Expanded View Figures

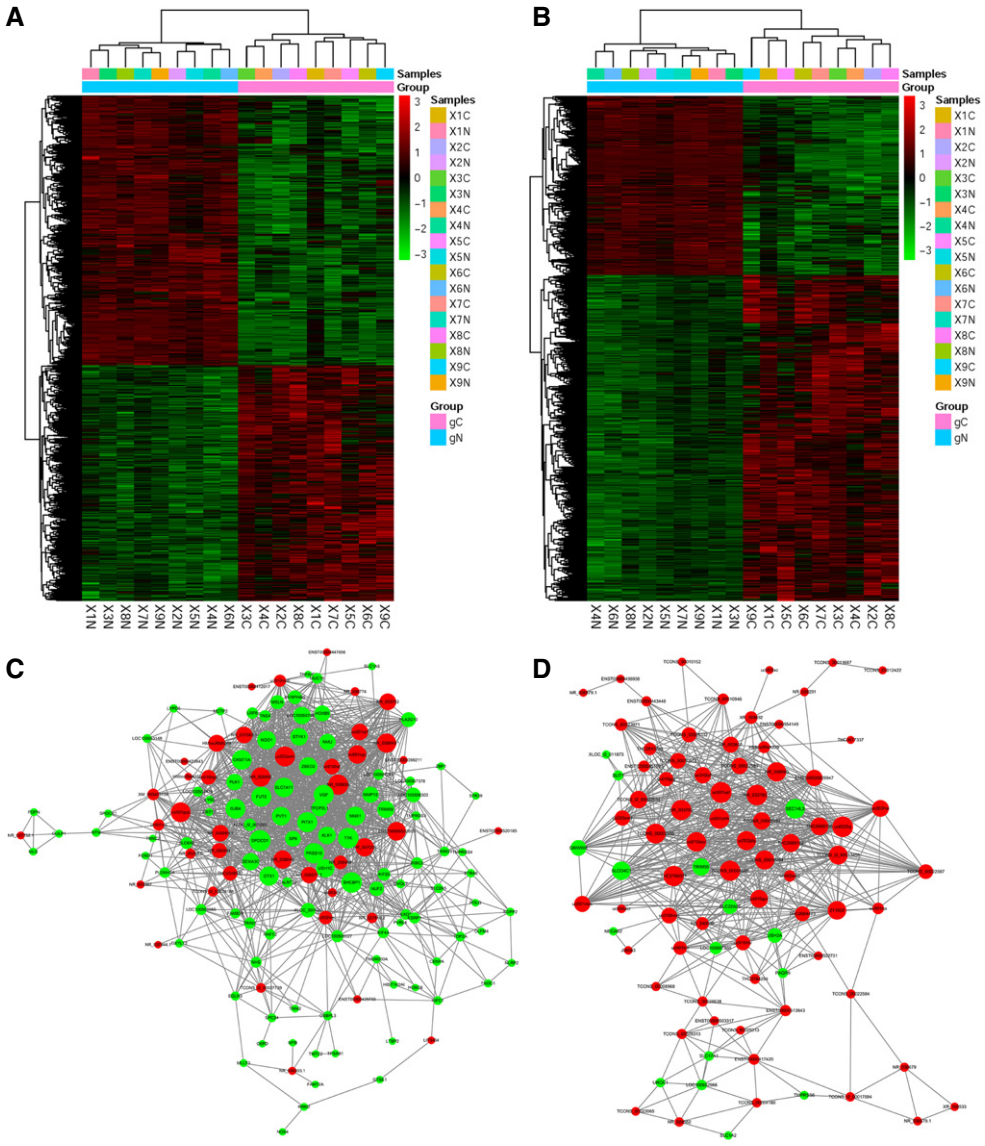

Figure EV1. Expanded information for differential expression of lncRNAs in GBC.

