

Figure S1. Workflow Diagram.

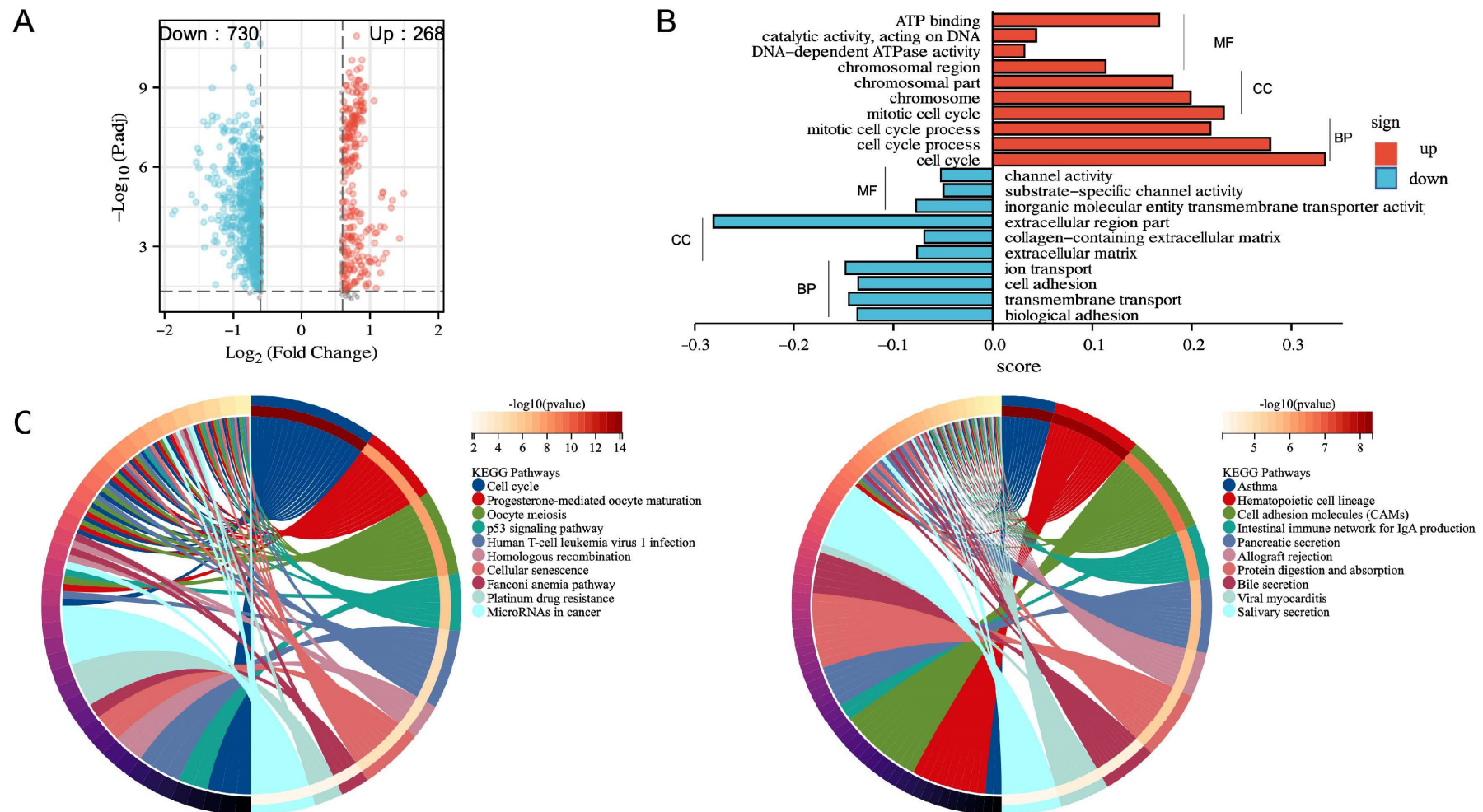


Figure S2. Identification of biological pathways associated with the risk of prognostic signature. (A) DEGs between different risk groups. (B) GO analysis of DEGs between different risk groups into three functional groups, including BP, CC and MF. (C) KEGG between the high-risk and low-risk groups of TCGA cohort. BP: biological process.

