

STAT gene family mRNA expression and prognostic value in hepatocellular carcinoma

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Background: Signal transducer and activator of transcription (STAT) proteins are well-known transcription factors that play an important role in the progression of cancer. However, the association between STAT family genes and hepatocellular carcinoma (HCC) remains unclear. This study investigates the expression level, the prognostic value and the potential mechanism of STAT family genes in HCC.

Methods: Data from 365 HCC patients in The Cancer Genome Atlas (TCGA) database and 241 HCC patients in the Gene Expression Omnibus (GEO) database were used to investigate the diagnostic and prognostic values of STAT genes by survival analysis and nomogram. Gene set enrichment analysis (GSEA) was used to investigate the potential mechanism of the STAT genes in the development of HCC.

Results: Our results showed that *STAT4/5B* mRNA expression levels in HCC tissues were lower than those in normal tissues. Importantly, our results indicated that high expression of *STAT5A*, *STAT5B* and *STAT6* was associated with better overall survival in HCC patients. Joint effects analysis of *STAT5A*, *STAT5B* and *STAT6* suggested that the prognosis difference for any combination of genes was more significant than that for any individual gene. Then, we developed a risk score model could predict HCC prognosis and the nomogram visualized gene expression and clinical factors of probability for HCC prognosis. The ROC and calibration curves showed good performance in survival prediction in both the TCGA and the GEO databases. GSEA suggested that high expression of *STAT5A*, *STAT5B* and *STAT6* were involved in immune-related biological processes, drug metabolism cytochrome P450, JAK-STAT signalling pathway, and PPAR signalling pathways.

Conclusion: Our data suggest that *STAT5A*, *STAT5B* and *STAT6* expression may be potential prognostic markers of HCC and, in combination, have a better predictive value for HCC prognosis.

Keywords: hepatocellular carcinoma, signal transducer and activator of transcription, prognosis, TCGA, GSEA

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Introduction

Liver cancer is the second leading cause of cancer-related deaths worldwide, with an estimated 782,500 new diagnoses and 745,500 deaths occurring worldwide in 2012.¹⁻³ Approximately 383,000 people die from liver cancer every year in China, accounting for 51% of the deaths from liver cancer worldwide.⁴ Hepatocellular carcinoma (HCC), the predominant form of liver cancer, can be triggered by a variety of causes, including hepatitis virus infections, alcohol abuse, autoimmune hepatitis, obesity, and several metabolic diseases.^{1,3,5} Although surgical resection, liver transplantation, percutaneous ablation, targeted therapy, and radiotherapy have

been used as clinical treatments, the prognosis of HCC patients remains unsatisfactory due to the high postoperative recurrence rate and metastasis.⁶ Therefore, the identification of prognostic biomarkers and drug targets is crucial to provide better prognosis and more effective personalized treatments for HCC patients.

Signal transducer and activator of transcription (STAT) proteins are intracellular transcription factors that regulate the expression of genes related to cell cycle, cell survival, and immune response associated with cancer progression.⁷ Seven STAT family members have been identified as follows: *STAT1*, *STAT2*, *STAT3*, *STAT4*, *STAT5A*, *STAT5B*, and *STAT6*.⁸ Some studies have shown that *STAT1* and *STAT2* activated by IFN play a key role in inhibiting hepatitis C virus (HCV) replication.⁹ Enhancing activation of these STATs could be an attractive strategy to improve IFN- α therapy for the treatment of HCV. It has been demonstrated that *STAT3* is a promising therapeutic target for converting cancer-promoting inflammation to anti-tumour immunity.¹⁰ *STAT3* has hepatoprotective activities and prevents liver injury-associated HCC initiation during the early stage of chronic liver injury; however, *STAT3* also promotes liver tumour cell survival and proliferation when tumour cells have developed during the end-stage of liver cirrhosis and HCC.^{11,12} Hennighausen Lother, et al found that liver-specific *STAT5* knockout mice were more susceptible to chronic CCl₄-induced liver fibrosis and HCC development.¹³ These studies suggested that STAT genes play an important role in the development and progression of HCC. However, the potential application value and mechanism of STAT genes for the prognostic prediction of HCC patients remains unclear.

