**Supplementary figure legend**

**Supplementary Figure 1:** **Flow chart of the method.**

**Supplementary Figure 2:** **Kaplan Meier curves unveil the correlation between PTTG1 expression levels and OS.**

(A) CESC, (B) GBMLGG, (C) KIRP, (D) LAML, (E)LGG, (F) LIHC. OS, overall survival.

**Supplementary Figure 3: Kaplan Meier curves reveal the relationship between PTTG1 expression lewels and DSS, DFS.**

1. GBMLGG, (B) KIPAN, (C) KIRP, (D) LGG. DSS, disease-specific survival.

(E) BRCA, (F) KIPAN, (G) KIRP, (H) LIHC. DFS, disease-free survival.

**Supplementary Figure 4: Kaplan Meier curves reveal the relationship between PTTG1 expression lewels and PFS.**

(A)GBMLGG, (B) KIRC, (C) LGG, (D) PRAD. PFS, progression-free survivel.

**Supplementary Figure 5: Nomogram models were established and evaluated in KIRC LUSC, and LIHC.**

(A) Establishment of a nomogram model incorporating PTTG1 expression in KIRC. (B) Calibration curves were used to evaluate the nomogram model in KIRC at 1-year, 3-year, and 5-year. (C) Building a nomogram model containing PTTG1 expression in LUSC. (D) The 1-year, 3-year and 5-year calibration curves were used to evaluate the prediction accuracy of the nomogram model in LUSC. (E) Building a nomogram model containing PTTG1 expression in LIHC. (F) The 1-year, 3-year and 5-year calibration curves were used to evaluate the prediction accuracy of the nomogram model in LIHC.

**Supplementary Figure 6: Correlation of PTTG1 with the level of immune infiltrating cells.**

(A) PTTG1 was closely related to the immune infiltration level in cancers analyzed via QUANTISEQ algorithms.

(B) PTTG1 was closely related to the immune infiltration level in cancers analyzed via EPIC algorithms. The asterisks indicate a statistically significant p-value calculated using spearman correlation analysis. (∗p<0.05, ∗∗p<0.01, and ∗∗∗p<0.001.)

**Supplementary Figure 7: Correlation analysis between PTTG1 expression and TME (tumor microenvironment).**

**(A-H)** PTTG1 expression was the highest in CD8 T cells, conventional CD4 T cells, exhausted CD8 T cells, monocytes and macrophages, and proliferating T cell fibroblasts in AEL, AML, ALL, BCC, BRCA, CHOL, CRC, and Glioma.

**Supplementary Figure 8: PTTG1 promotes the proliferation of neuroblastoma cells and inhibits apoptosis.**

(A) qPCR and western blotting were used to verify the interference efficiency of siPTTG1 in the SK-N-SH cell lines. (B) Growth curve was used to measure the effect of PTTG1 on the proliferation of SK-N-SH cells. (C) EdU-labeled flow cytometry was used to detect the proliferation function of PTTG1 in vitro; (D) Flow cytometry was used to detect cell apoptosis after PTTG1 knockdown. (\*P<0.05, \*\*P<0.01, and \*\*\*\*P<0.0001; bar graphs represent the mean ± SEM).