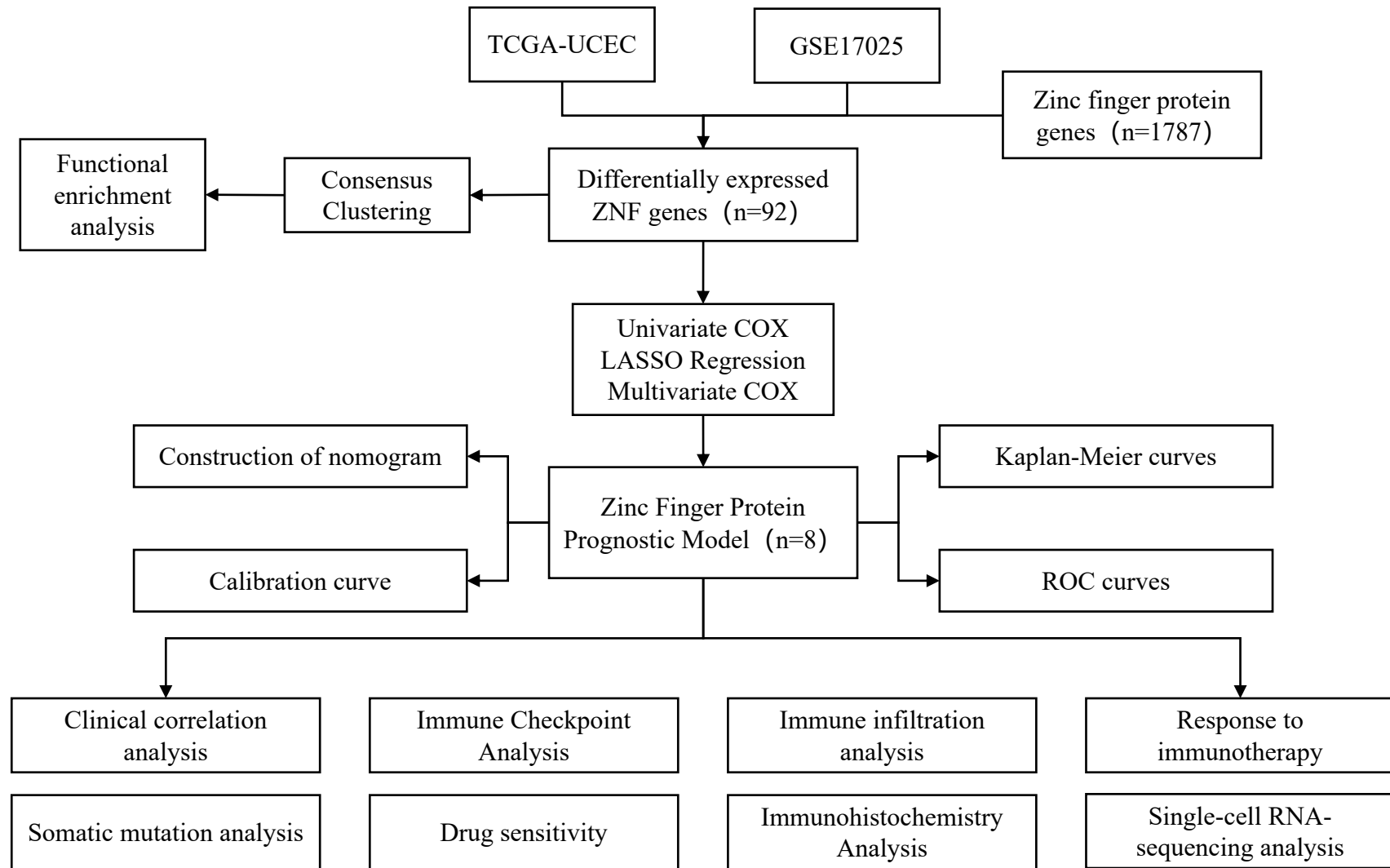




S1 Fig. Schematic workflow of ZNF score model construction.

Volcano plot showing differentially expressed genes. The y-axis represents $-\log_{10} P\text{-Value}$ (0 to 100) and the x-axis represents $\log_2 FC$ (-5 to 5). A legend indicates the regulation status: Down (blue), Normal (grey), and Up (red). Dashed lines indicate significance thresholds at $\log_2 FC = \pm 1$ and $-\log_{10} P\text{-Value} = 1.3$. Labeled genes include ZFPM2, ZEB2, WT1, PEG3, ZNF334, ZNF229, ZNF25, ZBTB38, KLIF4, ZDHHC12, ZNF540, ZNF165, RNF12, SPN2, ESCO2, NEIL3, UHRF1, MCM10, MELK, and ZIC1.

