

Table S1. Detailed information of included clinical cohorts with RNA-seq profiles

Cohorts	RNA-seq/ Proteomic data	Survival data	Country	Year	Platform
TCGA- LIHC	YES/NA	Yes	USA	2017	Illumina HiSeq RNAseqV2
ICGC- LIRI-JP	YES/NA	Yes	Japan	2016	Illumina HiSeq
CHCC	YES/Yes	Yes	China	2019	Illumina HiSeq X Ten

NA, not available

Table S2. The clinical characteristic information of the HCC patients in TCGA cohort

TCGA cohort (n = 363)		
Variable	Number	%
Age		
< = 55	122	33.6
> 55	241	66.4
Gender		
Female	118	32.5
Male	245	67.5
Histologic grade		
G1	55	15.2
G2	175	48.2
G3	116	32
G4	12	3.3
Vascular invasion		
None	205	66.3
Micro	90	29.1
Macro	14	4.5
Virus infection		
No	194	53.4
Yes	151	41.6
Alcohol consumption		
No	229	63.1
Yes	116	32
TNM stage		
I	170	46.8
II	84	23.1
III	81	22.3
IV	4	1.1

Table S3. The clinical characteristic information of the HCC patients in ICGC cohort

ICGC cohort		
(n = 229)		
Variable	Number	%
Age		
< = 55	25	10.9
> 55	204	89.1
Gender		
Female	60	26.2
Male	169	73.8
Family history		
No	141	65.9
Yes	73	34.1
TNM stage		
I	35	15.3
II	104	45.4
III	71	31.0
IV	19	8.3

Table S4. The clinical characteristic information of the HCC patients in CHCC cohort

CHCC cohort		
(n = 159)		
Variable	Number	%
Age		
<= 55	88	55.3
> 55	71	44.7
Gender		
Female	31	19.5
Male	128	80.5
Tumor number		
1	117	73.6
>1	42	26.4
Tumor size		
<=5cm	76	47.8
> 5cm	83	52.2
Liver cirrhosis		
No	47	29.6
Yes	112	70.4
Tumor thrombus		
No	122	76.7
Yes	37	23.3
AFP		
Low (<=300ng/ml)	98	61.6
High (>300ng/ml)	61	38.4
BCLC stage		
A	68	42.8
B	52	32.7
C	39	24.5
TNM stage		
I	91	57.2
II	14	8.8
III	52	32.7
IV	2	1.3

