

# Esophageal carcinoma cell-excreted exosomal uc.189 promotes lymphatic metastasis

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## ABSTRACT

Most cancers are old age-related diseases. Patients with lymphatic metastasis have an extremely poor prognosis in esophageal cancers (ECs). Previous studies showed ultraconserved RNAs are involved in tumorigenesis and ultraconserved RNA 189 (uc.189) served as an oncogene in cervical cancer, but the effect of exosomal uc.189 in esophageal squamous cell carcinoma (ESCC) remains undefined. This study revealed that uc.189 is closely correlated with lymph node (LN) metastasis and the number of lymphatic vessels in ESCC. ESCC-secreted exosomal uc.189 is transferred into human lymphatic endothelial cells (HLECs) to promote its proliferation, migration and tube formation to facilitate lymph node metastasis. Mechanistically, uc.189 regulated EPHA2 expression by directly binding to its 3'UTR region through dual-luciferase reporter assay. Over-expression and knockdown of EPHA2 could respectively rescue and simulate the effects induced by exosomal uc.189. Especially, the uc.189-EPHA2 axis activates the P38MAPK/VEGF-C pathway in HLECs. Finally, ESCC-secreted exosomal uc.189 promotes HLECs sprouting *in vitro*, migration, and lymphangiogenesis. Thus, these findings suggested that exosomal uc.189 targets the EPHA2 of HLECs to promote lymphangiogenesis, and may represent a novel marker of diagnosis and treatment for ESCC patients in early stages.

## INTRODUCTION

Squamous cell carcinoma of oesophagus is one of the most common malignant digestive system tumors, and it is also a common disease related to cancer death in China every year [1]. The combination of early detection, early diagnosis, and early treatment has effectively prolonged the survival time of ESCC patients; however, esophageal squamous cell carcinoma (ESCC) is easy to metastasize and relapse again [2]. Cancer mainly includes carcinoma and sarcoma. The metastasis of cancer is mainly through lymphatic vessels, while the metastasis of sarcoma is mainly through blood vessels. Cancer cells can secrete lymphatics/angiogenic factors to promote local

lymphangiogenesis or angiogenesis, and then the cells invade lymph/blood vessels to distant organs. ESCC is a type of carcinoma. This project focuses on the molecular mechanism by which ESCC cells promote lymphangiogenesis.

Ultraconserved RNAs (UCRs) are a set of 483 segments that are absolutely conserved in the homologous sequences of higher organisms, which regulate transcription and/or translation of other RNAs [3]. UCRs are a kind of non-coding protein RNAs that modulate the development of tumors [4]. Uc.189 is a member of UCRs, which is located on human chromosome 6p21. In 2016, Jiang et al. found that the expression of uc.189 is increased in spinal cord tissue of

neuropathic pain by Arraystar ucRNA Array [5]. Wang et al. detected that the expression of uc.189 is increased in female malignant tumors, including cervical squamous cell carcinomas, terminal adenocarcinomas, and cystoadenocarcinomas. The overexpression of uc.189 suggested that the prognosis of patients with cervical squamous cell carcinomas or terminal adenocarcinomas was poor [6]. Guo et al. [7] showed that the uc.189 expressions of ESCC were up-regulated, which was closely related to the invasion depth, metastasis and stage, suggesting that the higher the uc.189 expressions, the worse the prognosis of patients. In brief, uc.189 is involved in the development of tumor, but its role as an exosome has not been reported yet, which is the purpose of our study.

Exosomes are a class of tiny membranous vesicles with diameters of 60 to 150nm, which contain protein-coding genes and non-coding RNA (miRNAs and long noncoding RNAs) [8–9]. Recent studies have shown that cancer-secreted exosomal ncRNAs are crucial messengers for cancer metastasis in the tumor microenvironment. For example, exosome of miR-221 promotes lymphangiogenesis of cervical cancer by regulating VASH1 [10]. Exosome of miR-1247-3p targets for B4GALT3 and activates  $\beta$ 1-integrin-NF- $\kappa$ B signaling to promote lung metastasis [11]. And exosomal lncRNA LNMMAT2 promotes lymphatic metastasis via PROX1 signaling in the bladder [12]. EPHA2 is an oncogene, which is up-regulated in a variety of cancers, including breast cancer [13–15], colon adenocarcinoma [16], prostate cancer [17], non-small cell lung cancer [18] and melanoma [19, 20]. It has been reported that EPHA2 is an important mediator of angiogenesis mimicry *in vitro* and down-expression of EPHA2 can inhibit angiogenesis [21]. At the same time, EPHA2 is also an important negative regulator in formation of lymphatic vessels by the Gene Ontology Consortium [10].

In the current study, uc.189 was up-regulated by quantitative reverse transcription polymerase chain reaction (qRT-PCR) in ESCC tissues and highly enriched tiny exosomes in ESCC cells, and promoted lymphangiogenesis. Therefore, this project focuses on the mechanism of uc.189 promoting lymphangiogenesis to provide the theoretical basis for clinical diagnosis and treatment of ESCC.

## MATERIALS AND METHODS

### Clinical specimens' collection

66 pairs of ESCC specimens and matched normal esophageal tissues were from the Affiliated Hospital of Yangzhou University (Yangzhou, China) between 2018

and 2019. ESCC was confirmed by two pathologists. All fresh specimens were stored in liquid nitrogen before use. This study was approved by the Medical Ethics Committee of the Affiliated Hospital of Yangzhou University. Written informed consent was also provided for the patients.

### Cell culture

Esophageal carcinoma (EC) cell lines (TE-1, Eca109, EC9706, and KYSE150), HEE-1 (a normal esophageal epithelial cell) and Human lymphatic endothelial cells (HLECs) were all purchased from Shanghai Xinyu Biotechnology Co., LTD. (Shanghai, China) and cultured according to their culture protocol. HLECs were cultured in endothelial cell medium (ScienCell, USA) with 5% fetal bovine serum (Gibco, USA). All these cell lines were incubated in 37° humidified incubators with 5% CO<sub>2</sub>.

### Identification of exosomal uc.189

A total of 12 ml medium containing EC cells was mixed with ExoQuick™ exosome precipitation solution, and then exosomes were extracted from the mixture according to the instructions. Isolated exosomal uc.189 was immobilized on carbon membrane after 2% glutaraldehyde fixation, which was visualized by transmission electron microscopy (TEM).

