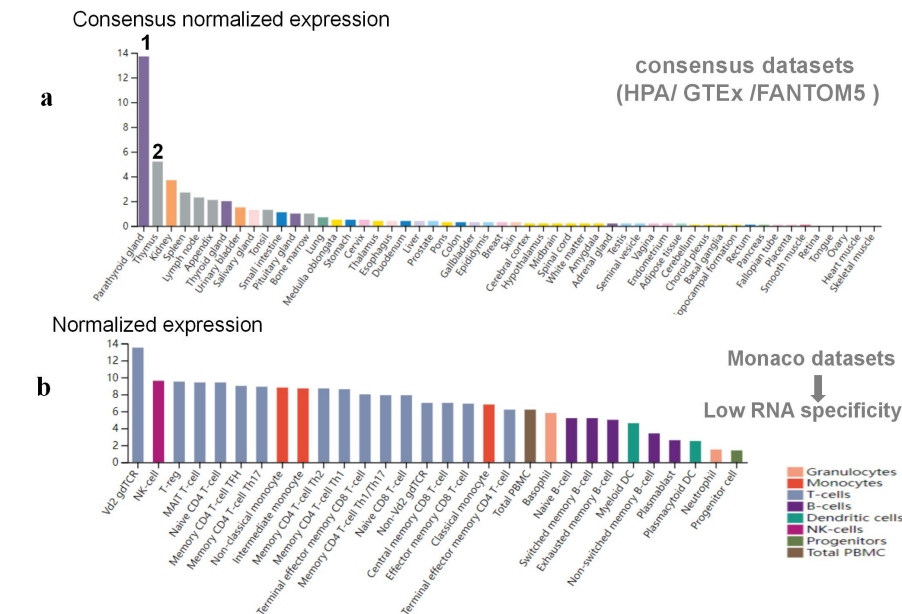


A Prognostic and Immunological Analysis of KLHDC7B in Pan-Cancer: A Potential Target for Immunotherapy and Survival

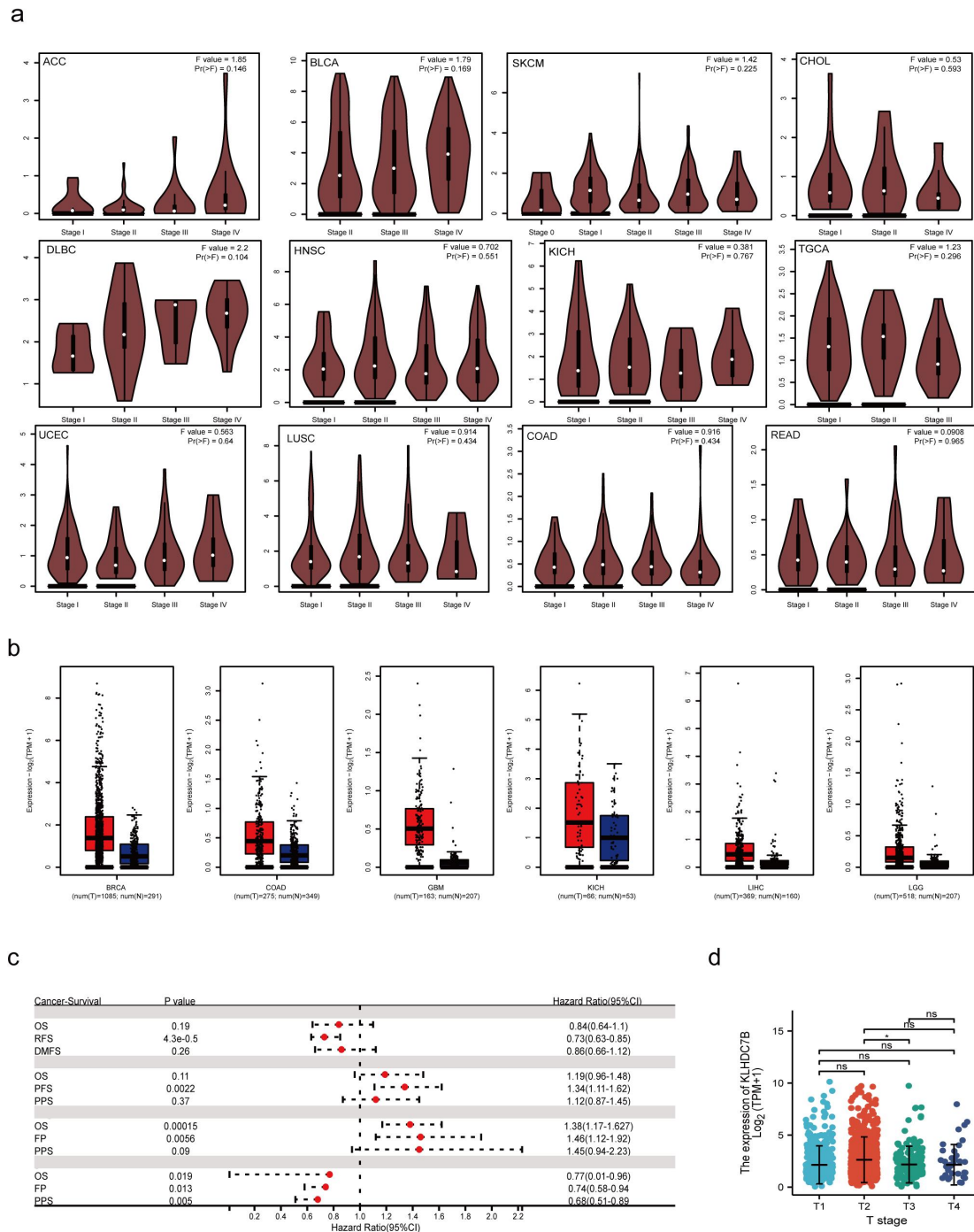
Supplementary data



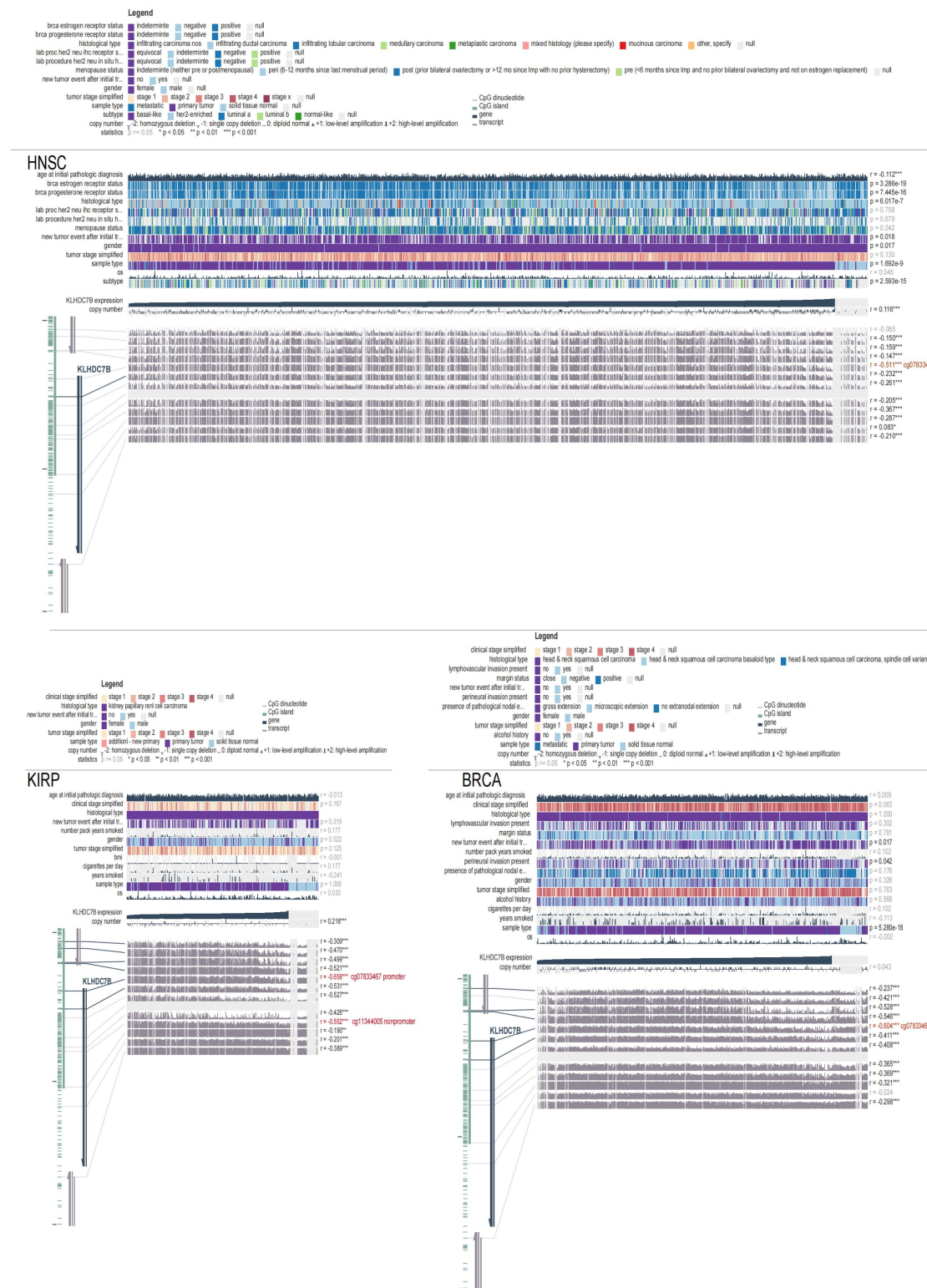
Supplementary Fig.S1 Structural characteristics of KLHDC7B in different species. (a) Genomic location of human KLHDC7B; (b) Conserved domains of KLHDC7B protein among different species



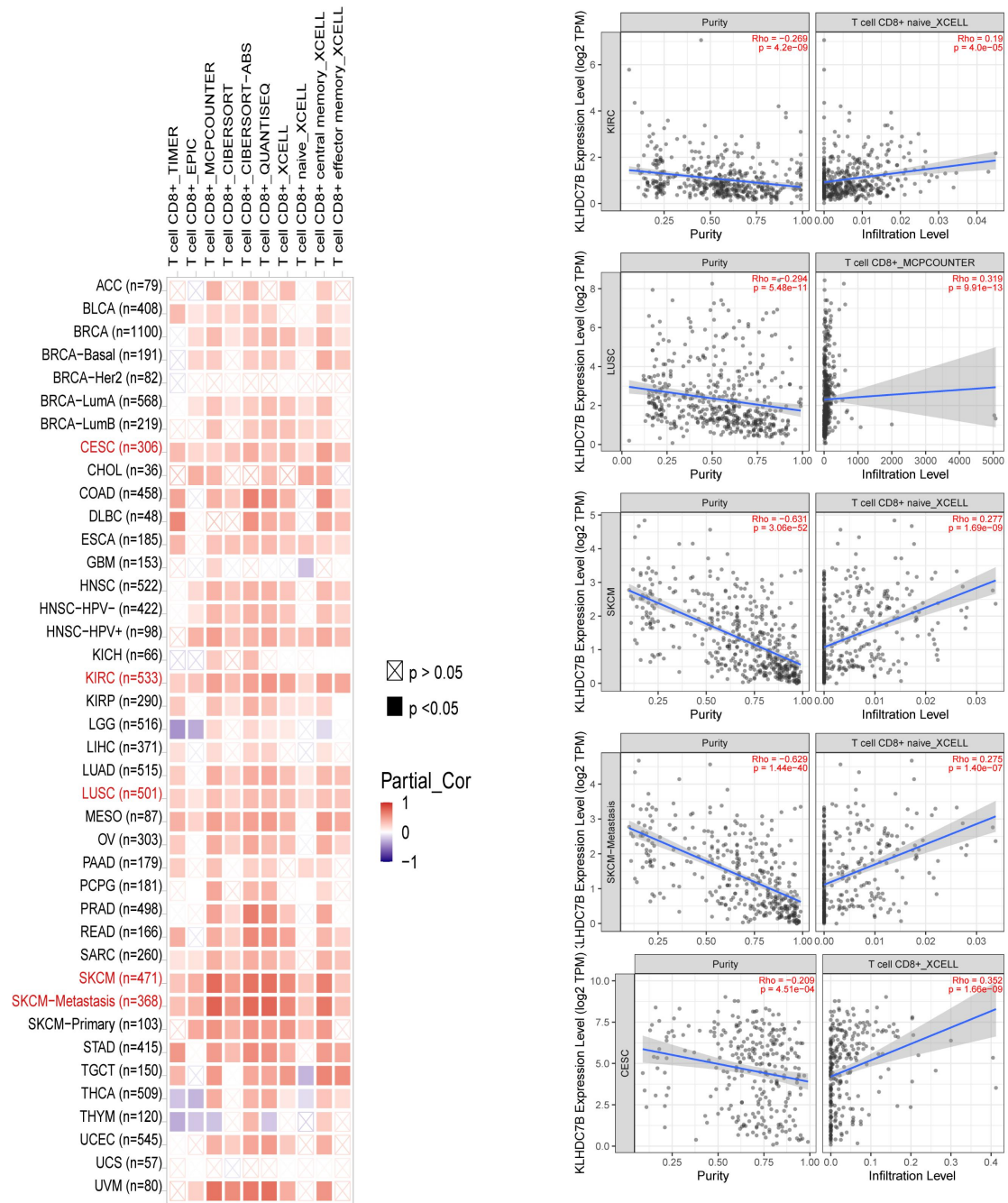