In this study, the HCC mRNA expression data were downloaded from The Cancer Genome Atlas (TCGA) and Gene Expression Omnibus (GEO) databases. The corresponding clinical information was downloaded from the University of California, Santa Cruz Xena (UCSC Xena) browser. Survival analysis, risk score model, nomogram, and gene set enrichment analysis (GSEA) were used to investigate the prediction value and potential mechanism of STAT genes in HCC prognosis.

Materials and methods

Public database mining of STAT genes

First, the Genotype-Tissue Expression (GTEx) website was used to investigate the mRNA expression distribution of STAT genes in normal organ tissues. Then, we used the

Metabolic gEneRApid Visualizer (MERAV) to study the expression distribution of STAT genes between HCC and adjacent normal tissues. Alteration of the status of STAT genes in HCC patients was obtained from the online cBioPortal for Cancer Genomics database.

Then, the level 3 mRNA expression data of HCC was downloaded from The Cancer Genome Atlas (TCGA) database, and the gene expression data were normalized by the *edgeR* package according to the user guide. The corresponding clinical information was downloaded from the UCSC Xena database, which included race, gender, age, body mass index (BMI), TNM stage, survival time (days), and survival status. In addition, the gene expression dataset (GSE14520) of HCC was also downloaded from the Gene Expression Omnibus (GEO) database. The GSE14520 dataset contained expression profiles generated from [HT_HG-U133A] Affymetrix HT Human Genome U133A and [HT_HG-U133A_2] Affymetrix HT Human Genome U133A_2.0 arrays. To avoid a batch effect, we selected a profile from the former array that had more patients (n=241 HCC patients) than the latter array.

Expression and association analysis

The comparison of STAT gene expression between tumour tissue and adjacent normal tissues was done by an analysis using TCGA and GEO databases, respectively. Pearson correlation coefficient was used to evaluate correlations among genes in coexpression analysis.

Survival analysis

In order to evaluate the prognostic value of a specific gene, the patients were divided into two groups according to the median expression of the gene (high vs low expression) in the TCGA and GEO database, respectively. The median survival time (MST) was used to evaluate the prognosis of HCC patients in TCGA database, whereas overall survival (OS) and recurrence-free survival (RFS) were used to assess that of patients in the GEO database. Survival analysis was carried out using the Kaplan–Meier method with the log-rank test to compare clinical factors and gene expression groups. Univariate and multivariate Cox proportional hazards regression analysis was conducted to further calculate the crude or adjusted hazard ratio (HR), 95% confidence interval (CI) and *P*-value. In addition, clinical characteristics of HCC patients were also analysed by Kaplan–Meier method in TCGA and GEO database, respectively.

Joint effects analysis of STAT5A, STAT5B, and STAT6

On the basis of the results of survival analysis, we also investigated the joint effects of significant prognostic-related STAT genes in HCC. Joint effects analysis was conducted with the following combinations: (1) *STAT5A* and *STAT5B*; (2) *STAT5A* and *STAT6*; (3) *STAT5B* and *STAT6*; and (4) *STAT5A*, *STAT5B*, and *STAT6*. The combinations of *STAT5A* and *STAT5B* were composed of four groups as follows: group 1 (low *STAT5A* and low *STAT5B* expression), group 2 (low *STAT5A* and high *STAT5B* expression), group 3 (high *STAT5A* and low *STAT5B* expression), and group 4 (high *STAT5A* and high *STAT5B* expression).

The combinations of *STAT5A* and *STAT6* were composed of four groups as follows: group I (low *STAT5A* and low *STAT6* expression), group II (low *STAT5A* and high *STAT6* expression), group III (high *STAT5A* and low *STAT6* expression), and group IV (high *STAT5A* and high *STAT6* expression).

The combinations of *STAT5B* and *STAT6* were composed of four groups as follows: group a (low *STAT5B* and low *STAT6* expression), group b (low *STAT5B* and high *STAT6* expression), group c (high *STAT5B* and low *STAT6* expression), and group d (high *STAT5B* and high *STAT6* expression).

