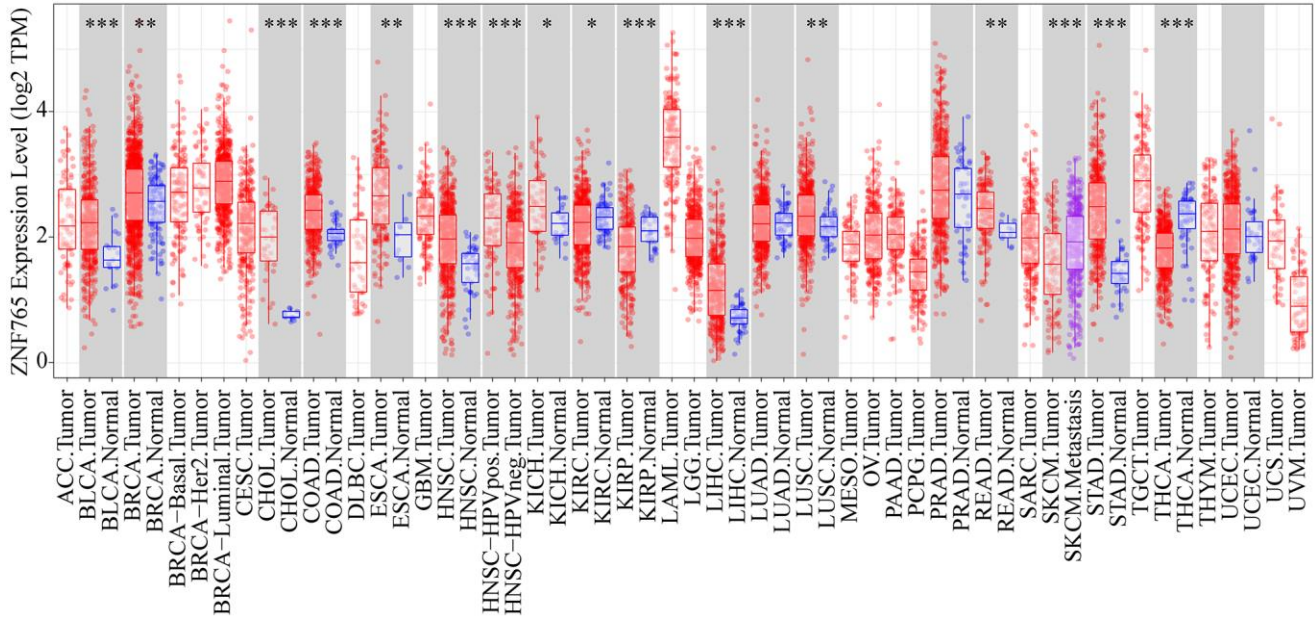
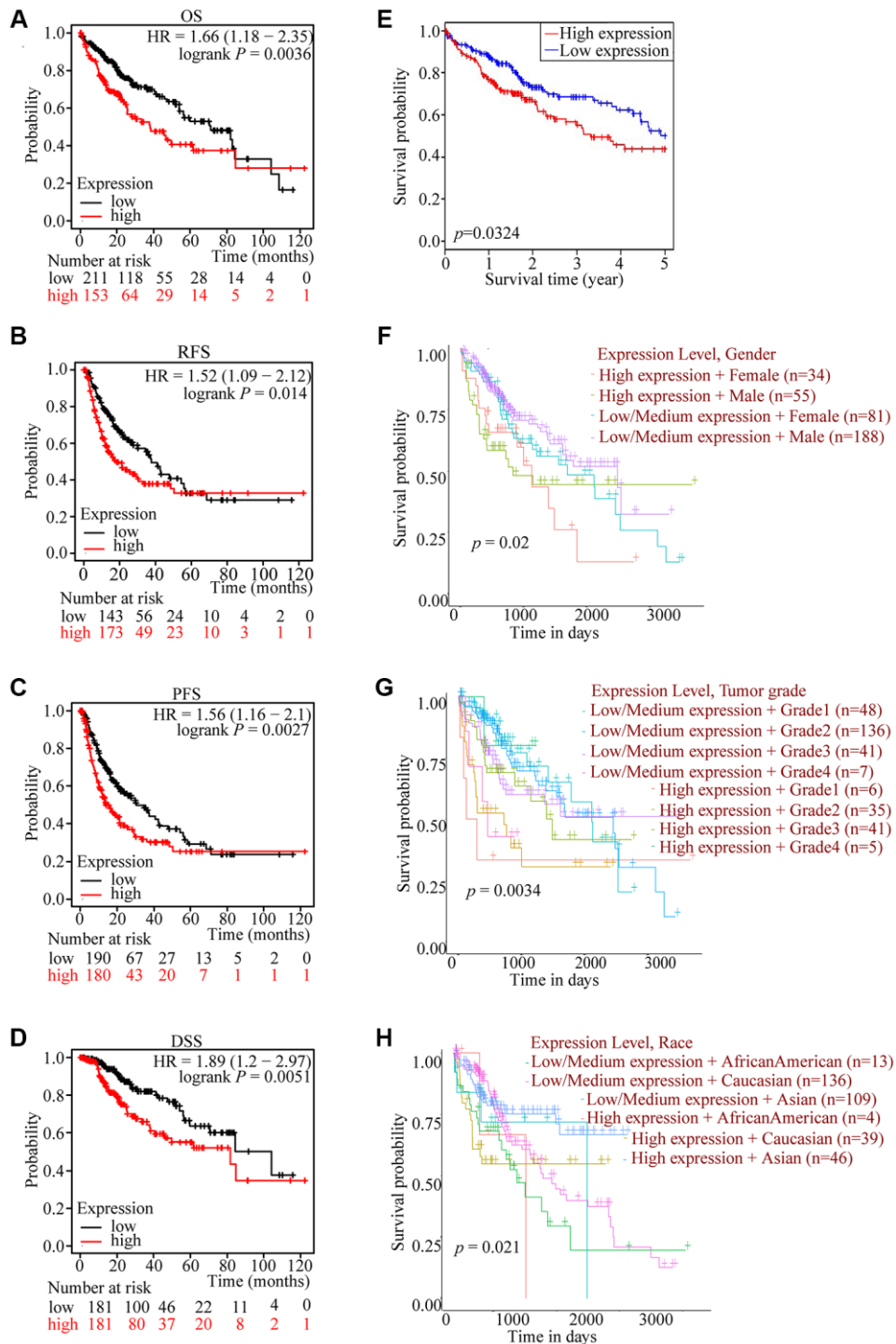


