Figure S1. Bodymap distribution of key genes of the JAK/STAT pathway using Gene Expression Profiling Interactive Analysis. (A) JAK1, (B) JAK2, (C) JAK3, (D) TYK2, (E) STAT1, (F) STAT2, (G) STAT3, (H) STAT4, (I) STAT5A, (J) STAT5B and (K) STAT6. JAK, Janus kinase; TYK2, tyrosine kinase 2; STAT, signal transducer and activator of transcription.

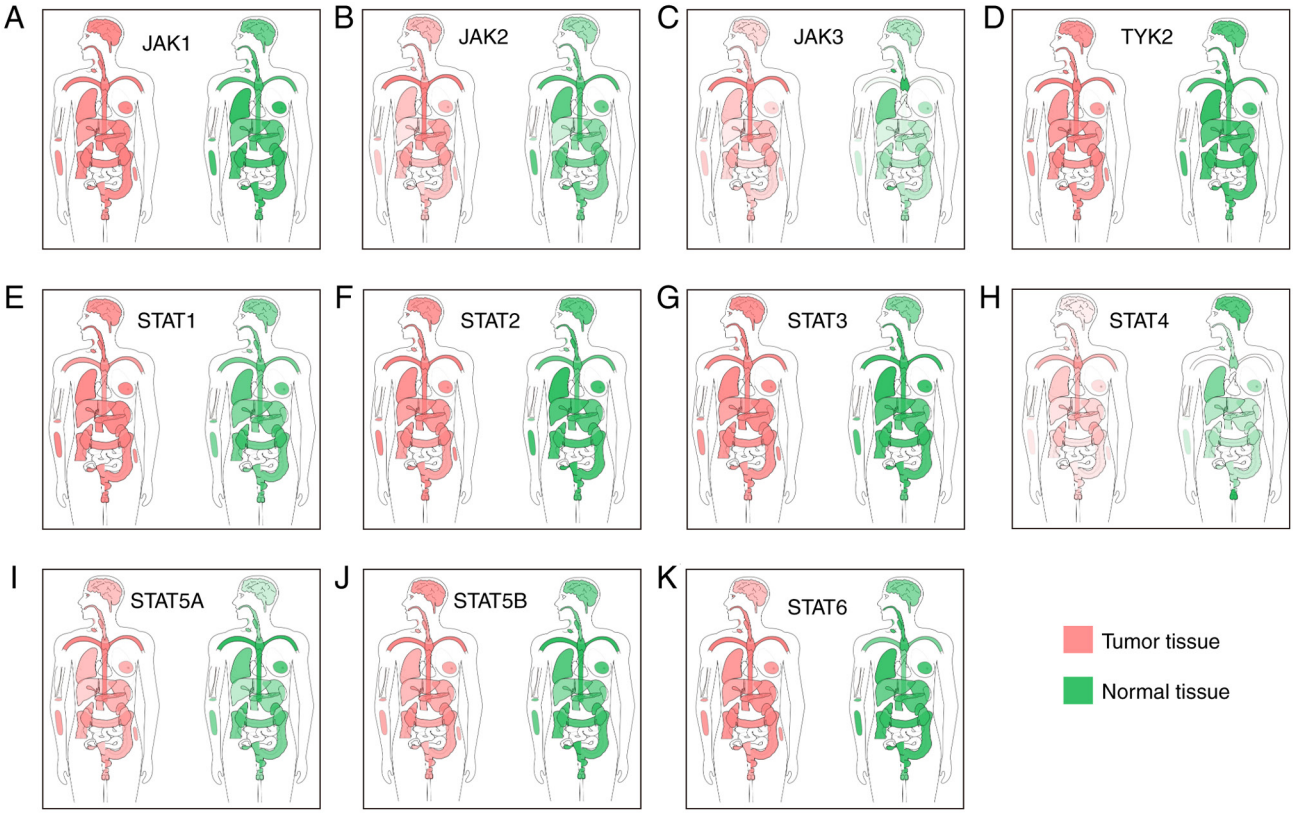

Figure S2. Protein expressions of key genes of JAK/STAT pathway in liver tissue from the Human Protein Atlas. (A) JAK1, (B) JAK2, (C) JAK3, (D) TYK2, (E) STAT1, (F) STAT2, (G) STAT3, (H) STAT4, (I) STAT5A, (J) STAT5B and (K) STAT6. JAK, Janus kinase; TYK2, tyrosine kinase 2; STAT, signal transducer and activator of transcription.

