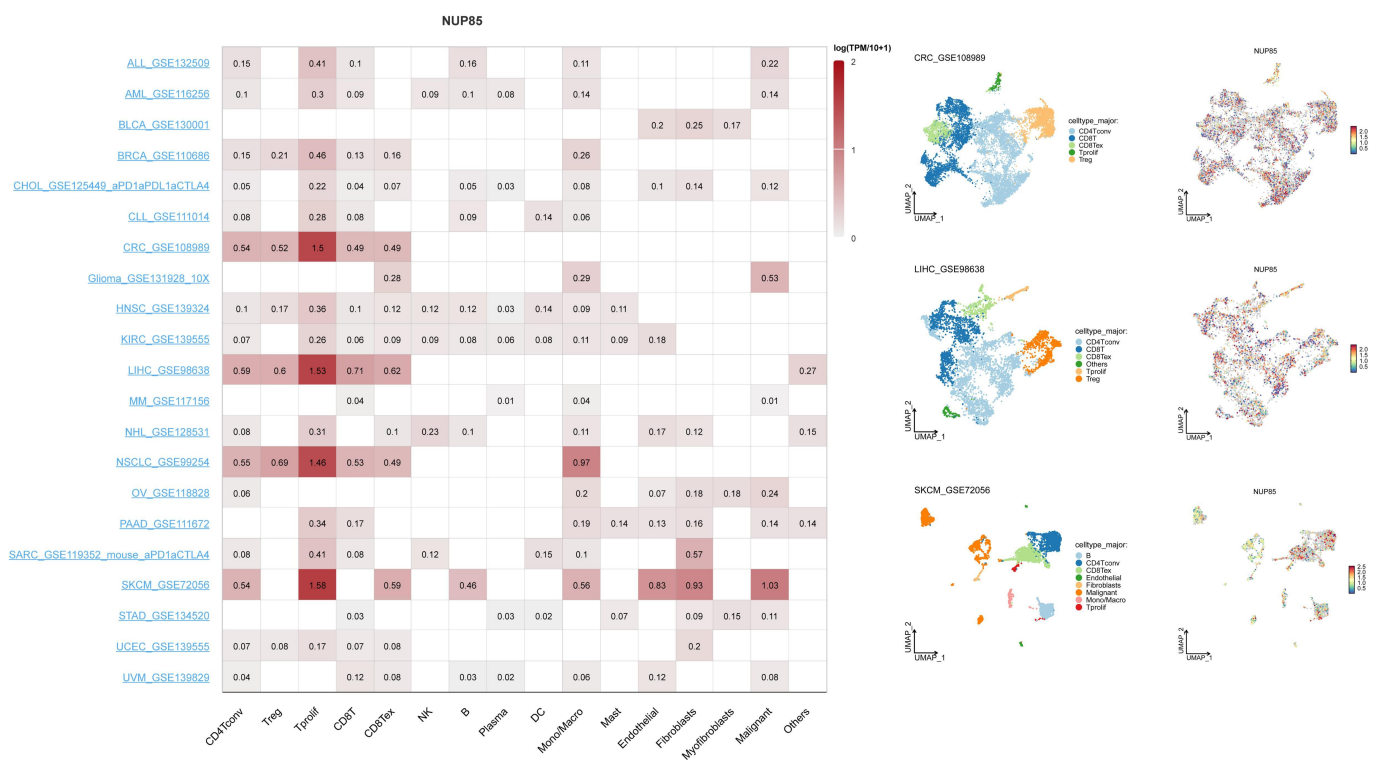
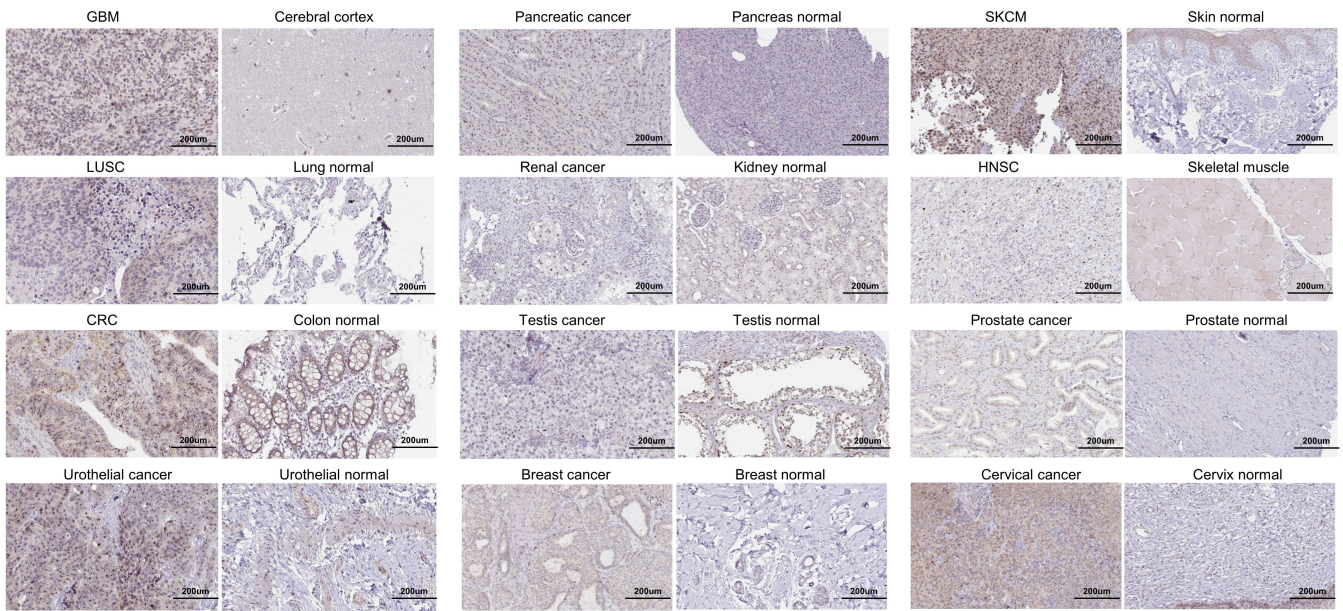


