

Figure S1 The validation set GSE167573 to assess the prognostic performance of phagocytosis-related genes. Panel (A) shows the KM survival curve of the sigScore high and low group (median grouping). Panel (B) displays ROC curve of the predictive performance of the phagocytosis regulatory gene model. Panel (C) reveals the sigScore ranking of samples from small to large. Figure (D) depicts the corresponding survival time and survival status according to the sample sorting of sigScore. Figure E displays the expression heatmap of phagocytosis regulatory genes. KM, Kaplan-Meier; ROC, receiver operating characteristic.

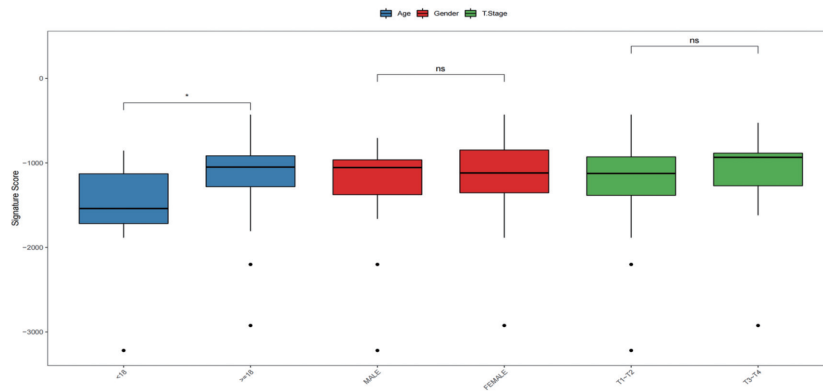


Figure S2 sigScore comparison of the validation set GSE167573 grouped by clinical features. The figure contains three clinical features: age (≥ 18 , < 18), gender (male, female), and stage (I-II, III-IV). *, $P < 0.05$; ns, not significant

Variable	N	Hazard ratio	p
Age	<18	Reference	
	≥ 18	0.01 (0.00, 0.21)	0.003
T.Stage	T1~T2	Reference	
	T3~T4	0.45 (0.05, 4.51)	0.498
Gender	FEMALE	Reference	
	MALE	0.95 (0.24, 3.69)	0.940
sigScore	high	Reference	
	low	0.01 (0.00, 0.22)	0.003

Figure S3 Multivariate Cox regression test for prognostic independence of phagocytosis factor-related genes. The figure depicts the results of multivariate Cox regression on the validation set GSE167573.

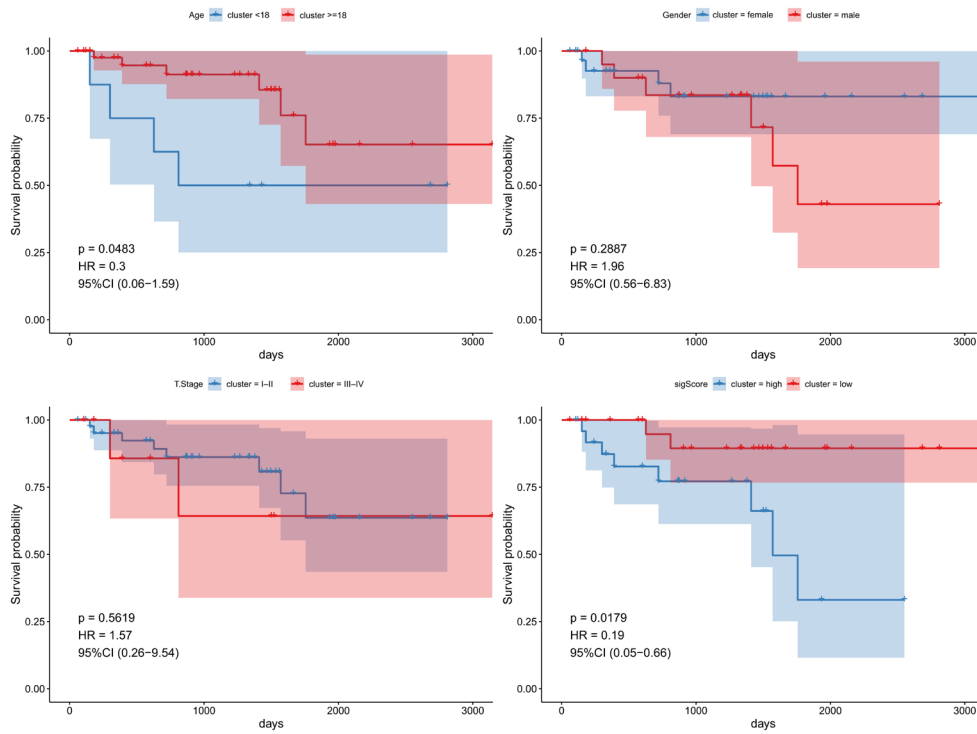


Figure S4 Kaplan-Meier survival analysis of clinical grouping versus median sigScore grouping. (A-D) The clinical characteristics of GSE167573, age (<18, ≥18), stage (I–II, III–IV), gender (male, female) and sigScore (high, low) for tumor sample grouping survival curve, log-rank test, and Cox hazard ratio.