Venn diagram illustrating the overlap of ZNFs, GSE17025_UP, and TCGA_UCEC_UP. The counts are as follows:

Region	Count
ZNFs only	1618
GSE17025_UP only	569
TCGA_UCEC_UP only	3872
ZNFs & GSE17025_UP	28
ZNFs & TCGA_UCEC_UP	123
GSE17025_UP & TCGA_UCEC_UP	540
All three (ZNFs & GSE17025_UP & TCGA_UCEC_UP)	18

Venn diagram illustrating the overlap of ZNFs, GSE17025_DOWN, and TCGA_UCEC_DOWN. The counts are as follows:

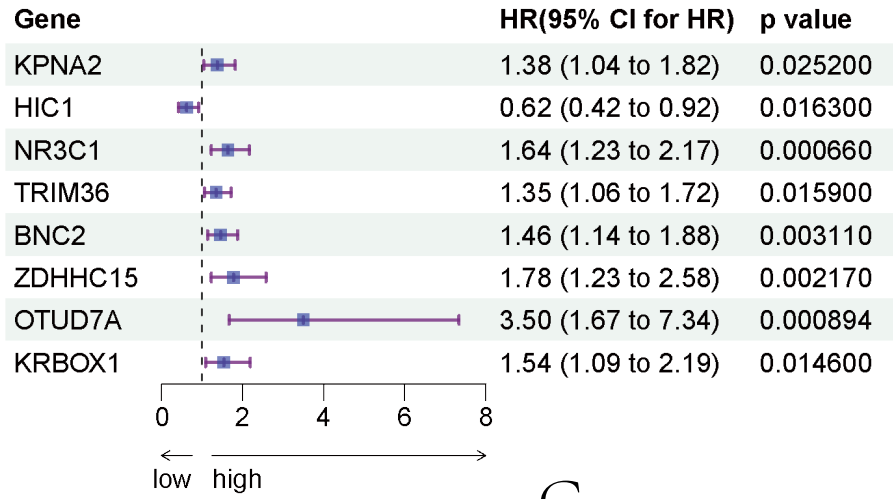
Region	Count
ZNFs only	1524
GSE17025_DOWN only	868
TCGA_UCEC_DOWN only	2391
ZNFs & GSE17025_DOWN	60
ZNFs & TCGA_UCEC_DOWN	129
GSE17025_DOWN & TCGA_UCEC_DOWN	498
All three (ZNFs & GSE17025_DOWN & TCGA_UCEC_DOWN)	74

A line plot titled "consensus CDF" showing the Cumulative Distribution Function (CDF) of the consensus index for different numbers of replicates (2, 3, 4, and 5). The x-axis is labeled "consensus index" and ranges from 0.0 to 1.0. The y-axis is labeled "CDF" and ranges from 0.0 to 1.0. The legend indicates that the red line represents 2 replicates, the green line represents 3 replicates, the cyan line represents 4 replicates, and the purple line represents 5 replicates. The plot shows that as the number of replicates increases, the CDF curve shifts to the left, indicating that a higher consensus index is required to achieve a given CDF value.

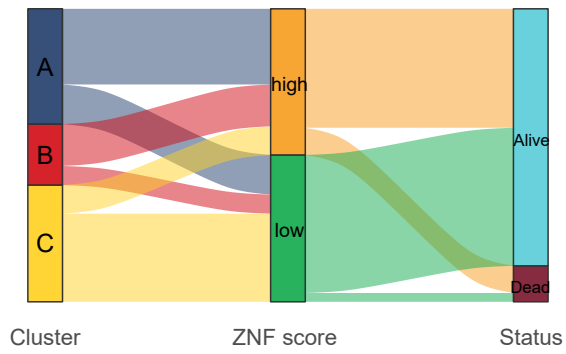
Scatter plot showing the frequency of CNVs (Copy Number Variations) across 100 genes. The y-axis represents 'Freq' (Frequency) from 0 to 15. The x-axis represents 'Gene' with 100 genes listed. The legend indicates two types of CNVs: 'Amp' (Amplification, red dots) and 'Del' (Deletion, blue dots). The plot shows a general downward trend in frequency across the genes, with some outliers.

S2 Fig. (A) Volcano plot of DEGs in TCGA-UCEC. (B) Volcano plot of DEGs in GSE17025. (C) Venn diagram of 18 upregulated ZNFs. (D) Venn Diagram of 74 downregulated ZNFs. (E) Relative area changes under the curve cumulative distribution function (CDF) curves from $k = 2$ to 5. (F) Prevalence of DE-ZNFs CNV alterations. Column height represents total alteration frequency, blue dots indicate deletion frequency, red dots denote amplification frequency.