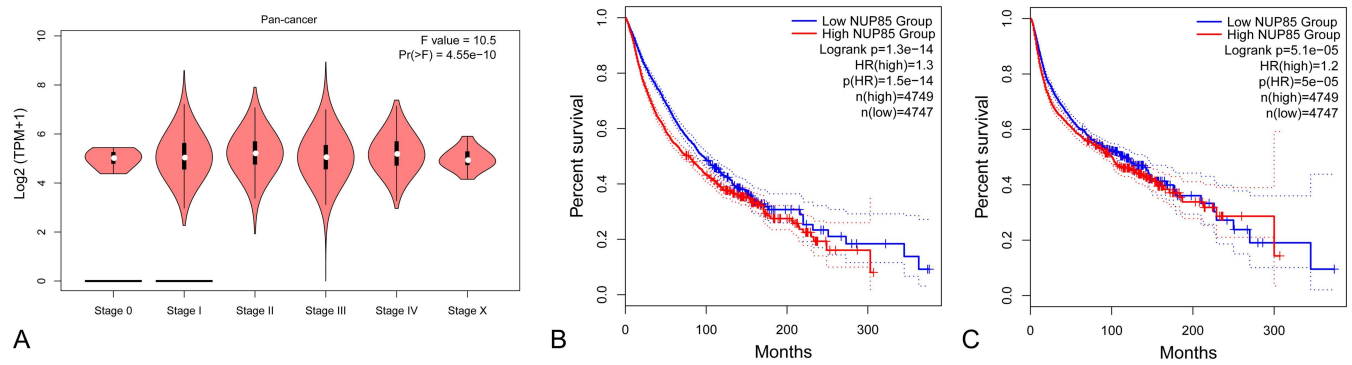
Supplementary Figure 1: The CERES values of NUP85 in various tumor cell lines sourced from the DepMap database. Note: More negative CERES values indicate a greater impact on cell proliferation upon gene knockout.



Supplementary Figure 2: The expression of NUP85 in single-cell sequencing datasets of different tumors sourced from the TISCH database.



Supplementary Figure 3: Immunohistochemical staining results of NUP85 in various tumor tissues and corresponding normal tissues.