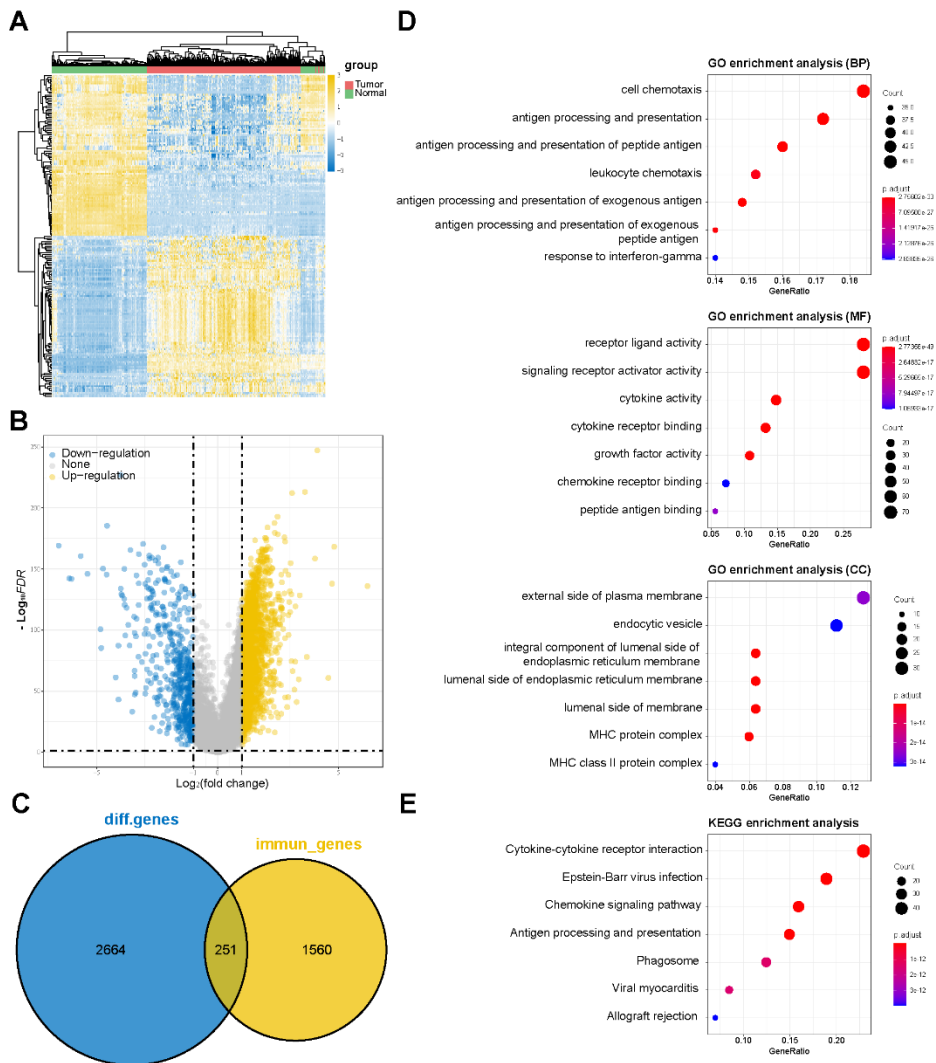


Figure S1. Identify the immune-related DEGs between HCC and normal liver tissues
A, Volcano plot of DEGs between HCC and normal tissues in TCGA data portal. **B**, Heatmap of DEGs between HCC and normal tissues. **C**, Venn diagram visualizing the intersections of DEGs with immune-related genes from ImmPort database. **D and E**, Enrichment analysis of 251 immune-related DEGs.

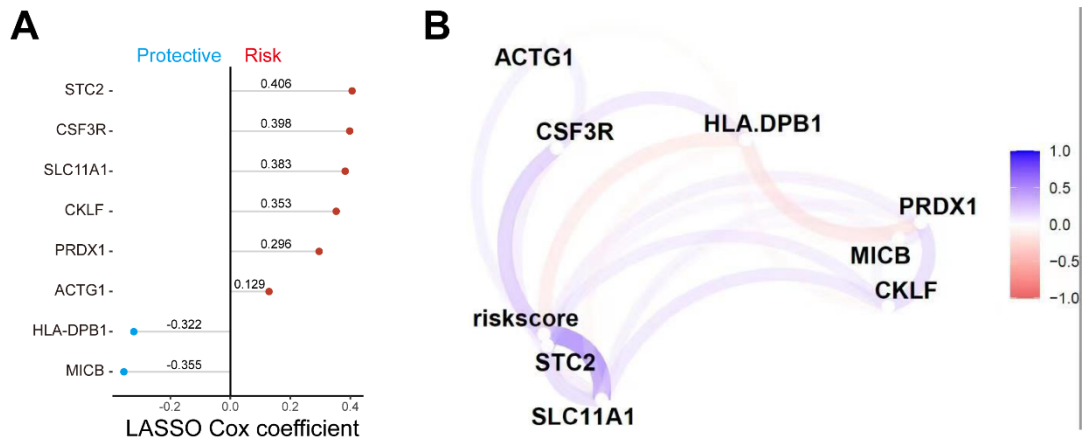


Figure S2. The coefficients and the corresponding correlations.

A, The lollipop map showing the coefficients of the IGS genes. **B**, The correlation network involving the 8 genes and risk score.