Supplementary Fig.S2 Expression level of KLHDC7B in different cells, tissues in the normal physiological state. We analyzed the expression of the KLHDC7B gene in different tissues using the consensus datasets of HPA, GTEx and FANTOM5 (a) or in different immune cells using the consensus dataset of HPA, Monaco and Schmiedel (b)



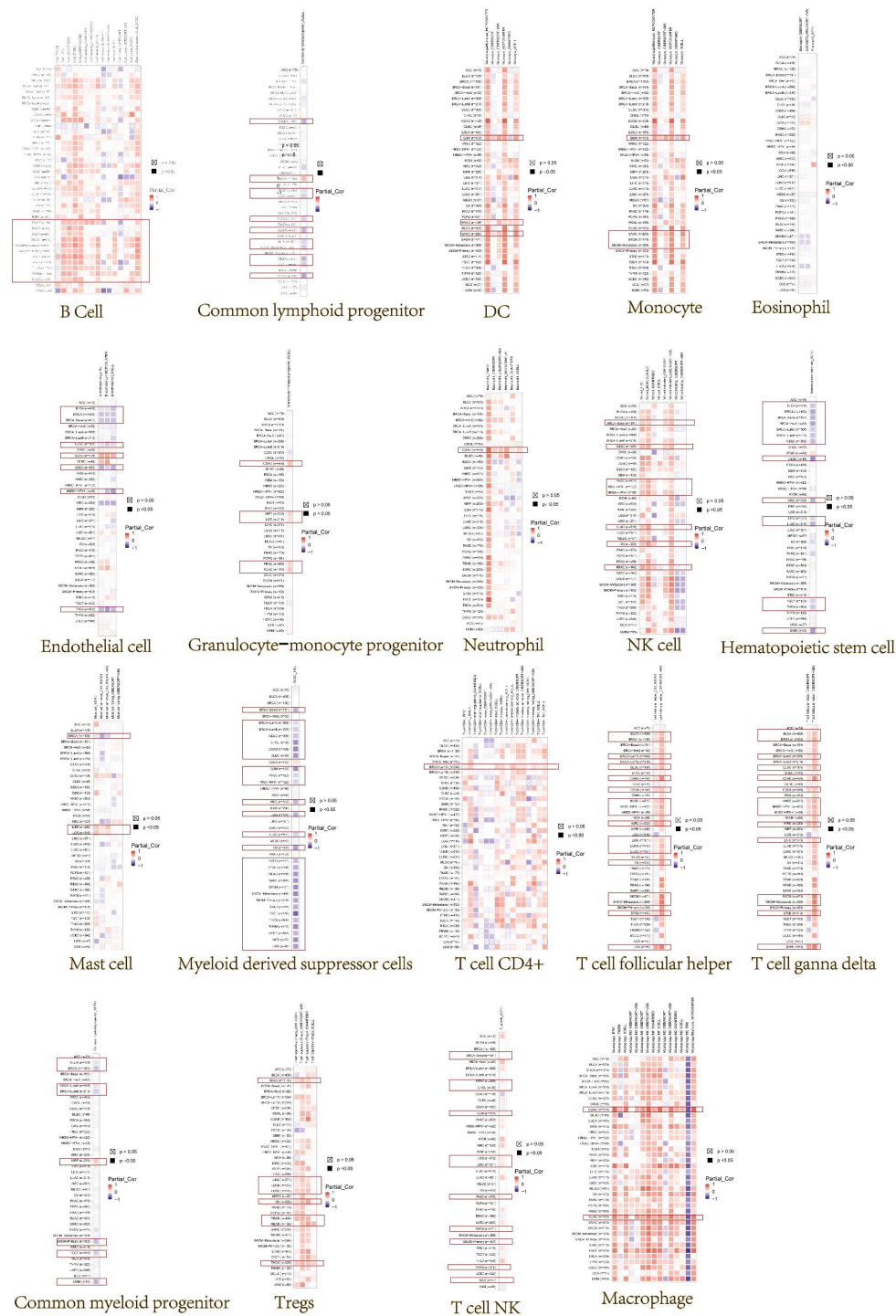
Supplementary Fig.S3 (a)Based on the TCGA data, the expression levels of the KLHDC7B gene