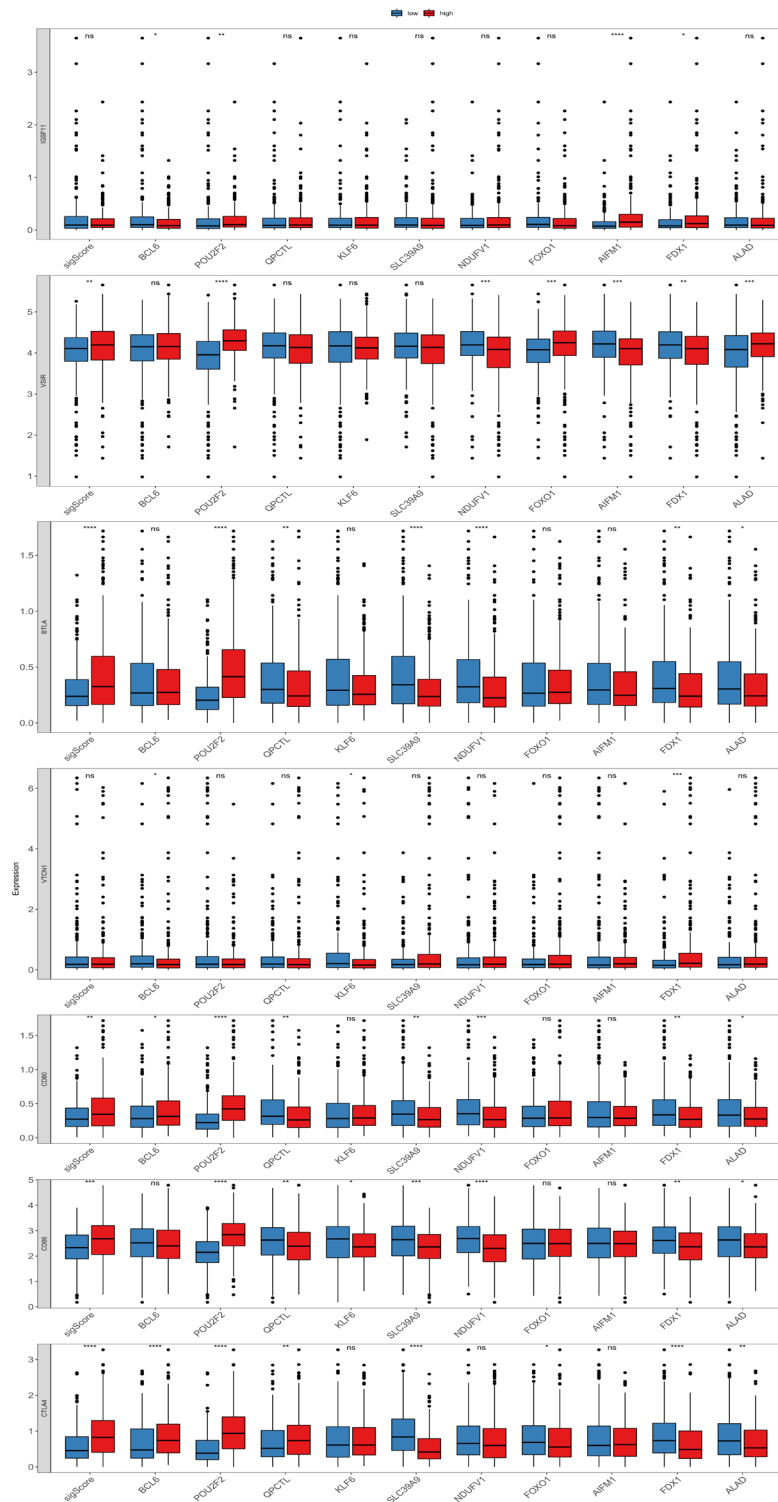


Figure S5 Association of phagocytosis regulatory genes with immune checkpoints. The figure demonstrates that the sigScore and signature gene expression is divided into two groups by the median value to evaluate the immune checkpoint genes IGSF11, VSIR, BTLA, VTCN1 and other genes in different groups and whether there is a difference in expression. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$; ns, not significant.

