

Figure S1. Differential expression of IRGs in Genotype-Tissue Expression database and The Cancer Genome Atlas samples. (A) Heatmap of differentially expressed IRGs. The green to red spectrum indicates low to high gene expression. (B) Volcano plot of differentially expressed IRGs. Green dots represent downregulated IRGs, red dots represent upregulated IRGs and black dots represent IRGs that were not significantly differentially expressed. FC, fold change; fdr, false discovery rate; IRG, immune-related gene.

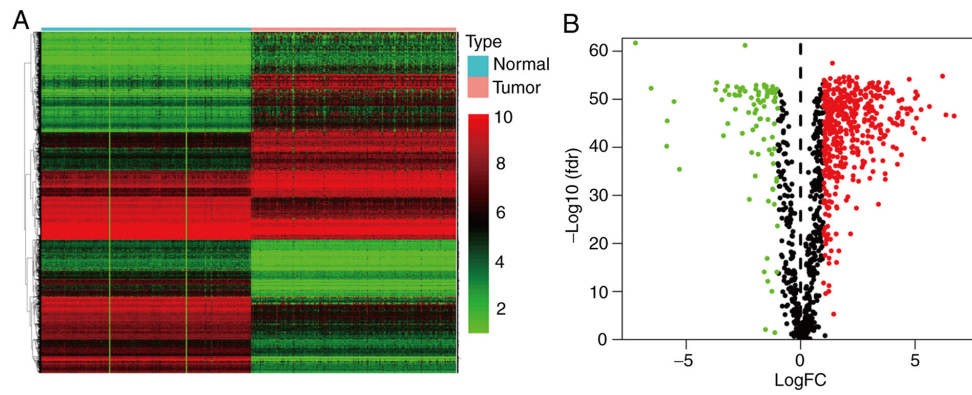


Figure S2. Prognostic analysis of high- and low-risk patients in the TCGA, ICGC and GEO cohorts. (A) Expression patterns of risk genes in TCGA training cohort. (B) Risk score distribution of patients in TCGA training cohort. (C) Survival time and status scatter plots of patients in TCGA training cohort. (D) Expression patterns of risk genes in the ICGC validation cohort. (E) Risk score distribution of patients in the ICGC validation cohort. (F) Survival time and status scatter plots of patients in the ICGC validation cohort. (G) Expression patterns of risk genes in the GEO validation cohort. (H) Risk score distribution of patients in the GEO validation cohort. (I) Survival time and status scatter plots of patients in the GEO validation cohort. Green dots represent low risk score and red dots represent high risk score. TCGA, The Cancer Genome Atlas; ICGC, International Cancer Genome Consortium; GEO, Gene Expression Omnibus; OAS1, 2'-5'-oligoadenylate synthetase 1; MET, MET proto-oncogene, receptor tyrosine kinase; IL1R2, interleukin 1 receptor type 2; IL20RB, interleukin 20 receptor subunit β .

