

Appendix: Supplementary methods

Small RNA sequencing

A total of 2 ml of pooled plasma derived from five or six patients per sample was used to perform exosome isolation using ultracentrifugation. miRNeasy Mini Kit (QIAGEN) was used to isolate total RNA from plasma exosomes following the manufacturer's instruction. Isolated RNA was loaded on 1.5% agarose gels to evaluate its degradation and contamination followed by quantitative determination in the NanoDrop 2000 Spectrophotometer (Thermo Fisher Scientific). A total of 2.5 ng RNA per sample was used to construct small RNA library. RNA libraries were sequenced on the platform of Illumina HiSeq2500. Clean reads filtered for ribosomal RNA (rRNA), transfer RNA (tRNA), small nuclear RNA (snRNA), small nucleolar RNA (snoRNA), other noncoding RNA (ncRNA) and repeats were compared with the miRBase database to assess miRNA expression.

Exosome isolation and identification

Exosomes were isolated from pooled plasma by ultracentrifugation for small RNA sequencing. Briefly, 2 ml of pooled plasma per sample was first centrifuged at 3,000 \times g and 4 °C for 15 min to obtain supernatant followed by dilution with PBS. The diluted supernatant was then centrifuged at 13,000 \times g and 4 °C for 30 min followed by filtration using a 0.22- μ m filter. The filtered sample was loaded into the ultracentrifuge and ultracentrifuged at 100,000 \times g and 4 °C for 2 hours to collect exosomes. Exosome pellet was washed by resuspending it in PBS and was then ultracentrifuged at 100,000 g and 4 °C for 2 hours. Next, the obtained exosome pellet was dissolved in 100 μ L PBS for RNA extraction.

For exosomes isolation from plasma in cohort 2, the Total Exosome Isolation (from plasma) Kit (Invitrogen) was applied according to the instructions, and the expression of plasma exosomal miRNA was validated.

To isolate exosomes from the cell culture supernatant, fresh culture medium (CM) supplying with 10% exosome-depleted fetal bovine serum (FBS) was added to cells and collected 48 hours later. The CM was processed for centrifugation at 500 \times g, 4 °C for 10 min, 2,000 \times g, 4 °C for 10 min successively to remove cells and dead cells, subsequently passed through a 0.22- μ m Vacuum Filter System (Corning, cat. No. 431097) to remove large particles. The filtered supernatant was further concentrated by the Vivaflow 200 filtration system (Sartorius, cat. No.

VF20P4) and then ultracentrifuged at 110,000 \times g and 4 °C for 70 min to precipitate exosomes. The exosome pellet was washed by dissolving it in PBS and ultracentrifuged once again, the final exosome sample was obtained by resuspending the second exosome precipitate in PBS and was stored at -80 °C for future use.

To characterize the isolated exosomes, transmission electron microscopy (JEOL-JEM1400, Tokyo, Japan) and ZetaView PMX 110 (Particle Metrix, Meerbusch, Germany) were used to capture the appearance and assess the diameter and number of exosomes, respectively. Western blotting was applied to identify exosome-related proteins, including CD9 and TSG101.

RNA isolation and qRT-PCR

TRIzol-based (Invitrogen, USA) traditional method was performed to isolate total RNA from cells, exosomes or serum. Specifically, for the isolation of RNA from exosomes or serum, cel-miR-39 was spiked in before adding chloroform to serve as the external reference gene, 0.1 mg/mL glycogen (Invitrogen) was added in the process of isopropanol precipitation to make the RNA pellet visible.

For miRNA, TransScript Green miRNA Two-Step qRT-PCR SuperMix (TransGen Biotech, Beijing, China) was used for the qRT-PCR of miRNA with a universal primer and a specific forward primer. RNU6 served as the internal reference gene in cell-miRNA PCR, while cel-miR-39 served as the external reference gene in exosome- or serum-miRNA PCR. For mRNA, TransScript II All-in-One First-Strand cDNA Synthesis SuperMix for qPCR and TransStart Top Green qPCR SuperMix (TransGen Biotech, Beijing, China) were used for mRNA RT-PCR and qRT-PCR, respectively. GAPDH served as the internal reference gene in mRNA PCR. All qRT-PCRs were conducted on an ABI 7900HT RT-PCR thermocycler (Life Technologies).

Western blotting

Proteins of exosomes or cells were harvested utilizing RIPA lysate buffer and protein concentrations were detected by the Bradford Protein Assay. Equivalent proteins from different samples were loaded for sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE). Separated proteins were then transferred to a polyvinylidene fluoride (PVDF) membrane followed by blocking with 5% milk for 1 hour at room temperature. After that, the diluted primary antibodies were added to incubate with the membranes

overnight at 4 °C. The next day, after incubation with HRP-conjugated secondary antibody for 1 hour at room temperature, the membranes were exposed and detected in an Amersham Imager 600. Antibodies used in this study were as follows: GAPDH (CST, #5174), claudin-11 (Abcam, ab175236), claudin-1 (CST, #13255), CD9 (Abcam, ab92726) and TSG101 (Abcam, ab83).

