Figure S1. SFXN1 expression in pan-cancer based on (A) The Cancer Genome Atlas and (B) Tumor Immune Estimation Resource. *P<0.05, **P<0.01 and ***P<0.001. ns, not significant; SFXN1, sideroflexin 1.

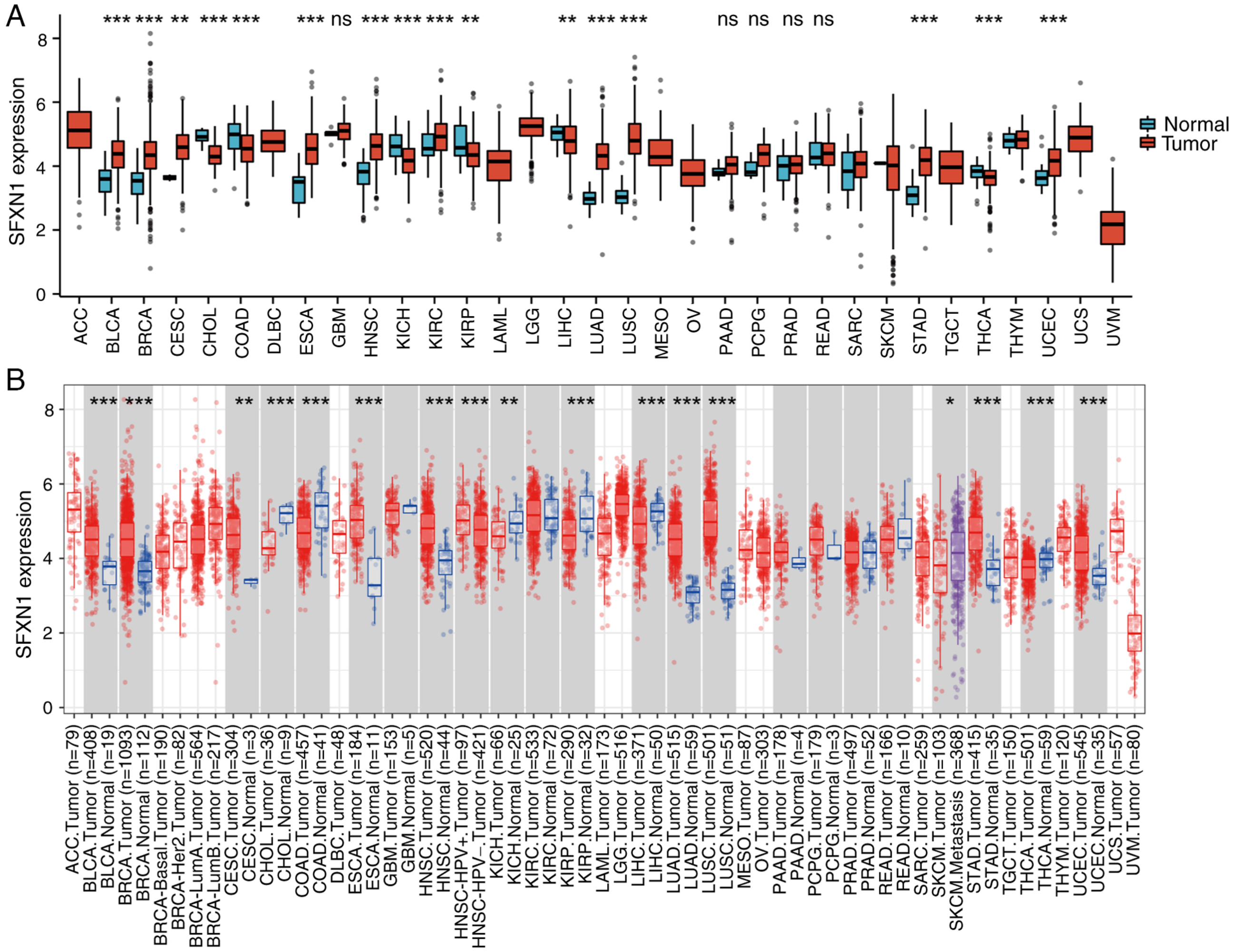


Figure S2. Prognostic value of SFXN1 in pan-cancer. OS of patients with (A) BRCA, (B) LAML and (C) KIRC based on Gene Expression Profiling Interactive Analysis, and (D) BRCA, (E) ESCA, (F) HNSC, (G) KIRC, (H) LIHC, (I) LUAD, (J) THCA and (K) UCEC based on Kaplan-Meier plotter. RFS of patients with (L) KIRC, (M) LUAD, (N) TGCT and (O) THCA based on Kaplan-Meier plotter. HR, hazard ratio; OS, overall survival; RFS, recurrence-free survival; SFXN1, sideroflexin 1; TPM, transcripts per million.