The combinations of *STAT5A*, *STAT5B* and *STAT6* were composed of four groups as follows: group A (low *STAT5A*, low *STAT5B*, and low *STAT6* expression); group B (high *STAT5A*, low *STAT5B*, and low *STAT6* expression; low *STAT5A*, high *STAT5B*, and low *STAT6* expression; and low *STAT5A*, low *STAT5B*, and high *STAT6* expression); group C (high *STAT5A*, high *STAT5B*, and low *STAT6* expression; high *STAT5A*, low *STAT5B*, and high *STAT6* expression; and low *STAT5A*, high *STAT5B*, and high *STAT6* expression); and group D (high *STAT5A*, high *STAT5B*, and high *STAT6* expression).

Construction of risk score model and nomogram

A risk score model was constructed based on the expression levels of prognosis-associated genes and the contribution coefficient (β) of the multivariate Cox proportional hazards regression model. The formula of the model was as follows: risk score = expression of *STAT5A* $\times \beta$ of *STAT5A* + expression of *STAT5B* $\times \beta$ of *STAT5B* + expression of *STAT6* $\times \beta$ of *STAT6*. The risk score was then divided into high and low risk groups with the optimal cut-off value of gene expression. The time-dependent receiver operating characteristic (ROC) curve was

drawn to evaluate the predictive value of the prognostic gene signature for overall survival. The Kaplan–Meier survival curve combined with a log-rank test was used to predict patient survival in the high- and low-risk group.

Nomogram is widely applied to predict cancer patients' prognoses. The nomogram was developed by the rms R package to assess the probability of the 3-, and 5-year OS rates for HCC patients, which was based on prognostic clinical indicators and prognostic-related STAT genes. Validation of the nomogram was assessed by discrimination and calibration. The discrimination of the nomogram was calculated using the concordance index (C-index) by a bootstrap method with 500 resamples. The calibration curve of the nomogram was evaluated graphically by plotting the nomogram prediction probabilities against the observed rates. Overlapping with the reference line demonstrated that the model was in perfect agreement.

Gene set enrichment analysis (GSEA)

Differences of biological process and pathways in transcriptome levels between high and low *STAT5A*, *STAT5B* and *STAT6* genes expression were analysed using GSEA, with reference to gene sets from the Molecular Signatures Database (MSigDB) of GO gene sets and KEGG gene sets, respectively. The number of permutations was set at 1,000. Enrichment results satisfying a nominal *P*-value < 0.05 and a false discovery rate (FDR) < 0.25 were considered statistically significant.

Statistical analysis

Kaplan–Meier survival analysis by log rank test was used to calculate the median survival time (MST). Univariate and multivariate Cox proportional hazards models were used to calculate the HR and 95% CI. Statistical analyses were performed using R software v3.5.0 (R Foundation for Statistical Computing, Vienna, Austria) and GraphPad Prism v7.00 (GraphPad Software Inc., USA). $P < 0.05$ was considered statistically significant.

Results

Public database mining of STAT genes

To make a complete analysis of the distribution and function of STAT genes in humans, the distribution of STAT genes in human normal organ tissues was investigated by GTEx. As shown in Figure 1A–G, the results suggested that the expression level of STAT1–6 genes was median in human liver tissues compared to other organ tissues. Then,