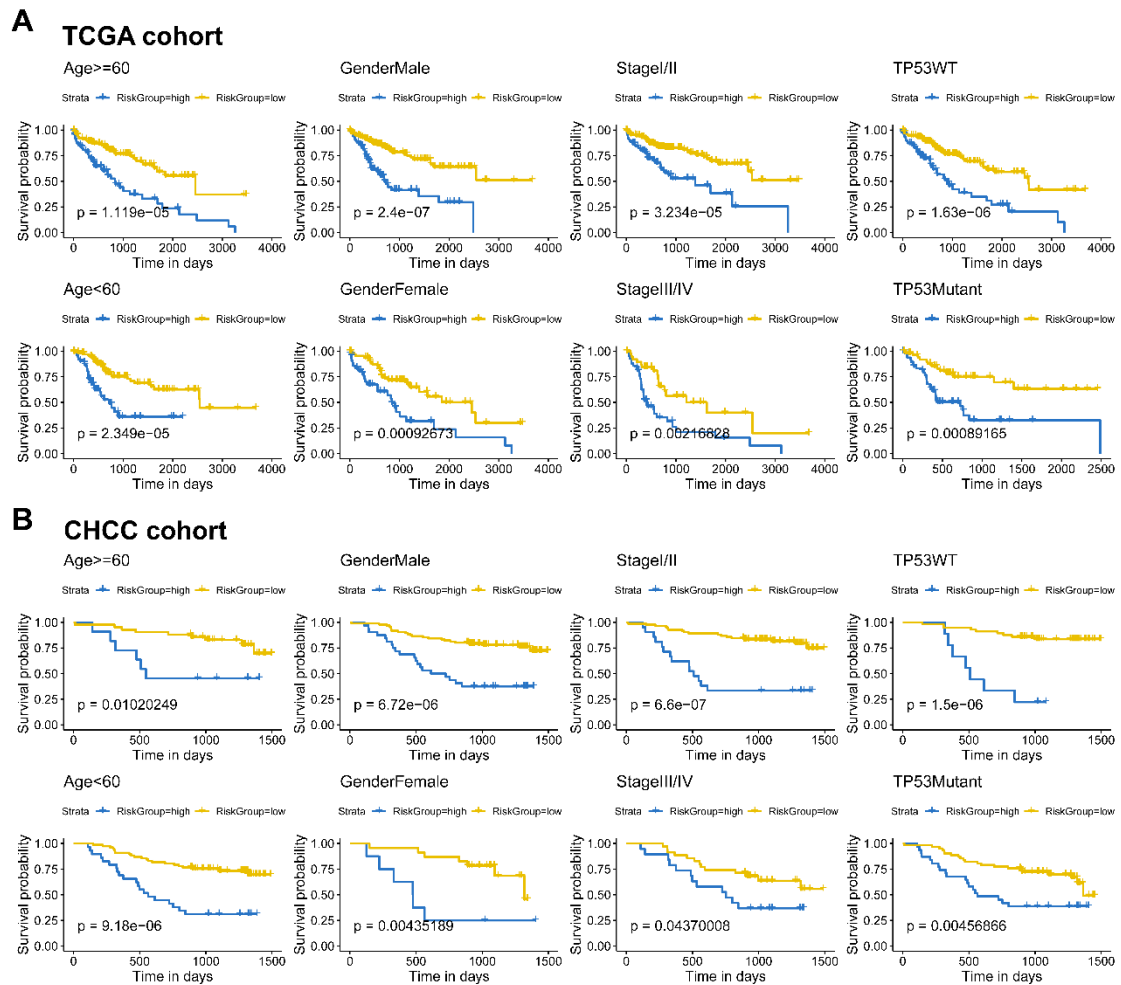


Figure S3. Stratified survival analysis of the high- and low-risk groups in the TCGA cohort and CHCC cohort.

The pooled TCGA or CHCC cohort was stratified into sub-groups based on the parameters including Age (≥ 60 or < 60), Gender, Stage (I/II or III/IV), and TP53 status (wide-type or mutated). **A**, Kaplan-Meier analysis with a log-rank test was conducted in the sub-groups of the TCGA cohort. **B**, Kaplan-Meier curves in the sub-groups of CHCC cohort.