A, B Hierarchical clustering analysis of lncRNAs (A) and protein-coding RNAs (B) that were differentially expressed between GBC samples (c, cancer tissues) and non-tumour samples (n, non-tumour samples). The colour scale shown on the right illustrates the relative expression level of RNA; red represents high expression and green represents low expression.

C Coexpression network in GBC tissues. Red nodes represent lncRNAs, and green nodes represent protein-coding genes.

D Coexpression network in non-tumour tissues. Red nodes represent lncRNAs, and green nodes represent protein-coding genes.

Source data are available online for this figure.

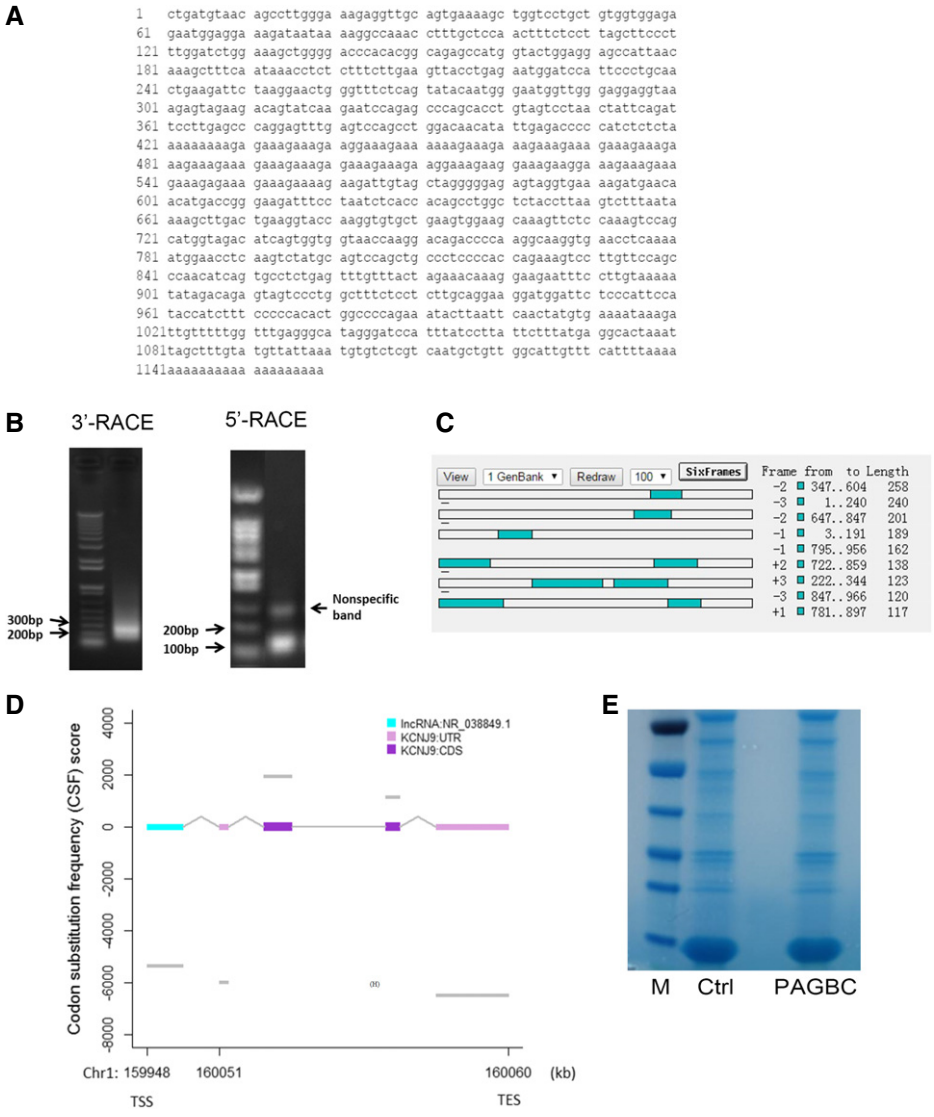

Figure EV2. Expanded information for lncRNA-PAGBC.

