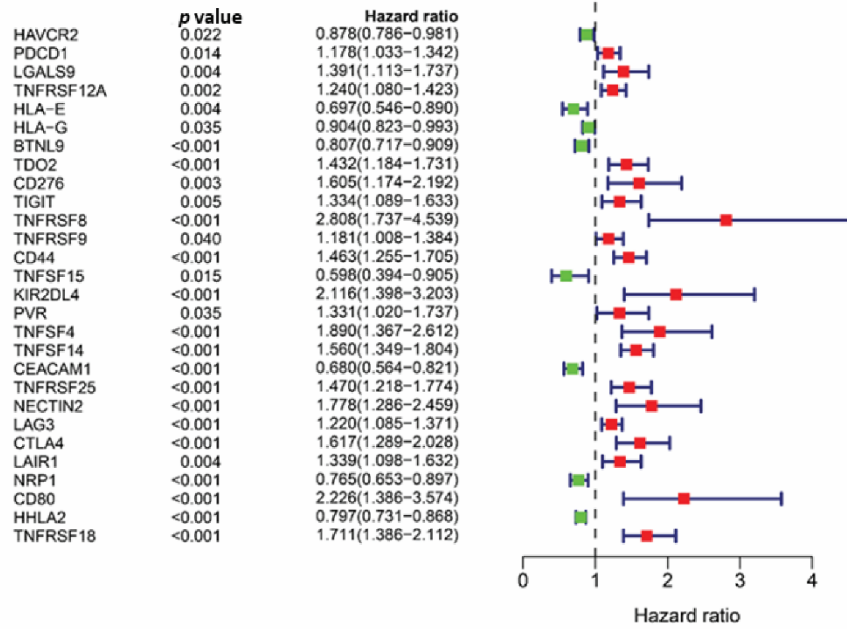


A



B

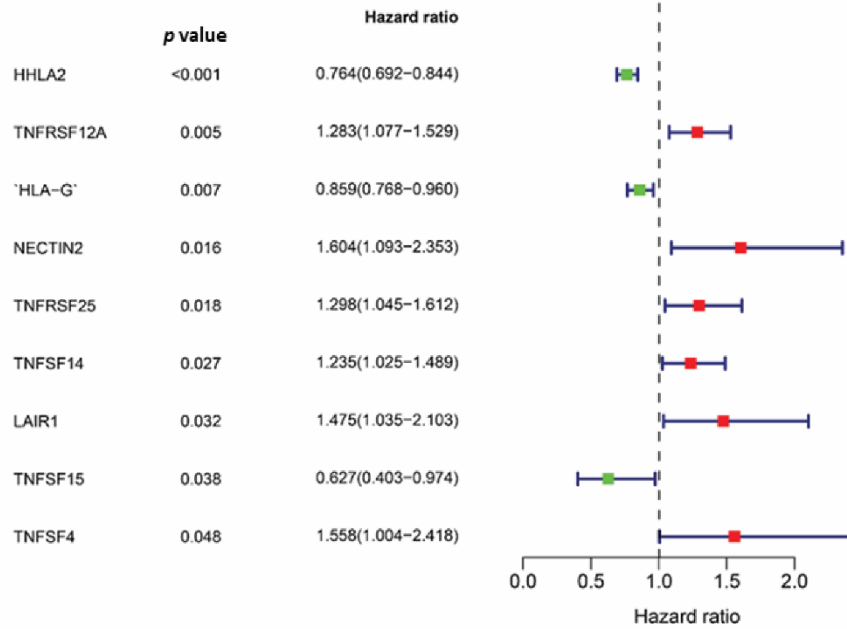


Figure S1. Construction of ICI-related gene signature. (A). Forest plot showing 28 ICIs prognostic genes for ccRCC identified by univariate with $p < 0.05$. (B). Forest plot showing 9 independent prognostic signature genes by multivariable Cox hazard regression model of ICI genes of the ccRCC cohort with $p < 0.05$.

