Supplementary

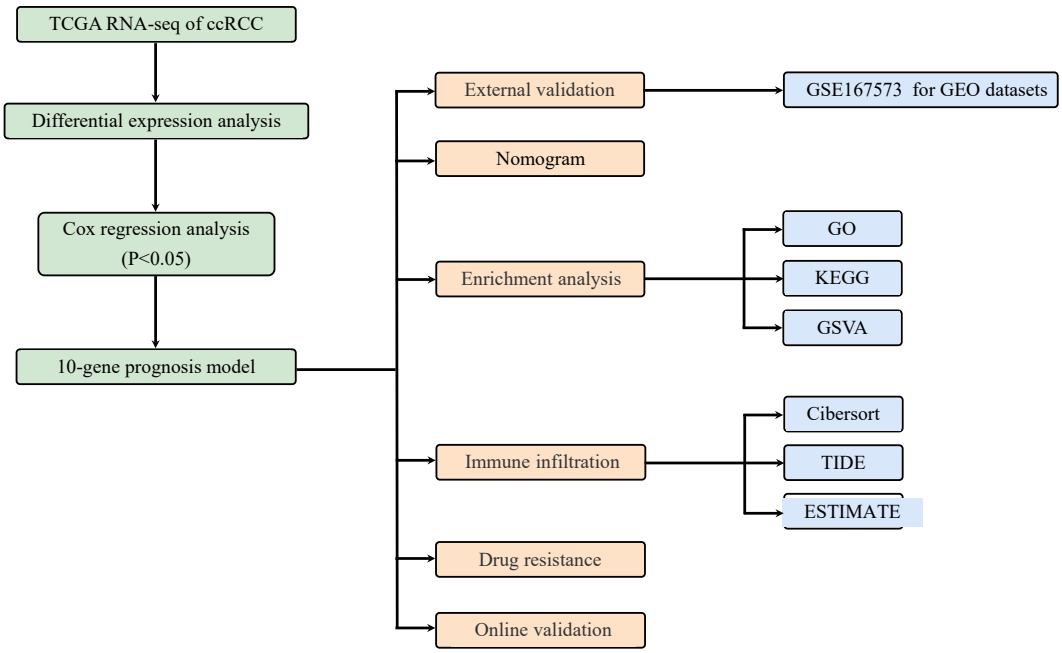

Figure S1 The workflow of this study. ccRCC, clear cell renal cell carcinoma; GEO, Gene Expression Omnibus; GO, Gene Ontology; GSVA, gene set variation analysis; KEGG, Kyoto Encyclopedia of Genes and Genomes; RNA-seq, RNA sequencing; TCGA, The Cancer Genome Atlas; TIDE, Tumor Immune Dysfunction and Exclusion.