### qRT-PCR

Total RNAs were isolated using TRIzol reagent (Invitrogen). RNAs were reverse-transcribed to cDNA using the PrimeScript First Strand cDNA synthesis kit (Takara) according to the instructions. qRT-PCR was performed on an Applied Biosystems 7500 Real Time PCR system. The related primers were in Supplementary Table 1. The expression of UCRs and mRNAs was normalized to U6 and GAPDH, respectively.

Total RNA was extracted from Trizol reagent (Invitrogen, USA). Total RNA was reverse-transcribed into cDNA using cDNA synthesis Kit (Takara, Japan) according to the instructions. qRT-PCR was performed with fluorescent quantitative Kit (2 × SYBR Green qPCR mastermix) on the Applied Biosystems 7500 real-time PCR instrument. The related primers are shown in Supplementary Table 1. U6 and GAPDH were used as internal parameters of uc.189 and EPHA2, respectively.

### RNA *in situ* hybridization (RISH)

Paraffin sections were dewaxed to water. Endogenous enzymes were eliminated by hydrogen peroxide treatment at room temperature. The exposed tissues

were digested with pepsin. Tissues were incubated in an incubator with pre-hybridizing solution. Next, RNAs were hybridized with uc.189 probe in 42°C for the night, the sections were added sealing fluid, biotinylated anti-digoxin (antidigoxin), and SABC. DAB was used for tissue staining. The sections were dyed hematoxylin, dehydrated, and sealed. Morphological changes of tissue were observed under a microscope. The hybridization solution containing the probe was replaced by pre-hybridization solution as blank control.

### Western blot assay

Western blotting has been described in the previous article [10]. The simple steps are as follows: Total protein extraction; Protein content determination; SDS-PAGE electrophoresis; Transfer membrane; Immune reaction; Final gel image analysis. The primary antibodies included CD9, CD81, EphA2, p38 MAPK, phosphorylated p38 MAPK, VEGF, phosphorylated VEGF and GAPDH; the second antibody was anti-rabbit immunoglobulin G antibody with horseradish peroxidase. CD9 (#ab2215), CD81 (#ab109201), EphA2 (#ab5386) and anti-rabbit immunoglobulin G antibody (#ab6721) were purchased from Abcam Biotechnology company; Phospho-P38 MAPK (#4511), P38 MAPK (#8690), phospho-VEGF (#2471), VEGF-C (#2445), and GAPDH antibody (#2118) were purchased from CST Biotechnology company.

### Immunofluorescence (IF) detection

IF Detection has been described in published literature [22]. Simple steps of IF are as follows: cell climbing film; 4% cold paraformaldehyde fixation; 0.2% Triton X-100 permeability; serum blocking; dripping primary antibody overnight; dripping secondary antibody; DAPI nuclei staining; fluorescence microscope observation and photography. The primary antibody is anti-EPHA2 (Abcam), Anti-rabbit IgG by fluorescence conjugation was purchased from Life Technologies Corporation (Shanghai, China). The fluorescence of tumor cells was observed by fluorescence microscope (Leica, Germany).

### Transient transfection

The assay was performed as we previously described [23]. The main steps of the assay are as follows: ESCC cells were transfected with uc.189 mimics or siRNA using Lipofectamine 2000 (Invitrogen, San Diego, CA, USA) and incubated for 36 hours at 37°C with 5% CO<sub>2</sub>.

### Dual-luciferase reporter assay

Bioinformatics method was used to predict the uc.189 binding sites in 3'UTR of EPHA2. The length 821

nucleotide of EPHA2 3'UTR was amplified and inserted into the luciferase reporter gene plasmid pGL3-BS. Plasmid of wild type (WT) and plasmid of mutation type (MUT) were co-transfected into 293 T cells (or cancer cells). The protein was extracted and used for luciferase detection. The activity of luciferase was determined by adding substrate. The relative fluorescence intensity was calculated, Firefly luciferase signal was used for normalization. The primers of EPHA2 3'-UTR are shown in Supplementary Table 1.

### Bioinformatic prediction

First, genes related to lymphangiogenesis were obtained by The Gene Ontology Consortium (GOC), and then the 3'-UTR binding sites of EPHA2 were matched by uc.189 by Blast.ncbi.nlm.nih.gov/Blast.cgi. Whether uc.189 can directly regulate the expression of e needs to be confirmed by Dual-luciferase reporter assay.

### Tube formation

50  $\mu$ l of the Matrigel mixture was covered in 96-well plates. After Matrigel solidification at 37°C incubator, HLECs were seeded on the wells and incubated for 10 hours under normal culture condition. Photos of tube formation were taken by a microscopic camera, and the tube lengths were quantified using Image J software.

### Transwell migration

In 180  $\mu$ l culture media of the upper wells, ten thousand of HLECs without serum were seeded on a fibronectin-coated polycarbonate membrane. In the lower wells, culture solutions contain 10% FBS. After 12 hours, the tumor cells migrated to the membrane' bottom surface and were fixed with methanol for 20 minutes, then stained with 0.1% crystal violet for 15 minutes, observed and photographed under a light microscope (10  $\times$  20).

### Cell counting kit-8 (CCK-8)

CCK8 assay has been described in published literature [22]. The main steps of the assay are as follows: the esophageal cancer cells transiently transfected with uc.189 overexpression or silencing expression were inoculated into 96 well plates with about 2000 cells in each well, and then the cell proliferation activity was detected every 24 hours. After incubation with 10  $\mu$ l CCK-8 reagents (Biotechnology Institute, Shanghai, China) for 2 hours, the absorbance of each well at 450 nm was measured in a microplate reader. The assay was performed in five replicate wells, and three parallel experiments were conducted for each sample.

## Statistical analysis

SPSS V.16 software and GraphPad Prism V.5 software were used for statistical analysis and all graphs. Students' *T* test was used to evaluate the differences between groups. The categorical variables were analyzed by chi square test ( $\chi^2$ -test).  $P < 0.05$  as a significant difference between the two groups.

