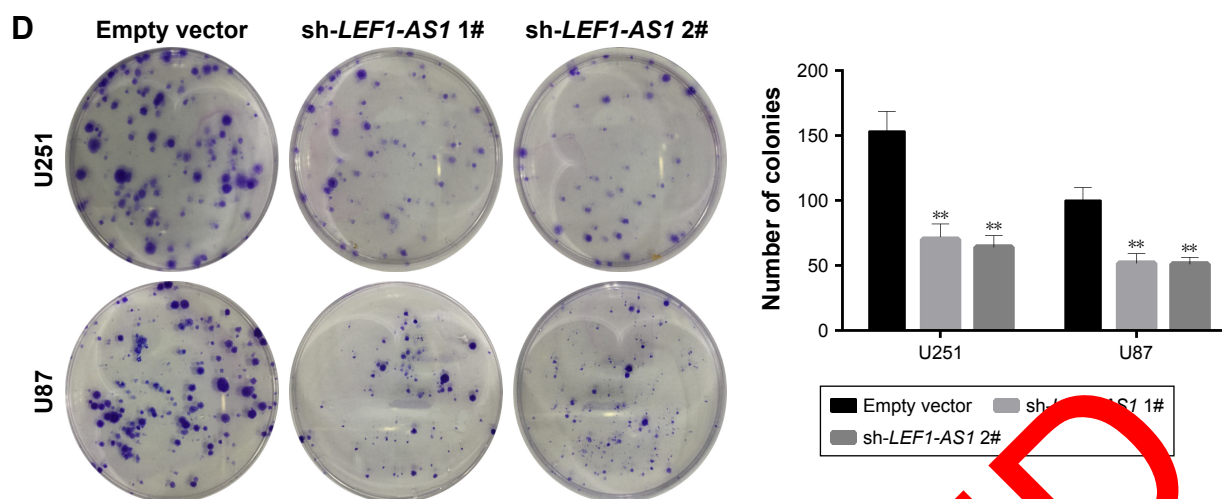

Figure 2 (*Continued*)

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Figure 2 Knockdown *LEF1-AS1* inhibits GBM cell proliferation in vitro.
Notes: (**A**) *LEF1-AS1* expression was downregulated by transfecting with si-*LEF1-AS1* 1# and si-*LEF1-AS1* 2# and determined by qRT-PCR in U251 and U87 cells. **P<0.01 versus si-NC. (**B**) After transfection with si-*LEF1-AS1* or negative control (si-NC), cell proliferation rates of U87 and U251 cells were determined by CCK8 assay. **P<0.01, *P<0.05 versus si-NC. (**C**) EdU assay detected the effect of *LEF1-AS1* knockdown on cell proliferation of U87 and U251. The click-it reaction revealed EdU staining (red). Cell nuclei were stained with DAPI (blue). All of the results are presented as mean ± SD from three independent experiments. **P<0.01 versus si-NC. (**D**) Relative ability of U87 and U251 cell proliferation after transfection with empty vector and sh-*LEF1-AS1* was detected by colony formation assay. **P<0.01 versus empty vector.
Abbreviations: *LEF1-AS1*, lymphoid enhancer-binding factor 1 antisense RNA 1; GBM, glioblastoma; si-*LEF1-AS1*, siRNA targeting *LEF1-AS1*; siRNA, small interfering RNA; qRT-PCR, quantitative real time polymerase chain reaction; si-NC, negative control siRNA; CCK8, Cell Counting Kit-8; EdU, 5-ethynyl-2-deoxyuridine; DAPI, 4′,6-diamidino-2-phenylindole; SD, standard deviation; sh, short hairpin; OD, optical density.

lower section were significantly reduced in the si-*LEF1-AS1* group compared with the si-NC group (Figure 3C). This indicated that the knockdown of *LEF1-AS1* inhibited cell invasion.