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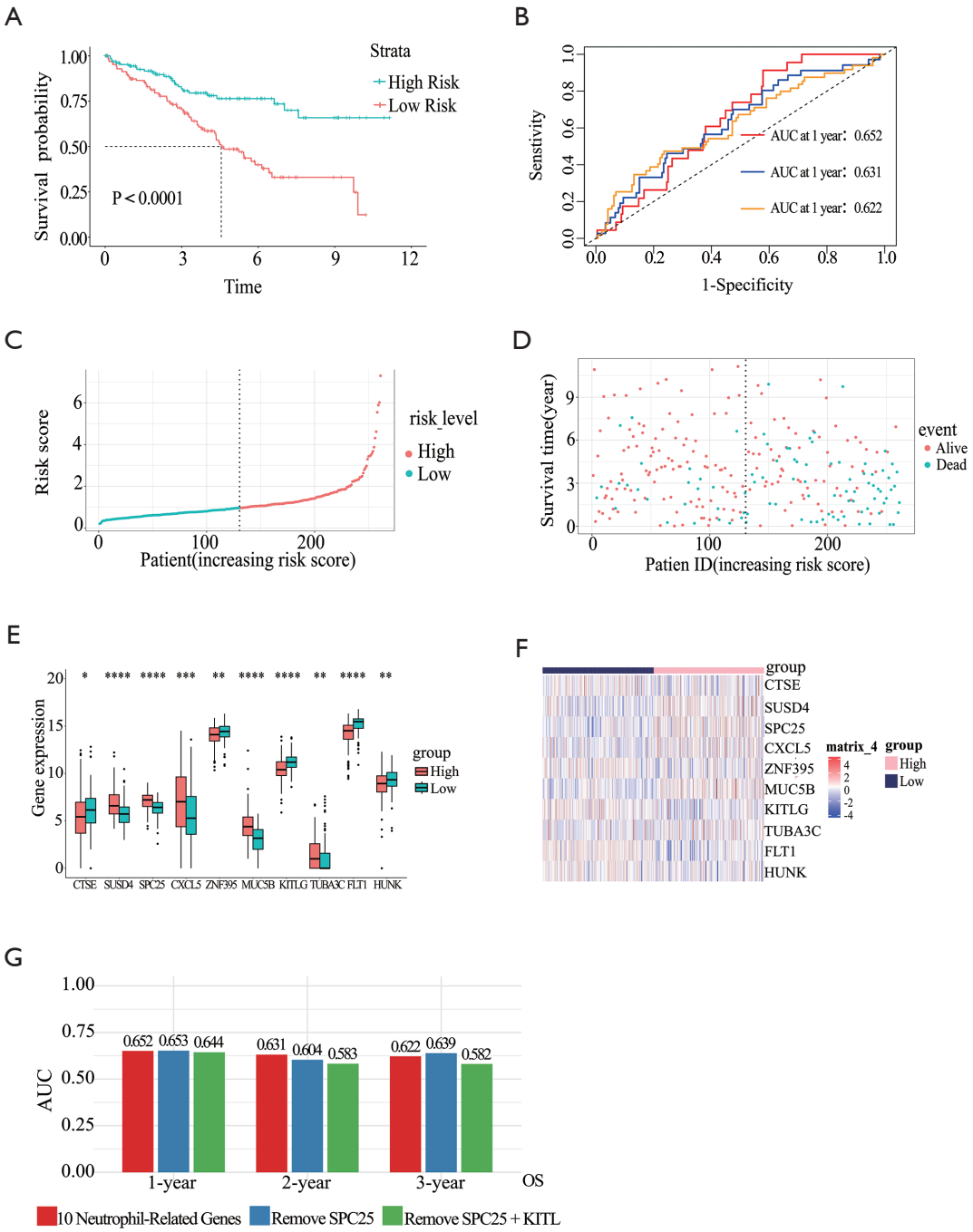

Figure S2 Construction and validation of a model based on neutrophil-related genes in ccRCC. (A) KM survival curves for OS in high and low risk groups in training set. (B) Time-dependent ROC curves (testing set, TCGA). The model demonstrated stable predictive accuracy for 1-, 2-, and 3-year OS, with AUCs (95% CI) of 0.652 (0.525–0.778), 0.631 (0.529–0.734), and 0.622 (0.534–0.710). (C) Distribution of risk factors in TCGA training set. (D) Survival status and risk score distribution (test set, TCGA). (E) Expression levels of 10 neutrophil-related genes (high- *vs.* low-risk groups). (F) Heatmap of neutrophil-related genes expression and clinical features. (G) Ablation study on prognostic characteristics in the TCGA test set. *, P<0.05; **, P<0.01; ***, P<0.001; ****, P<0.0001. AUC, area under the curve; ccRCC, clear cell renal cell carcinoma; CI, confidence interval; KM, Kaplan-Meier; OS, overall survival; ROC, receiver operating characteristic; TCGA, The Cancer Genome Atlas.

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Table S1 Comprehensive summary of the 10 neutrophil-related gene prognostic signature

Gene_symbol	Uni_HR	Uni_lower_95	Uni_upper_95	Lasso_coefficient	Multi_HR	Multi_lower_95	Multi_upper_95
CTSE	0.856758	0.780481	0.94049	−0.01754	0.922001	0.82902	1.025411
SUSD4	1.189877	1.06934	1.324001	0.009116	1.222319	1.073058	1.392342
SPC25	1.424402	1.135703	1.786489	0.042531	1.571107	1.266853	1.948433
CXCL5	1.135565	1.064371	1.211521	0.033506	1.068863	0.999605	1.142919
ZNF395	0.775216	0.659681	0.910985	−0.02894	0.757649	0.608377	0.943546
MUC5B	1.226864	1.091227	1.379362	0.024645	1.193073	1.062048	1.340262
KITLG	0.724359	0.615077	0.853058	−0.03934	0.662884	0.532392	0.825359
TUBA3C	1.169306	1.062731	1.286569	0.018014	1.128985	1.019421	1.250324
FLT1	0.779069	0.686716	0.883842	−0.01618	1.229957	0.949335	1.593532
HUNK	0.834856	0.75988	0.91723	−0.04198	0.83993	0.713168	0.989223