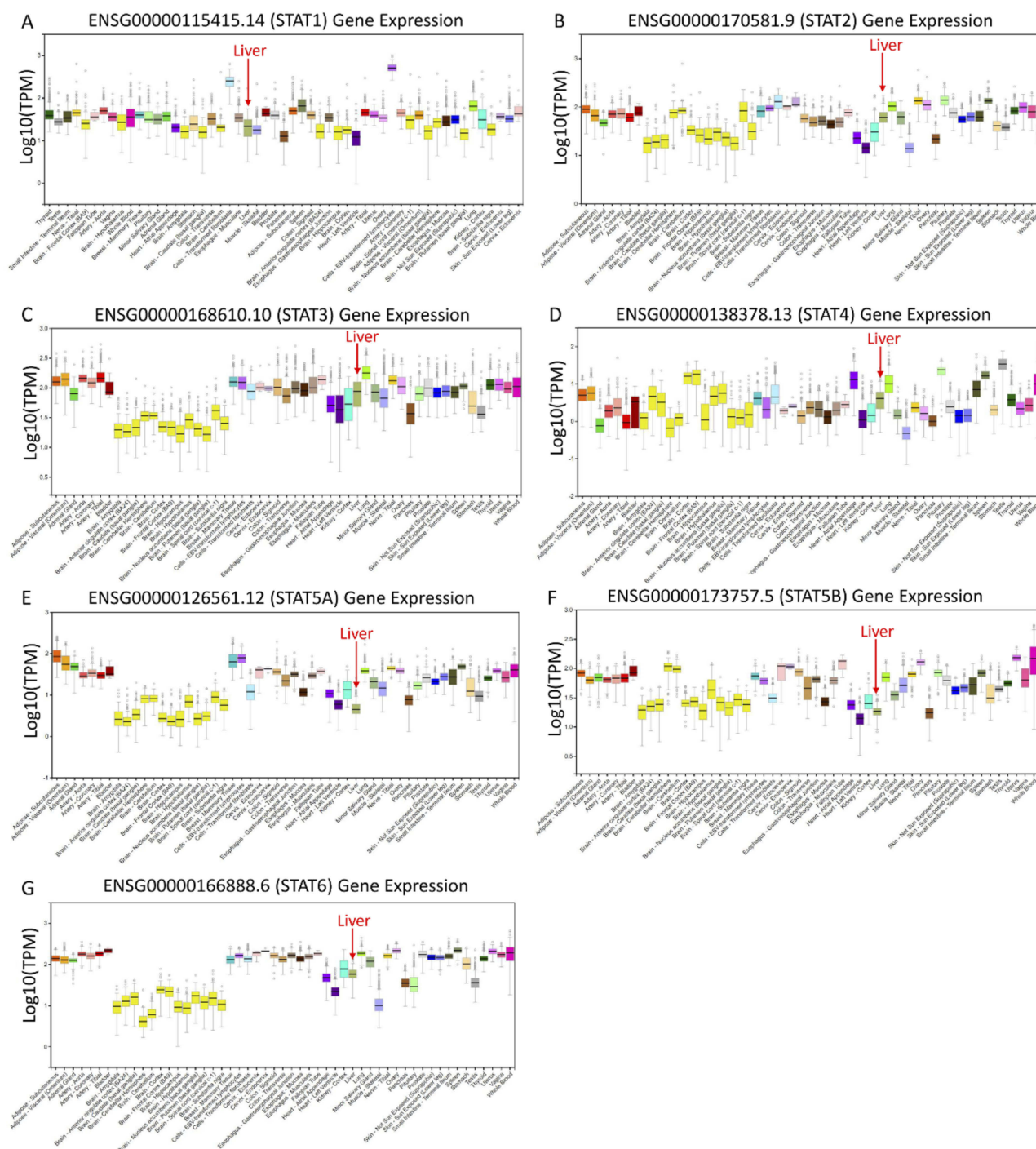


Figure 1 Expression distribution of STAT1-6 genes in human normal organ tissues. (A) *STAT1*; (B) *STAT2*; (C) *STAT3*; (D) *STAT4*; (E) *STAT5A*; (F) *STAT5B*; (G) *STAT6*.

the MERAV database showed that *STAT1* and *STAT5B* were upregulated in liver tumour tissue, whereas *STAT2*, *STAT3*, *STAT4*, *STAT5A*, and *STAT6* were downregulated in tumour tissue (Figure 2A–G). Furthermore, the protein expression of STAT genes obtained similar results by using clinical specimens from the Human Protein Profiles

(Figure 2H). Finally, we investigated the alteration percentage of STAT1-6 genes in HCC patients using the cBioPortal website (Figure 2I). The alteration percentage of the STAT genes signature in HCC varied from 2.9 to 13% (*STAT1*, 4%; *STAT2*, 6%; *STAT3*, 7%; *STAT4*, 6%; *STAT5A*, 2.9%; *STAT5B*, 13%; and *STAT6*, 7%).