Cell Immunofluorescence

miR-375-3p mimic-transfected or exosome-treated HUVECs were plated on chamber slides (Biologix, Shandong, China) and cultured for 24–48 hours. Then, HUVECs were washed in PBS twice to remove dead cells and fixed in 4% paraformaldehyde solution for 10 min. After that, 0.2% Triton X-100/PBS was added to the chamber slides for 5 min to permeabilize the cell membranes. 5% BSA/PBS was used to block the non-specific binding sites of HUVECs and the primary antibodies (claudin-1, CST, #13995) were added to incubate overnight at 4 °C. The next day, after incubation with secondary antibody (CST, #4412) in the dark, the slides were covered by ProLong™ Gold Antifade Mountant with DAPI (Invitrogen) and then photographed under a confocal microscope.

Liquid chromatography-mass spectrometry/mass spectrometry analysis (LC-MS/MS)

Proteins extracted from miR-375- or NC-transfected HUVECs (each group had three replicates) were processed for LC-MS/MS in Applied Protein Technology (Shanghai, China). Protein samples were digested to collect peptides by the filter-aided proteome preparation (FASP) method. A total of 100 µg peptides of each sample was used for tandem mass tag (TMT, Thermo Fisher Scientific) labeling following the instruction. TMT-labeled peptides of each sample were mixed in equal amounts followed by fractionation into 10 fractions by the High pH Reversed-Phase Peptide Fractionation Kit (Thermo Fisher Scientific). Each fraction was loaded onto a reversed-phase trap column (Thermo Scientific Acclaim PepMap100, 100 µm × 2 cm, nanoViper C18) and separated by a C18-reversed-phase analytical column (Thermo Scientific Easy Column, 10 cm long, 75 µm inner diameter, 3 µm resin) at a flow rate of 300 nL/min. A Q Exactive mass spectrometer (Thermo Scientific) was used to conduct LC-MS/MS in a data-dependent top10 manner with a survey scan of 300–1,800 m/z. MS/MS spectra data were searched in Proteome Discoverer 1.4 software for protein identification and quantitative analysis.

Table S1 The clinical and pathological characteristics of the pooled samples in cohort 1

		SCLC patients		Healthy volunteers	
		Sample 1	Sample 2	Sample 3	Sample 4
Sex	Female	4	2	4	2
	Male	1	4	1	4
Age	<60	2	6	3	6
	≥60	3	0	2	0
T	T1-T2	2	3	-	-
	T3-T4	3	3	-	-
N	N0-N1	0	0	-	-
	N2-N3	5	6	-	-
M	M0	0	6	-	-
	M1	5	0	-	-
Stage	III	0	6	-	-
	IV	5	0	-	-

SCLC, small-cell lung cancer.

Table S2 The clinical and pathological characteristics of samples in cohort 2 and cohort 3

		Cohort 2 (82)		Cohort 3 (147)		
		SCLC (57)	Normal (25)	SCLC (69)	NSCLC (LUAD 20, LUSC 26)	Normal (32)
Sex	Female	22	13	14	18	10
	Male	35	12	55	28	22
Age	<60	29	22	28	25	14
	≥60	28	3	41	21	18
T	T1-T2	26	-	28	26	-
	T3-T4	31	-	41	20	-
N	N0-N1	19	-	10	12	-
	N2-N3	38	-	59	34	-
M	M0	45	-	40	29	-
	M1	12	-	29	17	-
Stage	I	9	-	4	1	-
	II	8	-	1	5	-
	III	28	-	35	23	-
	IV	12	-	29	17	-

SCLC, small-cell lung cancer; NSCLC, non-small-cell lung cancer; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma.

Table S3 Sequences of primers used for PCR

Gene	Forward primer	Reverse primer
miR-375	CTTTGTTTCGTTCCGGCTCGC	-
Cel-miR-39	TCACCGGGTGTAATCAGCTTG	-
RNU6	CTCGCTTCGGCAGCACA	-
Pri-miR-375	CGACGTGTCAGCCGCAGATG	CCTCGGTGATCTCCTGGTCCTG
Claudin-11	GGCTGGTGTTTTGCTCATTCTGC	AGCACCAATCCAGCCTGCATAC
Claudin-1	GTCTTTGACTCCTTGCTGAATCTG	CACCTCATCGTCTTCCAAGCAC
GAPDH	GTCTCCTCTGACTTCAACAGCG	ACCACCCTGTTGCTGTAGCCAA