## RESULTS

### uc.189 is over-expression in ESCC

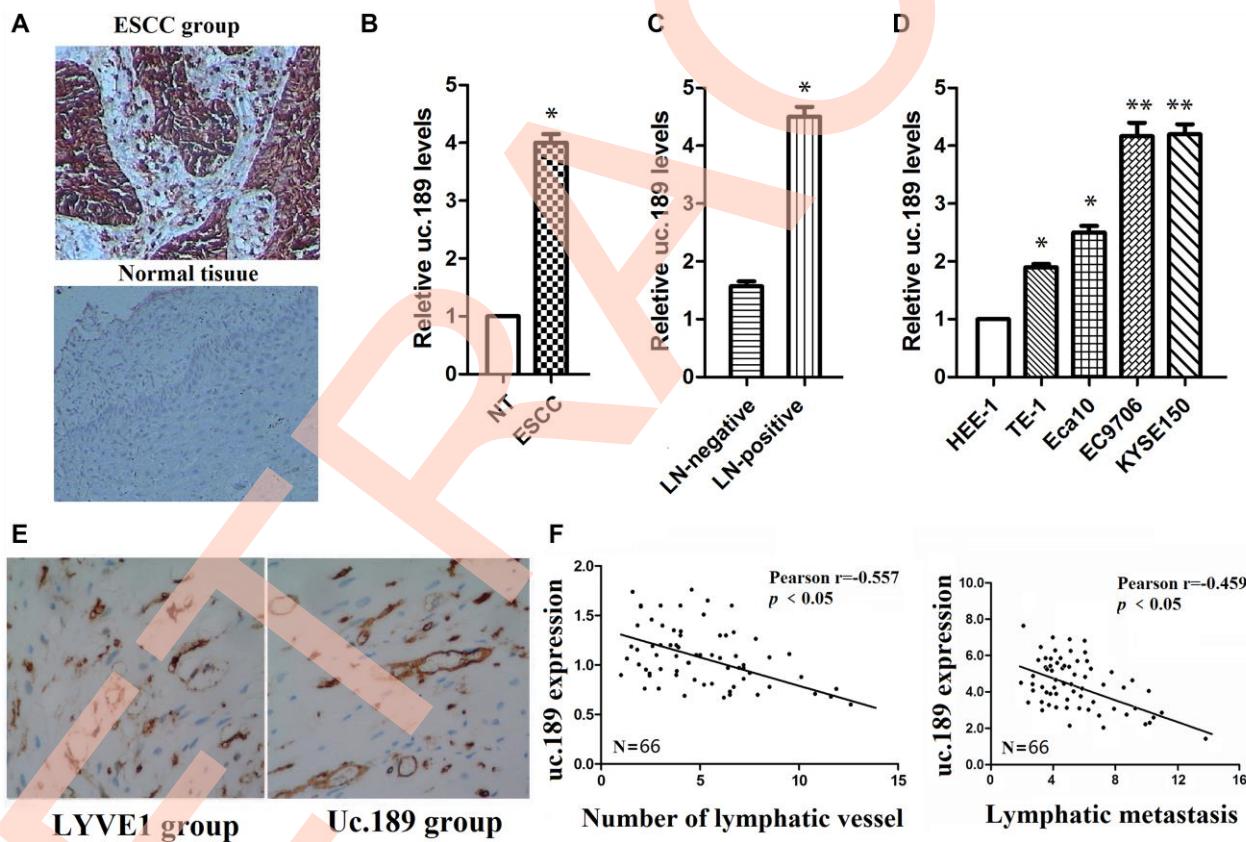
Since uc.189 was over-expression in gynecological cancers in our previous studies [6], we investigated whether uc.189 expressions are altered in human ESCC tissues.

Expression levels of uc.189 were detected in 66 specimens of ESCC using RISH and qRT-PCR. RISH results showed uc.189 expressions were positive

compared with the adjacent normal oesophagus tissues (negative group) in Figure 1A.

The expression levels of uc.189 in ESCC were significantly higher than that in negative group in Figure 1B, and the uc.189 levels in lymph node (LN) positive group were significantly higher than that in LN negative group (Figure 1C). Similarly, up-regulation of uc.189 was detected in four esophageal cancer cell lines (TE-1, Eca109, EC9706, and KYSE150) compared with a non-carcinoma esophageal epithelial cell HEE-1 by qRT-PCR (Figure 1D). Furthermore, uc.189 is also a positive expression in the peritumoral lymphatic vessel of ESCC specimens, and LYVE1 expression as a positive control (Figure 1E). Up-regulated uc.189 is positively correlated with the number of lymphatic vessels and LN metastasis (Figure 1F).

Collectively, these results suggest that overexpression of uc.189 promotes lymphangiogenesis and lymphatic metastasis of ESCC.



**Figure 1. Uc.189 expressions are detected in ESCC tissues and cell lines.** (A) uc.189 was a positive expression in ESCC and was a negative expression in normal tissue by ISH. (B) The uc.189 relative expression levels were determined by qRT-PCR in 66 paired human ESCC and normal tissue (NT) samples and normalized against an endogenous U6 RNA control. (C) The relative expression levels of uc.189 in ESCC with lymph-node metastasis (LN-positive;  $n = 58$ ) and non-metastasis (NM;  $n = 8$ ). (D) The relative expression levels of uc.189 in the four EC cell lines and normal cells (HEE-1). (E) uc.189 is a positive expression in the peritumoral lymphatic vessel (black arrow) of ESCC specimens and LYVE1 expression as a positive control. (F) Correlation analysis of ISH staining showing a negative correlation between uc.189 expressions and lymphatic vessel density indicated by anti-LYVE-S stain and uc.189 expressions are also a negative correlation with lymphatic metastasis in ESCC ( $n = 66$ ). \* $p < 0.05$ , \*\* $p < 0.01$ .