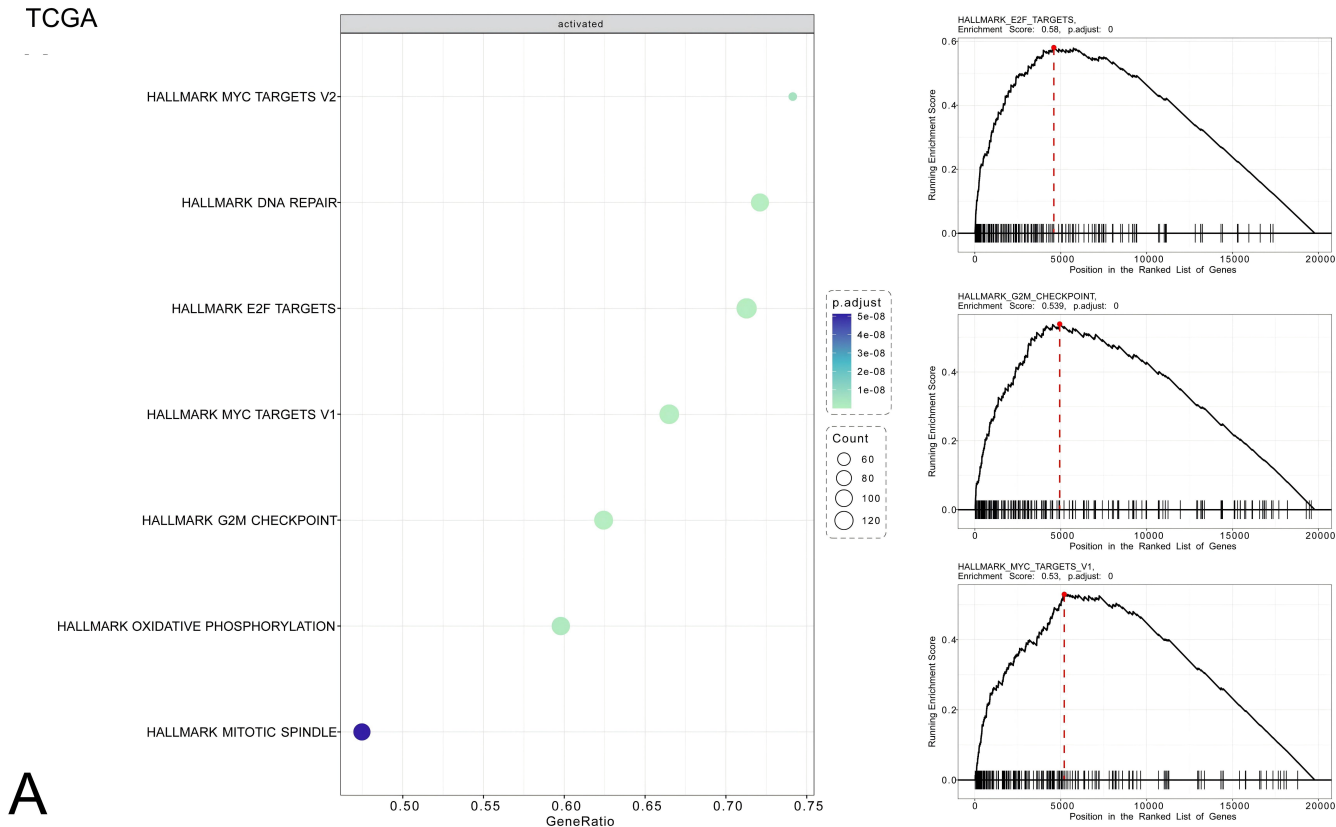
Supplementary Figure 4: The correlation of NUP85 with tumor stage and prognosis sourced from the GEPIA database.

(A) Stage Expression Differential Analysis of NUP85 Across All Tumors.