Knockdown of *LEF1-AS1* inhibited Akt/mTOR and MAPK pathway in GBM cells

To dissect the expression of genes downstream of lncRNA, Western blot assays were performed on *LEF1-AS1* responsible for si-*LEF1-AS1*-mediated inhibition of tumorigenicity. As known, the Akt/mTOR and ERK pathways are hyperactivated in many human cancers including GBM. They regulate many important functions for tumor initiation and apoptosis, proliferation, and invasion function.[15,16] The p-Akt, p-mTOR, and p-ERK expressions were significantly decreased in the si-*LEF1-AS1* group compared with the control (si-NC group), both in the U87 and U251 cell lines, while the Akt, mTOR, ERK1/2 and protein expressions were not changed obviously (Figure 4A). The result suggested that si-*LEF1-AS1* may exert inhibition of tumorigenicity function by downregulated ERK1/2- and Akt-mediated signaling pathway. The relative protein expressions of pro-invasion (MMP9 and MMP2), G1 phase arrest (cyclinD1), and anti-apoptosis protein were downregulated significantly compared with the control in the U87 and U251 cells, while cell-cycle regulatory protein p27 and pro-apoptosis protein Bax were up-regulated (Figure 4B). The findings of this study suggested that si-*LEF1-AS1* inhibited GBM cell proliferation and invasion and induced

apoptosis via regulation protein of MMP9, MMP2, cyclinD1, p27, Bcl-2, and Bax expression.

Knockdown of *LEF1-AS1* inhibited GBM cells' tumorigenesis in vivo

To assess whether si-*LEF1-AS1* can decrease tumorigenesis in vivo, U87 cells were inoculated with or empty vector into nude mice as xenografts. All the mice were sacrificed 24 days after the injection, and the tumors formed in the sh-*LEF1-AS1* group were substantially smaller than those in the control group (Figure 5A). Meanwhile, the tumor weight and volume of sh-*LEF1-AS1*-transfected group decreased significantly compared with those injected with control group (Figure 5B and C). In addition, the result of qPCR assays showed that the levels of *LEF1-AS1* expression in tumor tissues were significantly downregulated in the sh-*LEF1-AS1*-transfected cells compared with the control cells (Figure 5D). Hematoxylin-eosin staining of the tumor tissues from the two groups did not present any difference in histology, and the Ki-67-positive cells of tumors formed from the sh-*LEF1-AS1*-transfected U87 cells was obviously decreased compared with tumors formed from the control U87 cells (Figure 5E). These data suggested that the knockdown of *LEF1-AS1* reduced tumor growth in vivo.