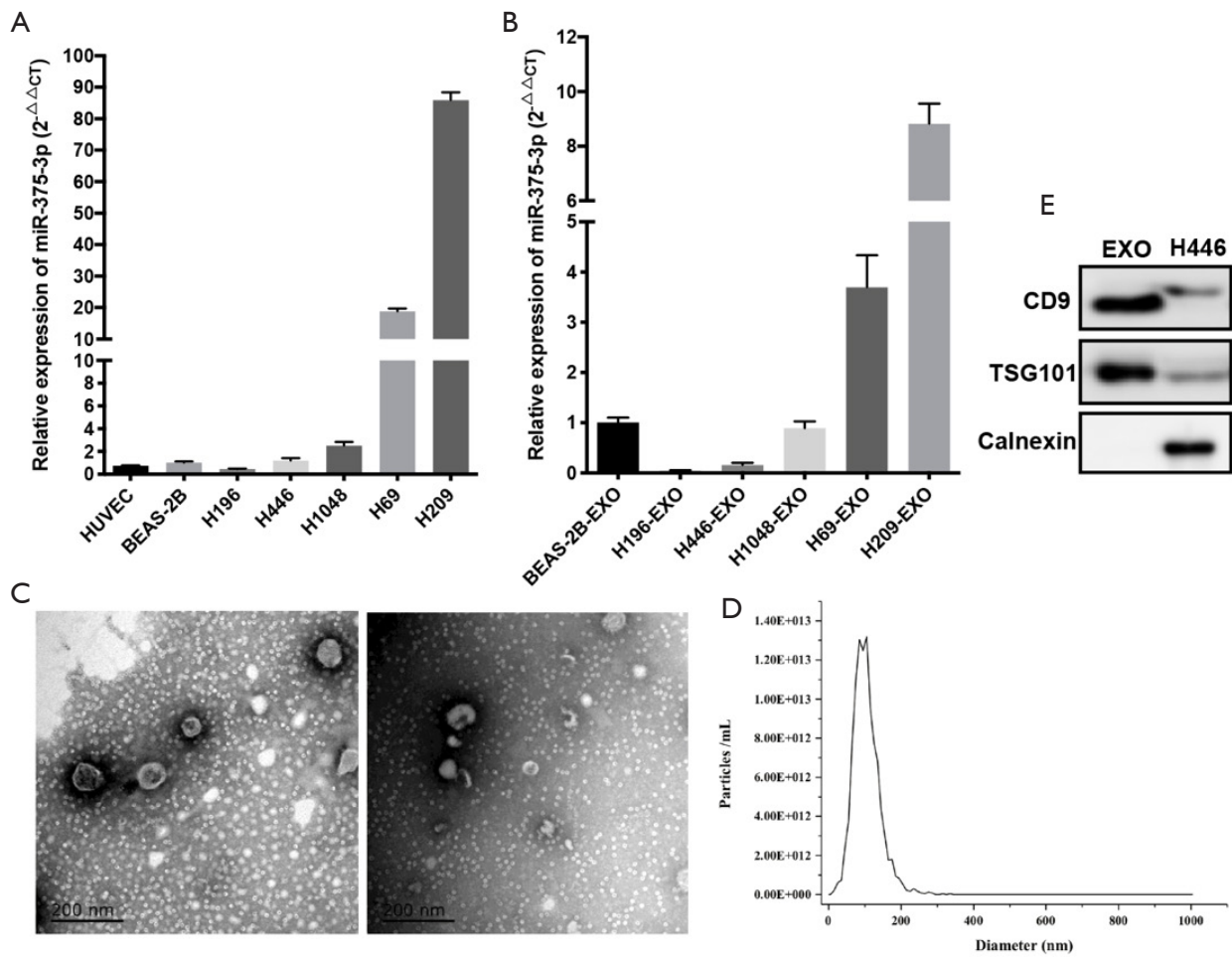


Figure S1 H446 and H1048 cells and their exosomes had low endogenous levels of miR-375-3p. (A,B) The level of miR-375-3p in HUVECs, BEAS-2B cells and SCLC cells (A) and SCLC-cell-secreted exosomes (B). (C) Representative images of H446-cell-secreted exosomes under TEM. (D) Distribution of the particle size of H446-cell-secreted exosomes. (E) Western blot analysis of TSG101, CD9 and Calnexin in H446 cell-secreted exosomes and H446 cells. TEM, transmission electron microscopy.