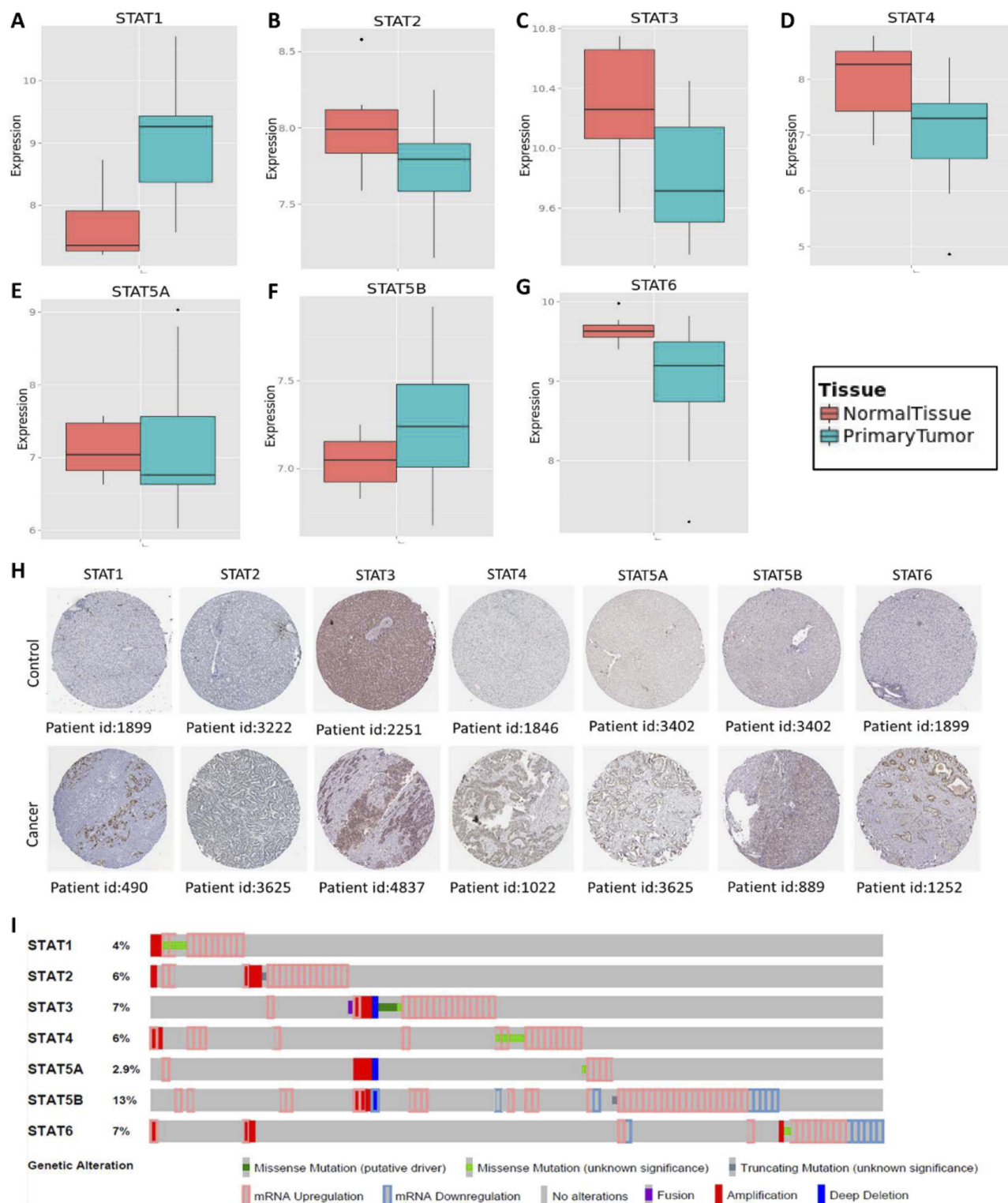


Figure 2 Gene expression and genetic alteration of STAT genes in HCC. (A–G) Comparison of *STAT1*, *STAT2*, *STAT3*, *STAT4*, *STAT5A*, *STAT5B* and *STAT6* mRNA expression in HCC and normal tissues using MERAV; (H) The protein expression of STAT genes in HCC using human protein atlas database; (I) Alteration frequency analysis of STAT genes in HCC using cBioPortal.