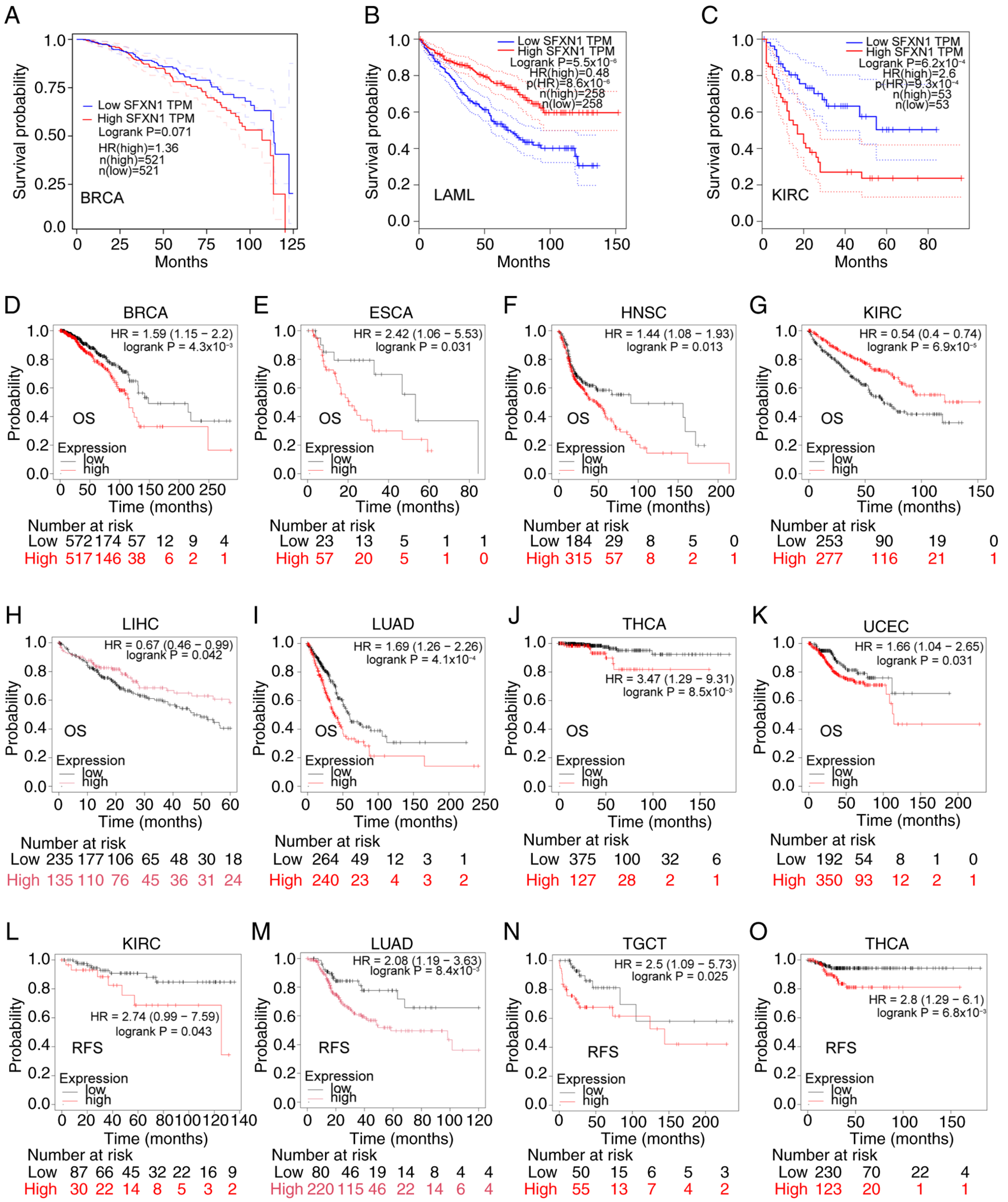


Figure S3. Correlation between SFXN1 expression and immune subtypes of pan-cancer in (A) ACC, (B) BLCA, (C) BRCA, (D) COAD, (E) GBM, (F) KIRC, (G) KIRP, (H) LIHC, (I) LUAD, (J) LUSC, (K) OV, (L) PAAD, (M) PRAD, (N) READ, (O) SARC, (P) SKCM, (Q) STAD, (R) TGCT, (S) THCA and (T) UCEC. CPM, counts per million; exp, expression; SFXN1, sideroflexin 1; C1, wound healing; C2, IFN-dominant; C3, inflammatory; C4, lymphocyte depletion; C5, immunologically quiet; C6, TGF-dominant.

