Figure S1. PCLAF exhibits differential expression levels in other cells, tissues, and plasma. We analyzed the expression of the *PCLAF* gene in (A) different tissues using the consensus datasets of HPA, GTEx, and FANTOM5 and (B) in other blood cells using the consensus dataset of HPA, Monaco, and Schmiedel. (C) Based on the consensus datasets of HPA, GTEx, and FANTOM5, PCLAF expression in different cell lines was also analyzed. PCLAF, PCNA clamp associated factor, also known as KIAA0101.

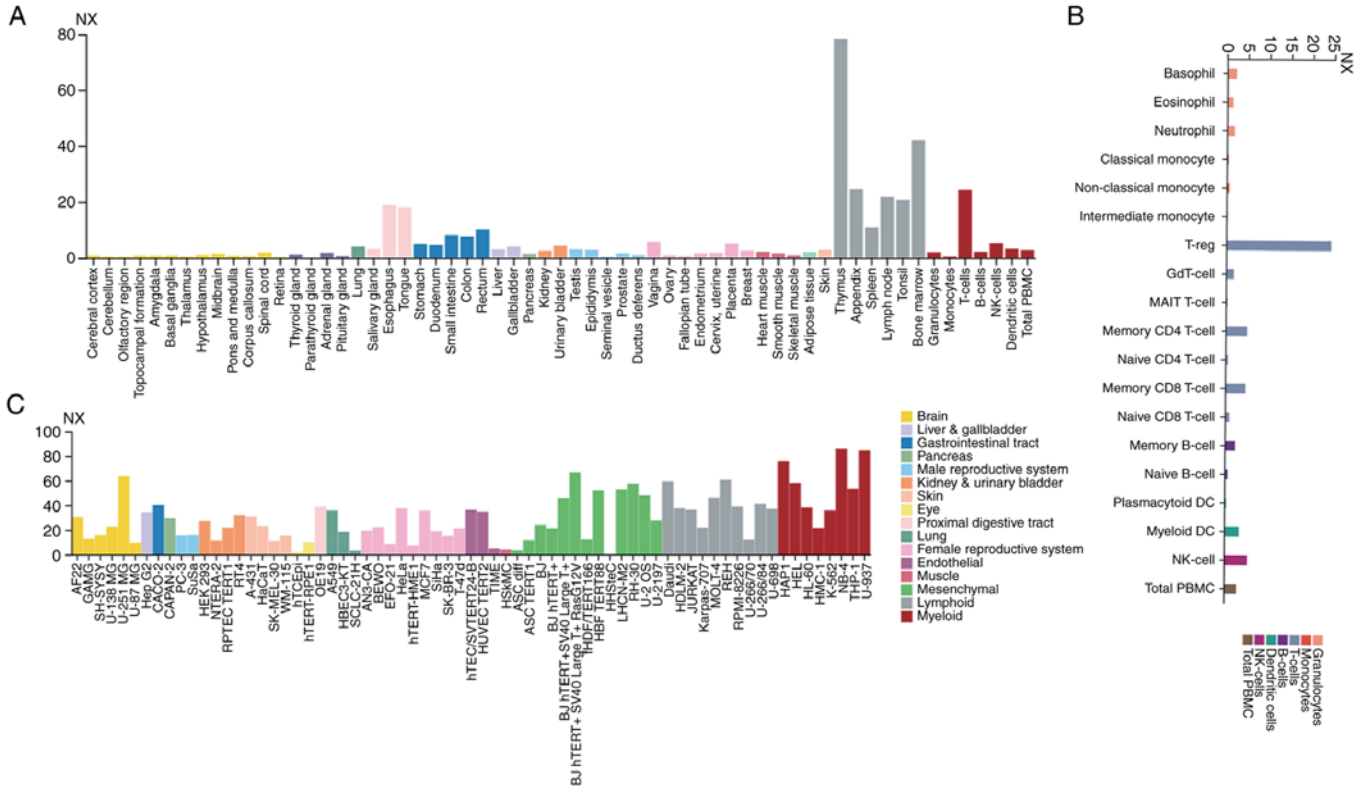

Figure S2. Expression level of the *PCLAF* gene in different pathological stages. (A) Based on TCGA data, the expression levels of the *PCLAF* gene were analyzed according to the main pathological stages (stage I, stage II, stage III, and stage IV) of ACC, KICH, KIRC, KIRP, LIHC, LUAD, LUSC, and PAAD. Log2 (TPM + 1) was applied for log-scale. (B) Kaplan-Meier database was used to analyze the expression levels of the *PCLAF* gene in breast, liver, and lung cancers to perform a series of survival analyses, including OS, DMFS, RFS, PFS, PPS, FP, and DSS. PCLAF, PCNA clamp associated factor, also known as KIAA0101. OS, overall survival; DMFS, distant metastasis-free survival; RFS, relapse-free survival; PFS, progression-free survival; FP, first progression; DSS, disease-specific survival.