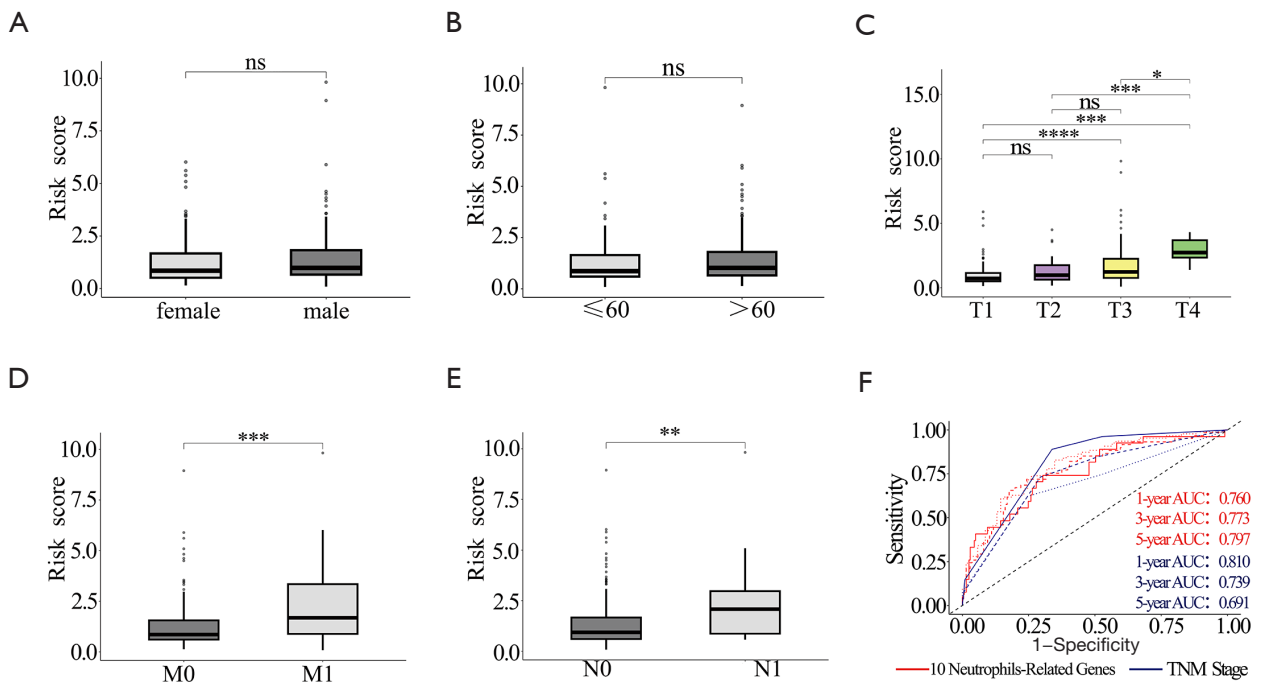

Figure S3 Relationship between risk score and clinical pathological characteristics of ccRCC patients. (A,B) Comparison of intergroup differences in risk scores by gender and age. (C-E) Comparison of intergroup differences in risk score in T stage, M stage, and N stage. (F) Time-dependent ROC curve comparison of the predictive performance between the risk score model and the TNM staging system. Statistical significance is denoted as ns, not significant (P≥0.05); *, P<0.05; **, P<0.01; ***, P<0.001; ****, P<0.0001. AUC, area under the curve; ccRCC, clear cell renal cell carcinoma; M, metastasis; N, node; T, tumor.