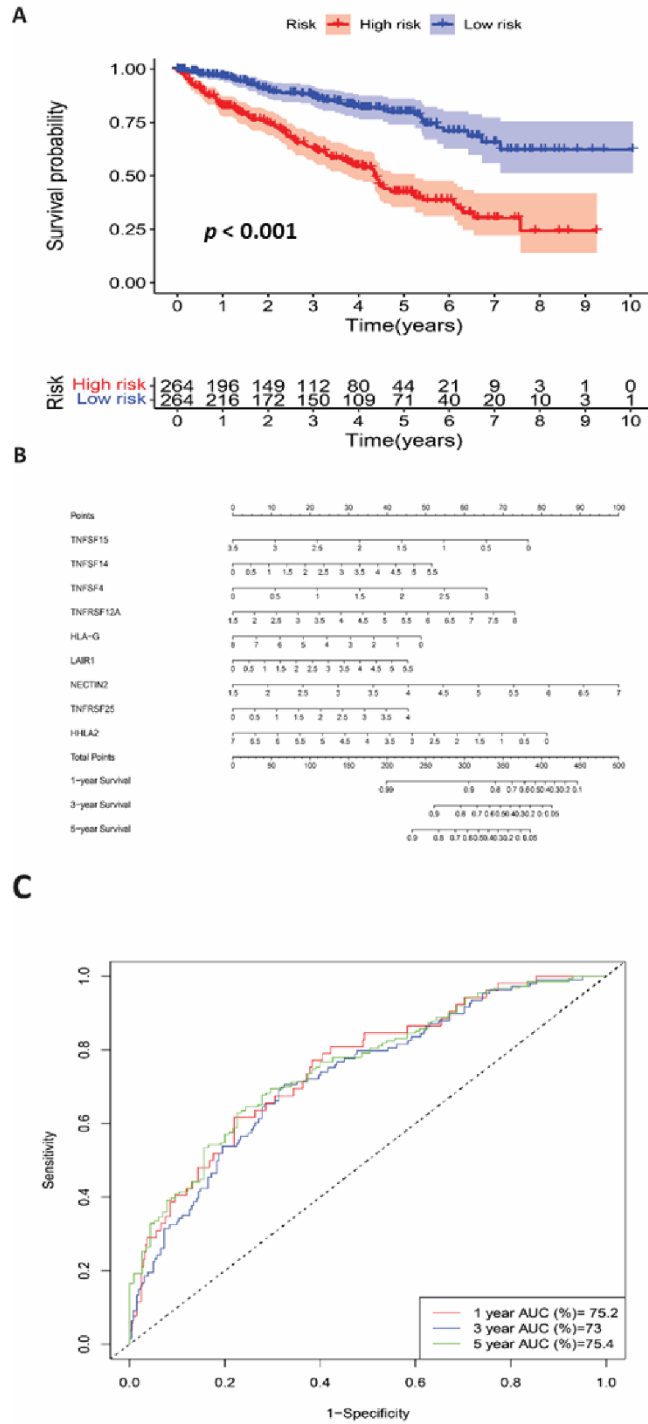


Figure S2. (A). Survival plot show significant OS differences between high and low risk group of ccRCC patients $p < 0.0001$. (B). Nomogram prediction of risk score signature genes in 1-yr, 3-yr, and 5-yr. (C). ROC curve that show predictive accuracy of risk score signature genes in 1-yr, 3-yr, and 5-yr (AUC; 75.2%, 73%, and 75.4%).