A The nucleotide sequence of full-length human lncRNA-PAGBC.

B A representative image of the PCR products of the 5′-RACE and 3′-RACE procedures.

C Putative proteins that may be encoded by lncRNA-PAGBC, as predicted by ORF Finder.

D Codon substitution frequency scores (CSF) of lncRNA-PAGBC.

E PAGBC translation reactions with PSPT19 backbone vector constructs: Molecular weight marker (M), TNT® SP6 Quick master mix control (Ctrl), 5 μl of the 50 μl *in vitro* translation reaction mixture with PSPT19-PAGBC (PAGBC).

Source data are available online for this figure.

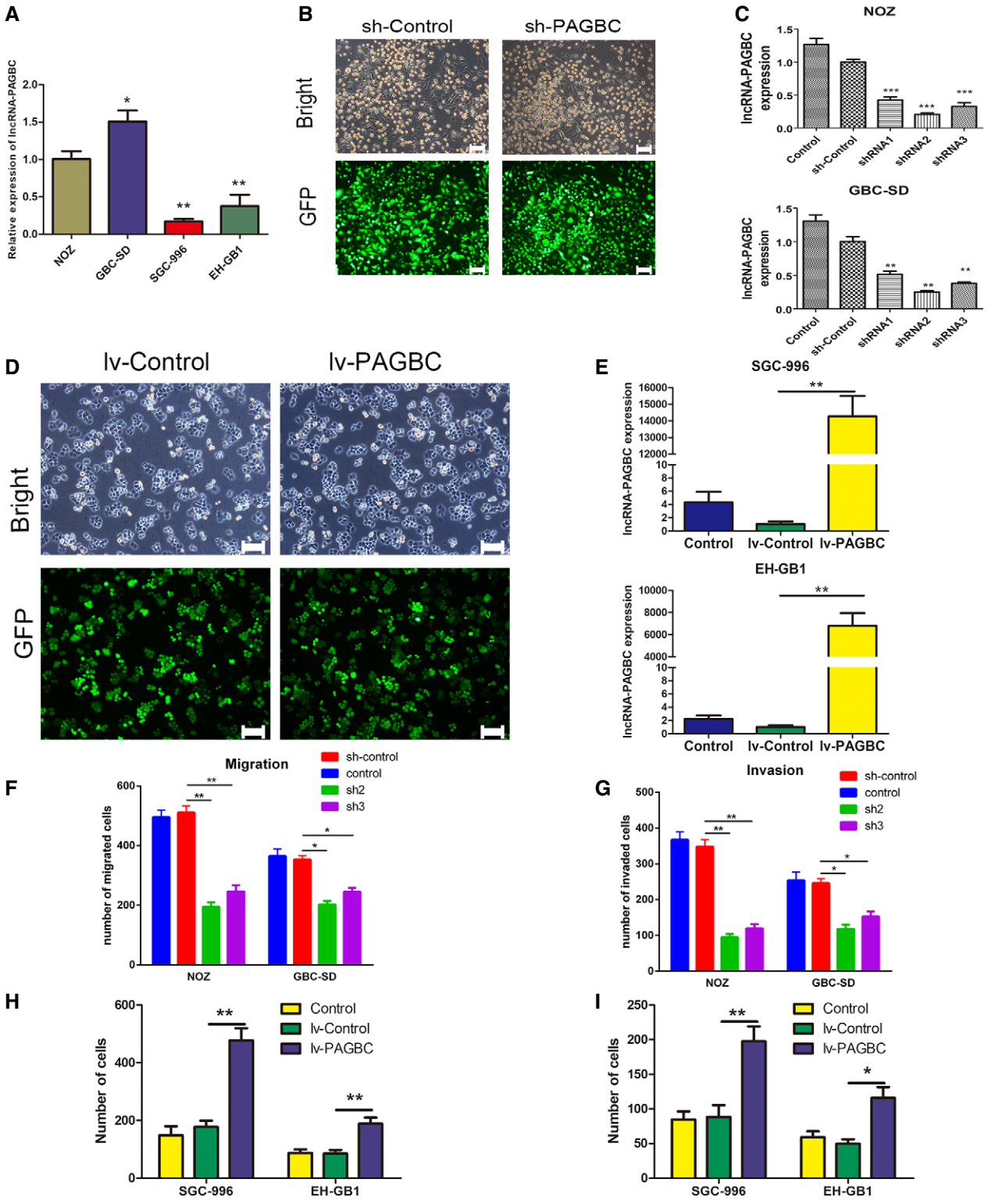

Figure EV3.

Figure EV3. lncRNA-PAGBC promotes the proliferation and metastasis of GBC cells.

A The relative PAGBC expression in different cell lines was determined using quantitative real-time PCR. The data were compared with NOZ cells. Data are mean ± SD (n = 3).

B The transfection efficiency was determined 3 days after incubation with the lentivirus. The GFP-labelled transfected cells were observed under a light microscope and a fluorescence microscope. Light micrograph (upper panel); fluorescence micrograph (lower panel). Scale bars represent 100 μm.

C Relative PAGBC expression was determined using quantitative real-time PCR. GAPDH was used as an internal control. The data were compared with the sh-Control. The data are shown as the means ± SD of triplicate samples.

D The transfection efficiency was determined 3 days after incubation with the lentivirus. The GFP-labelled transfected cells were observed under a light microscope and a fluorescence microscope. Light micrograph (upper panel); fluorescence micrograph (lower panel). Scale bars represent 100 μm.

E Relative PAGBC expression was determined using quantitative real-time PCR. GAPDH was employed as an internal control. The data are shown as the means ± SD of triplicate samples.

F, G A statistical plot of the average number of migrated (F) or invaded (G) NOZ and GBC-SD cells shown in Fig 3A. The data are shown as the means ± SD of triplicate samples.

H, I A statistical plot of the average number of migrated (H) or invaded (I) EH-GB1 and SGC-996 cells shown in Fig 3B. The data are shown as the means ± SD of triplicate samples.

Data information: ***$P < 0.001$, **$P < 0.01$, *$P < 0.05$ (Student's t-test).
Source data are available online for this figure.