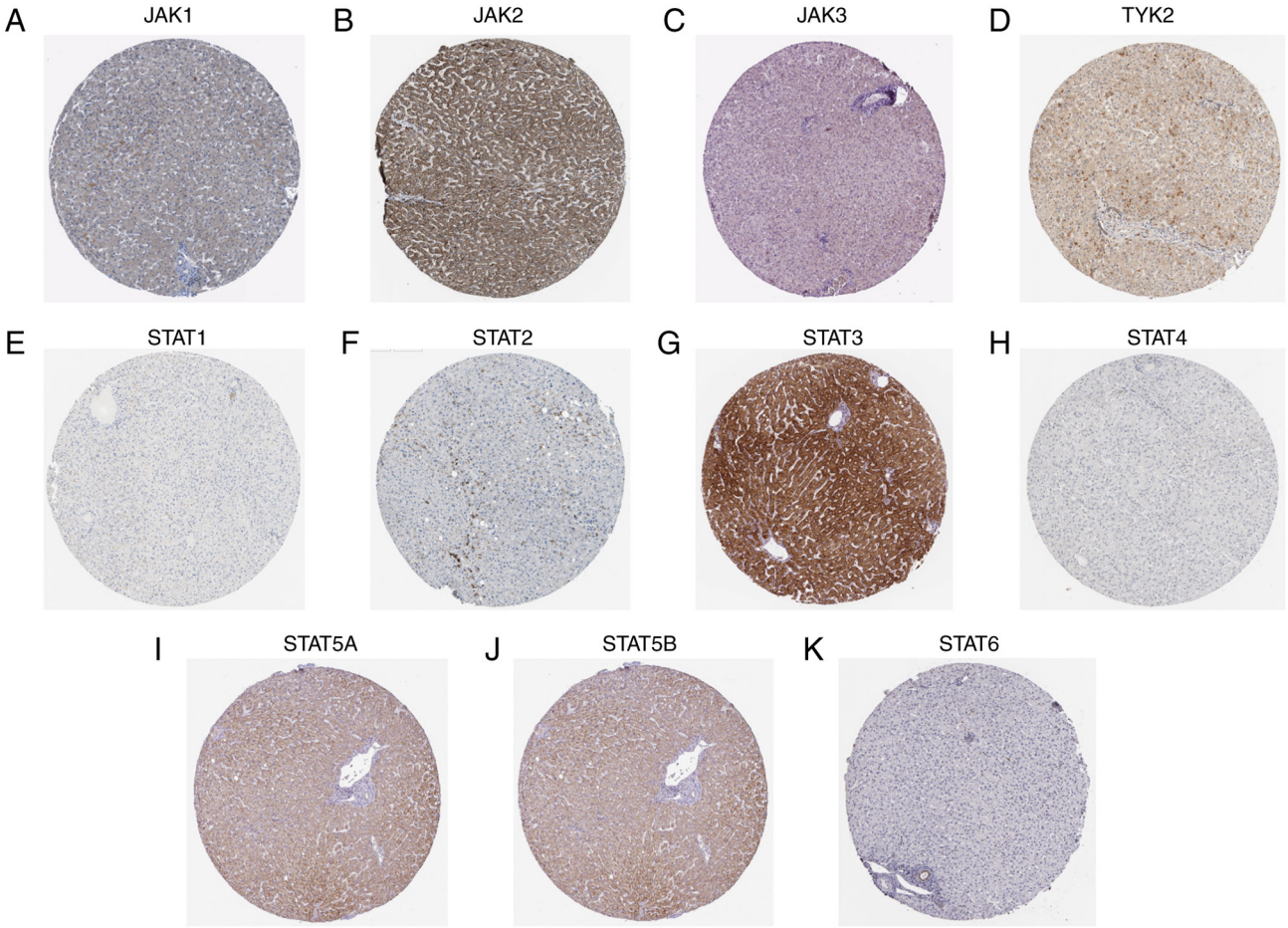

Figure S3. Nomograms constructed using overall survival-related clinical factors and JAK2, STAT5A and STAT6 in two cohorts. Nomograms constructed using overall survival-related clinical factors and genes in (A) the GSE14520 cohort and (B) The Cancer Genome Atlas (B) cohort. AFP, α-fetoprotein; BCLC, Barcelona Clinic Liver Cancer; JAK, Janus kinase; STAT, signal transducer and activator of transcription; HBV, hepatitis B.