Analysis of the expression of STAT genes and correlation in TCGA and GEO databases

To better understand the expression and clinical significance of STAT genes in HCC, the RNA-Seq dataset of HCC was downloaded from TCGA and GEO databases. After normalization of the RNA sequencing data, we found that the expression level of *STAT3*, *STAT4* and *STAT5B* were significantly lower in HCC tumour tissue than in normal tissue, but the differences in expression in the other genes did not reach statistical significance in the TCGA database (Figure 3A). As shown in Figure 3B, the expression levels of *STAT4*, *STAT5A*, *STAT5B*, and *STAT6* were significantly lower in HCC tissue than in non-tumour tissue. In addition, the Pearson correlation coefficients of the seven STAT genes were also calculated. In the TCGA database, *STAT5B* was negatively correlated with *STAT1*

($r=-0.10$, $P<0.05$) and *STAT4* ($r=-0.20$, $P<0.05$), but not significantly associated with *STAT5A* ($r=-0.03$, $P>0.05$). The other genes were positively and significantly correlated with each other (all $P<0.05$, Figure 3C). In the GEO database, *STAT5A* ($r=0.05$, $P<0.05$) and *STAT5B* ($r=0.31$, $P<0.05$) had a significantly positive correlation with *STAT6* (Figure 3D).

Survival analysis of STAT genes in TCGA and GEO databases

The clinical characteristics of HCC patients in the TCGA and GEO databases are summarized in Tables 1 and 2, respectively. As shown in Table 1, we found that tumour stage, and TNM stage were significantly associated with MST ($P<0.05$). In the GEO database, tumour size, cirrhosis, TNM stage, BCLC stage, and AFP level were related to OS (all $P<0.05$), while gender, TNM stage, and BCLC