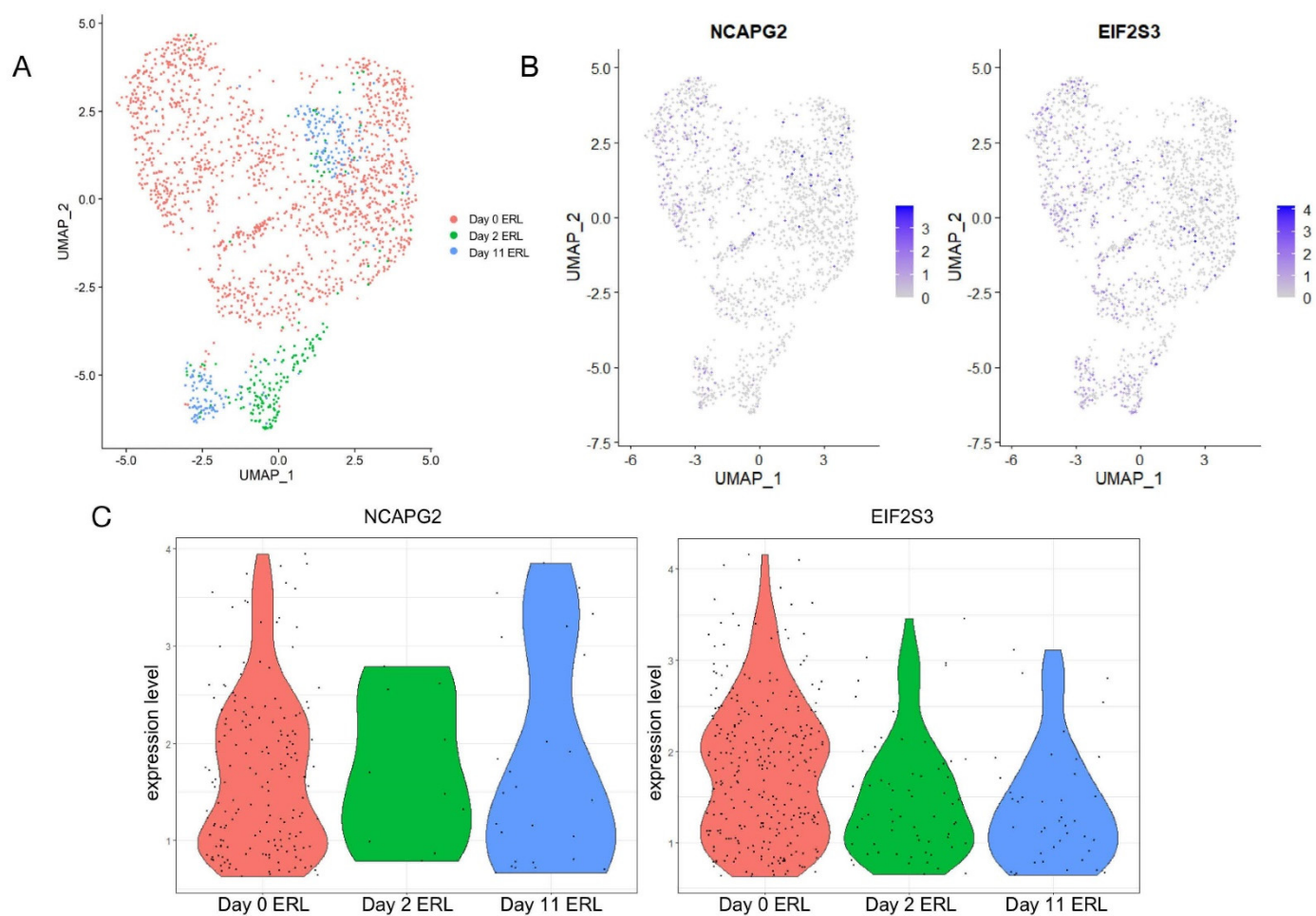


Figure S3. Single-cell RNA sequencing (scRNA-seq) analysis using GSE134839. (A) Visualization of scRNA-seq in three datasets using UMAP. (B,C) UMAP plots and violin plots showing the expression of NCAPG2 and EIF2S3 in cell populations.