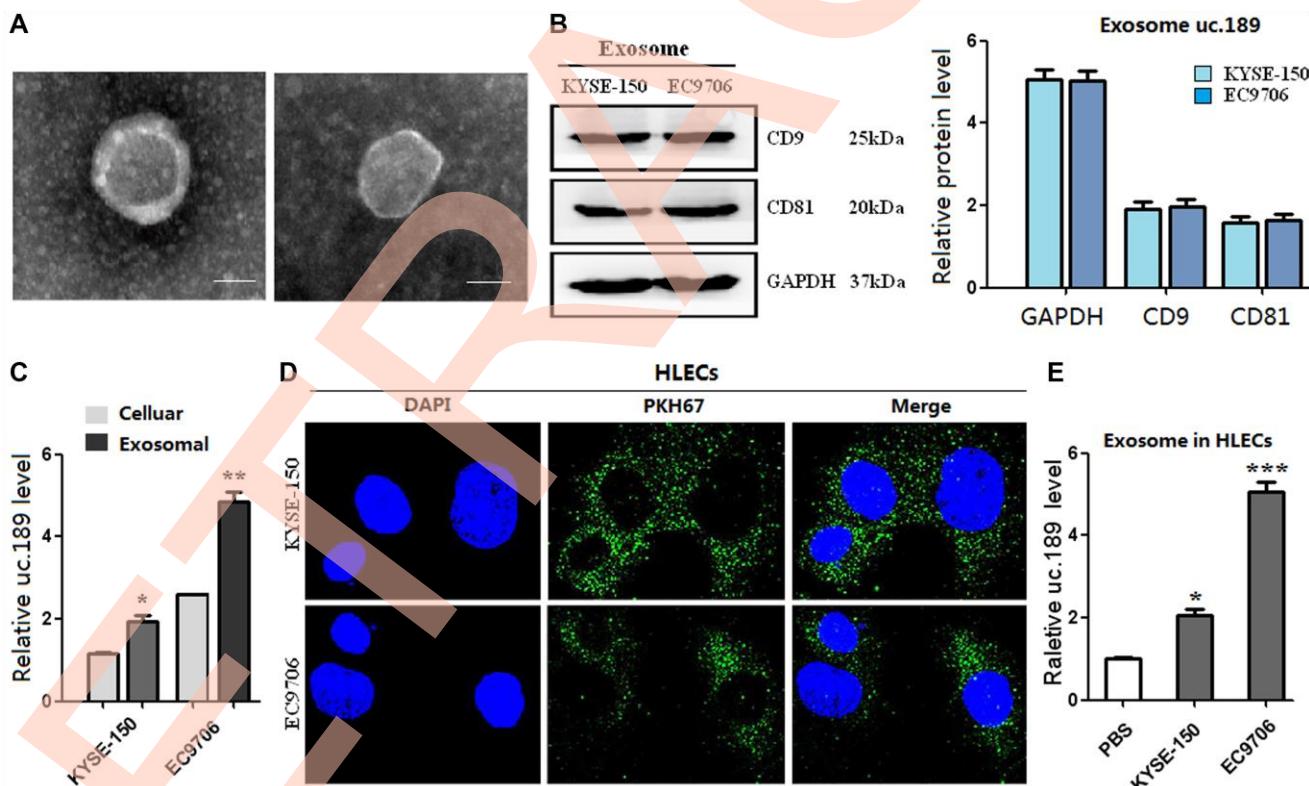
## Exosomal uc.189 can be enriched from EC cell lines and delivered to HLECs

Studies have confirmed that ncRNAs can be transferred between cells through exosomes [24]. Similarly, this study investigated whether uc.189 could form exosomes and transfer them from ESCC cells to HLECs. The exosomes were obtained from the supernatants of KYSE-150 and EC9706 cells by using ExoQuick™ exosome precipitation solution. The result showed that typical round or oval black ultrastructures with size ranging from 30 nm to 100 nm were observed in ECM (Figure 2A). Western blotting confirmed the presence of exosome positive markers of CD9 and CD81 (Figure 2B). Furthermore, qRT-PCR results showed that compared with KYSE-150 and EC9706 cells, uc.189 was highly enriched in the purified exosomes (Figure 2C). The exosomes labeled with green fluorescent membrane tracer of PKH67 showed green granular substance after incubation with HLECs for 48 hours, and the nuclei of HLECs were stained blue with DAPI (Figure 2D). Recipient HLECs with exosomes were observed having an increased level of uc.189 (Figure 2E). Taken together, these arrays suggest that uc.189

could form exosomes from ESCC cell lines and it passed from ESCC cells to HLECs via exosomes.

## Exosomal uc.189 promotes lymphangiogenesis, proliferation and migration of HLECs

To investigate whether the role of exosomal uc.189 on the proliferation, migration and lymphangiogenesis of HLECs cells, CCK-8, transwell and tube formation assay were used to test this effect. Firstly, we transfected the lentiviral vector with overexpressed or silenced uc.189 and control vector into EC9706, then cultured the purified exosomes with HLECs for 48 hours, and confirmed the expression level of uc.189 in EC9706 and HLECs by qRT-PCR. The results showed that the expression levels of uc.189 in EC9706 and HLECs were significantly higher than that in control group (Figure 3A, 3B). Then, CCK8, Transwell and tube formation assay were performed with HLECs containing uc.189 exosomes. The results showed that the overexpression of uc.189 significantly promoted the proliferation, migration and tube formation of HLECs, but the silencing of uc.189 suppressed the proliferation, migration and tube formation of HLECs. Compared with



**Figure 2. Exosomes of uc.189 can be secreted from ESCC cells and transferred to HLECs.** (A) Photo of exosomes secreted from KYSE-150 and EC9706 was confirmed by transmission electron microscopy (Scale bar, 50nm). (B) Positive markers (CD9 and CD81) of KYSE-150 and EC9706-secreted exosomes were detected by western blot. (C) Uc.189 levels in ESCC cells and paired exosomes were detected by qRT-PCR. (D) HLECs pre-treated with PKH67-labeled exosomes for 48 hours were stained with DAPI (blue) for confocal microscopy analysis. Scale bar, 20  $\mu$ m. (E) Uc.189 relative levels in HLECs pre-treated exosomes for 24 hours were detected by qRT-PCR. Error bars represent the mean  $\pm$  SD of three independent experiments. \* $P$  < 0.05, \*\* $P$  < 0.01, \*\*\* $P$  < 0.001.

the control group, there were significant differences between the two groups (Figure 3C–E). These results indicated that exosome of uc.189 is transmitted to HLECs and then promotes formation of lymphatic vessels, so that ESCC cells to pass through the lymphatic vessels to the adjacent lymph nodes and even to distant metastases.

