

Figure S1. IRF1 exhibited similar effects in a Chinese cohort of patients with CRC. (A) Kaplan Meier survival plots of the association between overall survival time and IRF1 expression in GSE71187 datasets. The association between IRF1 mRNA expression and the ratio of (B) M1 macrophages and activated (C) CD4⁺ memory T cells based on GSE71187 datasets. The histogram exhibits the frequency in the value. The violet dotted line represents the median value of log₂ (IRF1 expression) and the green dotted line indicates the median value of the ratio of (B) M1 macrophages or (C) activated CD4⁺ memory T cells. The blue line indicated the fit line of the association between the log₂ (IRF1 expression) and cell ratio of (B) M1 macrophages or (C) activated CD4⁺ memory T cells. IRF1, interferon regulatory factor 1; CRC, colorectal cancer.

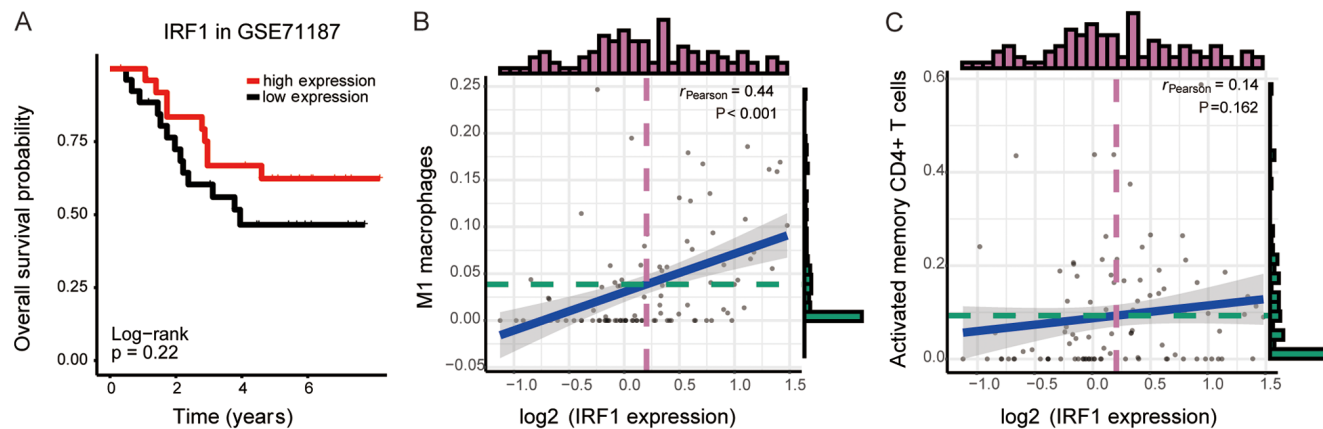


Table SI. Hub gene identification in the yellow module by a sum rank.

Gene symbol	Co-expression degree	PPI degree	Co-expression rank	PPI rank	Sum rank
IRF1	110	39	1	2	3
CCL5	108	27	2	9	11
UBE2L6	107	24	4	13	17
GBP1	100	33	16	5	21
IL2RB	104	22	8	20	28
STAT1	97	44	28	1	29
IFIT3	97	31	29	6	35
PSMB9	102	21	12	23	35
SAMD9L	103	20	10	25	35
GBP4	108	15	3	32	35
GBP5	100	23	17	19	36
CXCL10	95	37	35	3	38
PARP9	100	21	18	24	42
IDO1	102	17	13	29	42
IFI35	93	28	39	8	47
CD2	99	18	22	27	49
OAS2	92	27	41	10	51
GZMA	99	15	23	33	56
PSMB10	100	13	19	37	56
PSME1	104	8	9	48	57
PSMB8	89	24	45	14	59
NLRC5	100	10	20	43	63
TAP1	103	7	11	52	63
WARS	107	6	5	58	63
CXCL9	91	22	43	21	64
USP18	86	24	50	15	65
GNLY	102	7	14	53	67
CD247	99	10	24	44	68
APOL3	105	5	6	62	68
IFIH1	80	36	65	4	69
DHX58	83	24	59	16	75
TRIM21	85	22	53	22	75
CTLA4	75	31	70	7	77
RTP4	83	24	60	17	77
PARP14	89	16	46	31	77
IL15RA	101	5	15	63	78
RARRES3	105	3	7	73	80
CXCL13	96	8	32	49	81
CXCL11	85	18	54	28	82
CD3D	93	9	40	47	87
CXCR6	88	10	49	45	94
OAS3	68	24	77	18	95
CMPK2	82	15	63	34	97
LAP3	96	5	33	64	97
BIRC3	91	7	44	54	98
TAP2	97	4	30	68	98
APOBEC3G	98	3	26	74	100
CD38	82	12	64	38	102
TNFRSF9	84	10	56	46	102
CD7	89	7	47	55	102
CASP1	68	19	78	26	104
GZMB	48	27	95	11	106
ADAR	75	14	71	35	106
DTX3L	78	12	67	39	106
BTN3A1	100	1	21	85	106
IL12RB1	84	8	57	50	107
FAM26F	94	4	38	69	107
IRF8	43	26	98	12	110
RASGRP1	95	3	36	75	111

Table SI. Continued.

