

Figure S1. ERBB2 expression is upregulated in cervical cancer cell lines. (A) RT-qPCR analysis of ERBB2 mRNA expression and (B) WB analysis of ERBB2 protein expression in SiHa and HeLa cervical cancer cell lines compared with in the negative control, non-cancerous human H8 cervical epithelial cell line. GAPDH was used as the RT-qPCR housekeeping control and WB loading control. Data are expressed as the mean \pm SEM (n=3). **P<0.01 vs. H8; ††P<0.01 vs. SiHa analyzed via one-way ANOVA. WB, western blotting; RT-qPCR, reverse transcription-quantitative PCR; ERBB2, Erb-B2 Receptor Tyrosine Kinase 2.

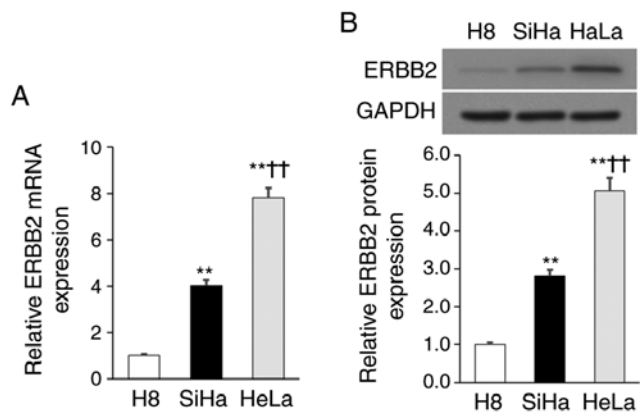


Figure S2. Validation of PIK3CA modulation in cervical cancer cell lines. Western blotting validation of (A) PIK3CA upregulation using a PIK3CA overexpression vector in HeLa cells and (B) PIK3CA knockdown using a PIK3CA-targeting siRNA in SiHa cells. GAPDH was used as the loading control. vec, vector; si, small interfering; PIK3CA, phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit α .

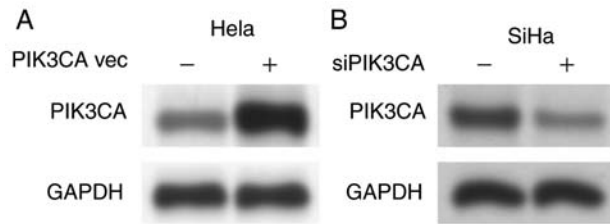


Figure S3. Validation of miR-3184 modulation in cervical cancer cell lines. Reverse transcription-quantitative PCR validation of (A) miR-3184-5p upregulation using a miR-3184-5p mimic in HeLa cells and (B) miR-3184-5p downregulation using a miR-3184-5p inhibitor in SiHa cells. U6 was used as the housekeeping control. Data are expressed as the mean \pm SEM (n=3). **P<0.01 analyzed via Student's t-test. Ctrl, control; miR, microRNA; inhib, inhibitor.

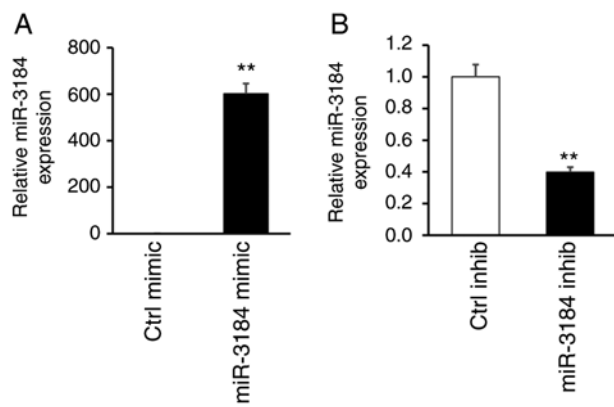


Figure S4. Low miR-3184-5p expression in patient-derived cervical cancer tissues is associated with a poor prognosis. miR-3184 expression values are reported relative to those of the housekeeping control U6. (A) miR-3184-5p expression in patient-derived cervical cancer vs. matched healthy cervical tissues. Data were analyzed via Wilcoxon signed-rank test. miR-3184-5p expression in (B) stage I/II vs. III/IV patient-derived cervical cancer biopsies and (C) lymph node metastatic vs. non-metastatic patient-derived cervical cancer biopsies. Data were analyzed via Mann-Whitney U test. (D) Survival analysis using the Kaplan-Meier method according to high (above the median) or low (below the median) miR-3184-5p expression. P-value was calculated using the log-rank test. Data in box plots are expressed as the median \pm IQRs (boxes) and absolute ranges (whiskers). **P<0.01. miR, microRNA.

