**Figure S1. Kaplan–Meier survival analysis of cervical cancer samples based on the pathologic N stage.**

The Kaplan–Meier curve of the pathologic N0 stage is indicated with a blue line and that of the pathologic N1 stage is indicated with a purple line. LogRank P-value indicates the statistical significance of difference.

**Figure S2. lncRNA-miRNA (A) and miRNA-mRNA (B) regulation network.**

Upregulated lncRNAs, miRNAs, and mRNAs are indicated as red squares, diamonds, and regular triangles, respectively. Downregulated lncRNAs, miRNAs, and mRNAs are indicated as green squares, diamonds, and inverse triangles, respectively. Regulatory relationships between the nodes are indicated as gray lines with arrows.

**Figure S3. Expression levels of *WNT2*, *BMP7*, *FGF7*, *FN1*, and *SV2A* and *CXCL12* in TCGA (A) and GSE44001 (B) datasets.**

Expression levels of ***WNT2*, *BMP****7*, *FGF7*, *FN1*, and *SV2A* and *CXCL12* in TCGA (A) and GSE44001 (B) datasets in the recurrent samples are indicated as red histograms; non-recurrent samples are indicated as green histograms.

p < 0.1, \*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001