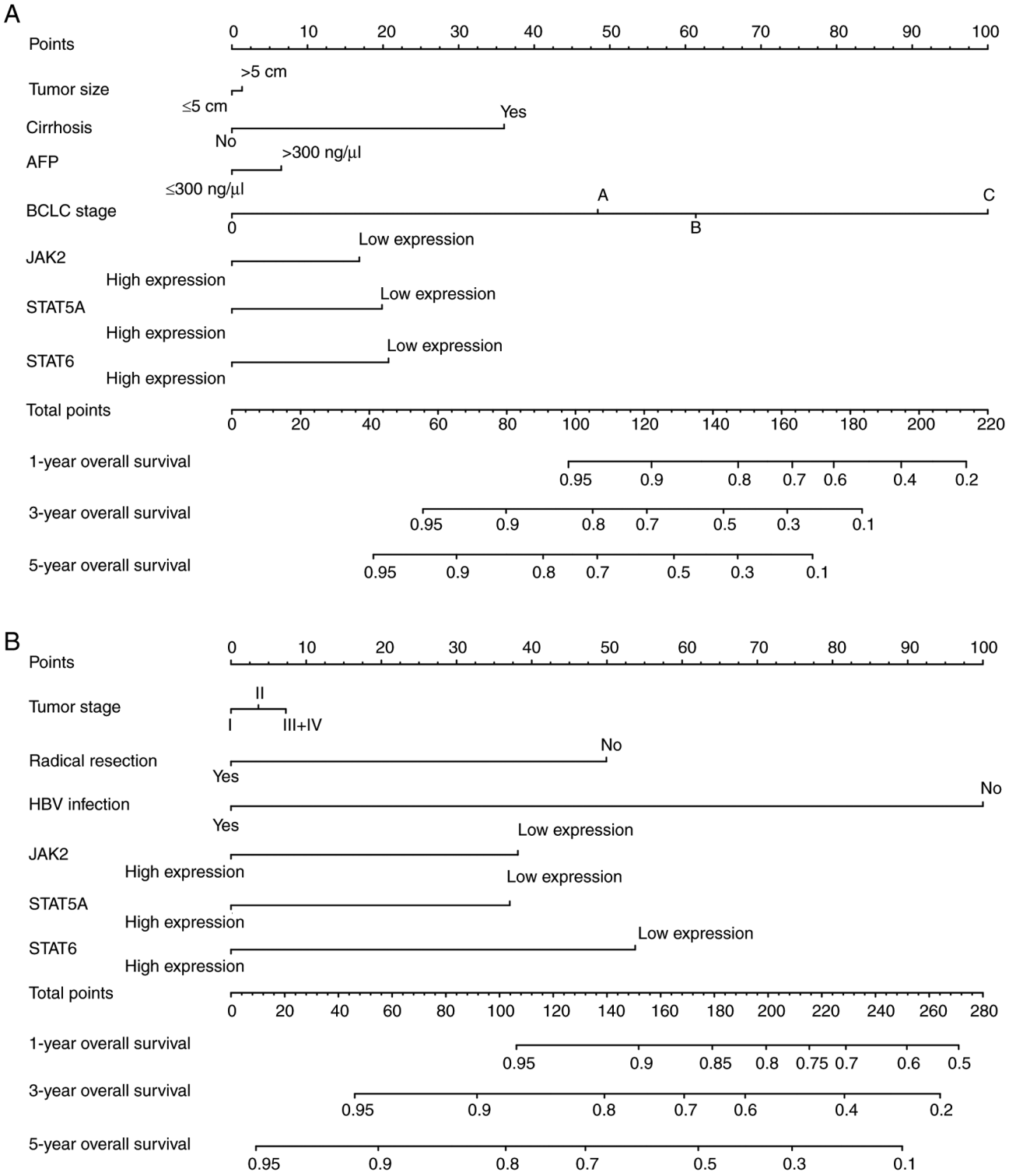

Figure S4. Enriched Gene Ontology terms of key genes of the JAK/STAT pathway. (A) Biological process, (B) cellular component and (C) molecular function. JAK, Janus kinase; STAT, signal transducer and activator of transcription.