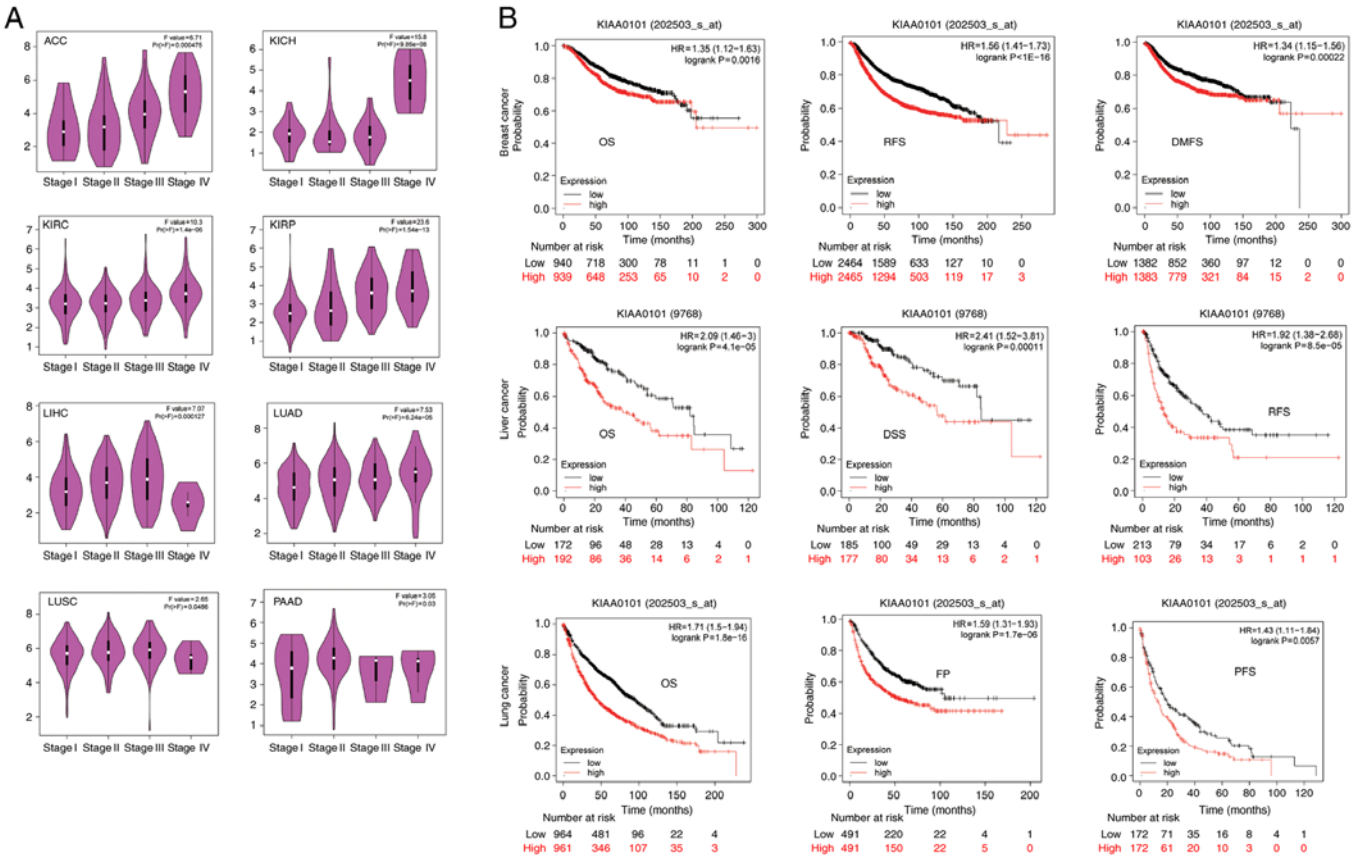

Figure S3. Forest plot shows the correlation of *PCLAF* mRNA expression with OS (n=1925) and PFS (n=982) in LUAD with different clinicopathological features. PCLAF, PCNA clamp associated factor, also known as KIAA0101. OS, overall survival; PFS, progression-free survival.

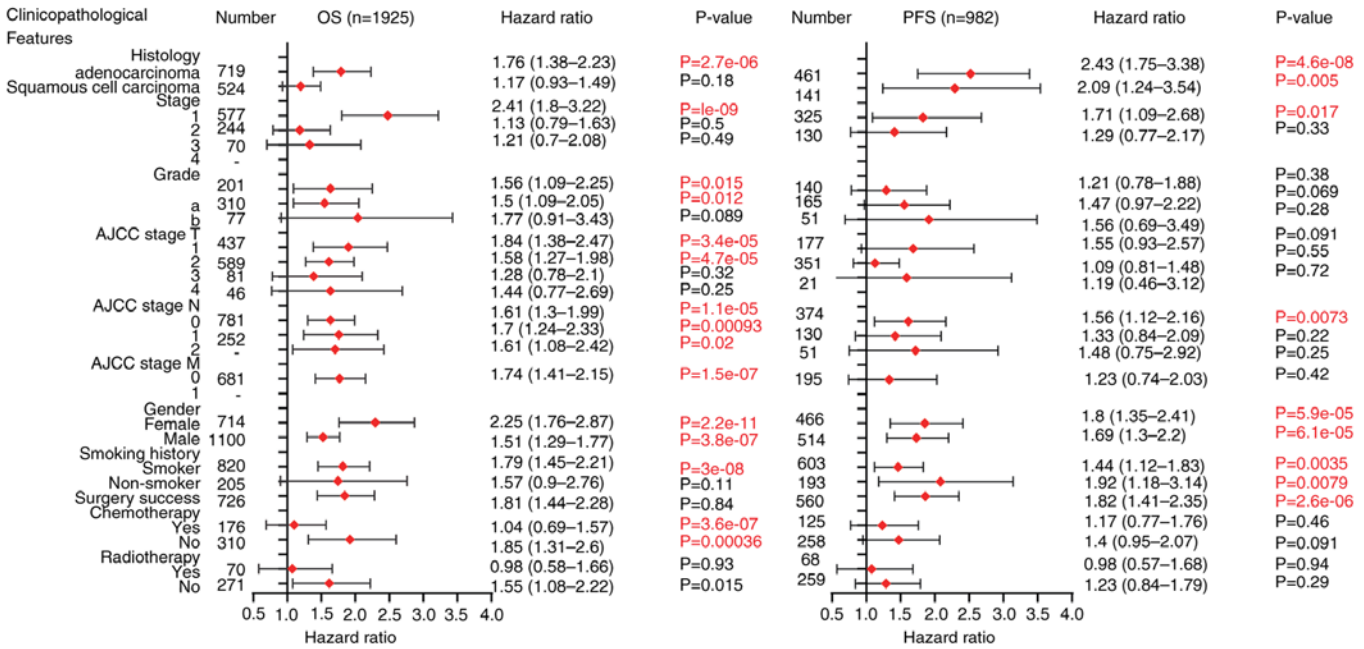

Figure S4. DNA methylation aberration of PCLAF in tumors. (A) Eight tumors with high PCLAF expression presented with a decreased DNA methylation level of PCLAF, including CHOL, CESC, GBM, PCPG, SARC, TGCT, STAD, UCEC. *P<0.05. (B) The DNA methylation level of KICH at different stages. (C) DNA methylation level of PCLAF in BRCA and COAD remained unchanged. PCLAF, PCNA clamp associated factor, also known as KIAA0101.