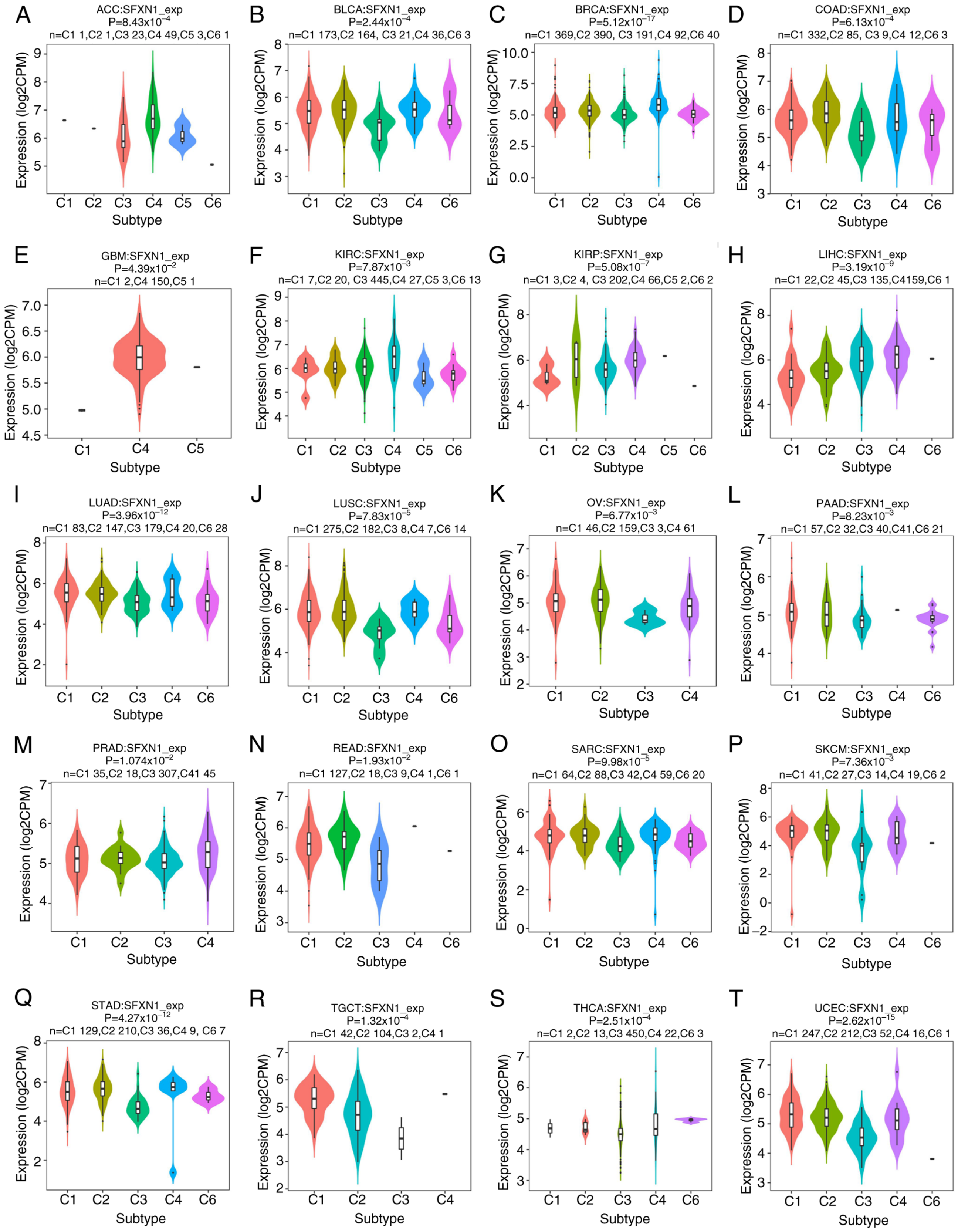


Figure S4. Mutation analysis of SFXN1 in pan-cancer. (A) Alteration frequency of SFXN1 in different tumor types. (B) Genetic alteration map of SFXN1 in pan-cancer. (C) Location of 58 SFXN1 mutations. Correlation between SFXN1 and (D) TMB and (E) MSI in pan-cancer. $^{*}P<0.05$, $^{**}P<0.01$ and $^{***}P<0.001$. CNA, copy number alteration; MSI, microsatellite instability; NSCLC, non-small cell lung cancer; NSGCT, non-seminomatous germ cell tumor; SFXN1, sideroflexin 1; SV, structural variant; TMB, tumor mutation burden.