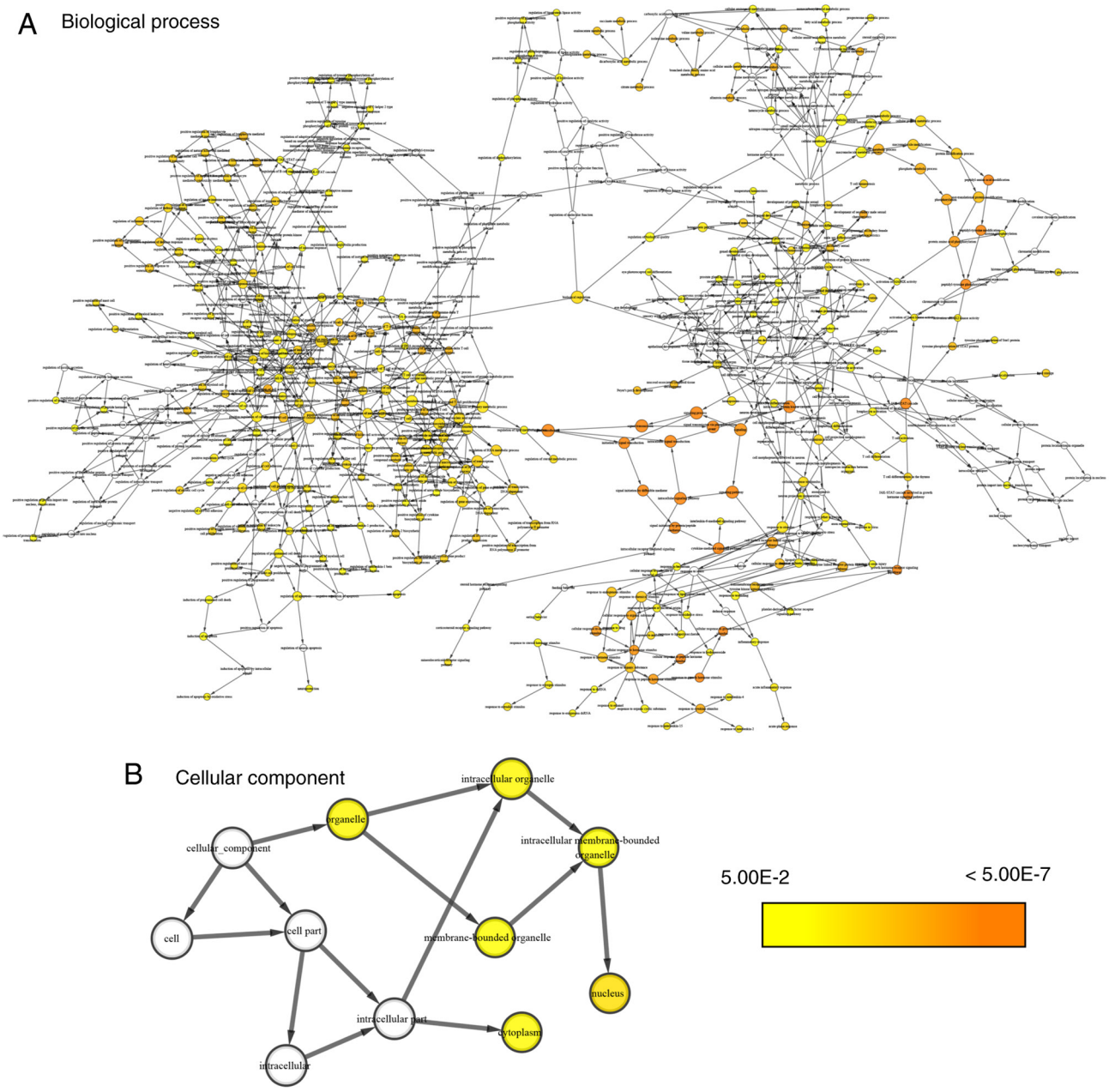

Figure S4. Continued.

