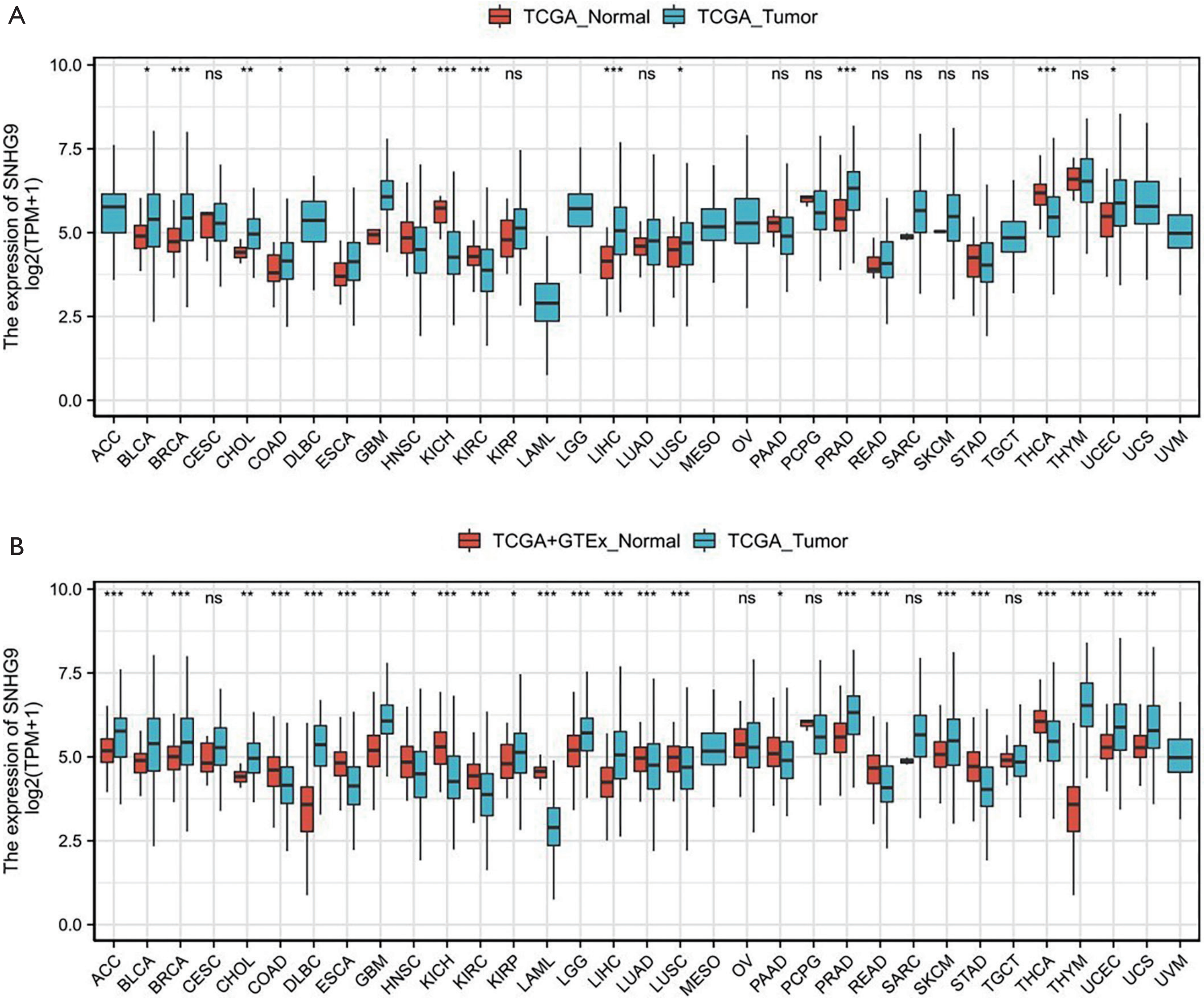

Figure S1 (A) Wilcoxon rank sum test was used to analyze the difference expression of SNHG9 in normal and tumor samples of TCGA. (B) Wilcoxon rank sum test was used to analyze the difference expression of SNHG9 in normal samples of GTEx combined with TCGA and tumor samples of TCGA. ns, $p \geq 0.05$; *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$.