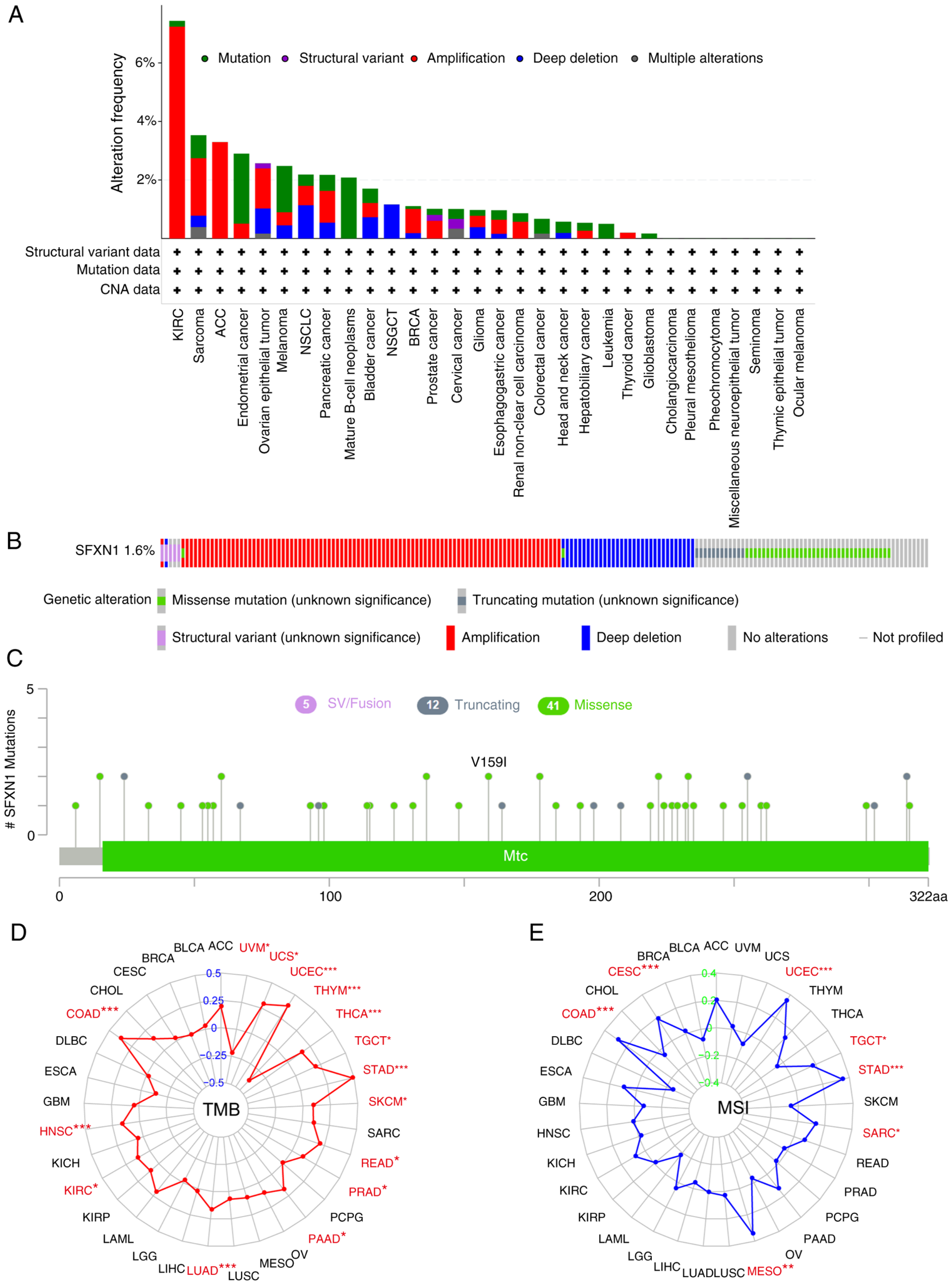
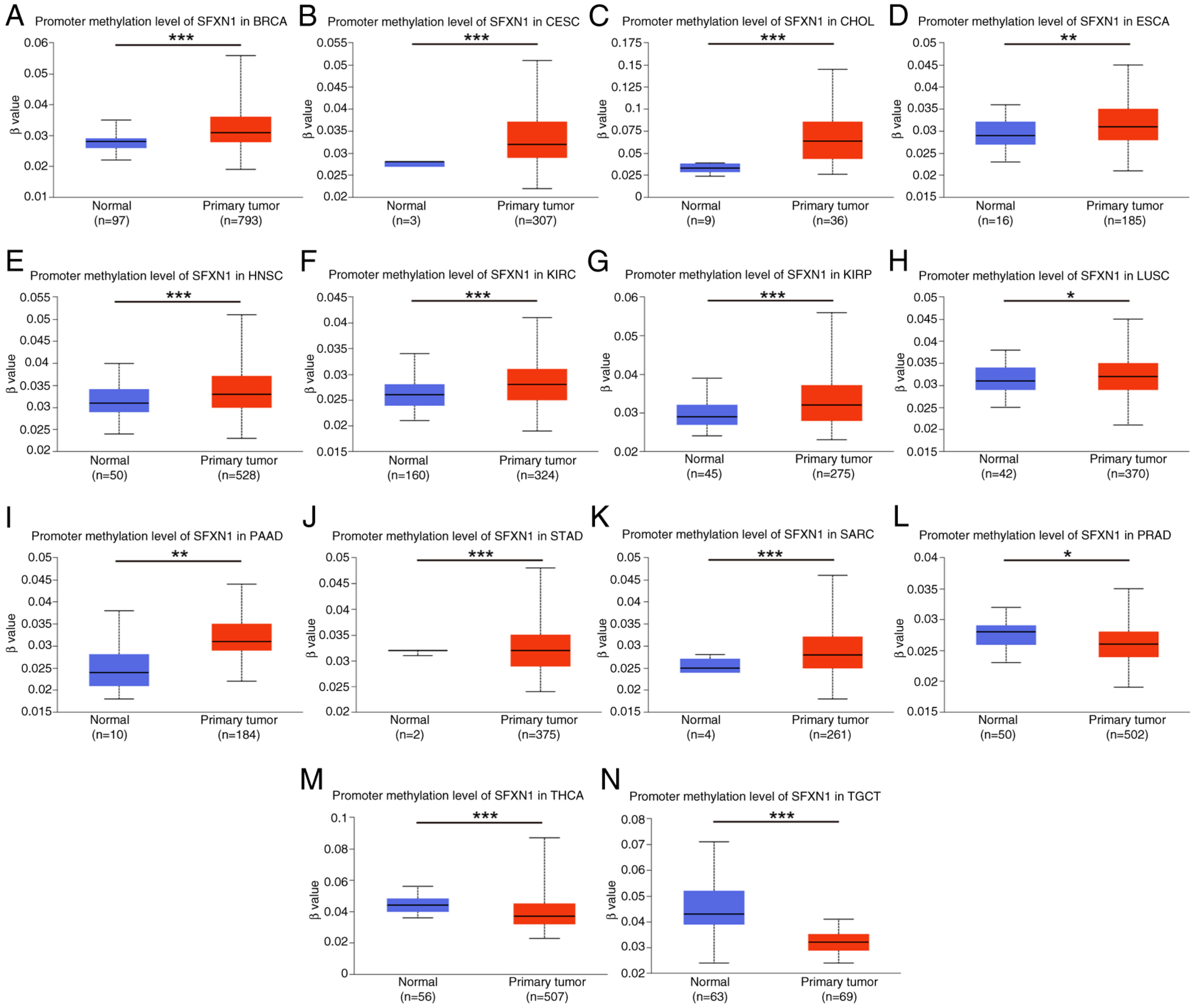