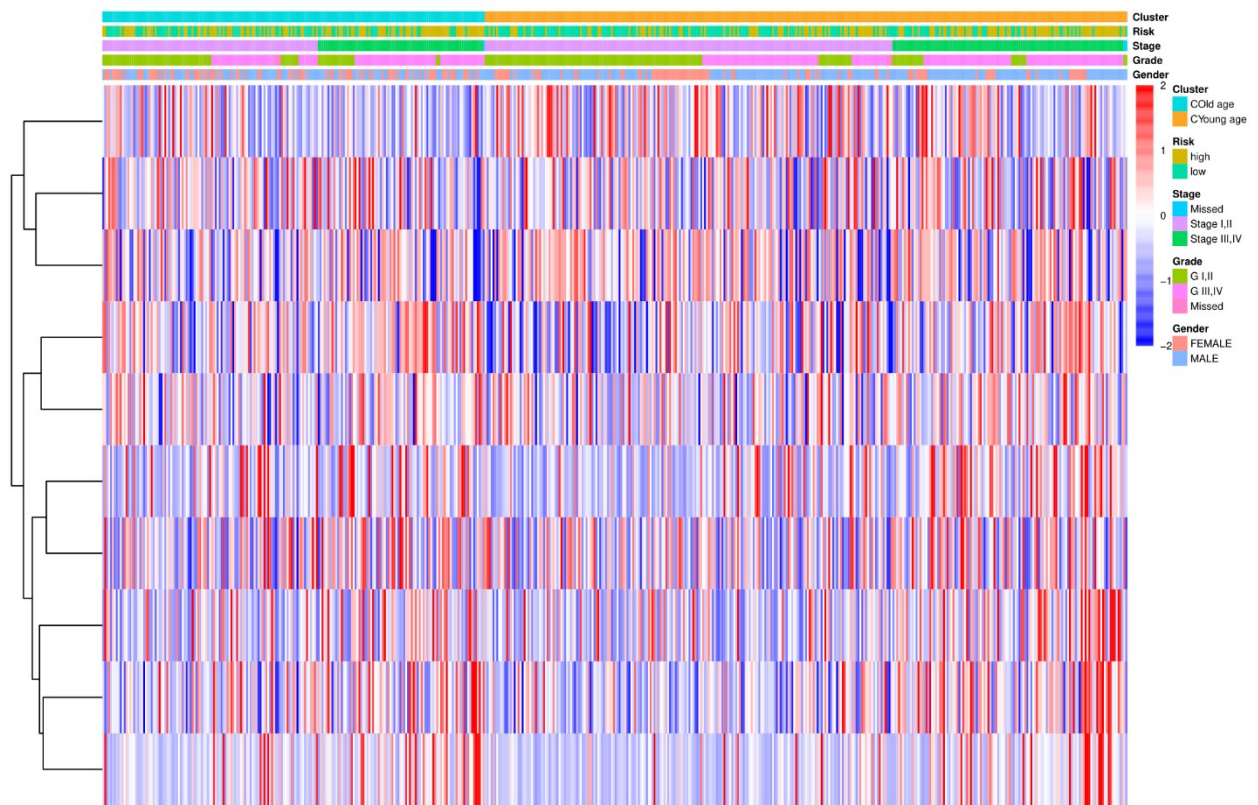


Figure S3. Heatmap showing young vs. old age group with clinicopathologic characteristics (gender, stage, and grade), risk score, and risk score signature genes.

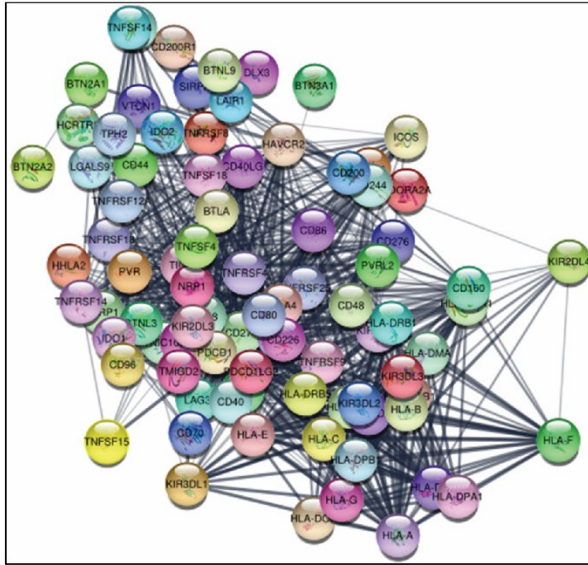
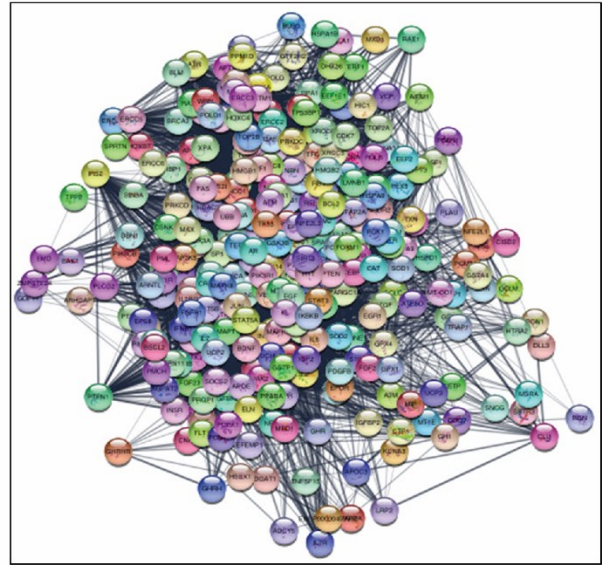
A**B**