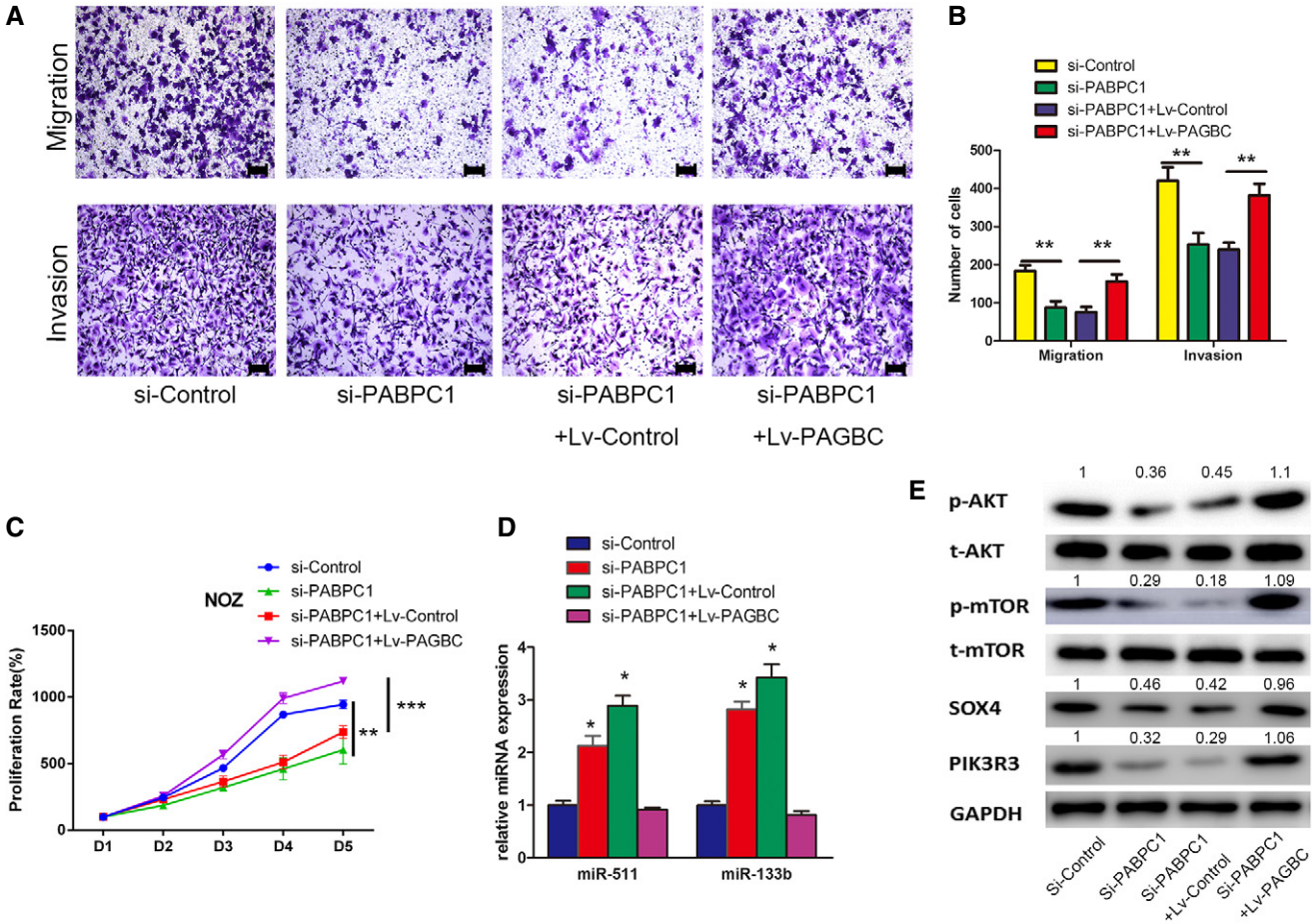

Figure EV4. The role of PABPC1 on the function of lncRNA-PAGBC.

A Transwell migration and invasion assays of NOZ transfected with siRNA against the indicated transcripts and transfected with the lentivirus encoding the indicated transcripts. Scale bars represent 100 μm.

B A statistical plot of the average number of migrated or invaded NOZ cells shown in (A). The data are shown as the means ± SD of triplicate samples.

C The proliferation of NOZ cells transfected with siRNA against the indicated transcripts and transfected with the lentivirus encoding the indicated transcripts was measured using CCK-8 assays. Data are mean ± SD (n = 3).

D qRT–PCR was performed to detect the expression of miR-133b and miR-511 in NOZ cells transfected with siRNA against the indicated transcripts and transfected with the lentivirus encoding the indicated transcripts. Data are mean ± SD (n = 3).

E Western blotting analysis of p-AKT, t-AKT, p-mTOR, t-mTOR, SOX4 and PIK3R3 in NOZ cells transfected with siRNA against the indicated transcripts and transfected with the lentivirus encoding the indicated transcripts.

Data information: ***$P < 0.001$, **$P < 0.01$, *$P < 0.05$ (Student's t-test).