Figure S5. DNA methylation of SFXN1 in pan-cancer. Promoter methylation level of SFXN1 in (A) BRCA, (B) CESC, (C) CHOL, (D) ESCA, (E) HNSC, (F) KIRC, (G) KIRP, (H) LUSC, (I) PAAD, (J) STAD, (K) SARC, (L) PRAD, (M) THCA and (N) TGCT. $^{*}P<0.05$, $^{**}P<0.01$ and $^{***}P<0.001$. SFXN1, sideroflexin 1.



A Promoter methylation level of SFXN1 in BRCA

B Promoter methylation level of SFXN1 in CESC

C Promoter methylation level of SFXN1 in CHOL

D Promoter methylation level of SFXN1 in ESCA

E Promoter methylation level of SFXN1 in HNSC

F Promoter methylation level of SFXN1 in KIRC

G Promoter methylation level of SFXN1 in KIRP

H Promoter methylation level of SFXN1 in LUSC

I Promoter methylation level of SFXN1 in PAAD

J Promoter methylation level of SFXN1 in STAD

K Promoter methylation level of SFXN1 in SARC

L Promoter methylation level of SFXN1 in PRAD

M Promoter methylation level of SFXN1 in THCA

N Promoter methylation level of SFXN1 in TGCT

Figure S6. SFXN1 expression in normal cells and tissues based on the Human Protein Atlas. SFXN1 expression in various cell types of the (A) bone marrow, (B) lungs, (C) lymph nodes, (D) PBMCs, (E) skin and (F) stomach at the single-cell level. NK, natural killer; nTPM, normalized transcripts per million; PBMC, peripheral blood mononuclear cell; SFXN1, sideroflexin 1; UMAP, uniform manifold approximation and projection.