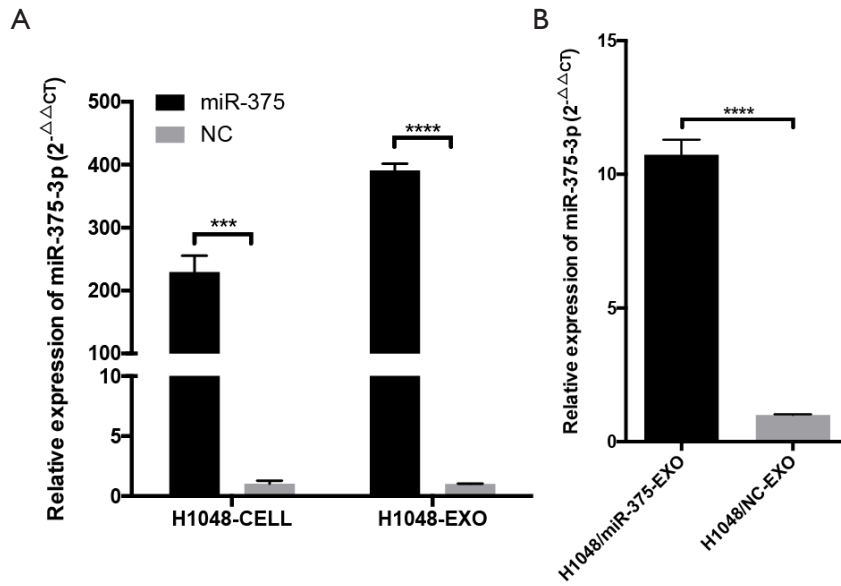


Figure S2 H1048-cell-secreted exosomal miR-375-3p was absorbed by HUVECs. (A) The level of miR-375-3p in H1048 cells or H1048-cell-secreted exosomes after transfection with miR-375-3p mimics (miR-375) or negative control mimics (NC). (B) The level of miR-375-3p in HUVECs after incubation with H1048/miR-375-EXO or H1048/NC-EXO for 12 hours. H1048/miR-375-EXO, exosomes derived from miR-375-transfected H1048 cells; H1048/NC-EXO, exosomes derived from NC-transfected H1048 cells. *** $P < 0.001$; **** $P < 0.0001$.

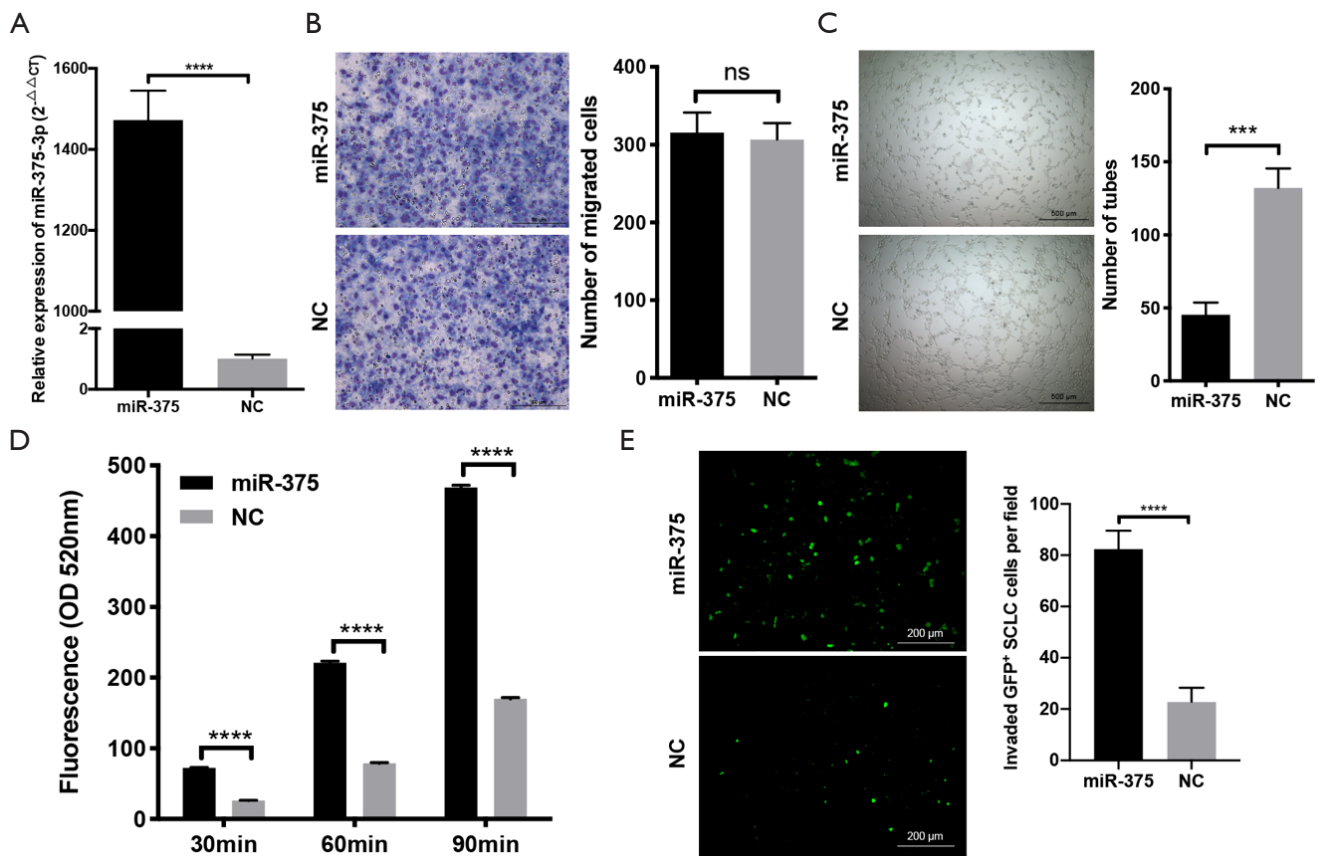


Figure S3 Mimics of miR-375-3p induced the permeability of HUVEC monolayers. (A) The level of miR-375-3p in miR-375-3p mimics (miR-375) or negative control mimics (NC) transfected HUVECs. (B) Representative images of migrated HUVECs after transfection with miR-375 or NC, with the right bar chart indicating the number of migrated cells. (C) Representative images of tubes formed by HUVECs after transfection with miR-375 or NC, with the right bar chart indicating the number of formed tubes. (D) Fluorescence intensity of FITC-dextran passing through HUVEC monolayers after transfection with miR-375 or NC. (E) Representative images of GFP+ SCLC cells migrated through miR-375- or NC-transfected HUVECs, with the right bar chart indicating the number of migrated cells. *, $P < 0.001$; **, $P < 0.0001$.