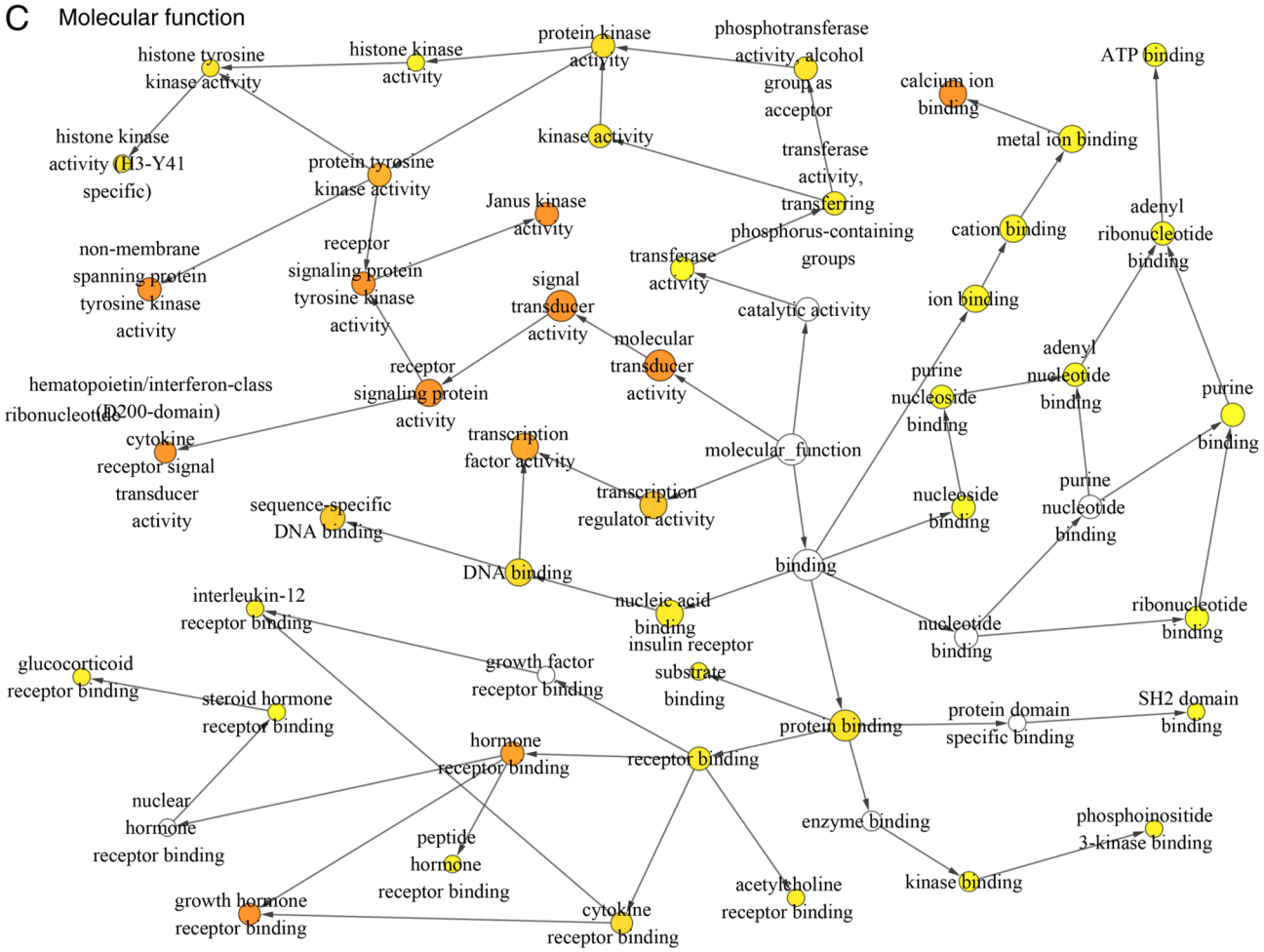

Figure S5. Schematic of the JAK/STAT signaling pathway. JAK, Janus kinase; STAT, signal transducer and activator of transcription; GF, growth factor; ECS, elongin-cullin-SOCS; p, phosphorylation; TC-PTP, T-cell protein tyrosine phosphatase; SHP1, tyrosine-protein phosphatase non-receptor type 6; STAM, signal-transducing adapter molecules; SHP2, protein tyrosine phosphatase non-receptor type 11; GRB, growth factor receptor bound protein; SOS, son of sevenless; IRF9, interferon regulatory factor 9; MAPK, mitogen-activated protein kinase; CBP/P300, Cbp/P300 interacting transactivator With Glu/Asp rich carboxy-terminal domain; PIAS, protein inhibitor of activated STAT; u, ubiquitination; SLIM, PDZ And LIM domain 2; CIS, cytokine-inducible SH2 protein; AOX, acyl-CoA oxidase; GFAP, glial fibrillary acidic protein; SOCS, suppressor of cytokine signaling; MCL1, myeloid cell leukemia 1; PIM1, Pim-1 proto-oncogene, serine/threonine kinase; CycD, cyclin D.