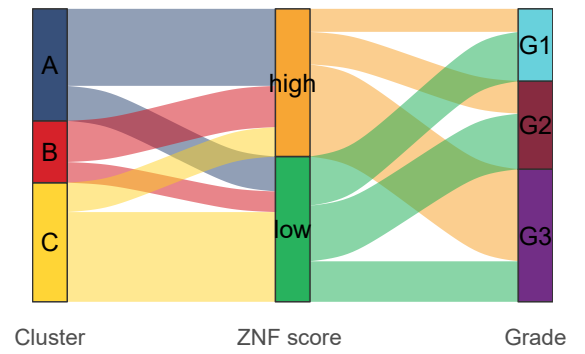
A



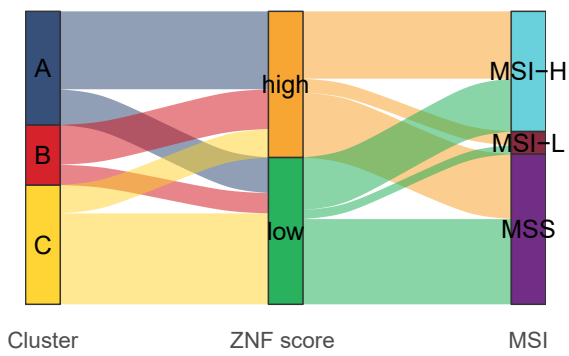
B



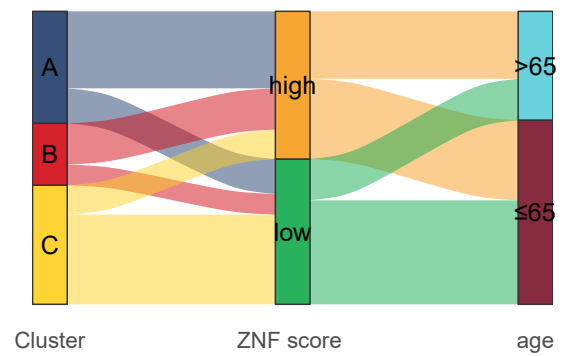
C



D

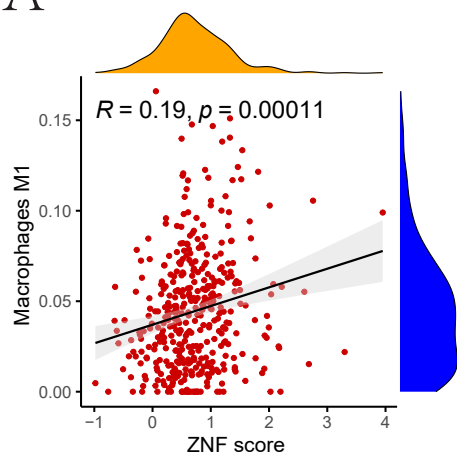


E

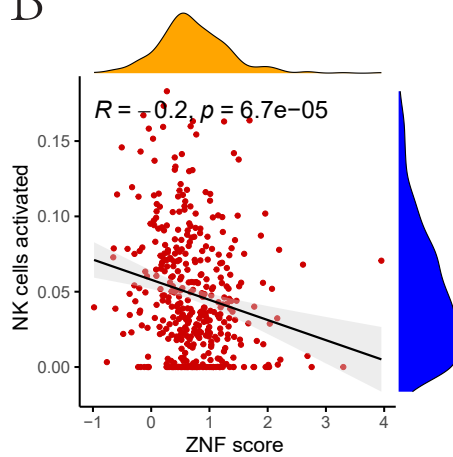


S3 Fig. (A) Forest plot of eight prognostic ZNFs. (B-E) Alluvial diagram depicting dynamic transitions among ZNF clusters, ZNF score stratification, survival outcomes, tumor grade, microsatellite instability status, and age distribution.