Discussion

Several publications have recently provided compelling evidence that the expression patterns of lncRNAs were of
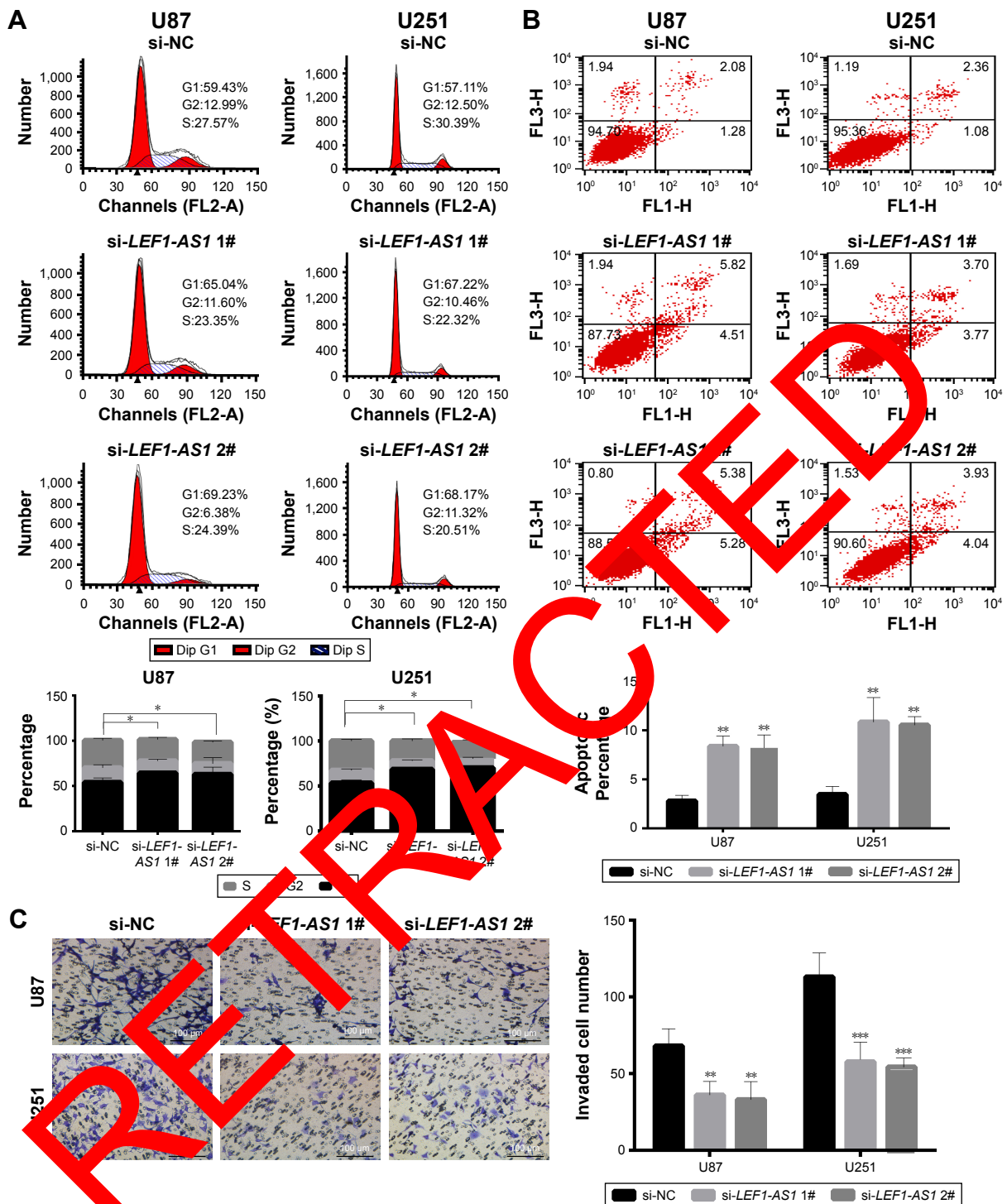
Figure 3 Knockdown *LEF1-AS1* induces G1 arrest and apoptosis and inhibits invasion in GBM cells.
Notes: After knockdown of *LEF1-AS1* for 24 hours in U87 and U251 cells, the flow cytometric histograms showed cell arrest in G1 phase of cell-cycle (**A**) and a dramatic increase of apoptosis (**B**). (**C**) Invasion capacities were investigated by Transwell assays. The numbers of invasion cells were calculated. Relative bar graphs are shown in right. ***$P<0.001$, **$P<0.01$, *$P<0.05$ versus si-NC. All of the results are presented as mean ± SD from three independent experiments.
Abbreviations: *LEF1-AS1*, lymphoid enhancer-binding factor 1 antisense RNA 1; GBM, glioblastoma; si-NC, negative control siRNA; si RNA, small interfering RNA; SD, standard deviation.