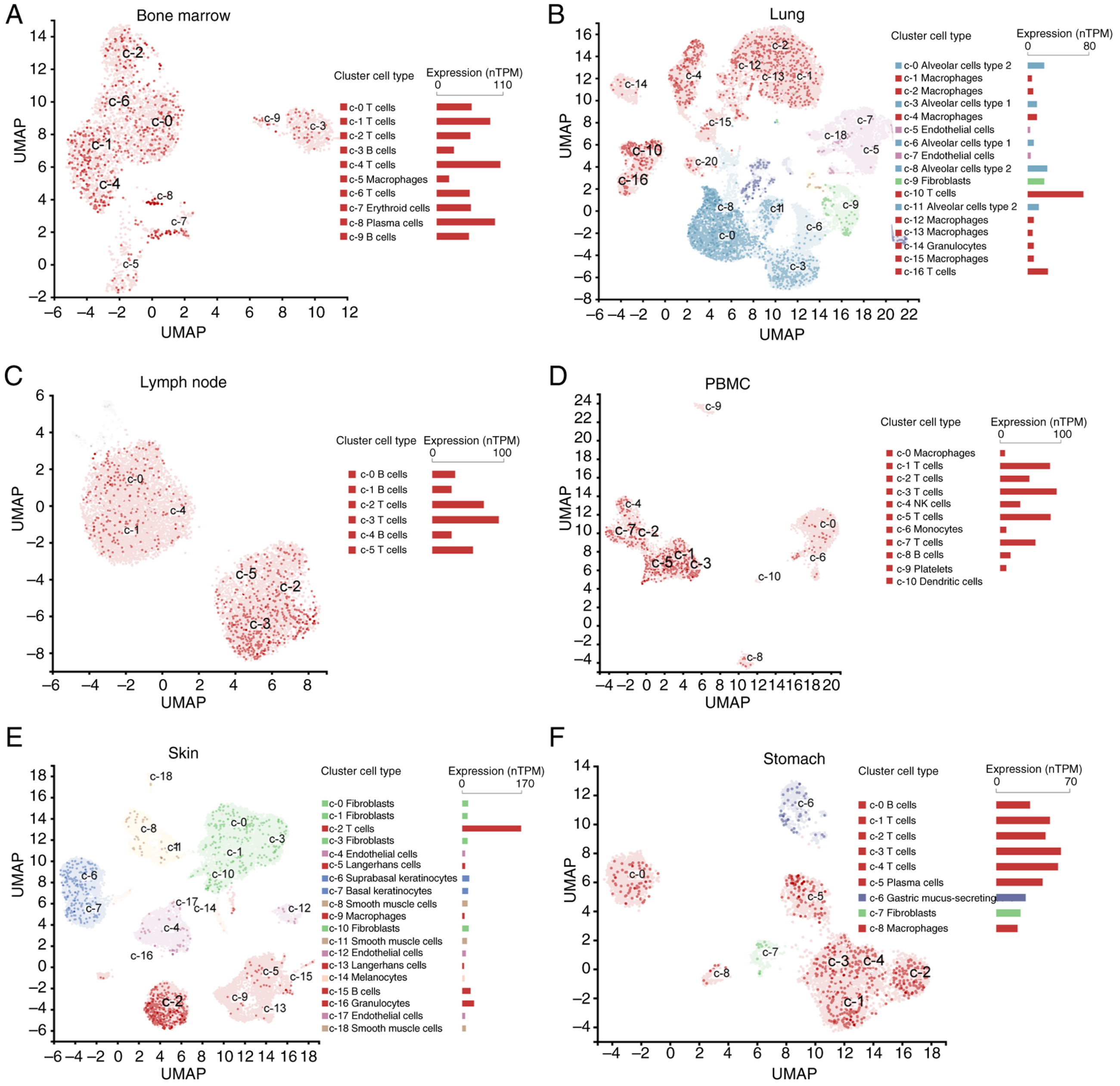


Figure S7. Protein-protein interaction network of sideroflexin 1-related genes in pan-cancer. Genes were colored red to yellow based on their degree in Cytoscape.