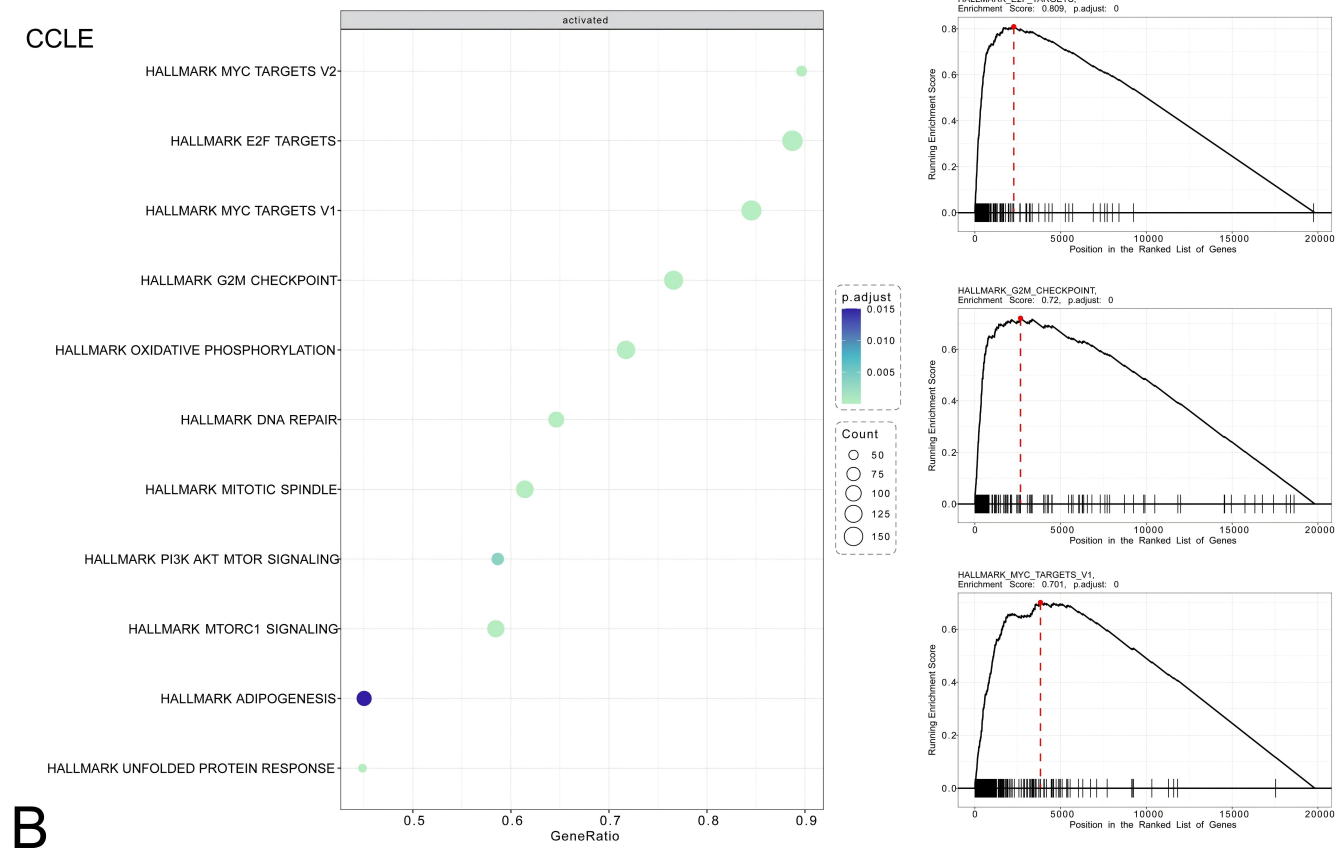
(B) Overall survival curve comparing high and low NUP85 expression groups in pan-cancer.

(C) Disease-free survival curve comparing high and low NUP85 expression groups in pan-cancer.