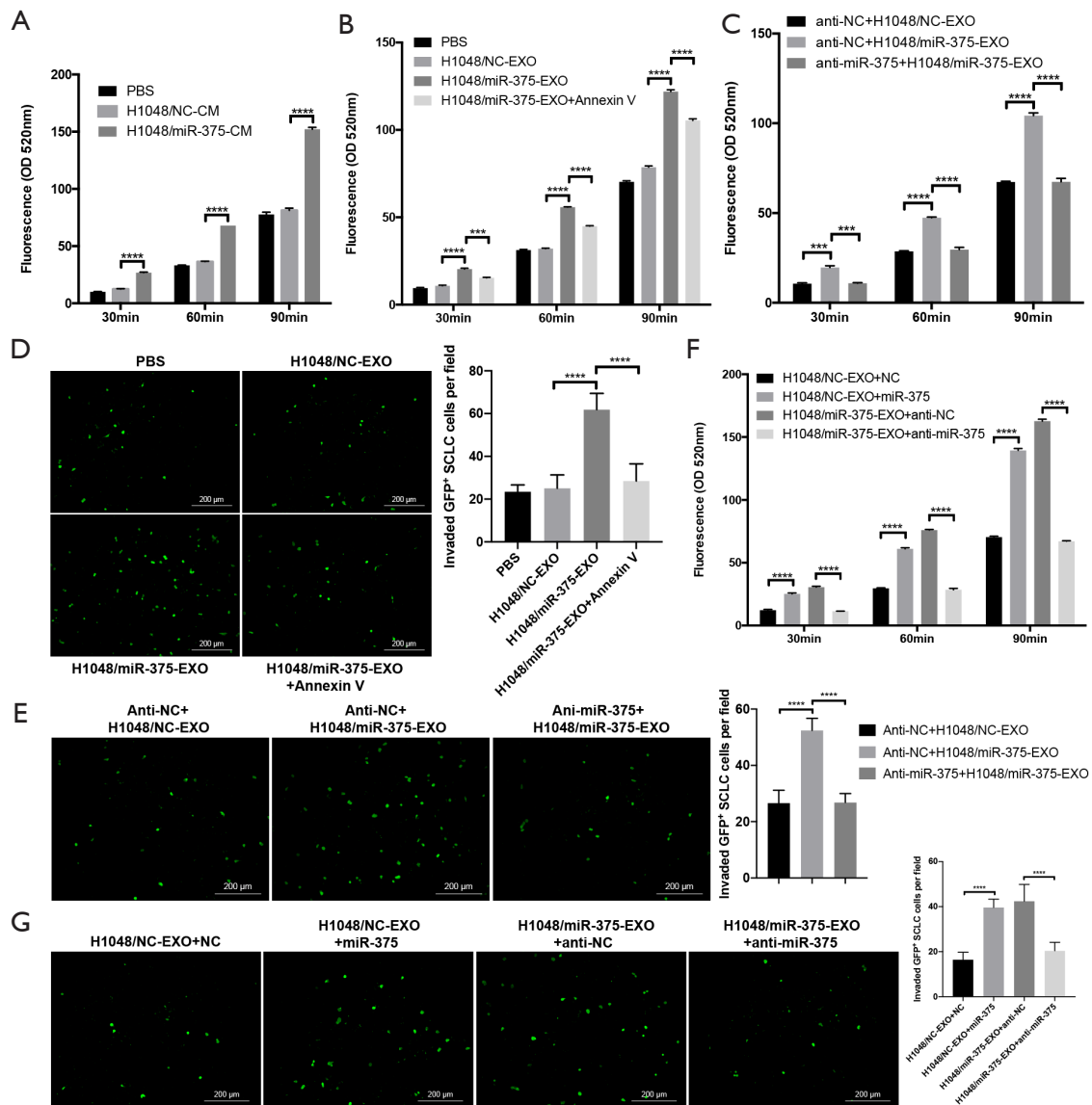


Figure S4 Exosomal miR-375-3p secreted by H1048 cells induced the permeability of HUVECs and promoted SCLC cell transendothelial migration in vitro. (A) Fluorescence intensity of FITC-dextran passing through HUVEC monolayers treated with H1048/miR-375-CM or H1048/NC-CM. (B) Fluorescence intensity of FITC-dextran passing through HUVEC monolayers treated with H1048/miR-375-EXO, H1048/NC-EXO or Annexin V-blocked H1048/miR-375-EXO. (C) Fluorescence intensity of FITC-dextran passing through H1048/miR-375-EXO- or H1048/NC-EXO-treated HUVEC monolayers pre-transfected with anti-miR-375 or anti-NC. (D) Representative images of GFP+ SCLC cells migrated through H1048/miR-375-EXO- or H1048/NC-EXO-treated HUVEC monolayers, the right bar chart indicated the number of migrated cells. (E) Representative images of GFP+ SCLC cells migrated through H1048/miR-375-EXO- or H1048/NC-EXO-treated HUVEC monolayers pre-transfected with anti-miR-375 or anti-NC; the right bar chart indicated the number of migrated cells. (F) Fluorescence intensity of FITC-dextran passing through HUVEC monolayers treated with miR-375-3p-mimic-loaded H1048/NC-EXO or miR-375-3p-inhibitor-loaded H1048/miR-375-EXO. (G) Representative images of GFP+ SCLC cells that migrated through HUVEC monolayers treated with miR-375-3p-mimic-loaded H1048/NC-EXO or miR-375-3p-inhibitor-loaded H1048/miR-375-EXO, the right bar chart indicated the number of migrated cells. H1048/miR-375-CM, culture medium derived from miR-375-transfected H1048 cells; H1048/NC-CM, culture medium derived from NC-transfected H1048 cells; H1048/miR-375-EXO, exosomes derived from miR-375-transfected H1048 cells; H1048/NC-EXO, exosomes derived from NC-transfected H1048 cells; anti-miR-375, miR-375-3p inhibitors; anti-NC, negative control inhibitors; *** $P < 0.001$; **** $P < 0.0001$.