vast importance associated with the pathogenesis of malignant tumors, including tumorigenesis, drug resistance, and metastasis.[17–19] The functions of lncRNAs can drive complex mechanisms on many important cancer phenotypes through

their interactions with other cellular macromolecules, which include epigenetic regulation of protein-coding genes and exploration of dysregulated lncRNAs.[20] Thus, the dysregulation of lncRNAs may not only affect the regulation of the
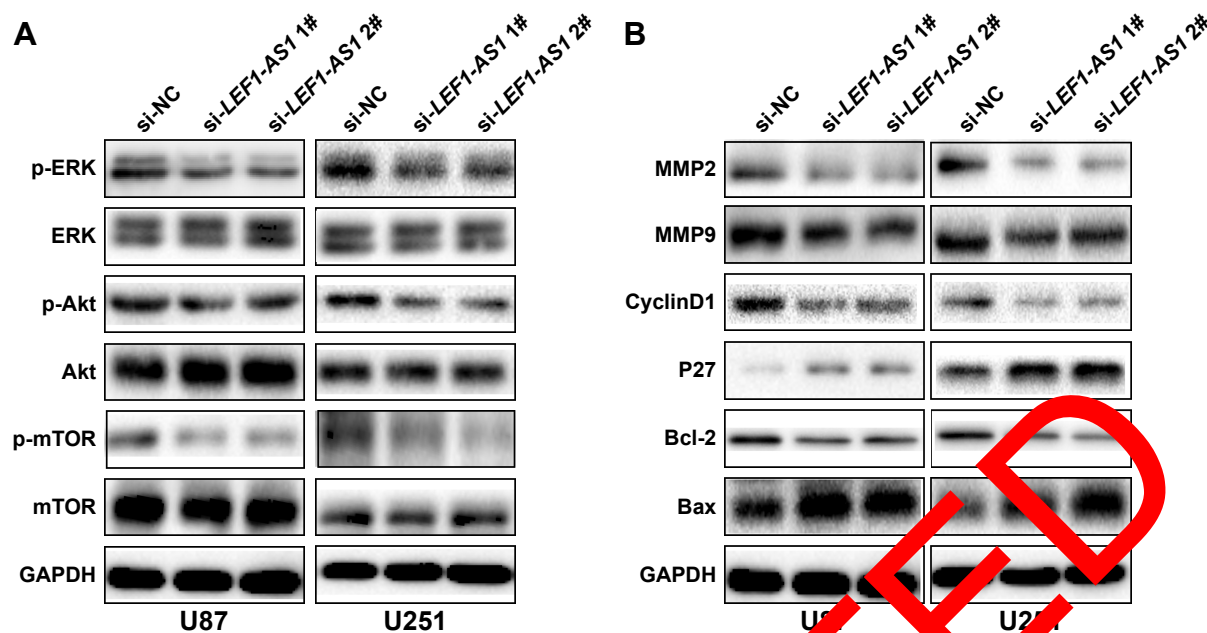
Figure 4 *LEF1-AS1* exerts its function on Akt/mTOR and MAPK pathways in GBM cells.
Notes: Cells were transfected with si-NC and si-*LEF1-AS1*. (**A**) Western blot analyzed the expression levels of p-ERK, ERK, p-Akt, Akt, p-mTOR, and mTOR in U87 and U251 cells. (**B**) The levels of cell-cycle, apoptosis, and invasion proteins were detected.