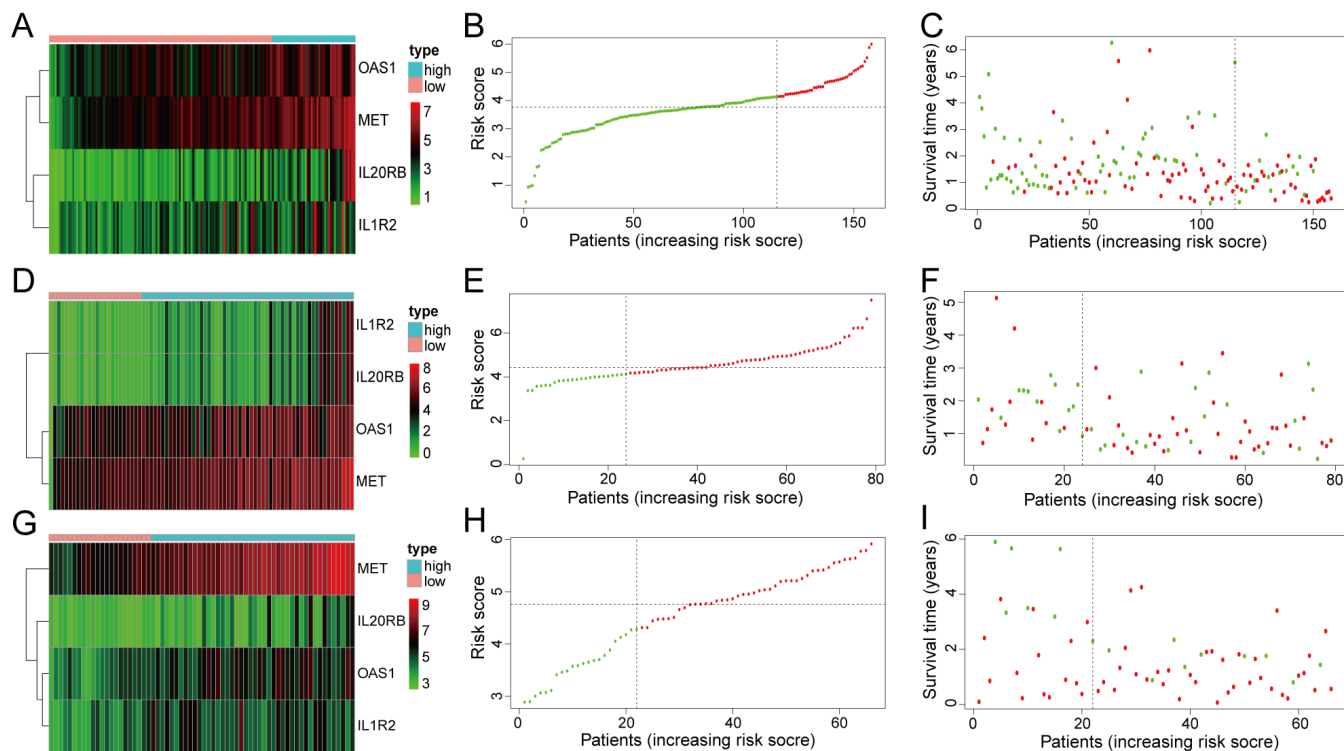


Table SI. Characteristics of patients in The Cancer Genome Atlas cohort.

Characteristics	Alive (n=68)	Dead, with tumor (n=82)	Dead, tumor-free (n=8)	Total (n=158)	P-value
Sex, n (%)					
Female	25(36.8)	38(46.3)	2(25)	65 (41.1)	0.3140
Male	43(63.4)	44(53.7)	6(75)	93 (58.9)	
Age, years					
Mean (SD)	62.6(10.2)	66(12.9)	73.6(5.8)	64.9 (11.8)	-
Median (min, max)	63.5(35, 84)	66(41, 88)	71(68, 84)	65(35, 88)	
Grade, n (%)					
G1	18 (26.4)	10 (12.2)	1 (12.5)	29 (18.3)	0.2040
G2	38 (55.9)	32 (39.0)	3 (37.5)	73 (46.2)	
G3	11 (16.2)	38 (46.4)	2 (25.0)	51 (32.3)	
G4	0 (0.0)	0 (0.0)	2 (25.0)	2 (1.3)	
Gx ^a	1 (1.5)	2 (2.4)	0 (0.0)	3 (1.9)	
Stage, n (%)					
Ia	3 (4.4)	2 (2.4)	1 (12.5)	6 (3.8)	0.0810
Ib	8 (11.8)	2 (2.4)	1 (12.5)	11 (7.0)	
IIa	15 (22.0)	10 (12.2)	2 (25.0)	27 (17.1)	
IIb	38 (55.9)	60 (73.2)	4 (50.0)	102 (64.5)	
III	1 (1.5)	4 (4.9)	0 (0.0)	5 (3.2)	
IV	3 (4.4)	4 (4.9)	0 (0.0)	7 (4.4)	
Tumor, n (%)					
T1	2 (2.9)	3 (3.7)	1 (12.5)	6 (3.8)	0.0834
T2	4 (5.9)	13 (15.8)	2 (25)	19 (12.0)	
T3	59 (86.8)	63 (76.8)	5 (62.5)	127 (80.4)	
T4	3 (4.4)	3 (3.7)	0 (0.0)	6 (3.8)	
Node, n (%)					
N1	30 (44.1)	9 (11.0)	3 (37.5)	42 (26.6)	0.0165
N2	38 (55.9)	73 (89.0)	5 (62.5)	116 (73.4)	
Metastasis, n (%)					
M0	37 (54.4)	52 (63.4)	5 (62.5)	94 (59.5)	0.0342
M1	1 (1.5)	5 (6.1)	1 (12.5)	7 (46.9)	
Mx ^a	30 (44.1)	25 (30.5)	2 (25.0)	57 (36.1)	