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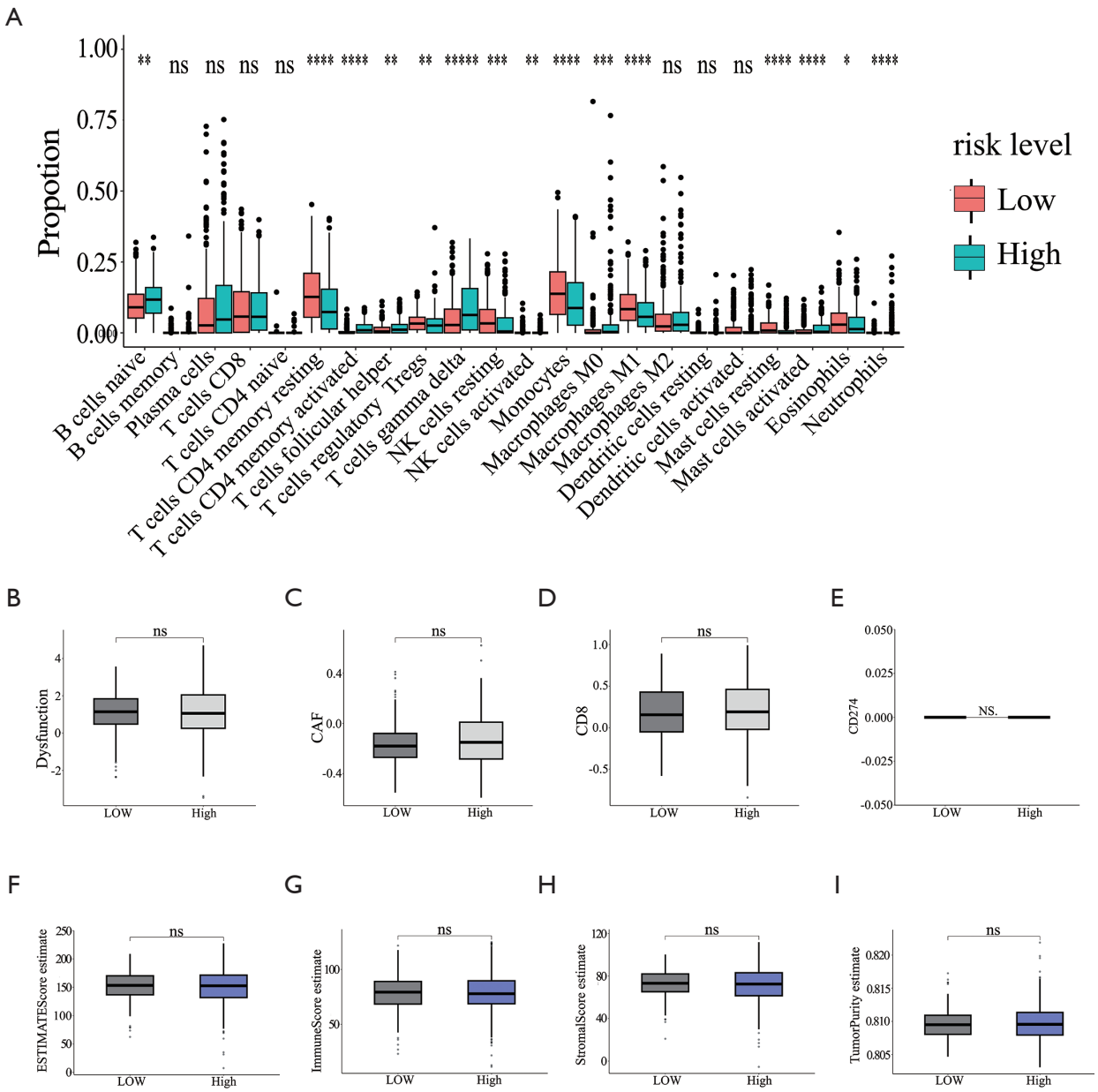

Figure S4 Supplementary Analysis of immune microenvironment in high- and low-risk groups. (A) Proportional distribution of 22 immune cell types estimated by ssGSEA, showing differences in immune cell infiltration between groups. (B) TIDE sub-scores, reflecting potential immune evasion mechanisms. (C) Enrichment of CAFs, indicative of stromal remodeling. (D) $CD8^+$ T cell infiltration expression levels. (E) CD274 (PD-L1) expression levels. (F-I) Boxplot for tumor microenvironment scores calculated by ESTIMATE in high- and low-risk groups: (F) combined ESTIMATE score, (G) immune score, (H) stromal score, and (I) tumor purity. Statistical significance is denoted as ns, not significant ($P \geq 0.05$); *, $P<0.05$; **, $P<0.01$; ***, $P<0.001$; ****, $P<0.0001$. CAF, cancer-associated fibroblast; NK, natural killer; ssGSEA, single-sample gene set enrichment analysis; TIDE, Tumor Immune Dysfunction and Exclusion.

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