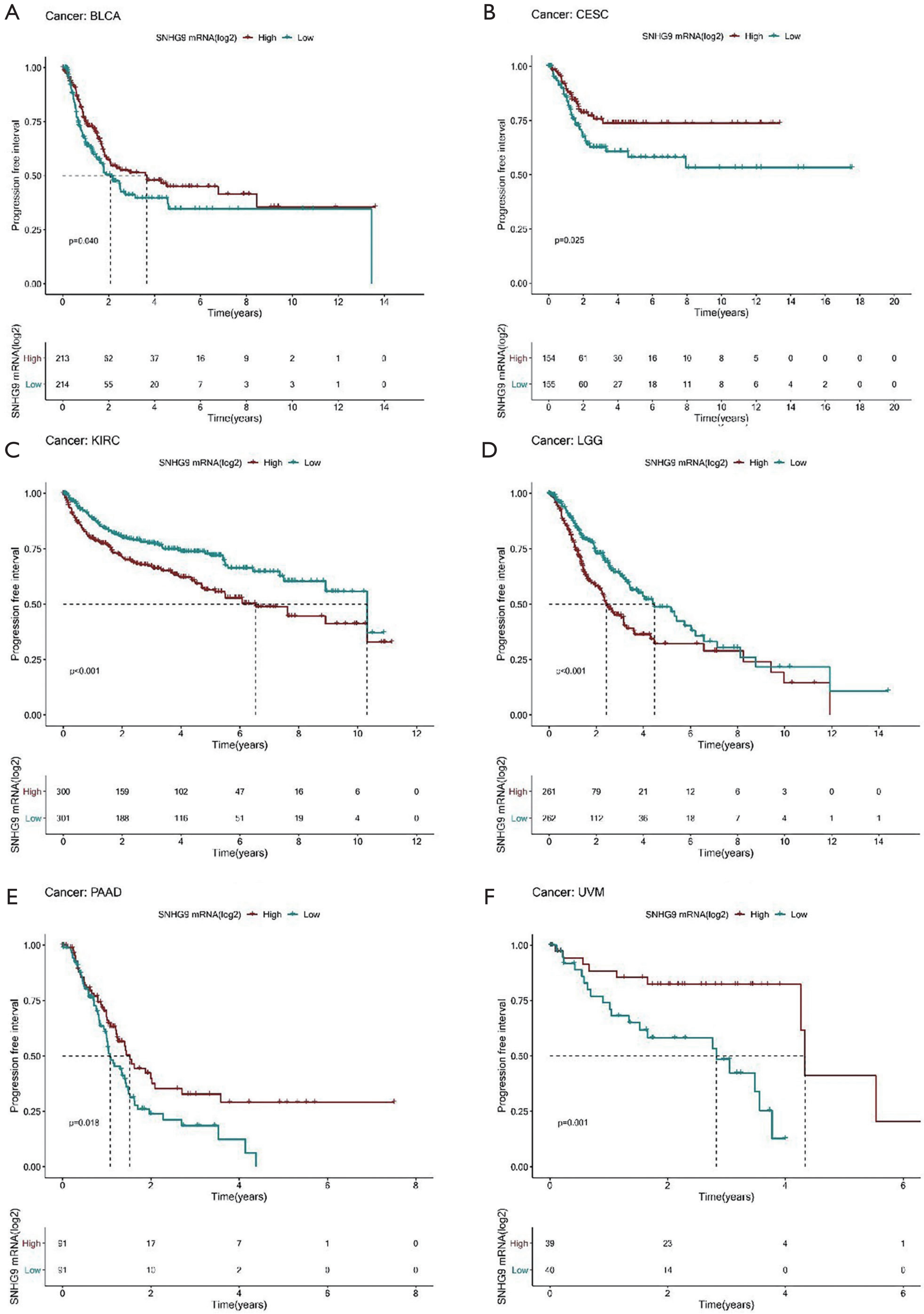

Figure S2 SNHG9 expression and prognosis in patients with other cancers. Kaplan-Meier curve was drawn using the R package survminer to evaluate the prognostic value of SNHG9 in PFS of some other cancer types. SNHG9 expression value was divided into high and low expression group according to median value.