TCGA



CCLC

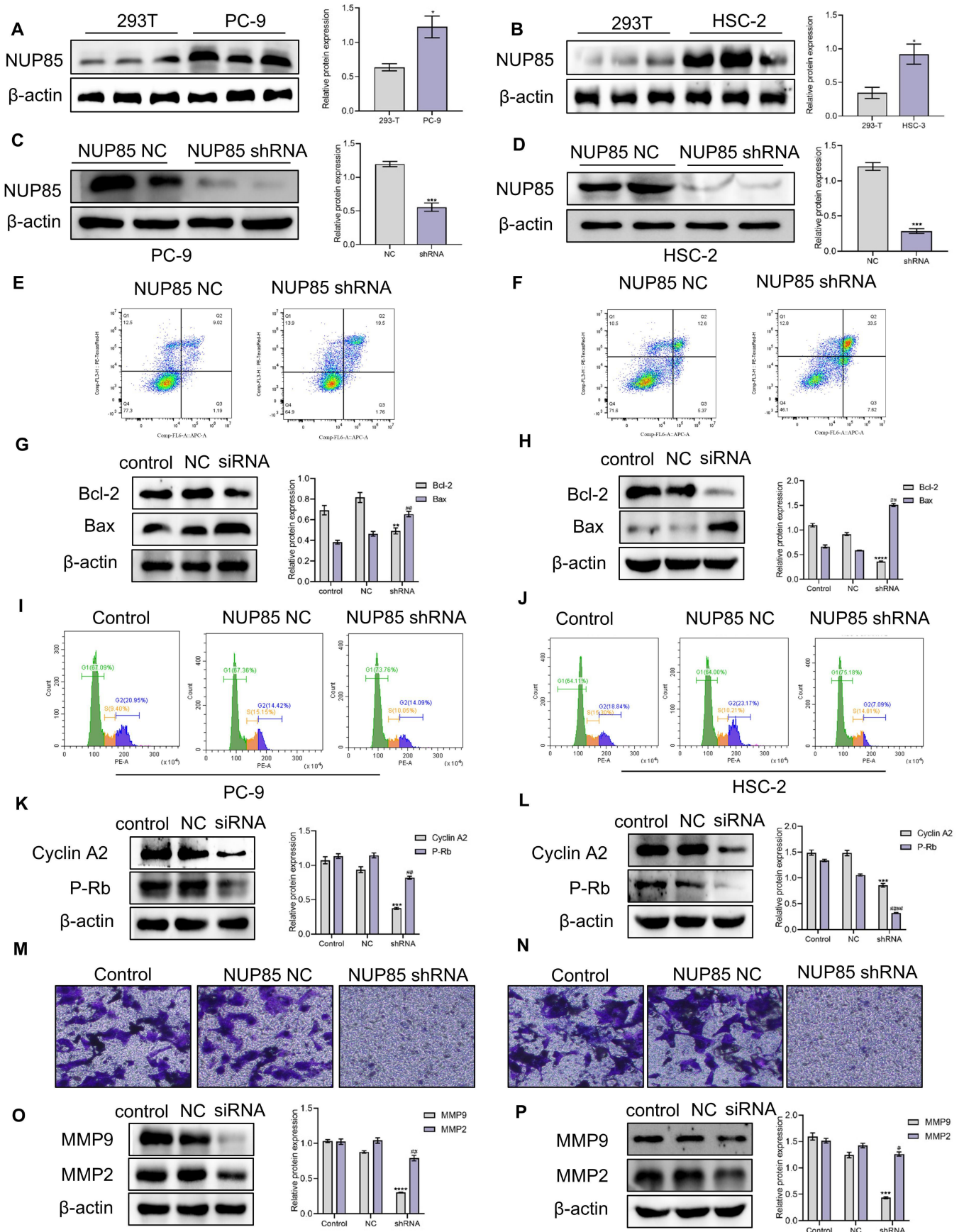


Supplementary Figure 5: Gene set enrichment analysis of NUP85 based on pan-cancer datasets.