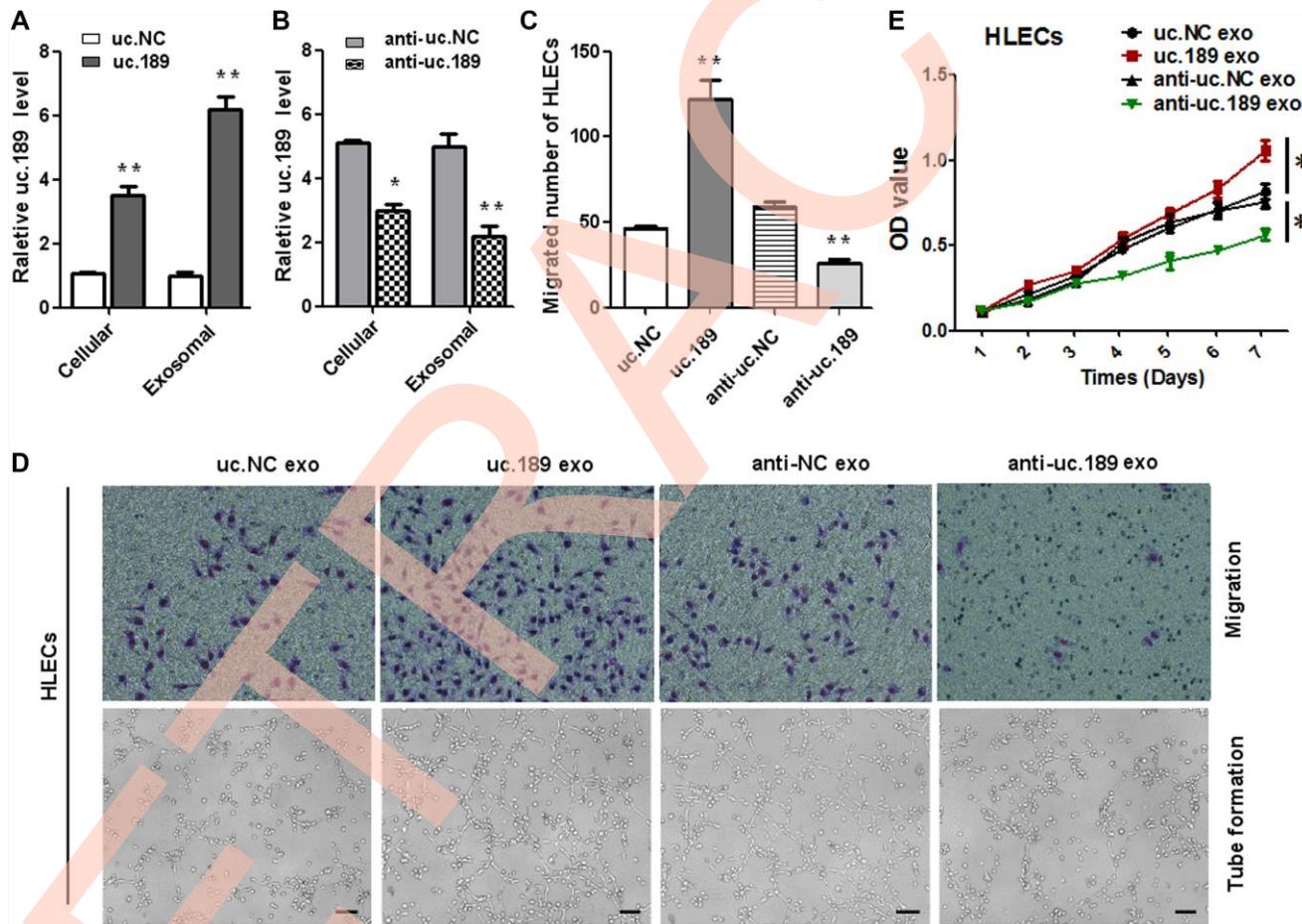
### EPHA2 is a direct target of exosomal uc.189

EPHA2, FOXC1 and Vasohibin-1 were confirmed as a negative regulator of lymph tube formation by GOC. By bioinformatics comparison, uc.189 only had two complementary binding sites with EPHA2 3' untranslated region (Figure 4A), but no binding sites with FOXC1 and Vasohibin-1. To confirm whether uc.189 directly targets EPHA2, dual luciferase reporter analysis was carried out. Figure 4A shows the

sequences of uc.189, EphA2 and mutated EPHA2 in the binding region. Compared with the control group, co-expression with EPHA2 3' UTR vector and uc.189 in HLEC resulted in a significant decrease in luciferase activity (Figure 4B). However, the luciferase activity did not change after co-expression with EPHA2 mutant vector (Figure 4B). Overexpression of uc.189 or exosomal uc.189 in HLECs inhibited mRNA and protein expression of EphA2, and vice versa (Figure 4C, 4D). These results indicated that uc.189 inhibited the protein translation of EPHA2 by binding to the 3'UTR of EPHA2.

### Uc.189 exerted its suppression on EPHA2

To determine whether EPHA2 can regulate lymphangiogenesis induced by uc.189, rescue assays were used. The result showed that overexpression of



**Figure 3. ESCC-secreted exosomal uc.189 promotes lymphangiogenesis.** (A) Relative uc.189 levels in EC9706 stably transfected with overexpression and negative control were detected verifiably by qRT-PCR in cells and exosomes. (B) Cellular and exosomal uc.189 levels after transfected with silencing of uc.189 and negative control lentivectors in EC9706 were detected by qRT-PCR. (C–D, upper panel) Migration assay of HLECs was treated previously with indicating exosomes. The average number of migrated cells was calculated under a light microscope. (D, lower panel) Tube formation assay in HLECs pretreated with indicated exosomes are shown. The average length of tubes per field was calculated. (E) CCK-8 proliferation assay in HLECs pre-treated with the indicated exosomes. Error bars represent the mean  $\pm$  SD of three independent experiments. \* $P$  < 0.05, \*\* $P$  < 0.01.

EPHA2 inhibited the up-regulation of EPHA2 by overexpression of exosomal uc.189, Knockdown of EPHA2 inhibited the down-regulation of EPHA2 by knockdown of uc.189 expression (Figure 5A, 5B). *In vitro* studies confirmed that up-regulation of EPHA2 can abrogate uc.189-mediated promotion of HLECs migration and tube formation, while down-regulation of EPHA2 can stimulate the ability of anti-uc.189 exosomes to induce HLECs migration and lymphangiogenesis (Figure 5C–5E). Collectively, these experiments showed that the exosomal uc.189 specifically inhibited the expression of EPHA2, and then promoted HLECs migration and lymphangiogenesis.