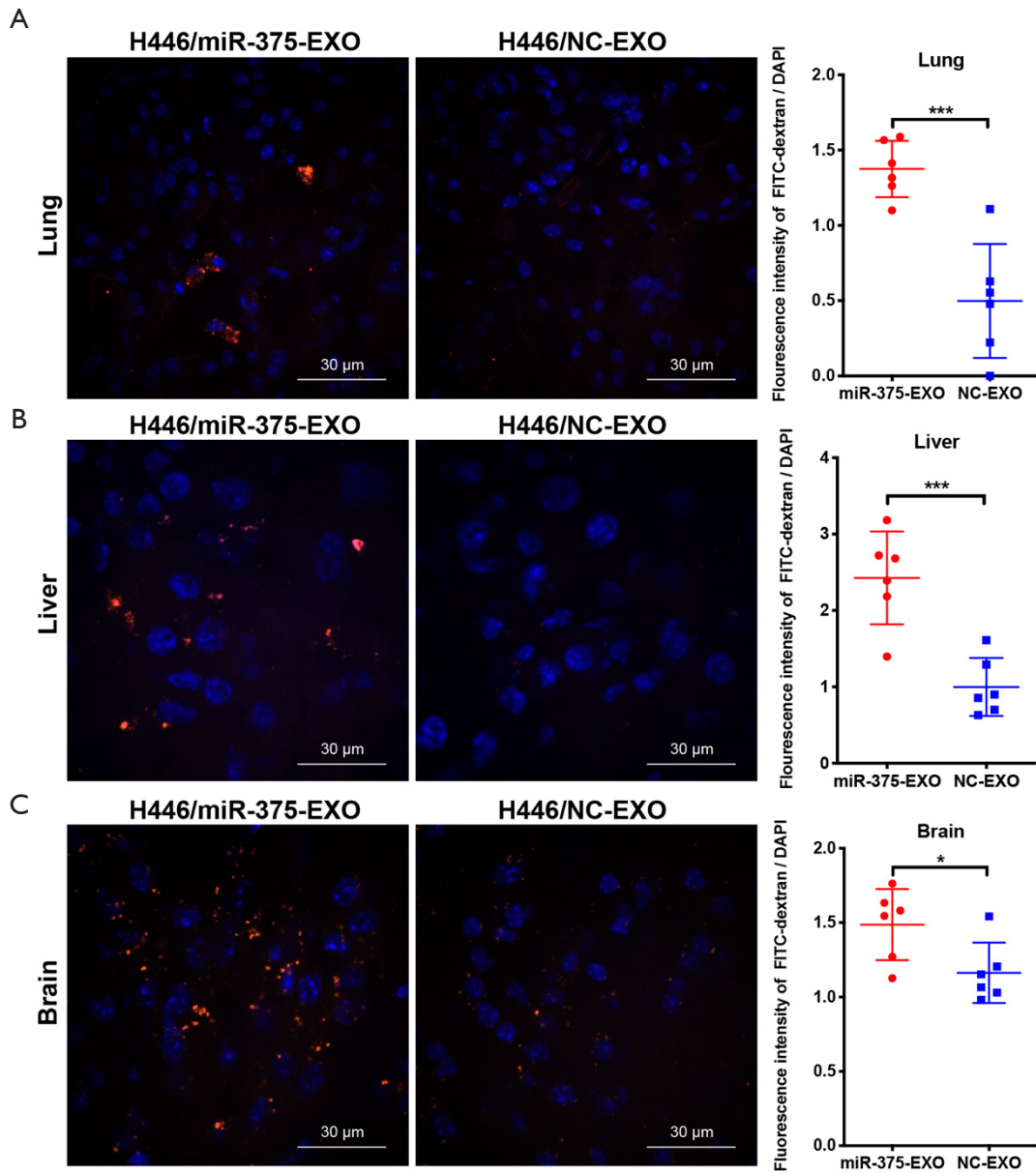


Figure S5 H446-cell-derived exosomal miR-375-3p induced the permeability of blood vessels *in vivo*. (A-C) Representative images of infiltrated FITC-dextran in the lung (A), liver (B) and brain (C) tissues of mice after treatment with H446/miR-375-EXO or H446/NC-EXO, with the red fluorescence indicating the infiltrated FITC-dextran, the blue fluorescence indicating the nucleus of cells and the right bar chart indicating the relative fluorescence intensity. H446/miR-375-EXO, exosomes derived from miR-375-transfected H446 cells; H446/NC-EXO, exosomes derived from NC-transfected H446 cells. * $P < 0.05$; *** $P < 0.001$.