Abbreviations: *LEF1-AS1*, lymphoid enhancer-binding factor 1 antisense RNA 1; GBM, glioblastoma; NC, negative control; siRNA; si RNA, small interfering RNA; si-*LEF1-AS1*, siRNA targeting *LEF1-AS1*; MMP, matrix metallopeptidase.
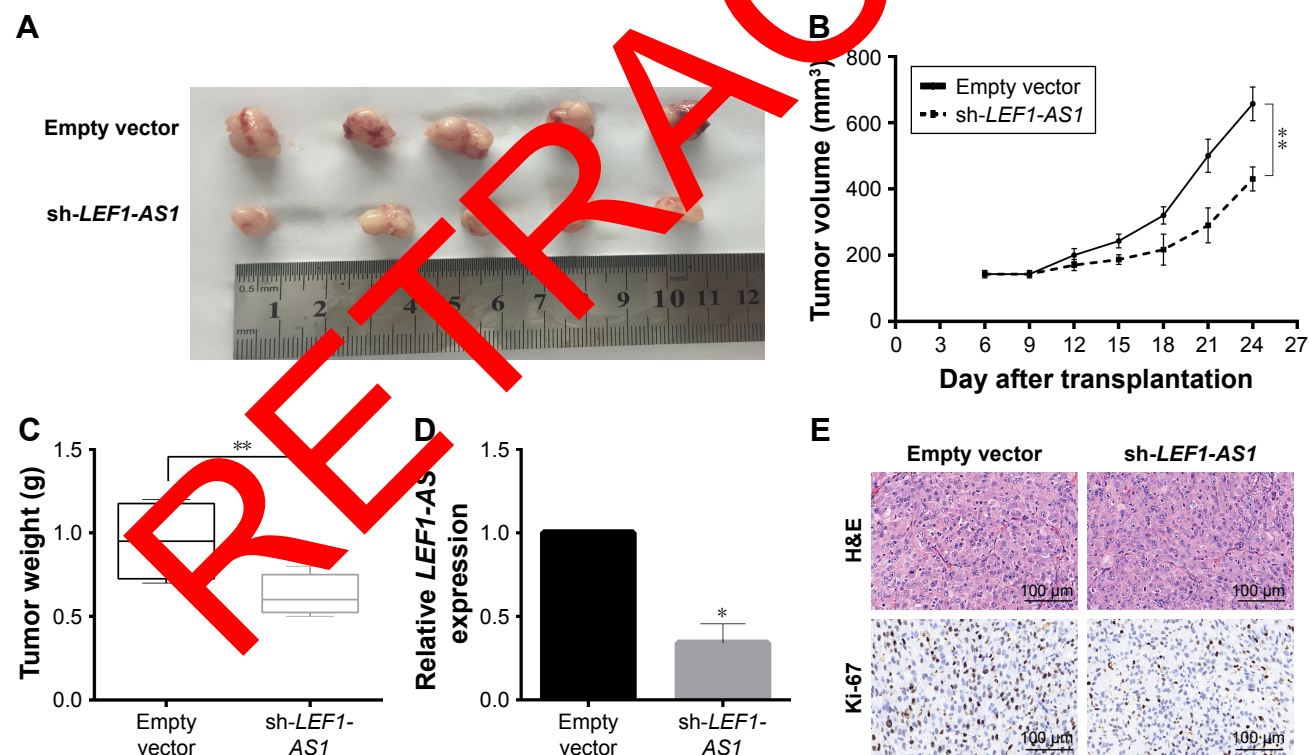
Figure 5 *LEF1-AS1* inhibits tumor growth in vivo.
Notes: (**A**) Nude mice inoculated were sacrificed 24 days after injection of U87 with sh-*LEF1-AS1* or empty vector. (**B**) The tumor size was measured every 3 days after injection. **P<0.01 versus empty vector. (**C**) The weight of tumor tissue resected from injected mice was measured. **P<0.01 versus empty vector. (**D**) qRT-PCR detected *LEF1-AS1* expression in tumor tissues formed. *P<0.05 versus empty vector. (**E**) Transplanted tumors with H&E staining and IHC showed expression of Ki-67.
Abbreviations: *LEF1-AS1*, lymphoid enhancer-binding factor 1 antisense RNA 1; qRT-PCR, quantitative real-time polymerase chain reaction; H&E, hematoxylin-eosin; IHC, immunohistochemistry; sh, short hairpin.