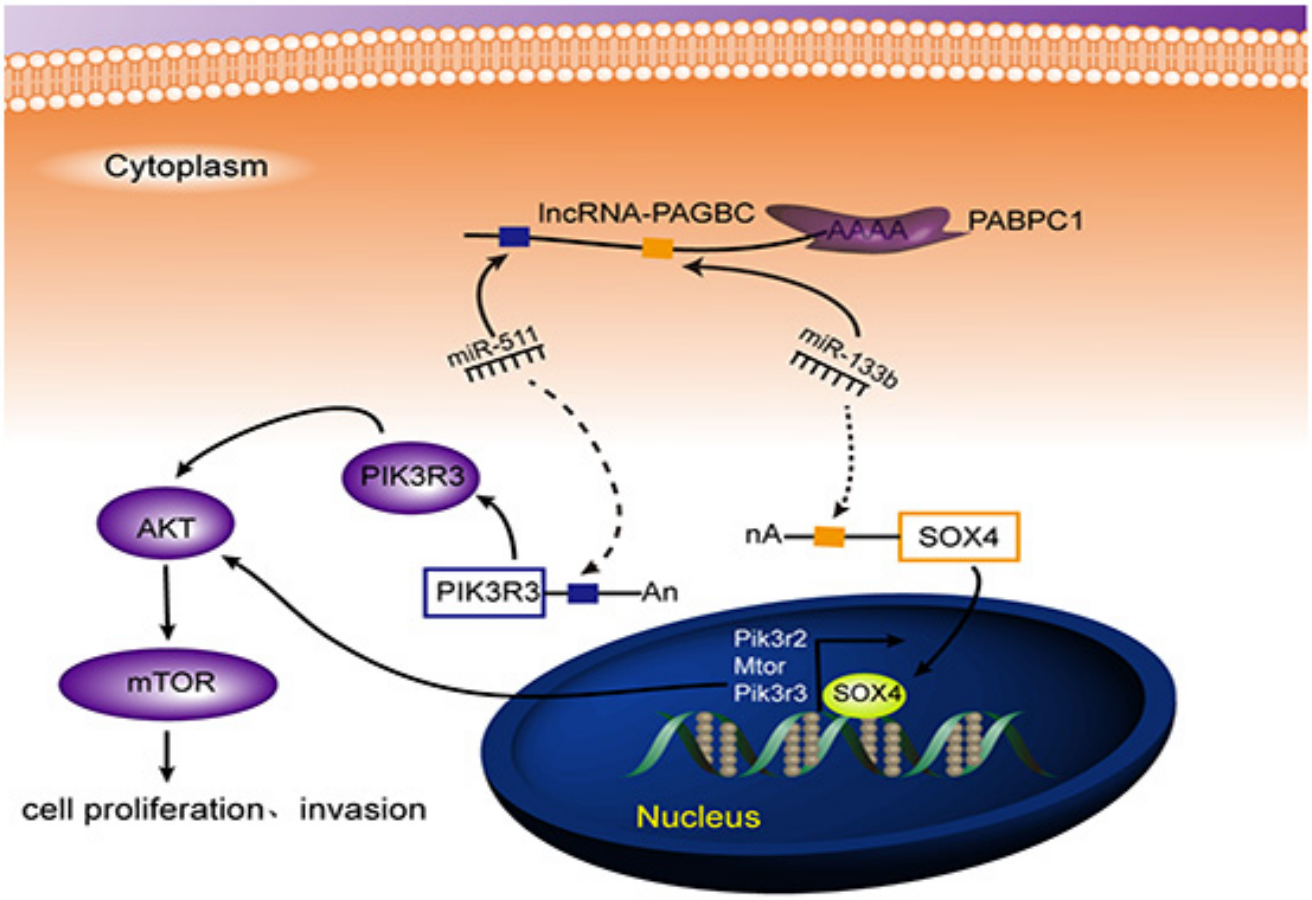

Figure EV5. Schematic model of the functions of lncRNA-PAGBC in GBC cells.

lncRNA-PAGBC, which is stabilized by PABPC1, promotes GBC cell proliferation and metastasis by competitively binding to miR-133b and miR-511, upregulating SOX4 and PIK3R3, and then activating the AKT/mTOR pathway.