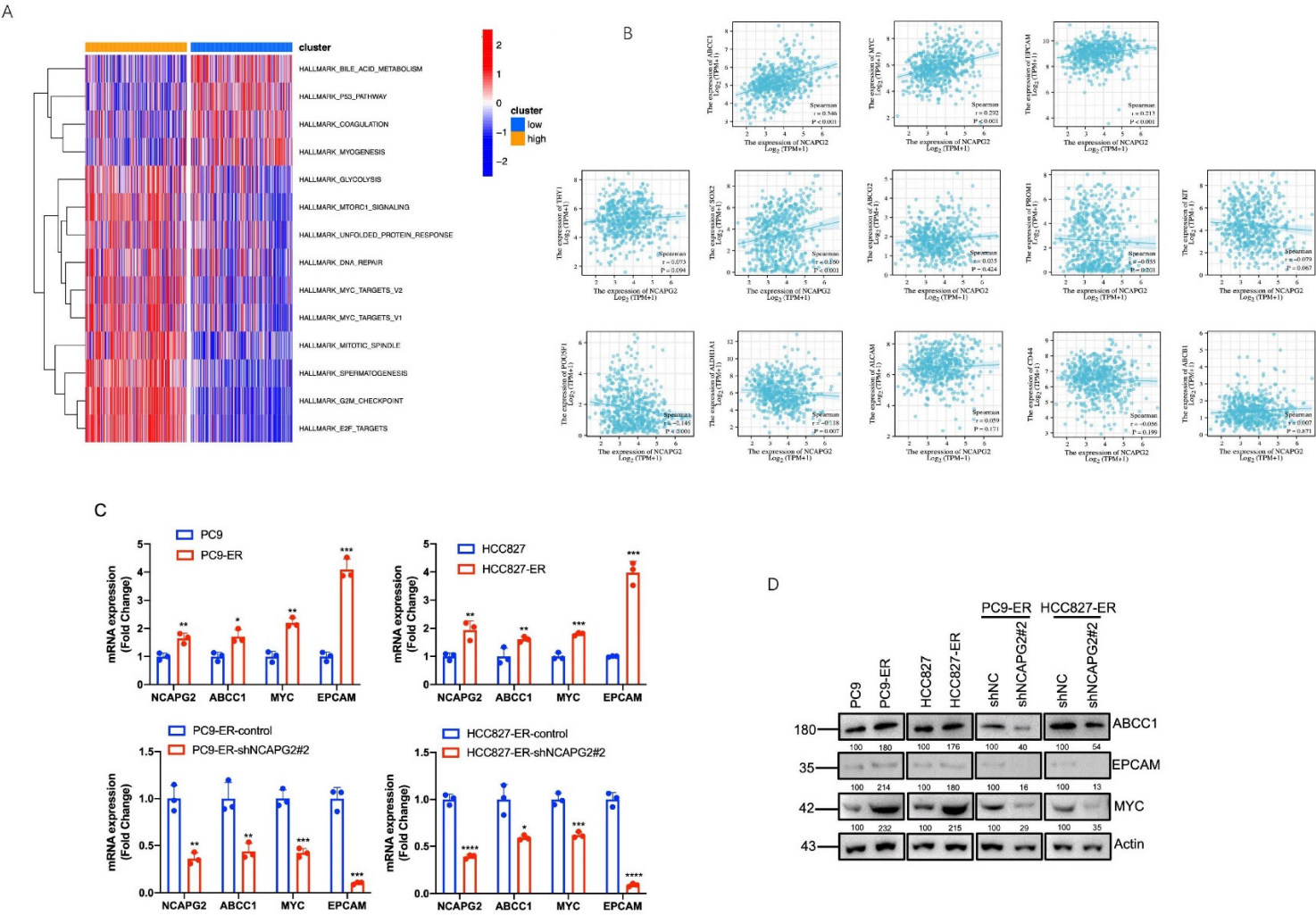


Figure S4. Relationship between NCAPG2 and stemness markers in LUAD. **(A)** GSEA of NCAPG2 expression. **(B)** Scatter plot shows the correlation between NCAPG2 and 13 stemness markers in lung cancer in TCGA database. **(C)** qPCR displays the expression of 3 stemness markers (ABCC1, EPCAM, MYC) in PC9-ER, HCC827-ER, PC9-ER control, PC9-ER shNCAPG2#2, HCC827-ER control and HCC827-ER shNCAPG2#2. **(D)** Western blot displays the expression of 3 stemness markers (ABCC1, EPCAM, MYC) in PC9-ER, HCC827-ER, PC9-ER control, PC9-ER shNCAPG2#2, HCC827-ER control and HCC827-ER shNCAPG2#2.

Table S1. Primers for qPCR.

Primer	Forward Sequence	Reverse Sequence
NCAPG2	5'-GGAAGTGGCATTGACACGAGC-3'	5'-GCTGCTCTAACAATGGGTGGCT-3'
ABCC1	5'-CCGTGTACTCCAACGCTGACAT-3'	5'-ATGCTGTGCGTGACCAAGATCC-3'
MYC	5'-CCTGGTGTCCATGAGGAGAC-3'	5'-CAGACTCTGACCTTTTGCCAGG-3'
EPCAM	5'-GCCAGTGTACTTCAGTTGGTGC-3'	5'-CCCTTCAGGTTTGCTCTTCTCC-3'
β-actin	5'-CACCATTGGCAATGAGCGGTTC-3'	5'-AGGTCTTTGCGGATGTCCACGT-3'

uncropped blots