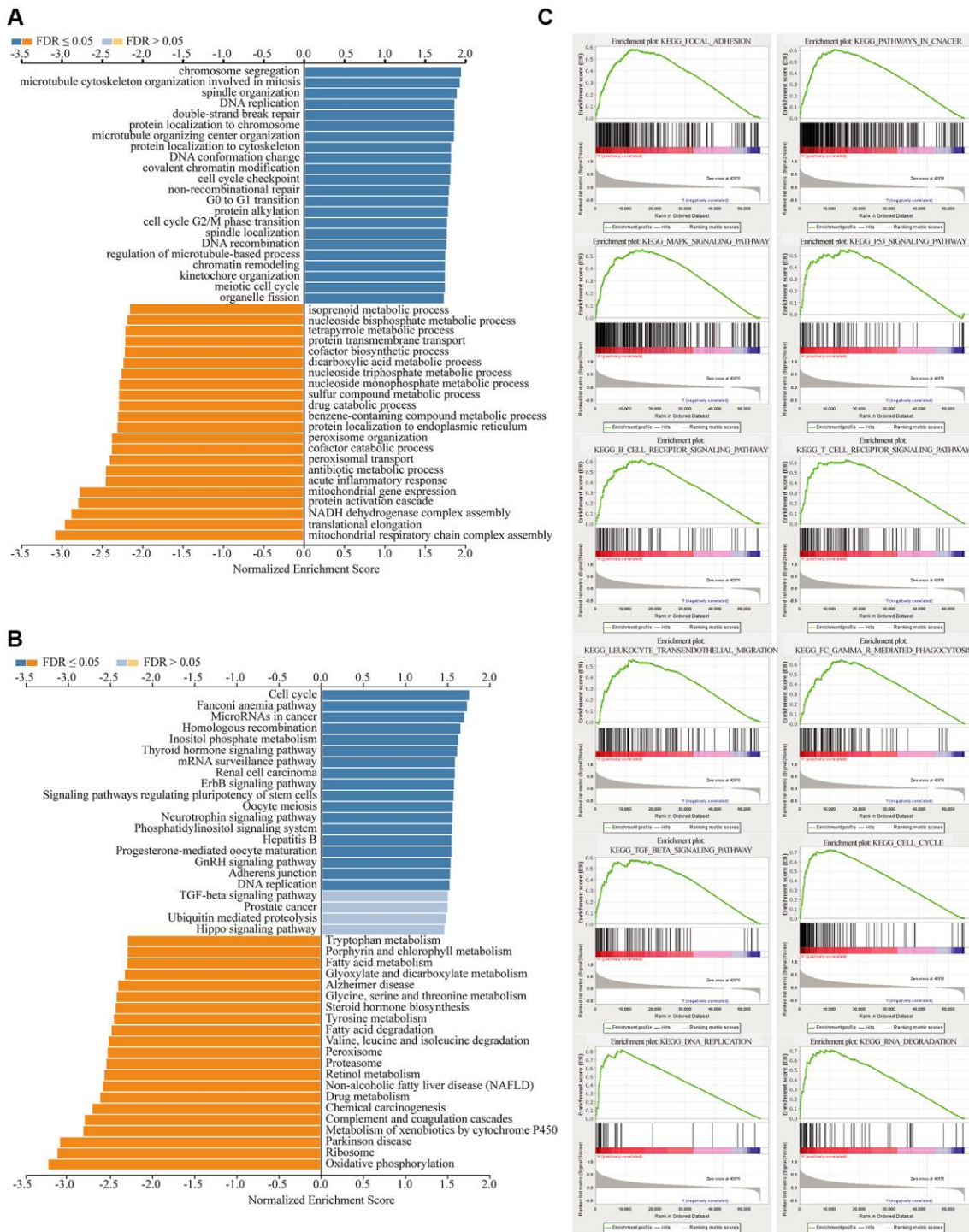
SUPPLEMENTARY FIGURES



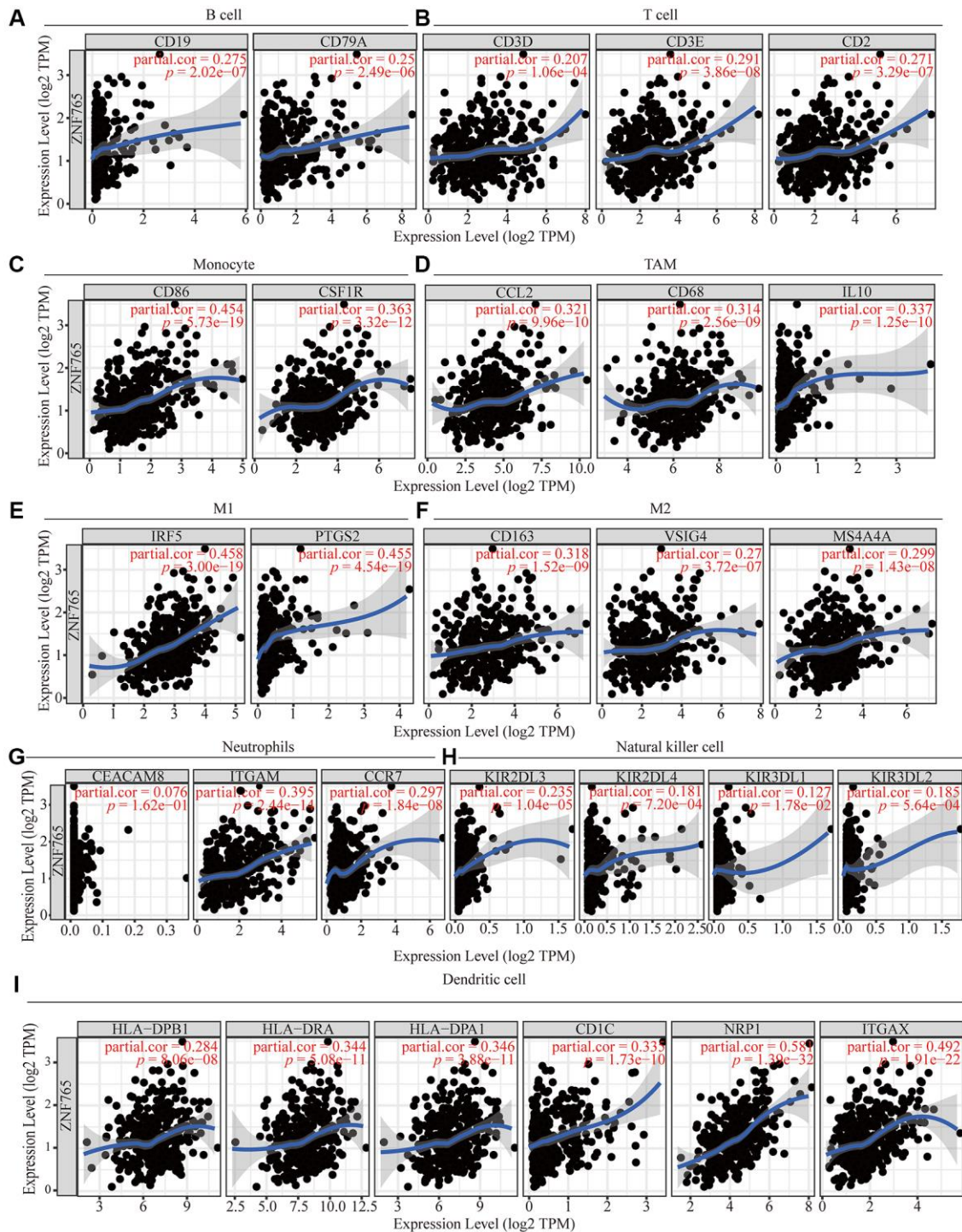
Supplementary Figure 1. The expression of ZNF765 in pan-cancers. Level of ZNF765 expression in a variety of cancer tissues (data from the TIMER database) (** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$).