eukaryotic genome, but may also provide a growth advantage to malignant cells, resulting in progressive and uncontrolled tumor growth.[21] For example, lncRNA AB073614 induces tumor progression and predicts poor prognosis through regulating ERK1/2 and Akt signaling pathways in ovarian cancer.[22] lncRNA CRNDE function a pro-oncogenic role through modulation of the mTOR signaling pathway.[23] In addition, several studies reveal that lncRNAs are exquisitely regulated and are restricted to specific cell types to a greater degree than protein-coding genes,[20,24,34,35] which indicates that lncRNAs may serve as more sensitive biomarkers of different cancers. Therefore, identification of GBM-associated lncRNAs, investigation of their clinical significance and biological function may new therapeutic targets for malignancy.

Benefits of the fast development of sequencing technique and bioinformatics in the past decades and genome-wide cancer mutation analyses are identifying an extensive landscape of functional mutations within noncoding RNAs' genome, with profound effects on the expression of lncRNAs in multiple cancer phenotypes. More and more novel lncRNAs have been discovered and biomarker of lncRNAs in multiple cancer phenotypes has been identified, which included GBM.[25,26] Dependent of some microarray platforms with a large group of lncRNA-specific probes, lncRNA profiling was performed initially on large cohort of GBM patients using data downloaded from TGA and GEO databases. In this study, a new lncRNA *LEF1-AS1* was demonstrated, which was most significantly upregulated in the GBM tissues, and the highest level of *LEF1-AS1* expression was correlated with poor prognosis and short survival time in the GBM patients. It was also confirmed that lncRNA *LEF1-AS1* was extremely upregulated in 10 GBM tissues, compared with 3 normal tissues. These findings indicate that lncRNA *LEF1-AS1* may serve as a novel prognostic marker and therapeutic target for GBM. To further determine the effect of lncRNA *LEF1-AS1*, a series of experiments was performed in vitro and vivo to investigate the loss of lncRNA *LEF1-AS1* function on various aspects of GBM-cell biology. The knockdown of lncRNA *LEF1-AS1* significantly reduced cell proliferation, migration, and invasion, and induced cell-cycle G1 phase arrest and apoptosis in the U87 and U251 cell lines. The in vivo studies also showed that the tumors derived from the knockdown of *LEF1-AS1* cells grew slower compared to those in the control group. Therefore, *LEF1-AS1* may exert tumorigenic activity in GBM, and promote growth and aggressive characteristics.

Akt and mTOR are important kinases that are activated by many cellular stimuli and regulate fundamental cellular functions including transcription, translation, proliferation, growth, and survival.[27] Inhibition of the phosphatidylinositol 3-kinase/Akt/mTOR pathway has served as a compelling therapeutic target for GBM in clinical trials.[28] Otherwise, it has been confirmed that ERKs promote cell proliferation, cell survival, and metastasis especially through upstream activation by the epidermal growth factor receptor and Ras small guanosine triphosphatases,[29] which is included GBM.[30] It was found that the knockdown of *LEF1-AS1* downregulated the expression of p-ERK1/2 and p-AKT, which indicated that lncRNA *LEF1-AS1* may exert its function by targeting ERK1/2 and Akt/mTOR signaling pathways. To the best of our knowledge, Akt/mTOR signaling pathway is one of the most important signaling pathways regulating apoptosis and cyclic protein of tumor cells.[31,32] Activated ERK1/2 could increase the production of MMPs.[33] As expected, *LEF1-AS1* knockdown decreased the cell pro-invasion protein (MMP9 and MMP2), G1 phase protein (cyclinD1), and Blc-2 significantly in both U87 and U251 cell lines, while it decreased the cell-cycle regulatory protein p27 and pro-apoptosis protein Bax significantly, indicating that *LEF1-AS1*-regulated GBM progression involved these genes.

In summary, it has been shown for the first time that *LEF1-AS1* expression was upregulated in GBM tissues and its overexpression might correlate with poor overall survival in GBM patients. The knockdown of *LEF1-AS1* exerted tumor suppressive functions through by reducing cell proliferation, migration and invasion as well as inducing apoptosis. Furthermore, the oncogenic mechanism of *LEF1-AS1* is partially through downregulating ERK and Akt/mTOR pathways. The findings suggest that lncRNA *LEF1-AS1* acts as a functional oncogene in GBM cell line and that the downregulation of lncRNA *LEF1-AS1* expression decreases GBM development. However, further studies are necessary to validate the findings in GBM cells, and finding out the underlying mechanism could provide a novel promising candidate for the treatment of GBM.

Acknowledgments

Disclosure

The authors report no conflicts of interest in this work.

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