were analyzed by the main pathological stages (stage I, stage II, stage III, and stage IV) of ACC, BLCA, BRCA, CESA, HNSC, KICH, LUHC, SKCM, READ, TGCA, UCEC. Log₂ (TPM + 1) was applied for log-scale. **(b)** Meta-analysis on the correlation between KLHDC7B expression and cancer prognosis. **(c)**Forest map showed the expression level of the KLHDC7B gene in breast cancer, ovarian cancer, lung cancer and gastric cancer.**(d)** Expression of KLHDC7B in different tumor stages



Supplementary Fig.S4 Association between KLHDC7B DNA methylation and gene expression for the KIRP, BRCA, HNSC cases of TCGA. We used the MEXPRESS approach to analyze the DNA methylation level of KLHDC7B of multiple probes. The promoter region probes are highlighted. The beta value of methylation, the Benjamini-Hochberg-adjusted P-value and the Pearson correlation coefficients (R) are displayed



Supplementary Fig.S5 Correlation analysis between KLHDC7B expression and immune infiltration of CD8+ T-cells. Different algorithms were used to explore the potential correlation between the expression level of KLHDC7B gene and the infiltration level of CD8+ T-cells across all types of cancer in TCGA



Supplementary Fig.S5 Correlation analysis between the KLHDC7B expression and immune infiltration with CIBERSORT, CIBERSORT-ABS, TIMER, xCell, McP-counter, quanTIseq, and EPIC algorithms. p-values <.05 were considered statistically significant