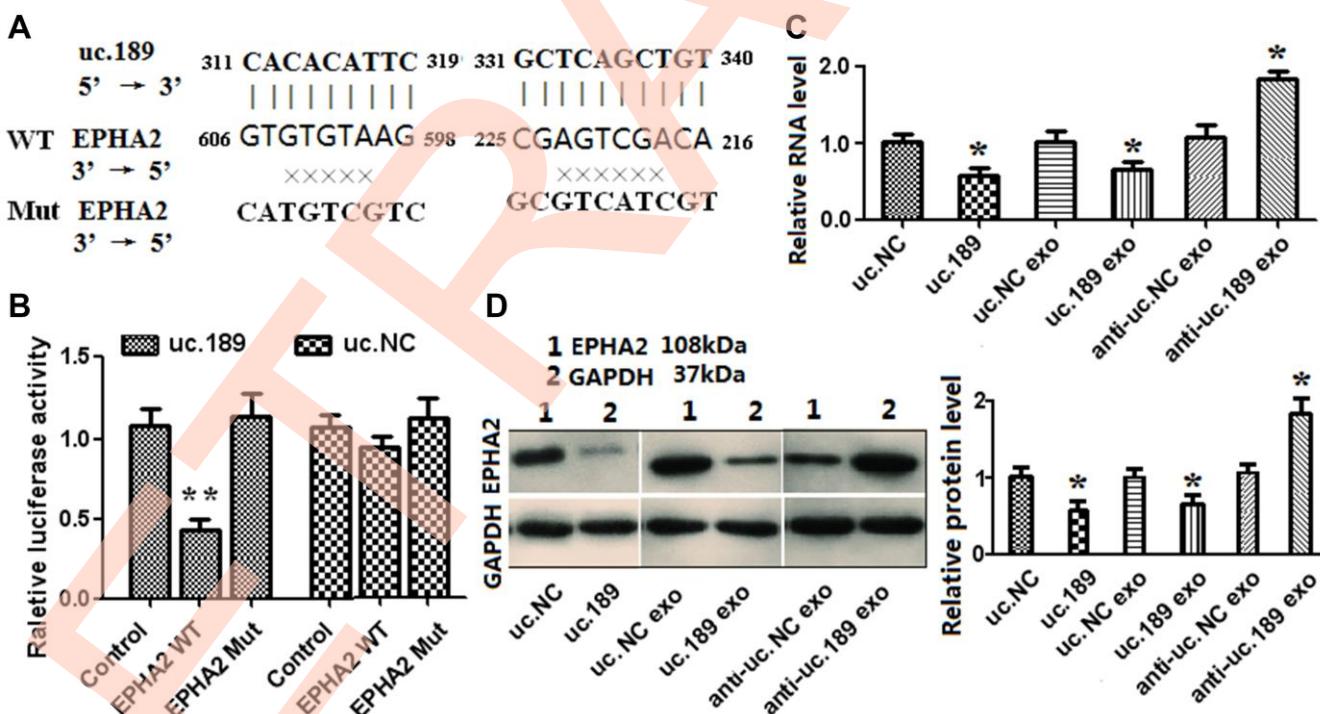
#### Exosomal uc.189 regulates lymphangiogenesis and metastasis through EPHA2/P38MAPK/VEGF-C pathway

Previous evidence has suggested that P38MAPK is a direct target of EPHA2 [25], the P38MAPK/VEGF-C pathways are involved in lymphangiogenesis [26]. So whether the P38MAPK and VEGF-C pathways could be activated by exosomal uc.189, qRT-PCR and western blotting were used to test this effect. qRT-PCR (Figure 6A–6C) and Western blotting (Figure 6D–6G) results showed that the phosphorylation of EphA2 was significantly decreased and the phosphorylation of

p38MAPK and VEGF-C was significantly increased after overexpression of uc.189 (Figure 6). When the expression of uc.189 was knocked down, the expression level of EphA2 increased significantly, and the phosphorylation of p38MAPK and VEGF-C decreased significantly (Figure 6). Previous studies have shown that tumor cells produce VEGF-C and activate p38MAPK signaling pathway in HLECs to induce lymphangiogenesis, and then promote tumor cell metastasis [26]. Therefore, this study concluded that exosomal uc.189 secreted by ESCC promoted lymphangiogenesis by down regulating EphA2 expression, and activated p38MAPK in HLEC plays a role in a VEGF-C-dependent manner, and then facilitated tumor cell migration to lymph tube (Figure 7).

## DISCUSSION

Growing evidences have suggested that tumor cell-induced proliferation and sprout of lymphatic endothelial cell and lymphangiogenesis promoted cancer cells spread to adjacent lymph nodes [27–28], which is one lethal cause of ESCC patient. So, we need to find new and effective molecular markers of ESCC to develop personalized diagnosis and treatment strategies for patients with different risk of progression.



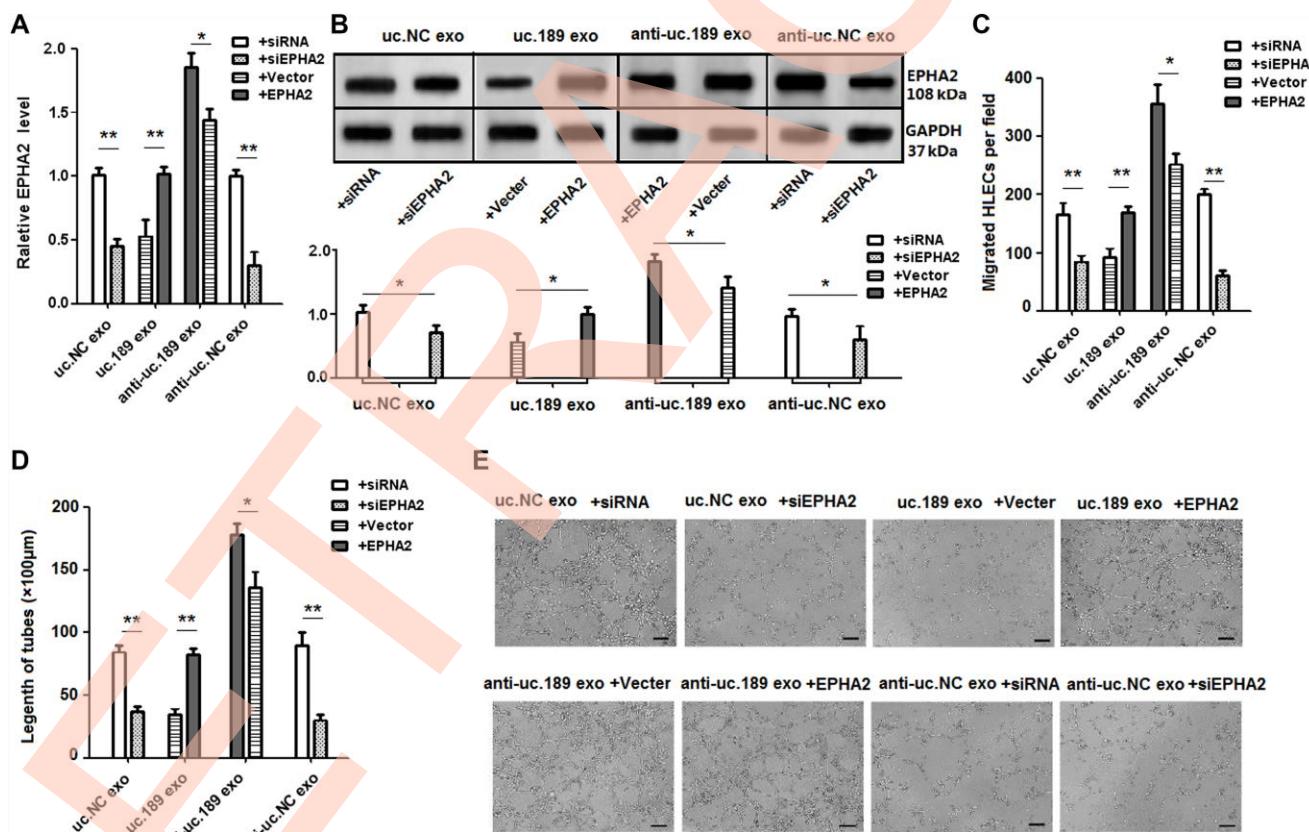
**Figure 4. Exosomal uc.189 targets EPHA2 inducing lymphangiogenesis in HLECs.** (A) DNA binding site sequence between uc.189 and the 3'-UTR of EPHA2 and the sequence of wild type (WT) or mutant type (MT) were shown. (B) The effect of uc.NC and uc.189 on the activity of the luciferase reporter containing either WT or MT were detected by dual-luciferase reporter assay. (C–D) RNA and protein levels of EPHA2 were, respectively, tested by qRT-PCR and western blot in HLECs transfected with uc.189 or negative control (NC) compared with those treated with the indicated exosomes. \*P < 0.05.