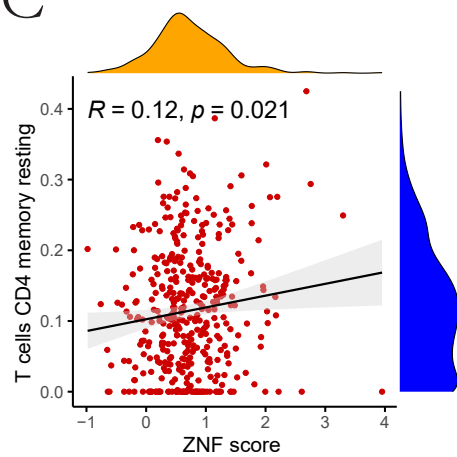
A



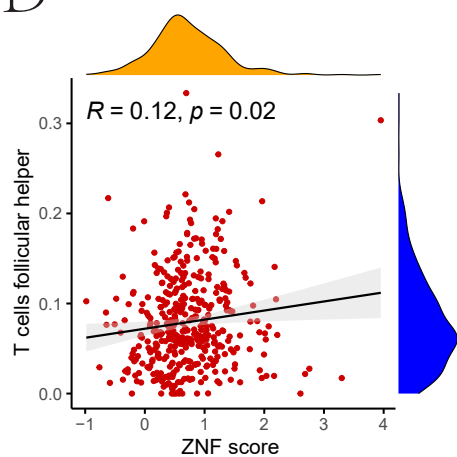
B



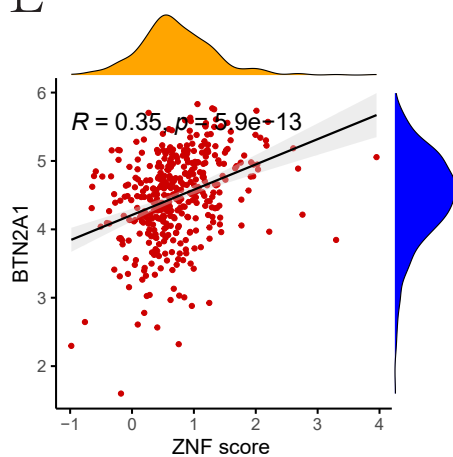
C



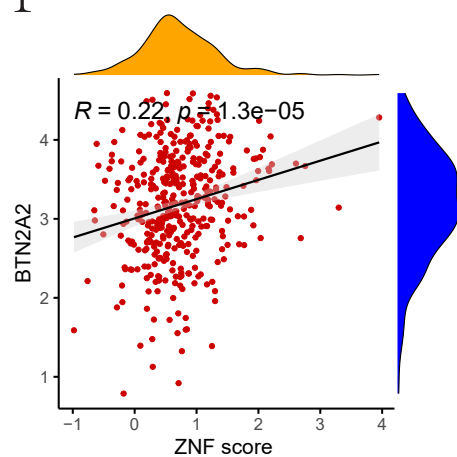
D



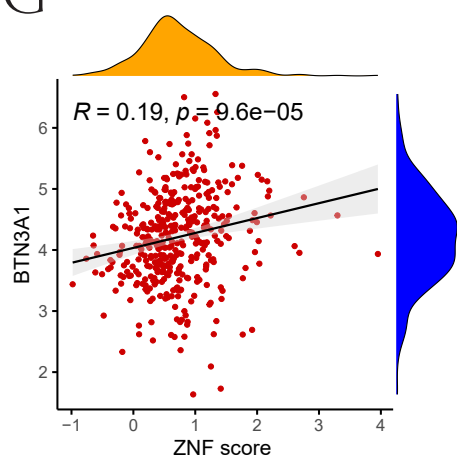
E



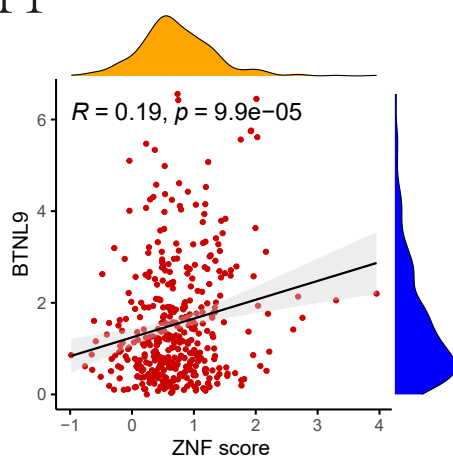
F



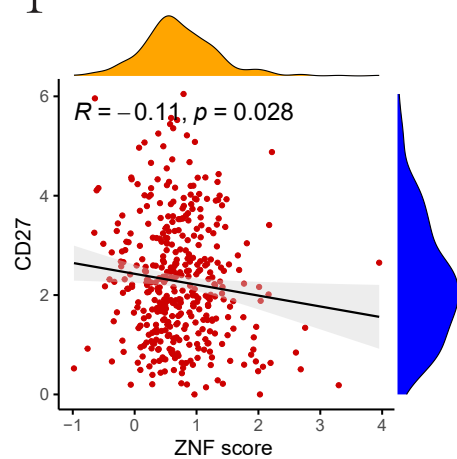
G



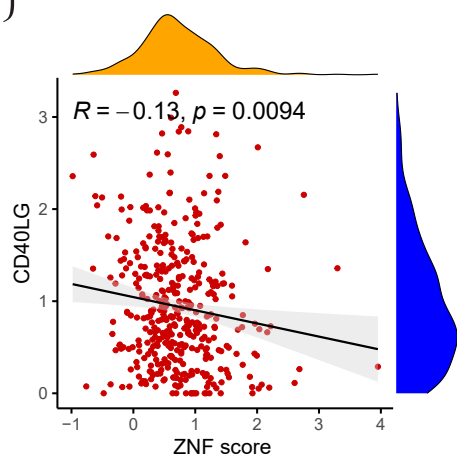
H



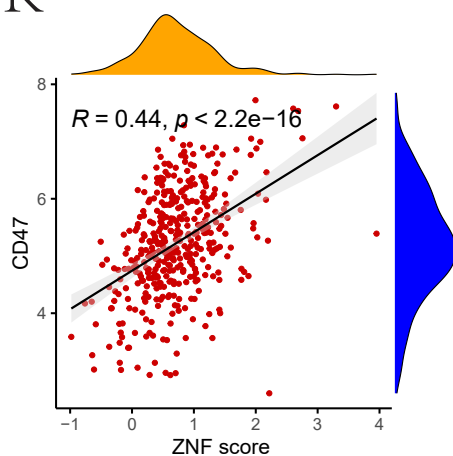
I



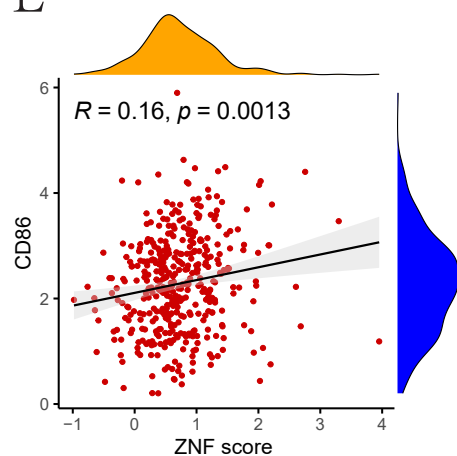
J



K