Figure S4. Protein–protein interactions (PPI) demonstrating TNFSF15 gene interplay with ICIs and aging genes. (A). ICI genes interaction with TNFSF15. (B). Aging genes list with TNFSF15.

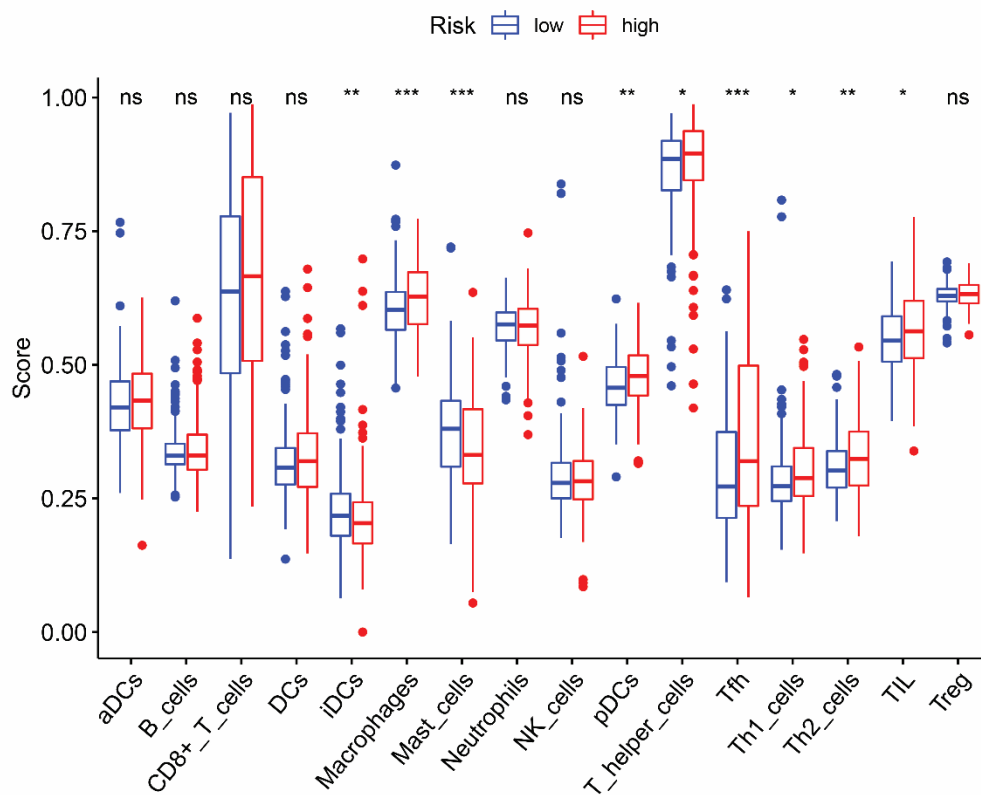
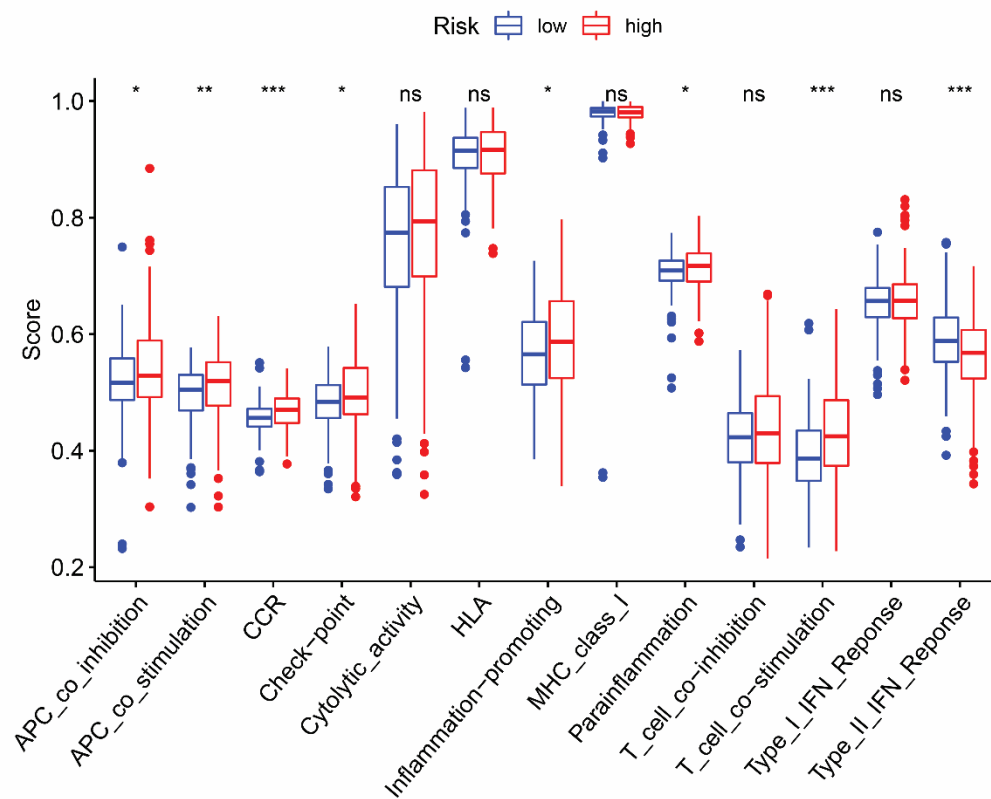
A**B**