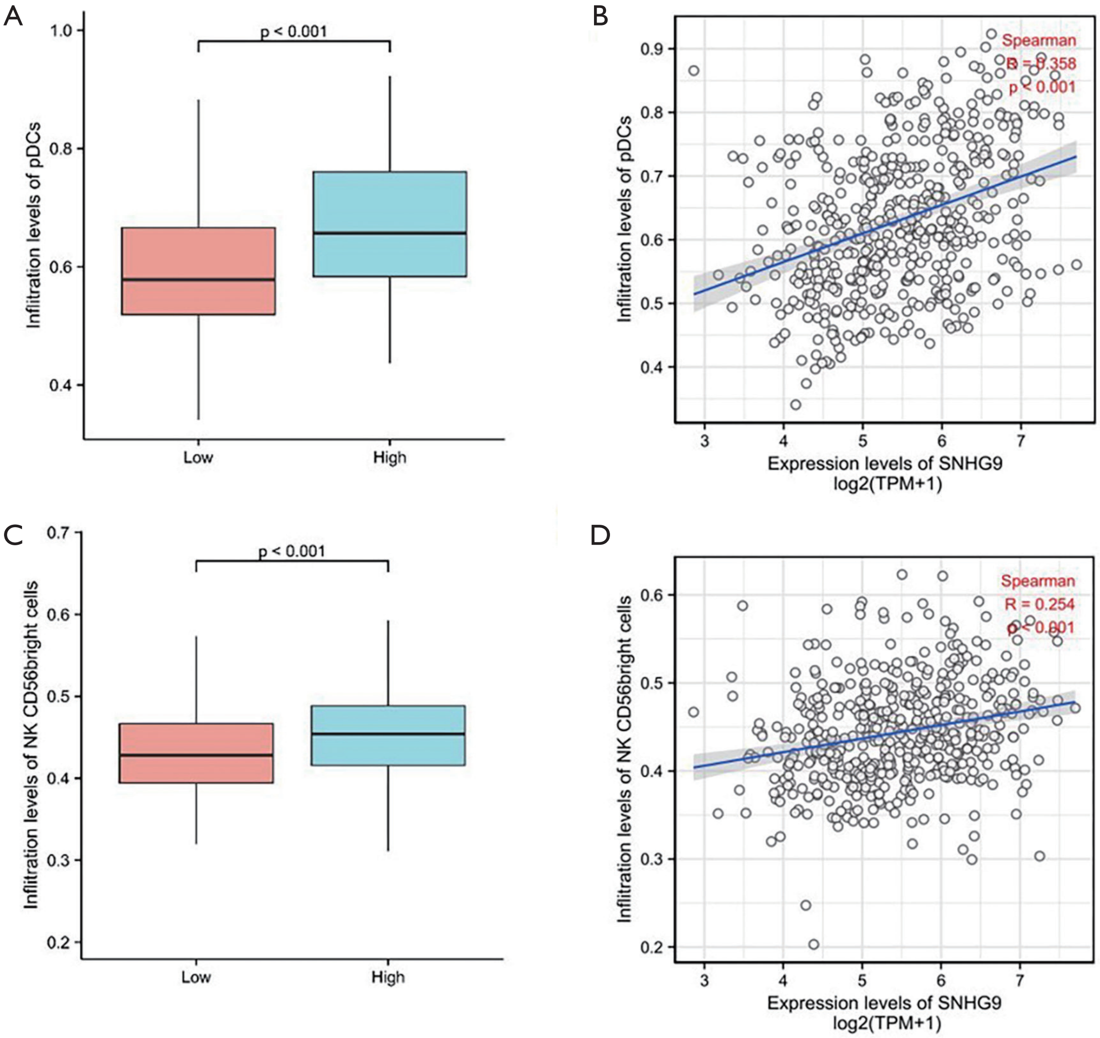

Figure S3 The Wilcoxon rank sum test was used to analyze the difference of pDCs infiltration level between SNHG9 high and low expression groups (A), and the correlation between SNHG9 expression and pDCs was detected by Spearman correlation method (B). The Wilcoxon rank sum test was used to analyze the difference of NK CD56bright cells infiltration level between SNHG9 high and low expression groups (C), and the correlation between SNHG9 expression and NK CD56bright cells was detected by Spearman correlation method (D). NK, natural killer; pDCs, plasmacytoid dendritic cells.