

**Figure S1.** Differentially expressed m7G-related genes between PC and normal tissues. (a) Different expressions of 35 m7G-related genes between PC tissues and normal tissues. (b) Volcanic map of m7G-related DEGs between PC and control samples with  $\log_2 FC > 1$  and  $p < 0.05$ . (c) Violin plot of 12 risk lncRNAs in low- and high-risk groups.

**Figure S2.** Prognostic value of m7G-related lncRNA risk model. (a) Survival analysis of 12 m7G-related lncRNAs between high- and low-risk groups. (b) Univariate and multivariate analysis of the clinical features and risk scores

**Figure S3.** Correlation between R0 resection rates and the expression of m7G-LPS and SNHG8. (a) Correlation between R0 resection rates and the expression of m7G-LPS. (b) Correlation between R0 resection rates and the expression of SNHG8.

**Figure S4.** In vitro functional verification in PC cells. (a) The proliferation ability of PC cell lines was detected by CCK-8 assays after overexpressing SNHG8. (b-c) Wound healing and Transwell assays were used to determine the migration capacities of PC cell lines after SNHG8 overexpressed. \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ , and \*\*\*\* $p < 0.0001$ . ns, no significant.