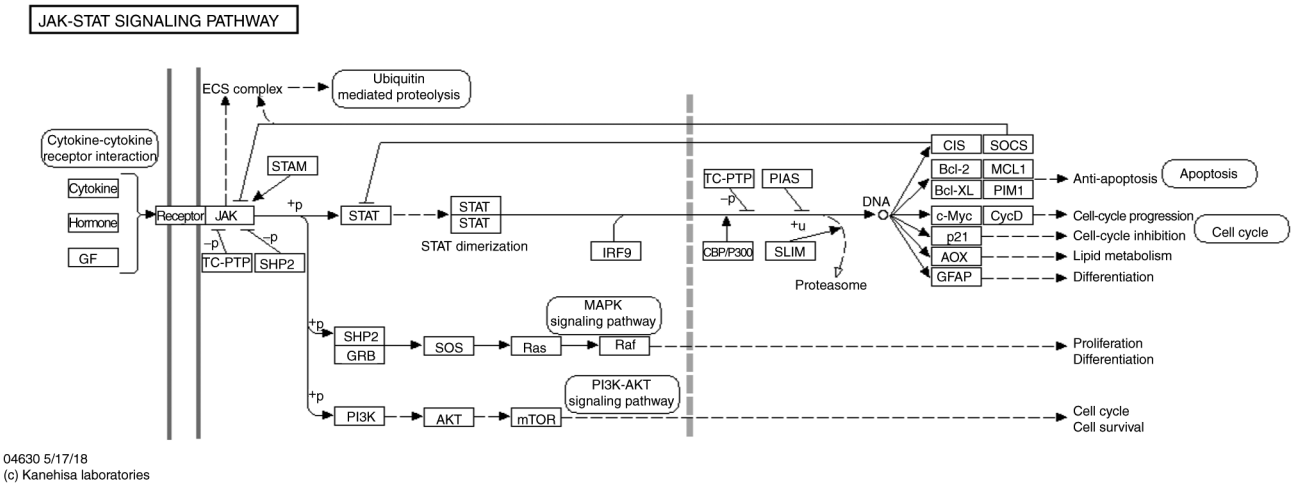

Figure S6. mRNA expression analysis of 21 pairs of hepatitis B virus-related tumor and non-tumor tissues. (A) JAK2, (B) STAT5A and (C) STAT6. JAK, Janus kinase; STAT, signal transducer and activator of transcription.

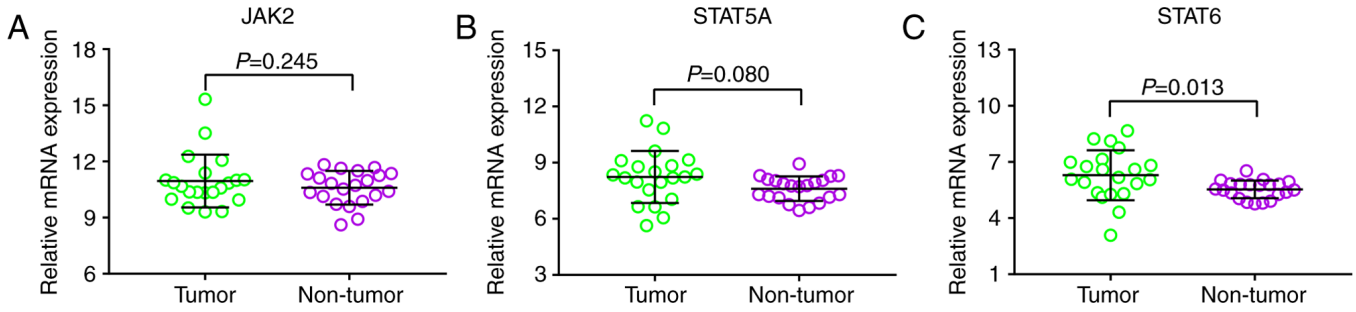

Table SI. Demographic characteristics of hepatocellular carcinoma patients in the GSE14520 dataset.