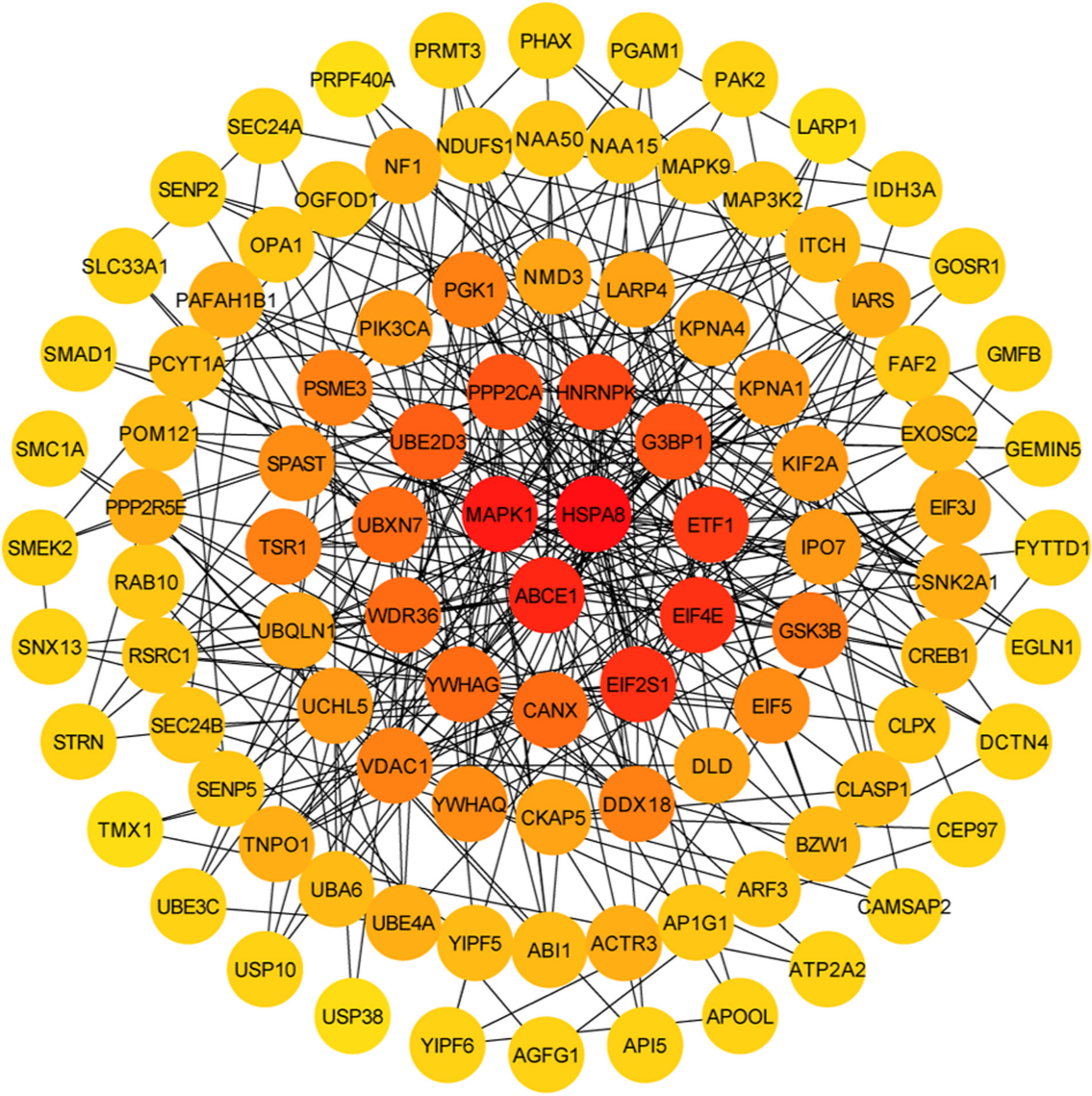


Figure S8. Heatmap of the positive correlation between sideroflexin 1 expression and the top 20 genes in pan-cancer from Gene Expression Profiling Interactive Analysis and visualized by Tumor Immune Estimation Resource 2.0.

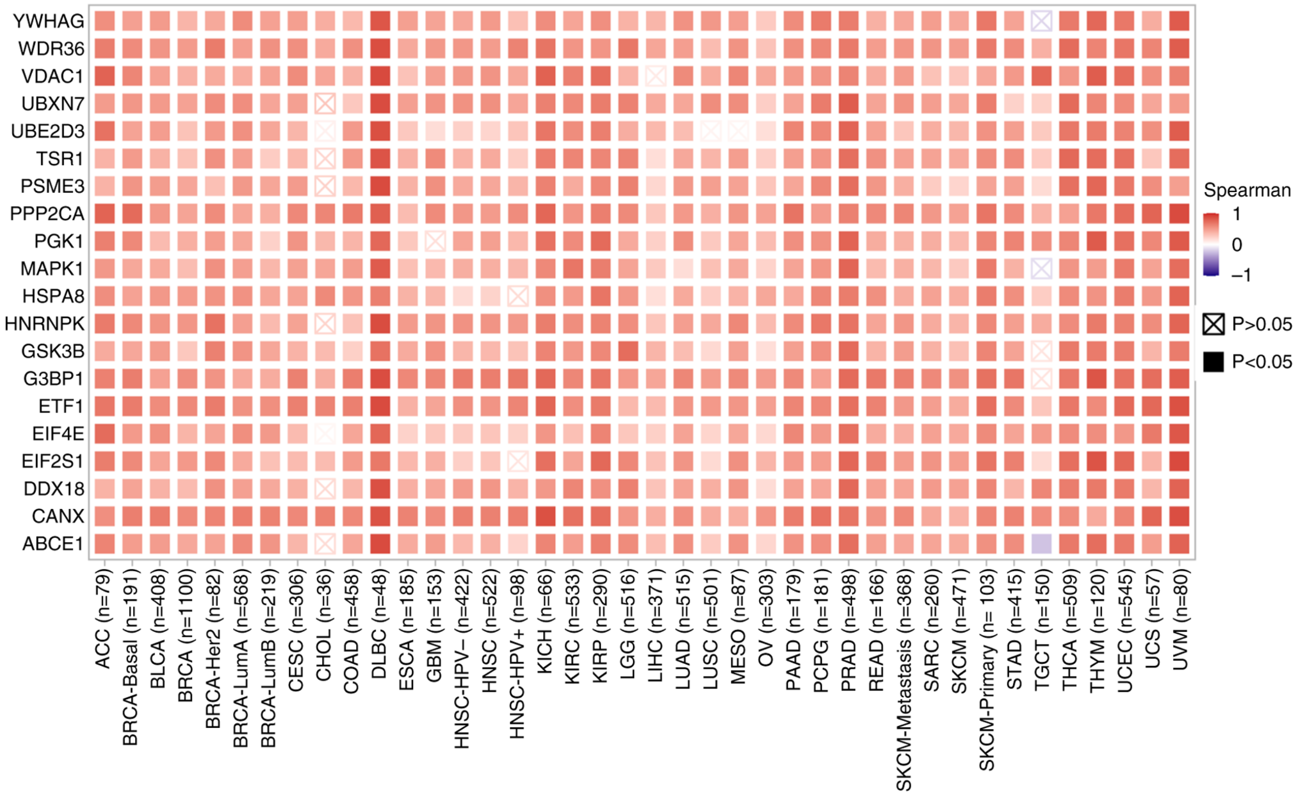


Figure S9. SFXN1 co-expressed gene heatmaps and enrichment analysis in LUAD. (A) Positively and (B) negatively co-expressed genes of SFXN1 in LUAD. Enrichment analysis of these associated genes for (C) biological processes, (D) cellular components, (E) molecular functions and (F) KEGG pathways. exp, expression; KEGG, Kyoto Encyclopedia of Genes and Genomes; LUAD, lung adenocarcinoma; SFXN1, sideroflexin 1.