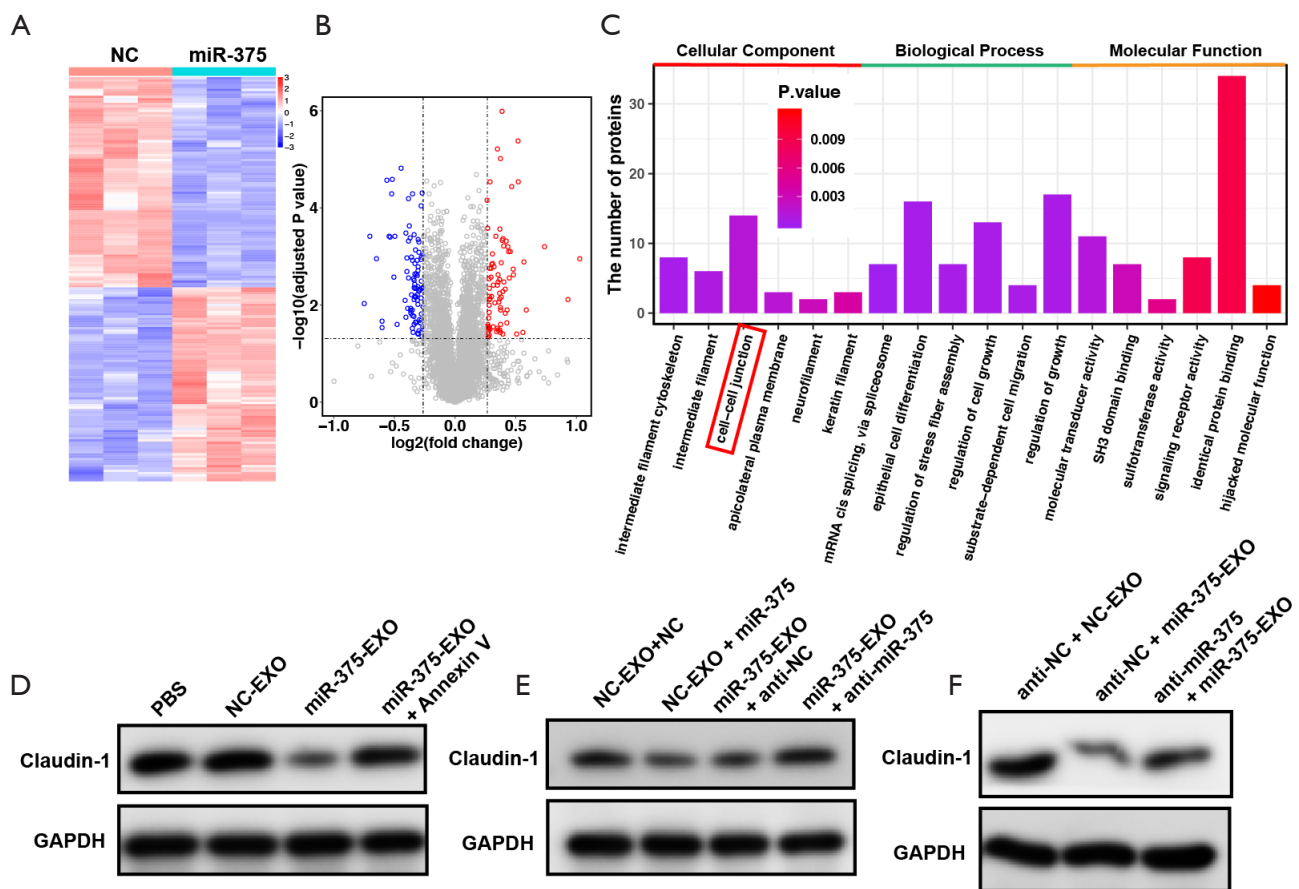


Figure S6 miR-375-3p inhibited the expression of tight junction protein claudin-1. (A,B) Heatmap (A) and volcano plot (B) of dysregulated proteins discovered by protein mass spectrometry analysis in miR-375-3p mimics (miR-375) or negative control mimics (NC) transfected HUVECs. (C) GO enrichment analysis in the dysregulated proteins discovered by protein mass spectrometry analysis. (D) Western blot analysis of claudin-1 in HUVECs that were incubated with PBS, NC-EXO, miR-375-EXO or Annexin V-pretreated miR-375-EXO. (E) Western blot analysis of claudin-1 in HUVECs after incubation with miR-375-3p-mimic-loaded NC-EXO (NC-EXO + miR-375) and its negative control (NC-EXO + NC), miR-375-3p-inhibitor-loaded miR-375-EXO (miR-375-EXO + anti-miR-375) and