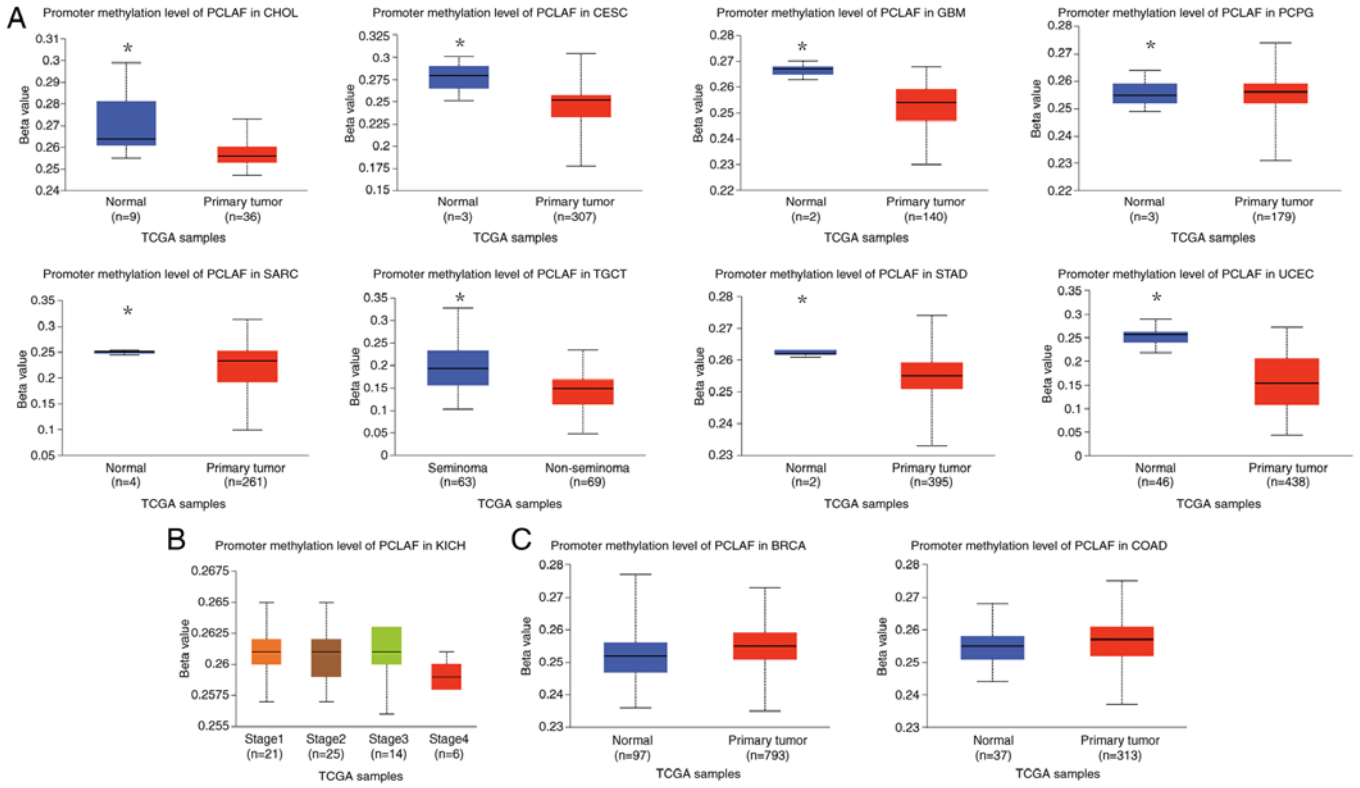

Figure S5. Correlations of PCLAF expression with the immune infiltration level. (A) Correlation of PCLAF and infiltration level of cancer-associated fibroblasts across THYM and TGCT. (B) Association between the expression of PCLAF and 28 types of tumor-infiltrating lymphocytes (TILs) across human cancers. (C) PCLAF was correlated with the abundance of activated CD4 T cell (Act CD4) and type 2 T helper (Th2) cells. PCLAF, PCNA clamp associated factor, also known as KIAA0101.