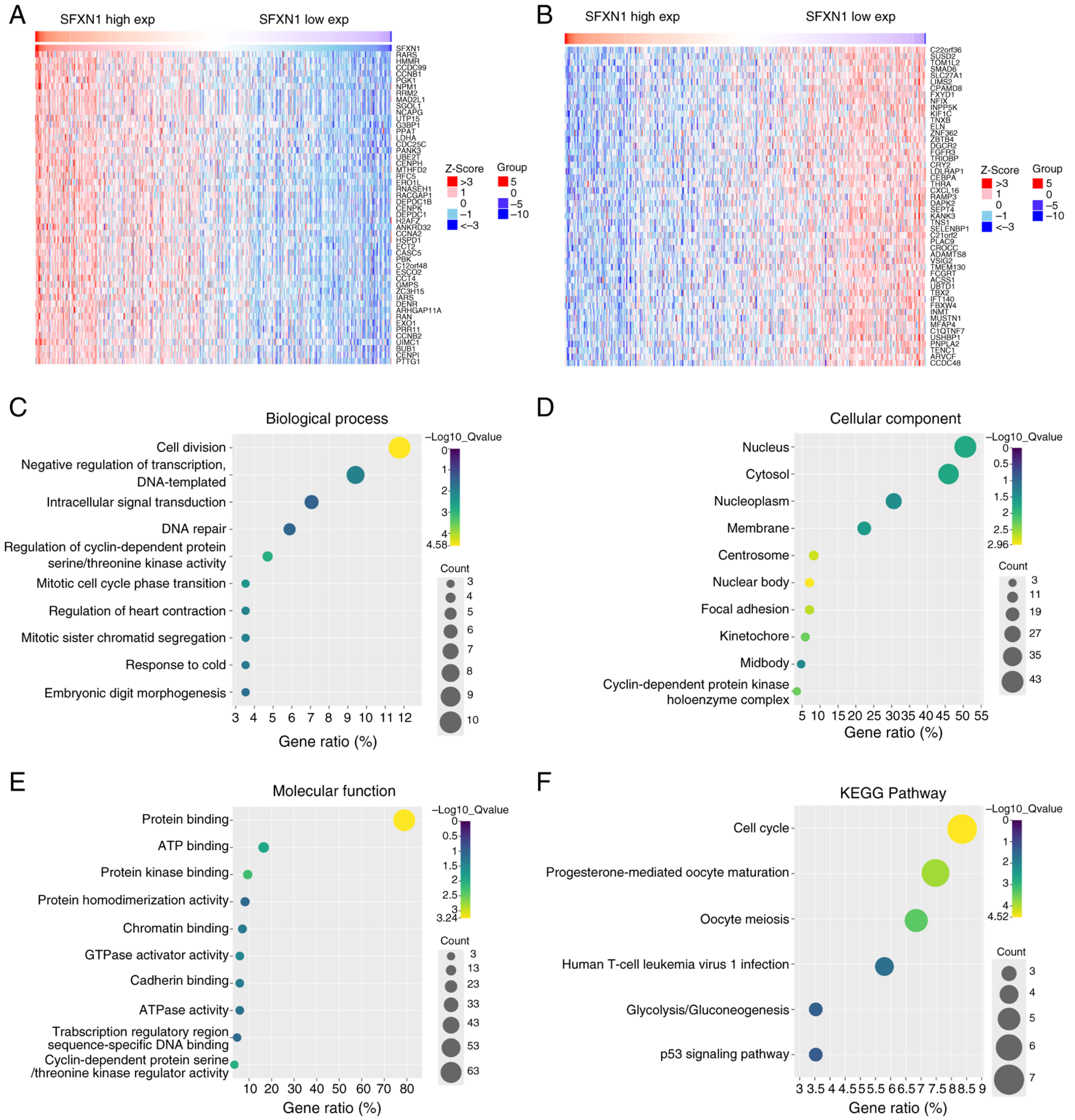


Figure S10. Gene set enrichment analysis of sideroflexin 1 co-expression genes in lung adenocarcinoma. (A) ‘Cell cycle’. (B) ‘PLK1 pathway’. (C) ‘Cell cycle checkpoints’. (D) ‘FOXM1 pathway’. (E) ‘G2 M checkpoints’. (F) ‘G1 S specific transcription’. (G) ‘Mitotic spindle checkpoint’. (H) ‘DNA strand elongation’. (I) ‘DNA replication’. FDR, false discovery rate; KEGG, Kyoto Encyclopedia of Genes and Genomes; NES, normalized enrichment score; P.adj, adjusted P-value; PID, Pathway Interaction Database; PLK1, polo-like kinase 1.