Figure S1. PLK4 mRNA expression is positively correlated with ECT2 mRNA expression and PIK3CA mRNA expression in patients with RCC. Correlation of PLK4 mRNA expression with (A) ECT2 mRNA expression and (B) PIK3CA mRNA expression in patients with RCC according to the data from the Gene Expression Profiling Interactive Analysis database. The data were analyzed using the Pearson test. ECT2, epithelial cell transforming sequence 2; PIK3CA, phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit α; PLK4, polo-like kinase; RCC, renal cell carcinoma; TPM, transcripts per million.
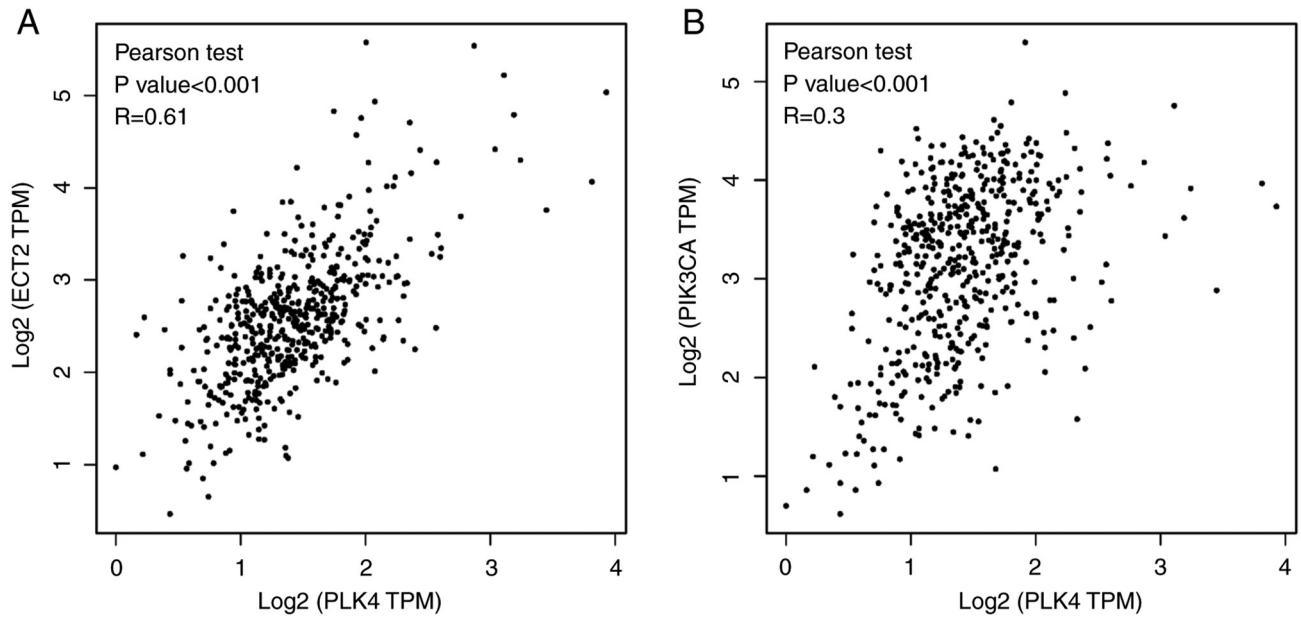
Figure S2. Further survival analysis confirmed that high PLK4 expression (vs. low PLK4 expression) is associated with shortened DFS and OS rates in patients with renal cell carcinoma. Further validation of the prognostic value of PLK4 using data from (A) GEPIA and (B) The Human Protein Atlas (derived from The Cancer Genome Atlas). DFS and OS rates were assessed using Kaplan-Meier curves and the significant differences were determined using the log-rank test. DFS, disease-free survival; GEPIA, Gene Expression Profiling Interactive Analysis; OS, overall survival; PLK4, polo-like kinase.