Figure S5. Cell infiltration and different immune function between high and low risk groups of ccRCC patients. (A). (iDCs) and mast cells were significantly higher in the low risk group $p < 0.05$. (B). Immune functional analysis. There was a significant infiltration score of type-II-IFN-response in the lower risk group than the high risk group. Checkpoint, inflammation-promoting, and T-cell-co-stimulation showed higher infiltration score in the high risk group than in the low risk group all $p < 0.05$. (ns = non-significant) * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

Table S1. Gene ontology and Kyoto Encyclopedia of Genes and Genomes pathways in ccRCC cohort.

GO	ONTOLOGY	Description	P value
	BP	Regulation of cellular senescence	0.020252379
	BP	positive regulation of cellular senescence	0.002568472
	BP	Regulation of T cell activation	3.30E-60
	CC	luminal side of endoplasmic reticulum membrane	4.01E-24
	CC	MHC class II protein complex	5.52E-23
	MF	Peptide antigen binding	2.54E-24
	MF	Immune receptor activity	2.75E-12
	MF	Tumor necrosis factor receptor superfamily binding	2.16E-09
KEGG	ID	Description	P value
	hsa04218	Cellular senescence	0.000271365
	hsa04658	Th1 and Th2 cell differentiation	1.56E-10
	hsa04060	Cytokine-cytokine receptor interaction	1.21E-09
	hsa05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	0.036436441

BP=biological process, CC=cellular component, MF=molecular function