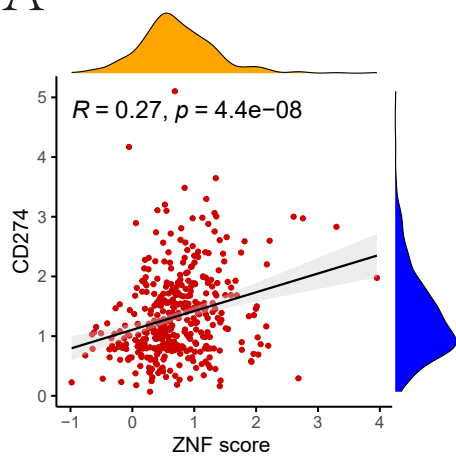


L

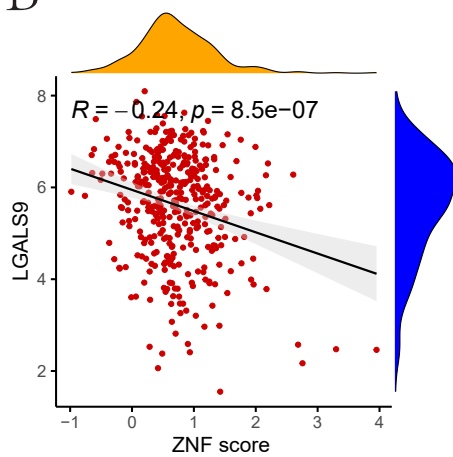


S4 Fig. (A-D) The correlation between the ZNF score and several immune cell infiltration, including (A)Macrophages M1, (B)NK cells activated, (C)T cells CD4 memory resting, (D) T cells follicular helper. (E-L) The correlation between the ZNF score and several immune check points, including (E)*BTN2A1*, (F)*BTN2A2*, (G)*BTN3A1*, (H)*BTNL9*, (I)*CD27*, (J)*CD40LG*, (K)*CD47*, (L)*CD86*.

