**Figure S1: Exhubition of the difference of all AS events and of the top 20 OS-related AS events of each type.**

(A) The volcano plot showed the all AS events, including the significant prognostic AS events (P value<0.05) and no significant AS events.

(B-H) the bubble graphs showed the top 20 OS-related AS events of each of the 7 types, respectively.

AA: alternate acceptor site, AD: alternate donor site, AP: alternate promoter, AT: alternate terminator, ES: exon skip, ME: mutually exclusive exons, and RI: retained intron.

**Figure S2: Evaluation of the riskScore prognostic signatures about OS-related AS events in ccRCC.**

(A) The results of the univariate independent survival analysis.

(B) The ROC curves of prognostic models for the clinical characteristics, red: risk, yellow: age, green: gender, azure: grade blue: stage, ROC: receiver operator characteristic, AUC: area under the curve.

**Figure S3: Establishment and evaluation of prognostic risk model in 7 types of OS-related AS events.**

(A) The results in the AA tpye of OS-related AS events. (a-b) The lambda graph and the cross validation graph from the LASSO regression, respectively. (c) The riskScore of each ccRCC samples, red: high risk, green: low risk. (d) The survival state of each ccRCC patients with riskScore, red: dead, green: alive. (e) The heat map of the PSI value of final OS-related AS events in high/low risk cohorts. (f) The Kaplan-Meier survival curve for ccRCC samples with high/low riskScore, red: high risk, blue: low risk, P<0,001. (g-h) The results of the univariate and multivariate independent survival analysis, respectively. (i) The ROC curves of prognostic models at 1, 2 and 3 years, red: 1 years, yellow: 2years, and green: 3 years, ROC: receiver operator characteristic, AUC: area under the curve. (j) The ROC curves of prognostic models for the clinical characteristics, red: risk, yellow: age, green: gender, azure: grade blue: stage, ROC: receiver operator characteristic, AUC: area under the curve.

(B-G) The results in the AD, AP, AT, ES, ME and RI tpye of OS-related AS events, respectively, all same as (A).

**Figure S4: The correlation between the riskScore and clinical characteristics of ccRCC patients.**

(A-B) The correlation between the riskScore and age, gender of patients, respectively. (P>0.05)

(C-G) The correlation between the riskScore and grade, stage, T, N, M of patients, respectively. (P<0.05)

**Figure S5: The predictive model of overall survival of ccRCC patients based on these riskScores from the 7 prognostic risk models.**

(A) The results based on the AA tpye prognostic risk model. (a) A nomogram for predicting OS of ccRCC patients. (b-d) The 1-, 2-, and 3-year OS calibration curves of the nomogram, respectively, red: real, gray: ideal.

(B-G) The results based on the AD, AP, AT, ES, ME and RI tpyes prognostic risk models, respectively, all same as (A).

**Figure S6: The GO and KEGG analysis in ccRCC** **subgroups based on these riskScores from the 7 prognostic risk models.**

(A) The results in subgroups with high/low risk based on AA tpye. (a, b) The top 10 GO enrichments in high/low risk subgroups, respectively. (c, d) The top 10 KEGG pathways enriched in high/low risk subgroups, respectively.

(B-G) The results in subgroups with high/low risk based on AD, AP, AT, ES, ME and RI tpyes, respectively, all same as (A), but in AT and RI types, the KEGG pathways only showed top 5 in high risk subgroup.

**Figure S7: The immune features in ccRCC cohorts with high/low risk.**

(A) The relationship between high/low clusters and the resting memory CD4+ T cell, (P<0.05).

(B-C) The relationship between high/low clusters and the macrophages M1/M2, respectively, (P<0.05).

(D) The relationship between high/low clusters and the regulatory T cells, (P<0.05).

(E-F) The relationship between high/low clusters and the PDCD1and CTLA4, respectively, (P<0.05).

**Figure S8: The immune features in ccRCC subgroups based on these riskScores from the 7 prognostic risk models.**

(A) The results in risk clusters based on AA tpye. (a) The relationship between high/low clusters and the stromal cell score. (b) The relationship between high/low clusters and the immune cell score. (c) The relationship between high/low clusters and the fractions of 22 types of immune cell infiltration. (d) The relationship between high/low clusters and the scores of immune cells and their functions by ssGSEA. (e) The heat map of the scores of immune cells and their function in each risk sample. (f) The correlation between the riskScore and significant immune checkpoint. (g) The expression of immune checkpoint related genes in the risk clusters. \*: P<0.05, \*\*: P<0.01, \*\*\*: P<0.001.

(B-G) The results in risk clusters based on AD, AP, AT, ES, ME and RI tpyes, respectively, all same as (A).

**Figure S9: The clinical features and immune features of C4orf19 in ccRCC.**

(A-E) The relationship between the C4orf19 expression and age, gender, T, N, and M, respectively.

(F-G) The ESTIMATEScore and Tumor purity in high/low clusters of C4orf19 expression, respectively.

**Figure S10: The clinical features and immune features of different** **parental genes of riskScore-related AS events in ccRCC.**

(A) The results based on the expression of ARHGAP24. (a) The expression of ARHGAP24 in ccRCC tumor samples and normal samples, red: tumor, blue: normal. (b-c) The relationship between the ARHGAP24 expression and grade and stage, respectively. (d) The Kaplan-Meier survival curve for ccRCC samples with high/low expression of ARHGAP24. (e) The ROC curves of ARHGAP24. (f-g) The stromal cell score and immune cell score in high/low clusters of ARHGAP24 expression, respectively. (h) The fractions of 22 types of immune cell infiltration in high/low clusters of ARHGAP24 expression. (i) The scores of immune cells and their functions in high/low clusters of ARHGAP24 expression by ssGSEA. (j) The expression of immune checkpoint related genes in high/low clusters of ARHGAP24 expression. \*: P<0.05, \*\*: P<0.01, \*\*\*: P<0.001.

(B-E) The results based on the expression of DNASE1L3, P4HA1, SLC39A14 and TAF1D, respectively, all same as (A).