Gene symbol	Co-expression degree	PPI degree	Co-expression rank	PPI rank	Sum rank
LAMP3	99	1	25	86	111
NMI	74	12	74	40	114
SLAMF7	85	6	55	59	114
APOL6	98	1	27	87	114
RNF213	66	14	80	36	116
BATF2	86	5	51	65	116
FBXO6	89	4	48	70	118
ICOS	75	8	72	51	123
ETV7	97	0	31	97	128
ZBP1	54	12	89	41	130
MICB	86	2	52	79	131
USP30-AS1	96	0	34	98	132
EPSTI1	52	11	91	42	133
TNFRSF14	76	5	69	66	135
RP1-93H18.6	95	0	37	99	136
TNFRSF18	59	7	85	56	141
IKZF3	83	2	61	80	141
TRBC1	92	0	42	100	142
IFITM1	20	17	113	30	143
SIRPG	84	1	58	88	146
BTN3A2	83	1	62	89	151
LGALS9	43	7	99	57	156
LYN	45	6	97	60	157
MMP12	60	3	84	76	160
IL18R1	50	4	92	71	163
MAX	65	2	82	81	163
ERAP1	34	6	103	61	164
LYSMD2	73	1	75	90	165
RFX5	69	1	76	91	167
APOL2	79	0	66	101	167
LAX1	58	2	86	82	168
CCDC109B	77	0	68	102	170
HSH2D	54	2	90	83	173
MLKL	38	4	102	72	174
IGFLR1	75	0	73	103	176
GSDMD	50	2	93	84	177
TAPBPL	19	5	115	67	182
TFAP2A-AS1	67	0	79	104	183
SLC25A28	66	0	81	105	186
GFI1	23	3	110	77	187
RP11-468E2.5	63	0	83	106	189
SOD2	43	1	100	92	192
C18orf8	56	0	87	107	194
ICAM3	17	3	117	78	195
PLA2G2D	55	0	88	108	196
JADE2	33	1	104	93	197
FAM46C	29	1	106	94	200
TRDV3	49	0	94	109	203
FREM2	21	1	111	95	206
PIM2	47	0	96	110	206
SP140L	40	0	101	111	212
GSTA4	7	1	119	96	215
LINC00944	33	0	105	112	217
BMS1P20	27	0	107	113	220
COL9A3	24	0	108	114	222
FGD3	24	0	109	115	224
NKD1	21	0	112	116	228
C1orf56	20	0	114	117	231
NUTM2A-AS1	18	0	116	118	234

Table SI. Continued.

Gene symbol	Co-expression degree	PPI degree	Co-expression rank	PPI rank	Sum rank
RP11-326I11.5	8	0	118	119	237
CTA-384D8.35	0	0	120	120	240

Co-expression degree indicates the number of connections that the indicated gene has to other genes in the co-expression network of the yellow module; PPI degree indicates the number of edges the indicated gene has to other genes in the yellow module; $N_{\text{co-expression rank}}$ and $N_{\text{ppi rank}}$ indicate the rank of the gene based on its rank of co-expression degree and PPI degree, respectively, among all genes listed in the yellow module. $N_{\text{sum rank}} = N_{\text{ppi rank}} + N_{\text{co-expression rank}}$. PPI, protein-protein interaction.

Table SII. Comparisons of the clinical variables between the Chinese and French cohort.

Clinical variable	Chinese cohort (GSE71187, n=52)	French cohort (GSE39582, n=585)	
Sex, ratio (n)			P>0.05 ^a
Male	0.577 (30)	0.550 (322)	
Female	0.423 (22)	0.450 (263)	
Age, year			P<0.001 ^b
Median (range)	58 (26-93)	69 (22-97)	
Tumor-Node-			P>0.05 ^c
Metastasis stage, ratio (n)			
I	0	0.067(39)	
II	0.365 (19)	0.466 (271)	
III	0.635 (33)	0.361 (210)	
IV	0	0.103 (60)	
NA, n	0	2	
Overall survival time, year			P>0.05 ^d
Median	3.865	4.333	
Survival state, ratio (n)			
Died	0.423 (22)	0.331 (194)	
Alive	0.577 (30)	0.658 (385)	
NA, n	0	6	

^aUnpaired t-test, ^b χ^2 test, ^cWilcoxon's rank sum test and ^dLog-rank test.