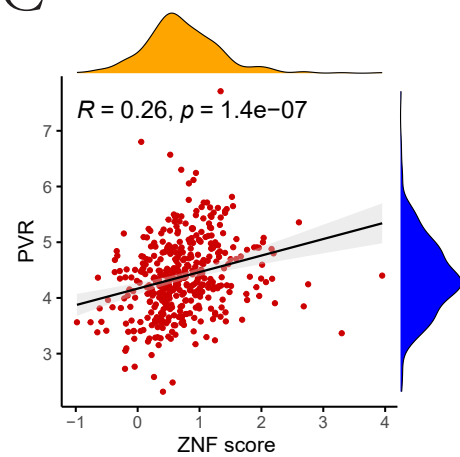
A



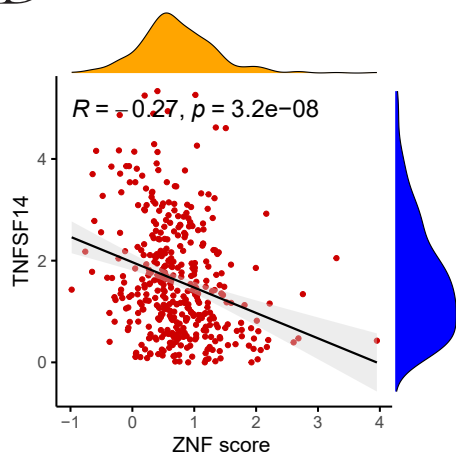
B



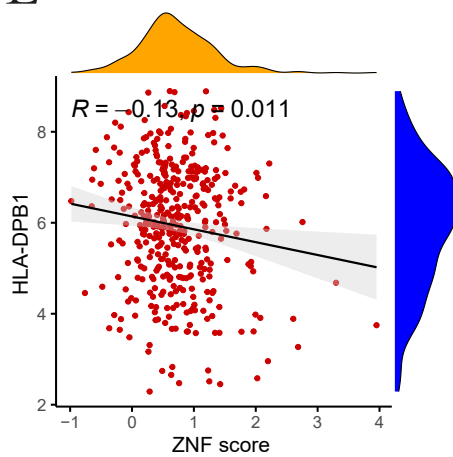
C



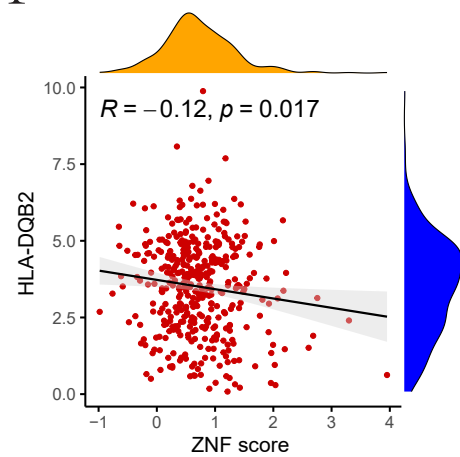
D



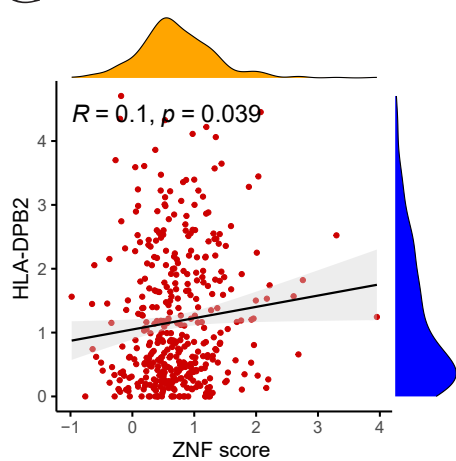
E



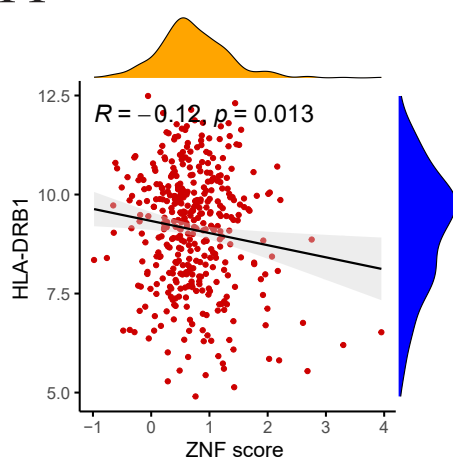
F



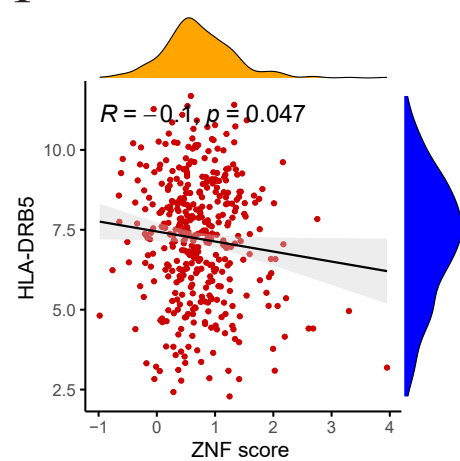
G



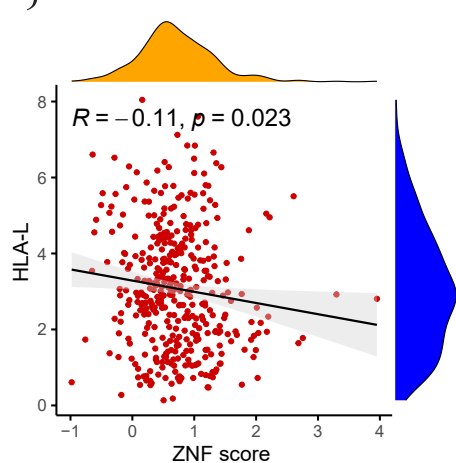
H



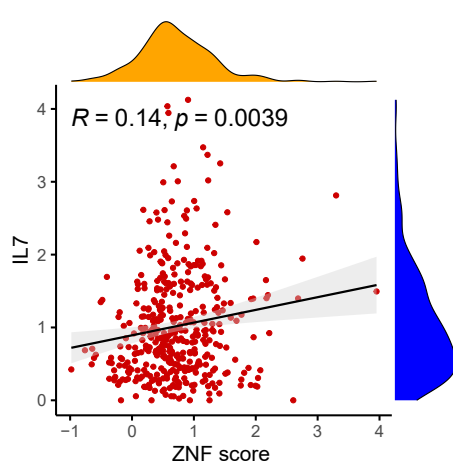
I



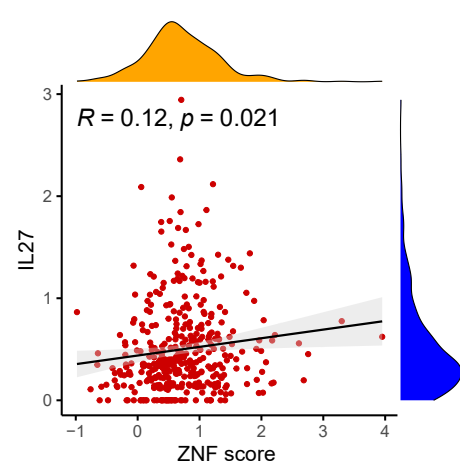
J



K

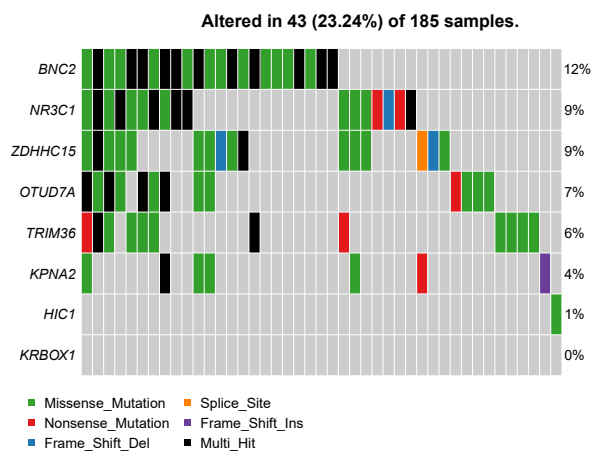


L

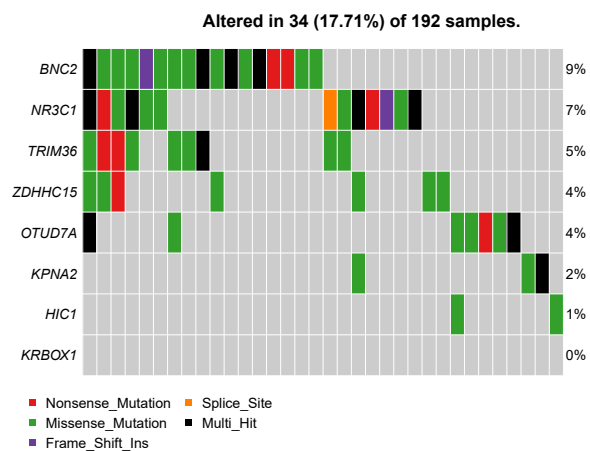