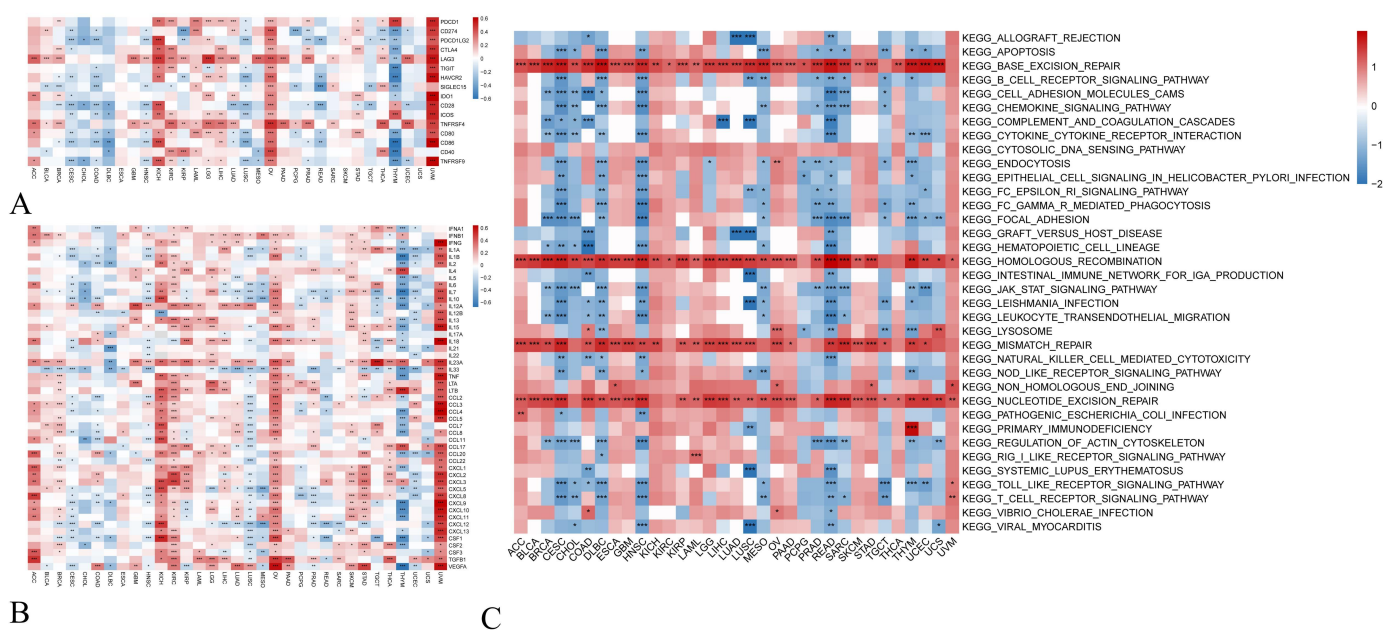
(A) Gene set enrichment analysis of NUP85 based on the TCGA dataset, displaying the top 3 results.

(B) Gene set enrichment analysis of NUP85 based on the CCLC dataset, displaying the top 3 results.