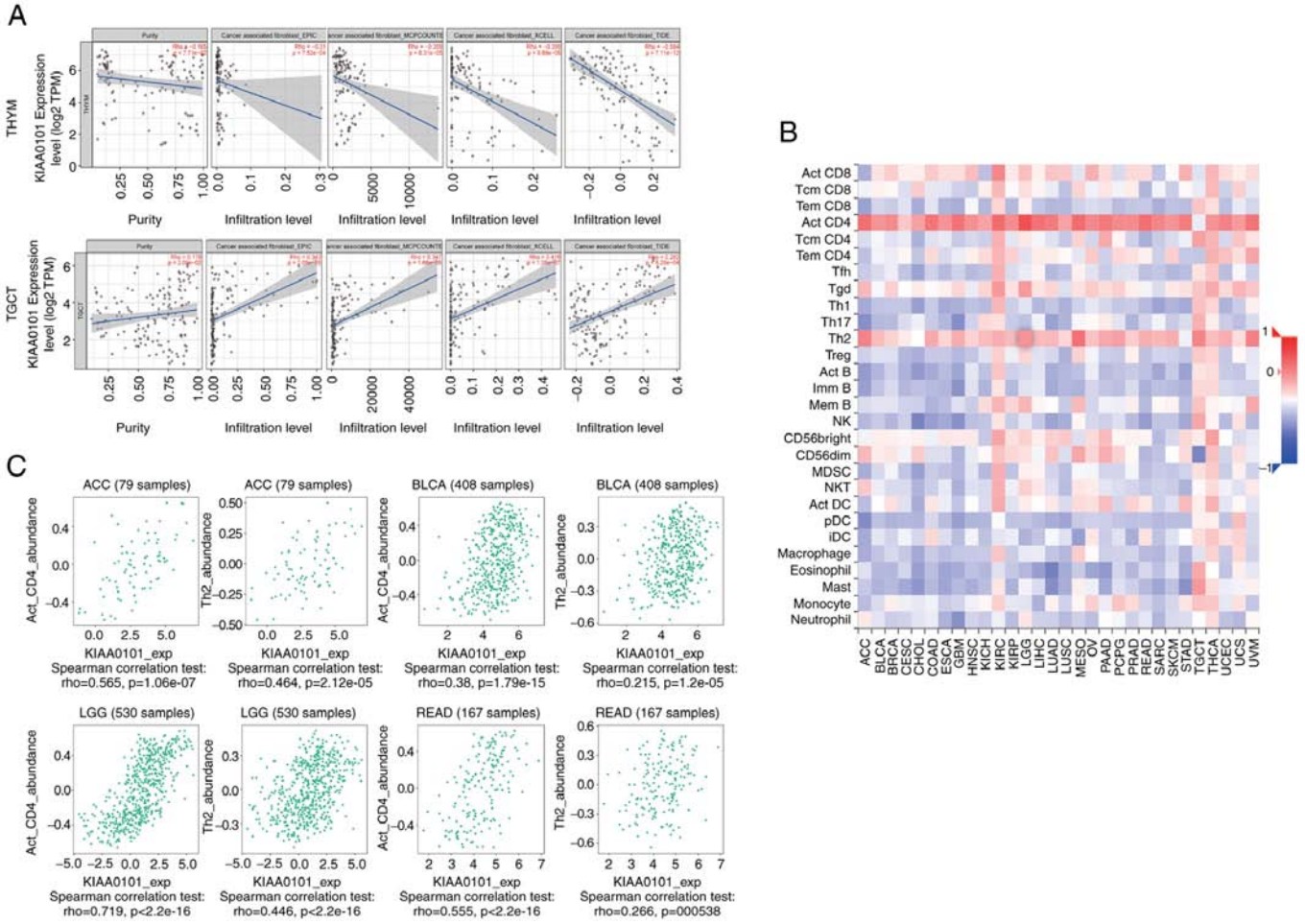

Figure S6. Transcription factor (TF) regulatory networks. (A) TF network. (B) Bubble plot of TF alterations in 14 cancers. (C) Enrichment score of TFs in 14 cancer types. (D) Heat map presents the percentage of cancers in which a gene has an effect (FDR ≤0.05) on the pathway among selected cancers types; the number in each cell indicates the percentage. PCLAF, PCNA clamp associated factor, also known as KIAA0101; DEGs, differentially expressed genes.