		Overall survival			
Variables	Patients (n=212)	No. of events	MST (month)	HR (95% CI)	P-value
Gender					
Male	183	74	NA	Ref.	
Female	29	8	NA	0.587 (0.283-1.218)	0.152
Age (years)					
≤60	175	69	NA	Ref.	
>60	37	13	NA	0.864 (0.478-1.564)	0.630
HBV					
AVR-CC	56	25	NA	Ref.	
CC	156	57	NA	0.747 (0.467-1.196)	0.225
Tumor size (cm)[a]					
≤5	137	46	NA	Ref.	
>5	74	36	53.30	1.975 (1.274-3.060)	0.002[c]
Cirrhosis					
Yes	195	80	NA	Ref.	
No	17	2	NA	0.231 (0.057-0.939)	0.041[c]
Multinodular					
Yes	45	23	47.90	Ref.	
No	167	59	NA	0.622 (0.384-1.008)	0.054
AFP (ng/ml)[b]					
≤300	115	39	NA	Ref.	
>300	94	43	NA	1.546 (1.002-2.385)	0.049[c]
BCLC stage					
0	20	2	NA	Ref.	<0.0001[c]
A	143	48	NA	4.119 (1.001-16.951)	0.050[c]
B	22	12	46.10	8.992 (2.005-40.320)	0.004[c]
C	27	20	13.60	18.993 (4.419-81.632)	<0.0001[c]

[a]Data from 1 patient were missing; [b]Data from 3 patients were missing; [c]significant P-values and 95% CI. MST, median survival time; HR, hazard ratio; 95% CI, 95% confidence interval; HBV, hepatitis B virus; AVR-CC, acute viral replication chronic carrier; CC, chronic carrier; AFP, α-fetoprotein; BCLC, Barcelona Clinic Liver Cancer.

Table SII. Demographic characteristics of hepatocellular carcinoma patients in The Cancer Genome Atlas database.

		Overall survival			
Variables	Patients (n=370)	No. of event	MST (days)	HR (95% CI)	P-value[k]
Gender					0.262
Female	121	51	1,490	Ref.	
Male	249	79	2,486	0.817 (0.573-1.164)	
Age (years)					0.217
≤60	177	55	2,532	Ref.	
>60	193	75	1,622	1.246 (0.879-1.766)	
Child pugh[a]					0.184
A	216	59	2,542	Ref.	
B + C	22	9	1,005	1.614 (0.796-3.270)	
HBV infection[b]					<0.0001[k]
No	247	104	1,210	Ref.	
Yes	104	20	NA	0.357 (0.221-0.578)[k]	
HCV infection[c]					0.730
No	295	105	1,791	Ref.	
Yes	56	19	1,229	1.090 (0.667-1.782)	
Histologic grade[d]					
G1	55	18	2,116	Ref.	0.750
G2	177	60	1,685	1.181 (0.697-2.000)	0.537
G3	121	43	1,622	1.233 (0.711-2.140)	0.456
G4	12	5	NA	1.693 (0.626-4.584)	0.300
Tumor stage[e]					
I	171	42	2,532	Ref.	<0.0001[k]
II	85	26	1,852	1.427 (0.874-2.330)	0.155
III + IV	90	48	770	2.764 (1.823-4.190)[k]	<0.0001[k]
Ishak fibrosis score[f]					
0	74	30	2,131	Ref.	0.874
1,2	31	9	1,372	0.917 (0.429-1.962)	0.823
3,4	28	6	NA	0.682 (0.281-1.654)	0.397
5	9	2	1,386	0.750 (0.177-3.167)	0.695
6	69	17	NA	0.766 (0.418-1.403)	0.388
AFP (ng/ml)[g]					
≤400	213	62	2,456	Ref.	0.832
>400	64	22	2,486	1.055 (0.645-1.724)	
Radical resection[h]					
R0	323	110	1,875	Ref.	0.007[k]
R1 + R2 + RX	40	17	837	2.030 (1.213-3.395)[k]	
Vascular invasion[i]					
No	206	60	2,131	Ref.	0.155
Yes	108	36	2,486	1.351 (0.892-2.047)	
Alcohol history[j]					
No	234			Ref.	0.896
Yes	117			1.026 (0.703-1.496)	

[a]Data of 132 patients were missing; [b]data of 19 patients were missing; [c]data of 19 patients were missing; [d]data of 5 patients were missing; [e]data of 14 patients were missing; [f]data of 159 patients were missing; [g]data of 93 patients were missing; [h]data of 7 patients were missing; [i]data of 56 patients were missing; [j]data of 19 patients were missing; [k]significant P-values and 95% CI. MST, median survival time; HR, hazard ratio; 95% CI, 95% confidence interval; Ref., reference; HBV, hepatitis B virus; HCV, hepatitis C virus; AFP, α-fetoprotein.