Supplementary Figure 2. The function of high ZNF765 expression in prognosis. (A–D) Kaplan-Meier analysis of OS (overall survival), RFS (relapse-free survival), PFS (progression-free survival), and DSS (disease-specific survival) in the HCC patients. (E) Effect of ZNF765 mRNA expression level on HCC patient survival by HCCDB ($p = 0.0324$). (F) Survival probability of HCC patients with different genders and ZNF765 expression. (G) Survival probability of HCC patients with different tumor grades and ZNF765 expression. (H) Survival probability of HCC patients between different races and ZNF765 expression.



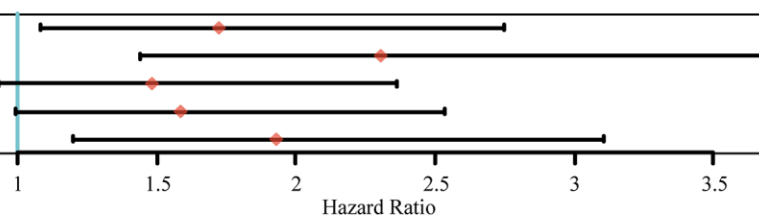
Supplementary Figure 3. Enrichment analysis of ZNF765 functional networks in HCC. (A) GO pathway analysis. Dark blue and orange indicate an FDR ≤ 0.05, whereas light blue and orange indicate an FDR greater than 0.05. FDR, false discovery rate. **(B)** KEGG pathway analysis. FDR ≤ 0.05 is indicated by dark blue and orange; FDR > 0.05 is indicated by light blue and orange. **(C)** GSEA analysis of ZNF765 based on expression in the TCGA-LIHC dataset. Abbreviation: NES: normalized enrichment score. NOM *p*-value: nominal *p* value; FDR *q*-val: false discovery rate.