its negative control (miR-375-EXO + anti-NC). (F) Western blot analysis of claudin-1 in NC-EXO- or miR-375-EXO-treated HUVECs that were pre-transfected with anti-miR-375 or anti-NC.

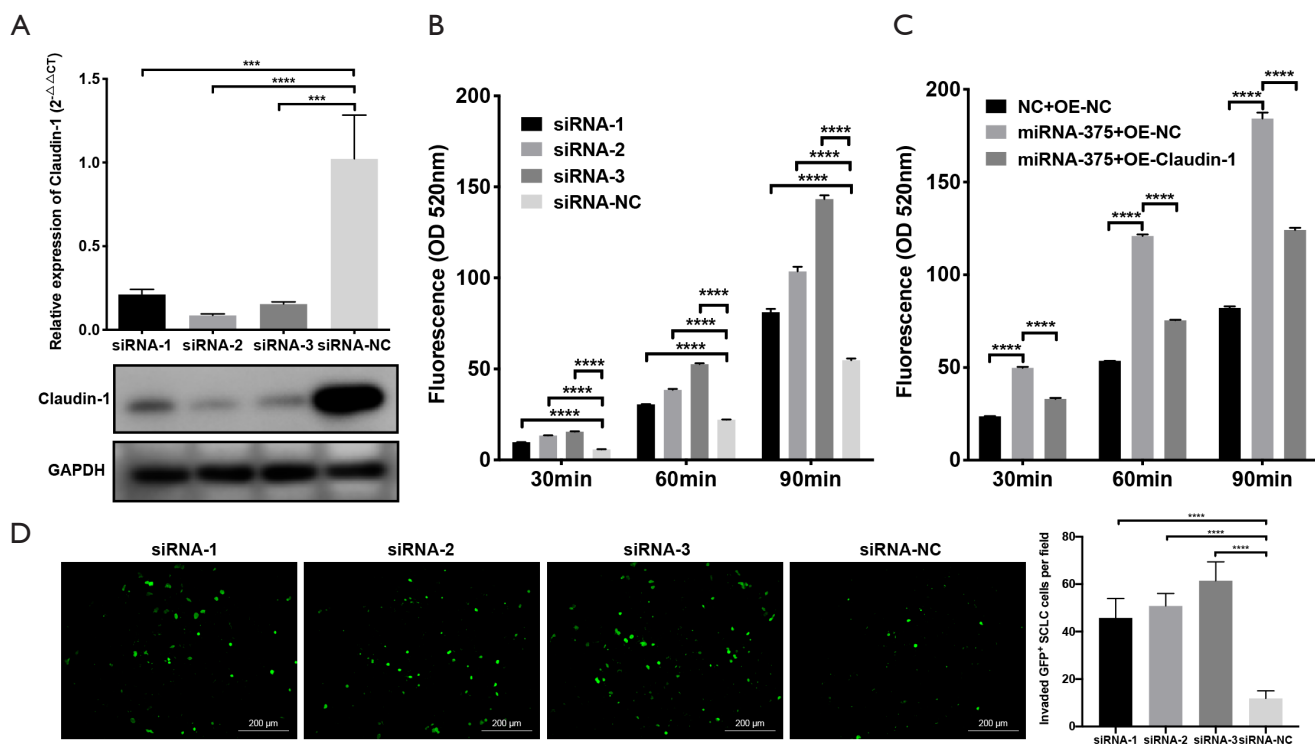


Figure S7 Knocking down the expression of claudin-1 increased the permeability of HUVECs monolayers. (A) Both the RNA and protein expression of claudin-1 in HUVECs were downregulated by three claudin-1-specific siRNAs. (B) The downregulation of claudin-1 in HUVECs induced the permeability of HUVEC monolayers. (C) The increased permeability of HUVEC monolayers induced by miR-375-3p was abrogated by the upregulation of claudin-1. (D) The downregulation of claudin-1 in HUVECs promoted the transendothelial migration of GFP + SCLC cells. *, $P < 0.001$; **, $P < 0.0001$.