^aGx and Mx were used to represent the unavailable data of grade and metastasis respectively.

Table SII. Characteristics of International Cancer Genome Consortium samples.

Variable	Alive (n=38)	Dead, with tumor (n=35)	Dead, tumor-free (n=6)	Total (n=79)	P-value
Sex, n (%)					
Female	19 (50.0)	14 (40.0)	1 (16.7)	34 (41.1)	0.275
Male	19 (50.0)	21 (60.0)	5 (83.3)	45 (58.9)	
Age, years					
Mean (SD)	65.4 (10.2)	66.3 (8.6)	68.2 (8.8)	66 (9.3)	-
Median (min, max)	65 (40, 87)	67 (51, 83)	67.5 (58, 80)	66.5 (40, 87)	
Tumor, n (%)					
T1	2 (5.3)	0 (0.0)	0 (0.0)	2 (2.5)	0.183
T2	4 (10.5)	2 (5.7)	3 (50.0)	9 (11.4)	
T3	32 (84.2)	32 (91.4)	3 (50.0)	67 (84.8)	
T4	0 (0.0)	1 (2.9)	0 (0.0)	1 (1.3)	
Node, n (%)					
N1	5 (44.1)	4 (11.0)	0 (0.0)	9 (11.4)	0.215
N2	33 (55.9)	31 (89.0)	6 (100.0)	70 (88.6)	

Table SIII. Characteristics of Gene Expression Omnibus samples.

Variable	Alive (n=16)	Dead (n=50)	Total (n=66)	P-value
Stage, n (%)				
Stage Ia	0 (0.0)	0 (0.0)	0 (0.0)	0.070
Stage Ib	0 (0.0)	4 (8.0)	4 (6.1)	
Stage IIa	5 (31.2)	6 (12.0)	11 (16.7)	
Stage IIb	9 (56.2)	26 (52.0)	35 (53.0)	
Stage III	0 (0.0)	10 (20.0)	10 (15.1)	
Stage IV	2 (13.6)	4 (8.0)	6 (9.1)	
Tumor, n (%)				
T1	1 (6.3)	1 (2.0)	2 (3.0)	0.180
T2	9 (56.2)	23 (46.0)	32 (48.5)	
T3	5 (31.2)	26 (52.0)	31 (47.0)	
T4	1 (6.3)	0 (0.0)	1 (1.5)	

Table SIV. IRGs in the prognostic model associated with overall survival in the cohort from The Cancer Genome Atlas.

IRGs	Coefficient	Hazard ratio	95% confidence interval	P-value
OAS1	0.221350	1.247760	0.984858, 1.580840	0.066717
MET	0.515099	1.673804	1.286910, 2.177010	0.000123
IL1R2	0.179351	1.196441	1.010572, 1.416495	0.037338
IL20RB	0.141478	1.151975	0.973111, 1.363715	0.100310

IRGs, immune-related genes; OAS1, 2'-5'-oligoadenylate synthetase 1; MET, MET proto-oncogene, receptor tyrosine kinase; IL1R2, interleukin 1 receptor type 2; IL20RB, interleukin 20 receptor subunit β .