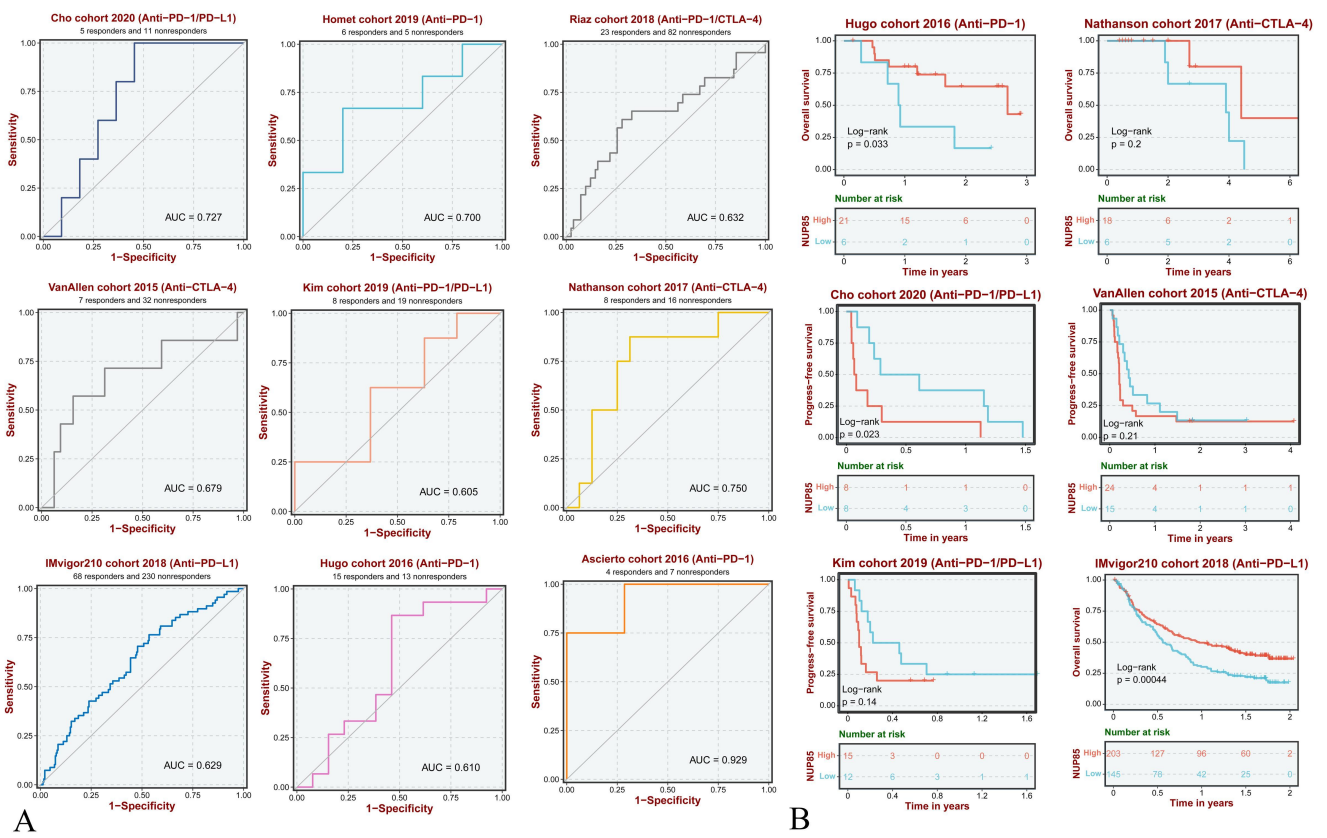
Notes: The red dashed vertical lines represent the position where the enrichment score reaches its highest point or the point of significant change in the enrichment profile. These lines mark the key positions of maximal enrichment, indicating the region where the gene set is most strongly associated with the phenotype being analyzed.



Supplementary Figure 6. Cell functional experiments was utilized to validate the impact of NUP85 on tumor cells(A) Western blotting was used to verify the expression of NUP85 in 293T cells and LUAD cells. (B) Western blotting was used to verify the expression of NUP85 in 293T cells and OSCC cells. (C-D) Verify the transfection efficiency of shRNA in LUAD and OSCC cells. (E) Flow cytometric apoptosis profiles of NC and NUP85 knockdown groups in LUAD. (F) Flow cytometric apoptosis profiles of NC and NUP85 knockdown groups in OSCC. (G-H) In LUAD cells and OSCC cells, the expression of Bcl-2 and Bax was detected by Western blotting. (I) In LUAD, the cell cycle images of MOCK, NC, and NUP85 knockdown groups were drawn by flow cytometry. (J) In OSCC, the cell cycle images of MOCK, NC, and NUP85 knockout groups were drawn by flow cytometry. (K-L) In LUAD cells and OSCC cells, the expression of Cycling A2 and P-Rb was detected by Western blotting. (M) Transwell images of migration and invasion in MOCK, NC, and NUP85 knockdown groups in LUAD. (N) Transwell images of migration and invasion in MOCK, NC, and NUP85 knockdown groups in OSCC. (O-P) Western blotting was used to detect the expression of MMP2 and MMP9 in LUAD and OSCC cells transfected with shRNA. Notes: * indicates comparison within the Bcl-2 group; # indicates comparison within the Bax group. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$; # $p < 0.05$, ## $p < 0.01$, ### $p < 0.0001$.



Supplementary Figure 7. The correlation of between NUP85 and immune indexes
 (A) Relationship between NUP85 expression and immune checkpoint genes in multiple cancers.
 (B) Relationship between NUP85 expression and cytokines/chemokines in multiple cancers.
 (C) Relationship between NUP85 expression and immune-related pathways in multiple cancers.
 Notes: Significance levels are denoted as * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, and **** $p < 0.0001$.



Supplementary Figure 8. The Predictive Value of NUP85 Across Different Immune Cohorts
 (A) The value of NUP85 in predicting response to immunotherapy in an immunotherapy cohort
 (B) The prognostic value of NUP85 across different immune cohorts