S5 Fig. (A-D) The correlation between the ZNF score and several immune check points, including (A)*CD274*, (B)*LGALS9*, (C)*PVR*, (D)*TNFSF14*. (E-J) Correlation analysis between ZNF score and HLA gene expression profiles, including (E)*HLA-DPB1*, (F)*HLA-DQB2*, (G)*HLA-DPB2*, (H)*HLA-DRB1*, (I)*HLA-DRB5* and (J)*HLA-L*. (K-L) The correlation between the ZNF score and several IL, including *IL7* (K) and *IL27* (L).

A

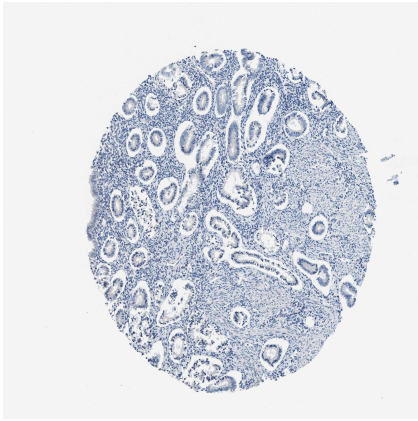


B

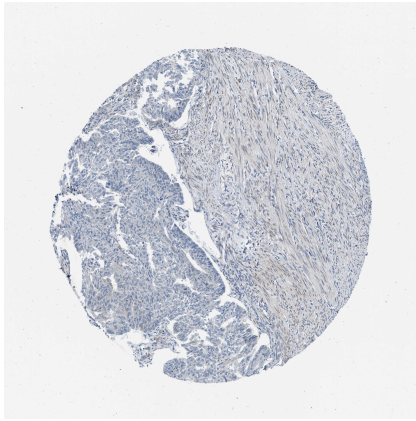


S6 Fig. (A-B) Mutational landscape of eight prognostic ZNF genes in the high (A) and low ZNF score groups (B).