Lymphatic metastasis is one of the spreading pathways for ESCC. The metastasis cascade not only needed ncRNAs alternations in tumor cells but also depended on interactions with peripheral cells to contribute to cancer development. The overwhelming mass of research supported ncRNAs had participated in cancer metastatic progress in various types of carcinoma [29–31]. Recently, tumor-secreted exosomes of ncRNAs have been confirmed as effective modulators in signal transmission of metastasis. For example, Yang et al. [32] showed that exosomal miR-130a from gastric cancer cells could deliver to vascular endothelial cells to promote angiogenesis acts as a monitor of gastric cancer development. LncRNA HOTAIR promoted exosome secretion from hepatocellular carcinoma cells by inducing MVB transport to the plasma membrane and induced the phosphorylation of SNAP23 through the mTOR signaling pathways [33]. Kang et al. [34] reported that up-regulated exosome lncRNA PART1 promoted gefitinib resistance as a competing endogenous RNA to bind competitively miRNA-129 to suppress the expression of Bcl-2 in ESCC cells, while knockdown of PART1 potently helped the gefitinib-

induced cell apoptosis. Chen et al. [12] demonstrated that exosomal LNMAT2 derived from BCa cell was directly interacting with hnRNPA2B1 and then was internalized by HLECs to promote lymphatic tube formation, ultimately resulting in lymphangiogenesis and lymphatic metastasis.

Ultraconserved RNAs (UCRs) is a class of ncRNAs. The existing data show that UCRs can not only be used as tumor biomarkers for diagnosis and prognosis [35–37], but also as regulators of other genes, participating in tumor biology and tumorigenesis [38–40]. However, UCRs might regulate tumor development in the form of an exosome, which has not been previously reported.

In this study, uc.189 was strongly up-regulated in ESCC tissues compared with matched normal oesophageal tissues, and the expression level of uc.189 in LN metastasis group was significantly higher than that in LN negative group. This conclusion is consistent with the results reported in the literature [7], indicating that uc.189 is an oncogene in ESCC. Up-regulated uc.189 could produce exosomal uc.189 in esophageal cancer

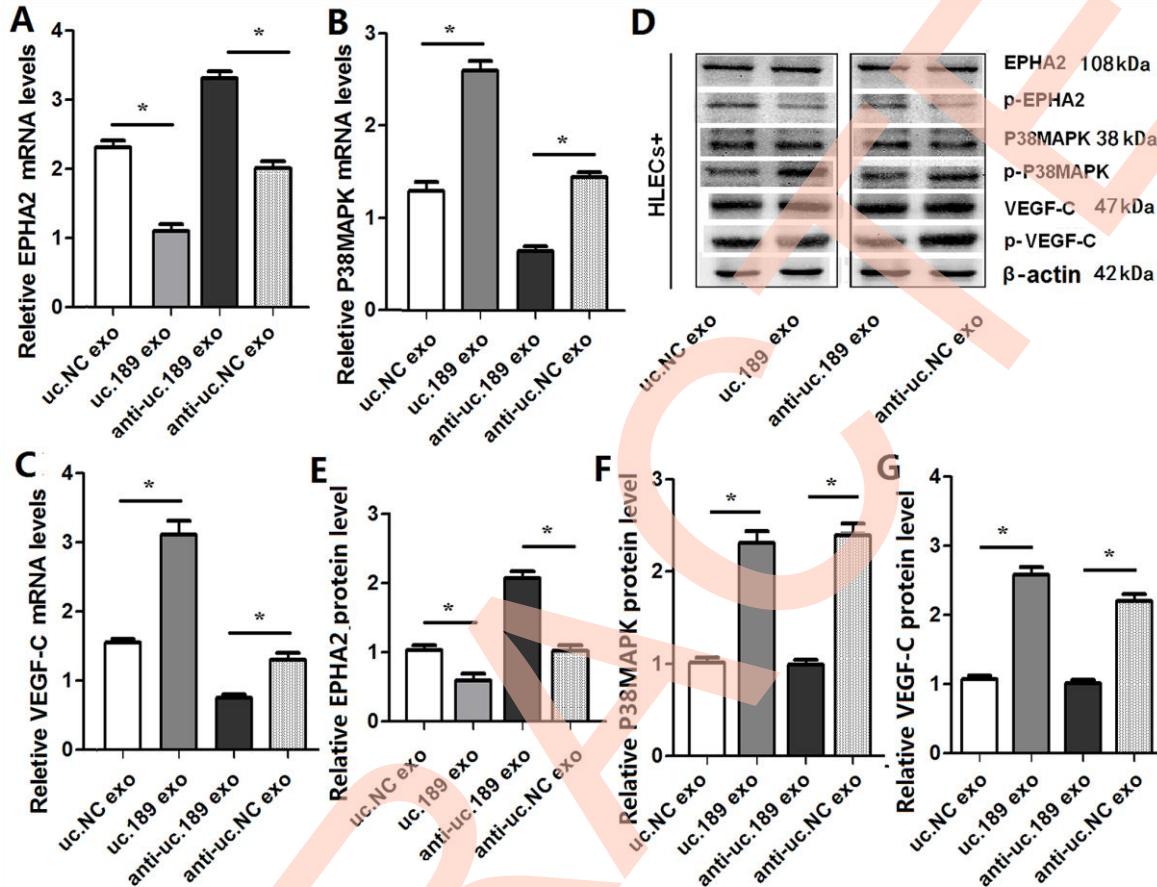


**Figure 5. Rescue assays detected the effects of EPHA2 regulated by uc.189 in lymphangiogenesis.** (A–B) RNA and protein levels of EPHA2 were detected respectively by qRT-PCR and western blot in HLECs with relative exosomes in the presence of EPHA2 overexpression or vector control and si-EPHA2 or siRNA control. (C–E) Overexpression of EPHA2 rescued the biologic effects via exosomal uc.189-induced, whereas knockdown of EPHA2 simulated the effects associated with exosomal uc.189 through cell migration and tube formation assays in HLECs. Error bars represent the mean  $\pm$  SD of three independent experiments. \* $P$  < 0.05, \*\* $P$  < 0.01, \*\*\* $P$  < 0.001.