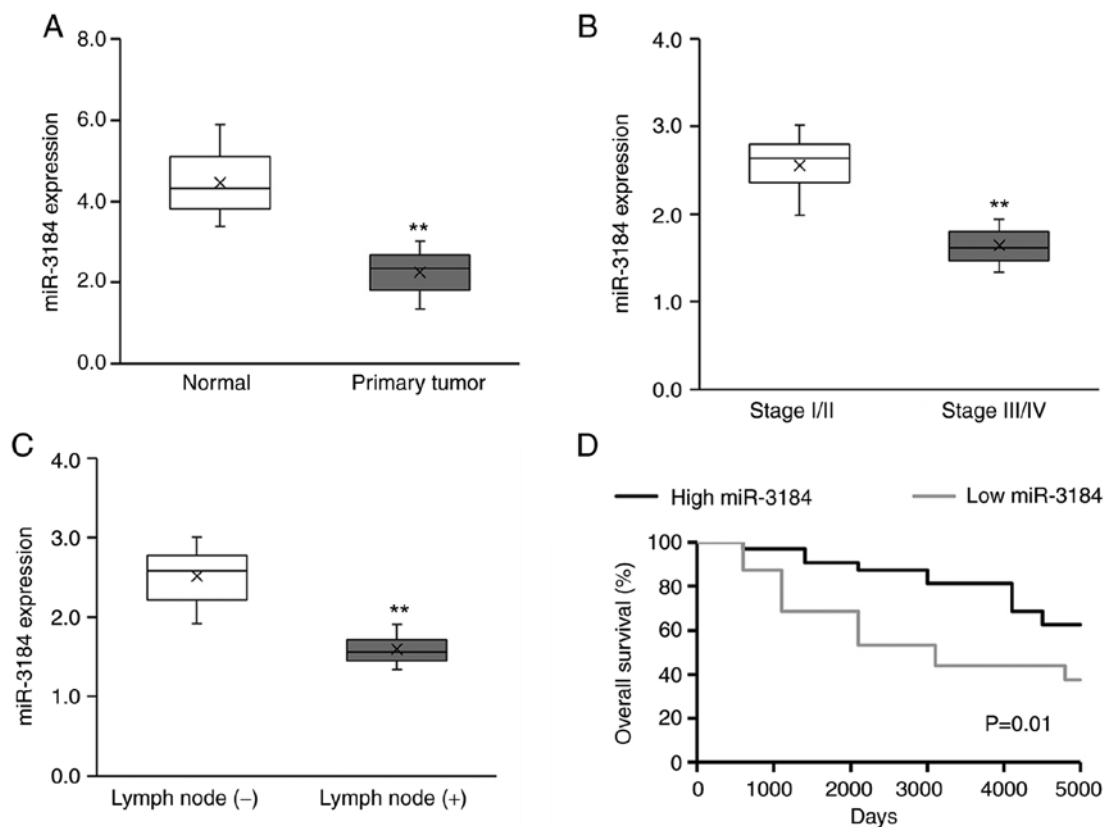


Table SI. Clinicopathological characteristics of recruited patients with cervical cancer (n=65).

Characteristic	No.	%
Age, years		
≤50	29	45
>50	36	55
Tumor size, cm		
≤4	45	69
>4	20	31
Histological type		
Squamous cell carcinoma	48	74
Adenocarcinoma	17	26
FIGO stage		
Stage I/II	43	66
Stage III/IV	22	34
Histological differentiation		
Well + moderate	50	77
Poor	15	23
Lymph node metastasis		
No	46	71
Yes	19	29

FIGO, International Federation of Gynecologists and Obstetricians.