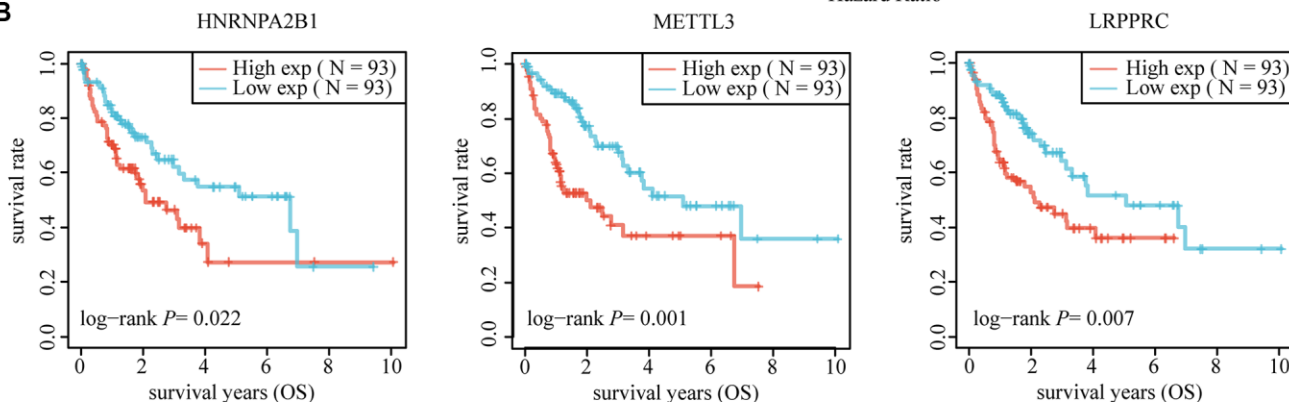
Supplementary Figure 4. Correlation of ZNF765 expression and the marker genes of infiltrating immune cells in HCC (TIMER). The scatter plots showed correlation between ZNF765 expression and the gene markers of (A) B cell (CD79A, CD19); (B) T cell (CD3D, CD3E, CD2); (C) Monocyte (CD86, CSF1R); (D) TAM cell (CCL2, CD68, IL10); (E) M1 cell (IRF5, PTGS2); (F) M2 cell (CD163, VSIG4, MS4A4A); (G) Neutrophils (ITGAM, CCR7, CEACAM8); (H) Natural killer cell (KIR2DL3, KIR2DL4, KIR3DL1, KIR3DL2); (I) Dendritic cell (HLA-DPB1, HLA-DRA, HLA-DPA1, CD1C, NRP1, ITGAX).

A *ZNF765* high expression

Names	<i>P</i> value	Hazard Ratio(95% CI)
HNRNPA2B1	0.0221	1.7235(1.0814,2.7467)
METTL3	0.0005	2.3047(1.4376,3.6947)
RBMX	0.0963	1.4829(0.9321,2.3592)
RBM15B	0.0540	1.5858(0.9921,2.5347)
LRPPRC	0.0068	1.9295(1.1993,3.1043)



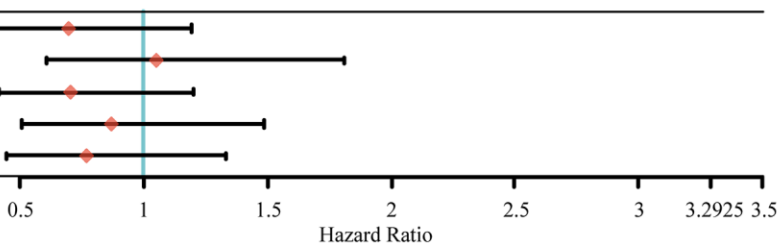
B



C

ZNF765 low expression

Names	<i>P</i> value	Hazard Ratio(95% CI)
HNRNPA2B1	0.1897	0.6989(0.4091,1.1938)
METTL3	0.8522	1.0529(0.6123,1.8105)
RBMX	0.1996	0.7068(0.4159,1.2011)
RBM15B	0.6154	0.8713(0.5091,1.4913)
LRPPRC	0.3515	0.7713(0.4466,1.3319)



Supplementary Figure 5. ZNF765 affects the prognosis of HCC patients by affecting some m6A regulators. (A) HNRNPA2B1, METTL3, and LRPPRC were risk factors for HCC when ZNF765 was highly expressed. **(B)** When ZNF765 was highly expressed, high expression of HNRNPA2B1, METTL3 or LRPPRC led to poor survival in HCC patients. **(C)** HNRNPA2B1, METTL3, and LRPPRC had no effect on the prognosis of HCC patients when ZNF765 was lowly expressed.