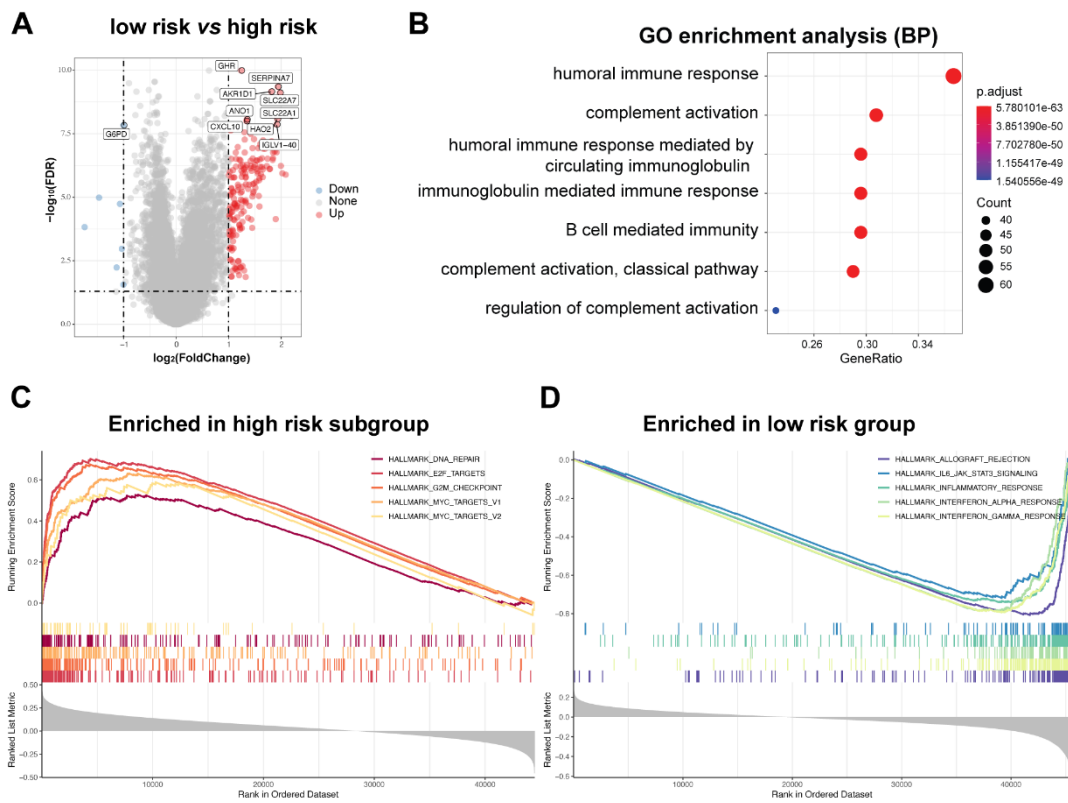


Figure S4. Molecular characteristics of different IGS subgroups. **A**, Volcano plot of the DEGs between IGS-low and -high groups in TCGA cohort. **B**, GO analysis of the DEGs above. **C**, GSEA analysis in high IGS risk subgroup ($P < 0.05$, $\text{FDR} < 0.25$). **D**, GSEA analysis in low IGS risk subgroup ($P < 0.05$, $\text{FDR} < 0.25$).

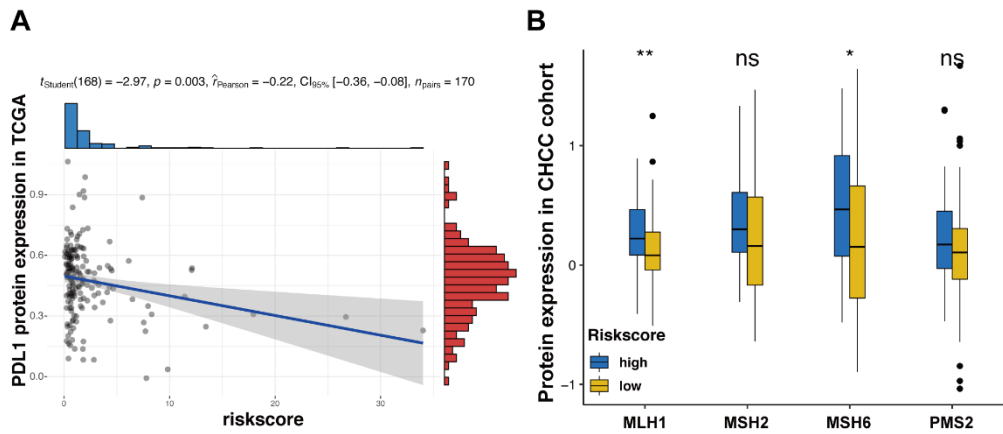


Figure S5. The correlation of IGS risk score with PDL1 and MSI genes.

A, the correlation of IGS risk score with PDL1 expression in LIHC TCGA cohort. **B**, the expression of MSI-related genes in IGS-high and IGS-low sub-group in CHCC cohort.