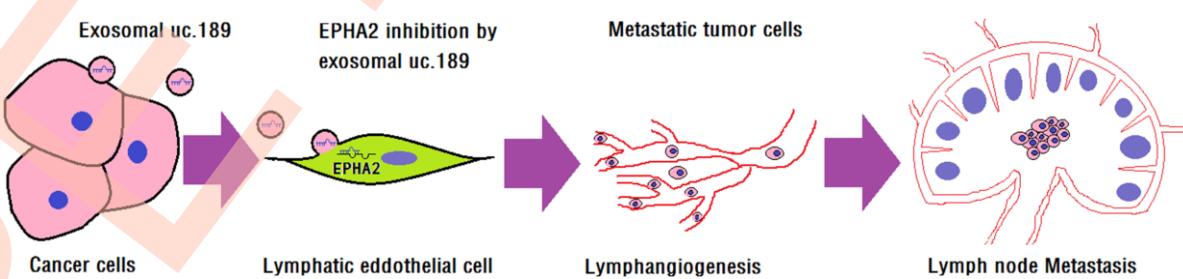
cells, which had not been shown before. The exosomes transferred to HLECs to help tumor proliferation, tumor migration, and lymphangiogenesis in cell level, suggesting that exosomal uc.189 could facilitate the lymphatic tube formation, so that ESCC cells migrate to adjacent lymph nodes. Therefore, this study suggested

that exosomal uc.189 can be used as an early serum diagnostic marker and therapeutic molecule for patients of ESCC metastasis.

In GOC group, EPH2 was confirmed to be the reverse regulator of lymphangiogenesis. There are two



**Figure 6. Exosomal uc.189 activated EPHA2/P38MAPK/VEGF-C pathways in HLECs.** (A) mRNA levels of EPHA2 were detected in HLECs of exosomal uc.189-overexpressing or exosomal uc.189-knockdown compared with the negative control (NC) by qRT-PCR. (B) mRNA levels of P38MAPK were detected in HLECs of exosomal uc.189-overexpressing or exosomal uc.189-knockdown compared with NC by qRT-PCR. (C) mRNA levels of VEGF-C were detected in HLECs of exosomal uc.189-overexpressing or exosomal uc.189-knockdown compared with NC by qRT-PCR. (D-F) Protein levels of EPHA2, P38MAPK, and VEGF-C were detected in HLECs of exosomal uc.189-overexpressing or exosomal uc.189-knockdown compared with NC by western blot. Error bars represent the mean  $\pm$  SD of three independent experiments. \* $P < 0.05$ .



**Figure 7. Exosomal uc.189 promotes lymphangiogenesis.** Illustrative model showing the mechanism whereby ESCC-secreted exosomal uc.189 promotes lymphangiogenesis by downregulating lymphatic EPHA2 expression that then facilitates lymphatic metastasis.

complementary binding sites between uc.189 and EPHA2 3'UTR region. By bioinformatics, so could uc.189 regulate EPHA2 via protein translation? Dual-luciferase reporter array showed that uc.189 inhibited the protein translation of EPHA2 by binding to the 3'UTR of EPHA2, so EPHA2 was regulated directly by uc.189. Previous researches suggest P38MAPK as a direct target of EPHA2 [25]. The P38MAPK/VEGF-C pathways are involved in lymphangiogenesis in a VEGF-C-independent manner [26]. Our results showed overexpression or inhibition of EPHA2 induced by exosomal uc.189 can inhibit or promote the expression of p38MAPK and VEGF-C in HLECs, respectively, so as to regulate lymphangiogenesis; uc.189-EPHA2 axis activated p38MAPK in a VEGF-C-dependent manner in HLECs. This result is different from that previous report [26]. It is of great significance to target the expression of VEGF-C in the treatment of metastatic esophageal squamous cell carcinoma.

In conclusion, uc.189 was highly expressed in esophageal squamous cell carcinoma and is transmitted to HLECs via the form of exosome. Exosomal uc.189 promoted the proliferation and lymphangiogenesis of HLECs by activating EPHA2/p38MAPK/VEGF-C signaling pathways, so as to facilitate the ESCC cells to metastasize to regional lymph nodes. The newly discovered results indicated that uc.189 is an important pro-metastasis oncogene in ESCC. This study provides a new theoretical basis for the diagnosis and treatment of metastatic ESCC.

## AUTHOR CONTRIBUTIONS

Zhiyan Ding and Chenghai Wang conceived and designed the whole experiments. Zhiyan Ding collected clinical data. Zhiyan Ding, Yun Yan, Yu Lian Guo performed the major work of the assays. Yun Yan and Cheng Hai Wang analyzed and did data statistics. Zhiyan Ding, Yun Yan, Yu Lian Guo And Cheng Hai Wang wrote this manuscript.

## CONFLICTS OF INTEREST

The authors declared no potential conflicts of interests with respect to the authorship and/or publication of this article.

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## SUPPLEMENTARY MATERIALS

### Supplementary Table

Supplementary Table 1. Sequences of the primers.

Primer name	Sequence (5'-3')
uc.189-f	Gatggtgtactgtggc
uc.189-r	Tggtcacatgacgctgaa
EPHA2-f	Gcctgttaccaaggatggacacca
EPHA2-r	Cgcagggtgacgcgttagacaatgt
P38MAPK-f	Tacaccaacctctcgatcatcgcc
P38MAPK-r	Gccagaggctgtctacttcaatc
VEGF-C-f	Atgcacttgctgggcttctct
VEGF-C-r	Catgtaattttggggcaggcttt
GAPDH-f	Caccacactccaccccttgc
GAPDH-r	Ccaccaccctgttgctgttag
U6-f	Cgttccggcagcacatatac
U6-r	Ttcacgaatttgcgtgtcat
EPHA2 3'-UTR-f	5'-tcggccaagaataactt-3'
EPHA2 3'-UTR-r	5'-tcgggttgaatcatct-3'