Figure S1. Survival analysis results of PTTG1 from TCGA dataset. (A) PTTG1 expression, survival time and survival status of TCGA dataset. The top scatterplot represents the gene expression from low to high. Different colors represent different groups. The scatter plot distribution represents the gene expression of different samples corresponding to the survival time and survival status. (B) Kaplan-Meier survival analysis of the gene signature from TCGA dataset, comparison among different groups was made using log-rank test. HR (high expression group) represents the hazard ratio of the low-expression sample relatives to the high-expression sample. HR>1 indicates the gene is a risk factor, and HR<1 indicates the gene is a protective factor. (C) Heatmap of PTTG1 expression. (D) Receiver operating characteristic curve of PTTG1. Higher AUC values correspond to a higher predictive power. TCGA, The Cancer Genome Atlas; HR, hazard ratio; AUC, area under the curve.

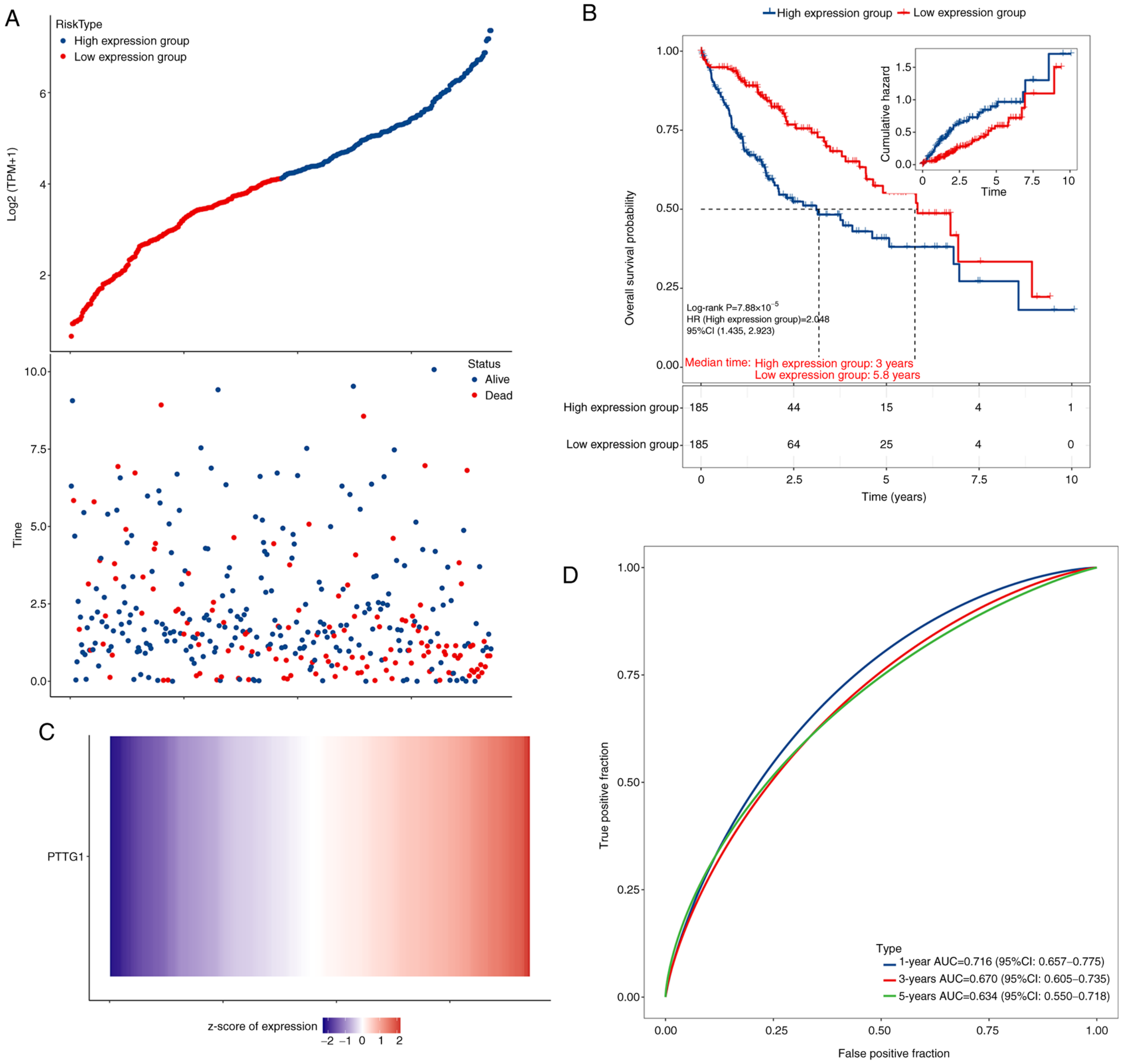

Figure S2. A schematic model of the functions of lncRNA PTTG3P during HCC tumor growth and metastasis. The lncRNA PTTG3P upregulates PTTG1, which then activates the PI3K/AKT signaling pathway. When PI3K/AKT signaling is activated, it elevates the expression of C-myc and CyclinD1, leading to increased levels of p-Rb and ultimately promoting cell proliferation in HCC. Additionally, the activation of PI3K/AKT inactivates Caspase3, thereby inhibiting cell apoptosis and accelerating tumor growth. Furthermore, PTTG3P promotes HCC cell migration and invasion by activating PI3K/AKT signaling, which upregulates Snail and Slug, downregulates E-cadherin, and induces the process of EMT HCC, hepatocellular carcinoma; p-, phosphorylated; EMT, epithelial-mesenchymal transition.