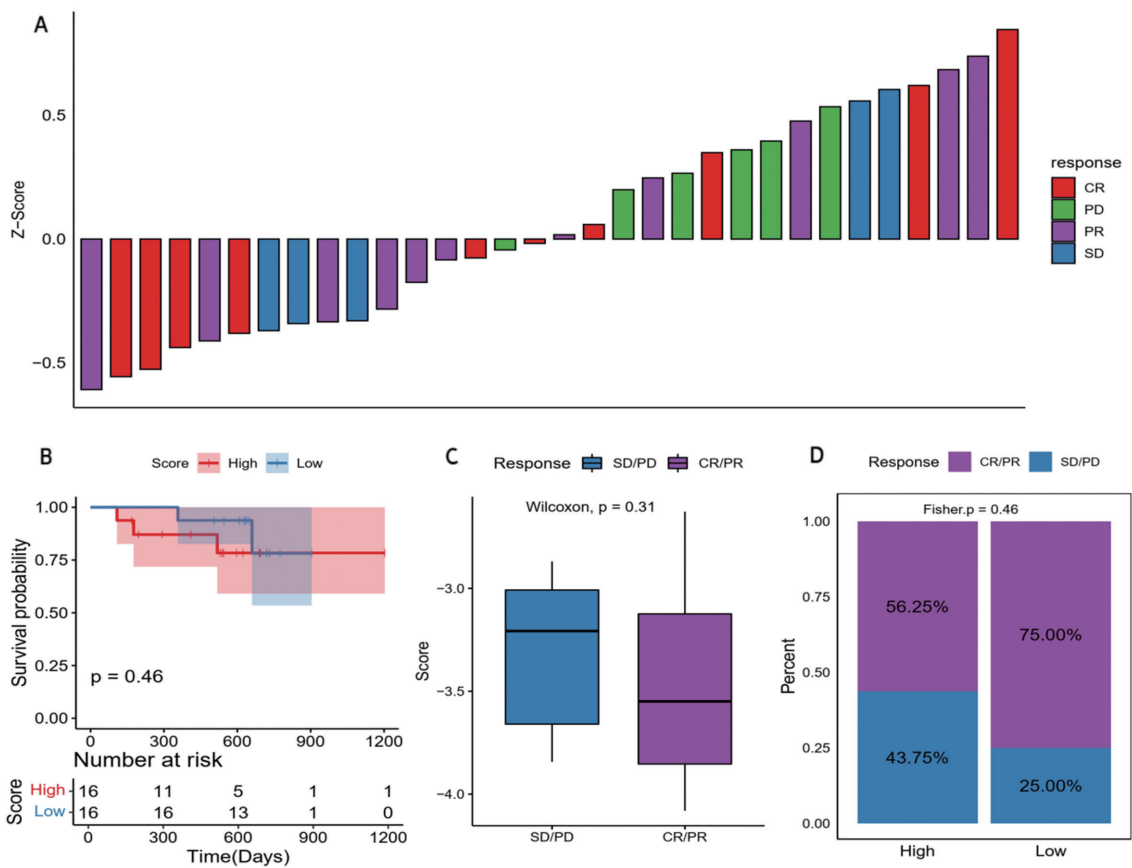


Figure S6 Correlation analysis of phagocytosis regulatory genes with immunotherapy outcomes. (A) The correlation between each patient's sigScore and clinical response to immunotherapy in the immunotherapy cohort. (B) Survival analysis of low-score and high-score patient groups in the immunotherapy cohort using Kaplan-Meier curves. (C) Differences in scores between different clinical response groups. (D) The proportion of patients responding to immunotherapy in the low-score or high-score groups. CR, complete response; PR, partial response; PD, progressive disease; SD, stable disease.

Table S1 GSE167573 clinical information for clear cell renal carcinoma samples

Parameter	Subtype	Patients
Gender	Female	276
	Male	235
T Stage	T1	278
	T2	120
	T3	80
	T4	25
	NA	8
Age (years)	≥18	361
	<18	140
	NA	10

Table S2 TCGA-KIRC Immune cell subtypes.

Parameter	Subtype	Patients
Immune subtypes	C1	7
	C2	19
	C3	442
	C4	26
	C5	3
	C6	13
	NA	16

NA, not application.