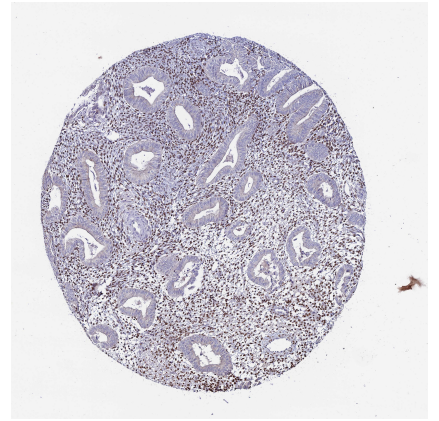
A



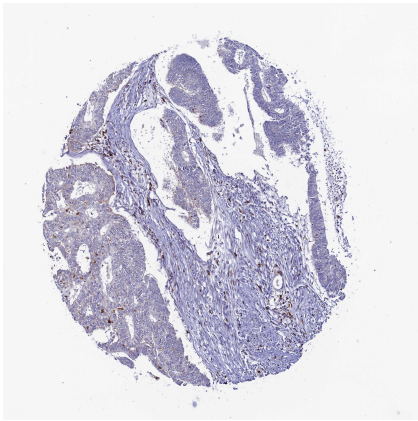
B



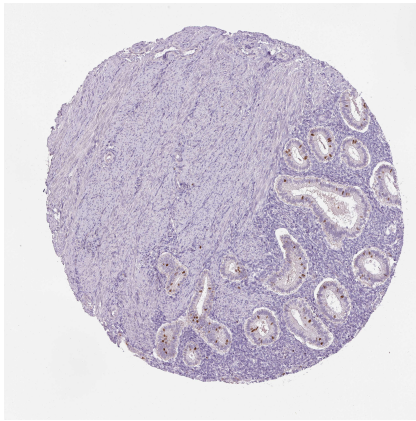
C



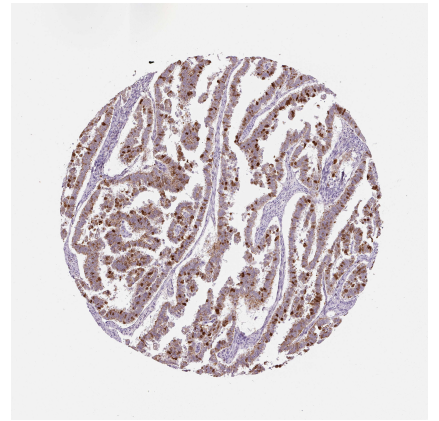
D



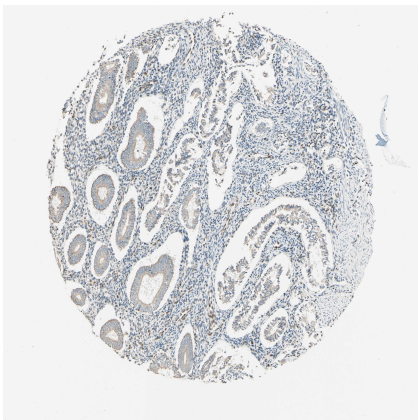
E



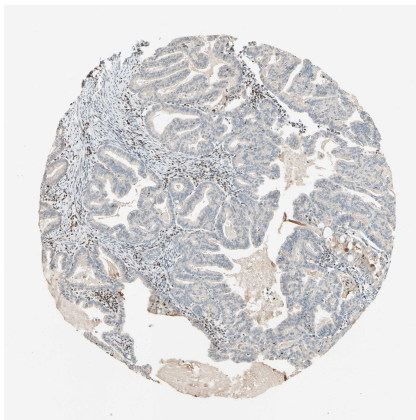
F



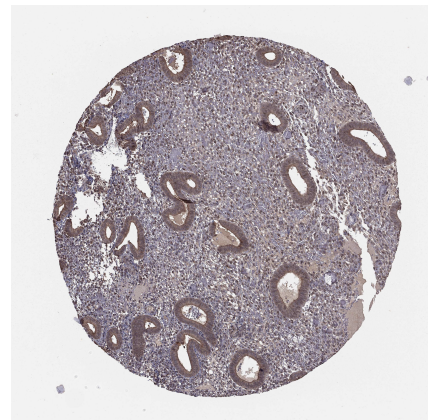
G



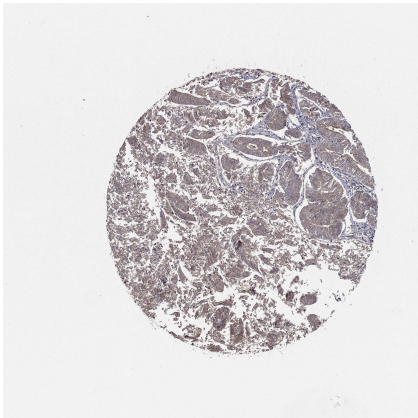
H



I



J



S7 Fig. (A-B) The expression of *BNC2* in normal tissue and UCEC; (C-D) The expression of *HIC1* in normal tissue and UCEC; (E-F) The expression of *KPNA2* in normal tissue and UCEC; (G-H) The expression of *NR3C1* in normal tissue and UCEC; (I-J) The expression of *ZDHHC15* in normal tissue and UCEC.