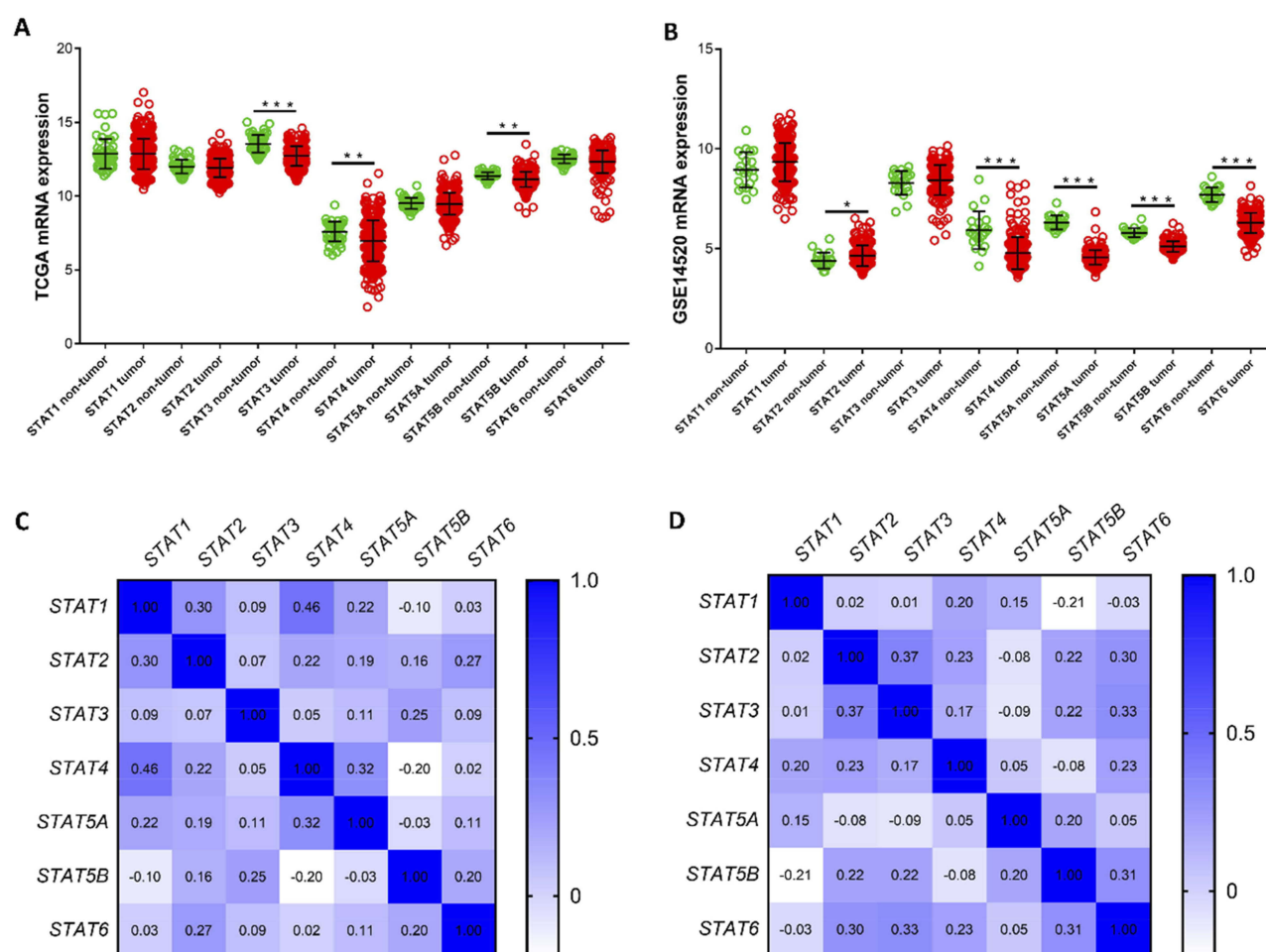


Figure 3 Gene expression distribution and coexpression heat map of STAT genes in the TCGA and GEO dataset. (A–B) Distribution of STAT genes expression between tumour tissue and adjacent normal tissue using the TCGA and GEO dataset, respectively. (C–D) Coexpression heat map of STAT genes in HCC tissue using the TCGA and GEO dataset, respectively. * $P<0.05$, ** $P<0.01$ and *** $P<0.001$.

Table I Clinical characteristics of 365 HCC patients in TCGA database

Variables	Events/total	MST (months)	HR (95% CI)	Log-rank P-value
Gender				0.263
Male	79/246	82.9	0.82 (0.57–1.16)	
Female	51/119	49.7		
Race				0.174
White	75/182	46.6	1.30 (0.89–1.89)	
Asian	44/155	NA		
Others	6/18	38.3		
Missing	10			
Age (years)				0.337
≤60	54/165	70.5	0.84 (0.59–1.20)	
>60	74/197	54.1		
Missing	3			
BMI				0.477
≤26	70/205	81.9	0.87 (0.59–1.28)	
>26	42/127	70.5		
Missing	33			
Tumour Stage				0.004**
Stage I	42/170	84.4	5.50 (1.70–17.84)	
Stage II	26/84	61.7		
Stage III	45/83	25.7		
Stage IV	3/4	18.6		
Missing	24			
Histological grade				0.392
G1	18/55	70.5	1.27 (0.74–2.18)	
G2	60/175	56.2		
G3/G4	48/130	54.1		
Missing	5			
Pathological T				<0.001***
T1/T2	76/271	81.9	2.54 (1.78–3.61)	
T3/T4	53/91	22.0		
Missing	3			
Pathological N				0.027*
N0	83/248	81.9	1.51 (1.05–2.18)	
N1/NX	46/116	37.8		
Missing Pathological M	1			
M0	84/263	81.9	1.68 (1.16–2.42)	0.005**
M1/MX	46/102	36.3		

Notes: * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$.

stage were related to RFS (all $P < 0.05$). Furthermore, we analysed the relationship between STAT genes and the OS of HCC patients. The prognostic-related characteristics in the TCGA database were analysed by univariate and multivariate Cox regression analysis, and the results revealed that low expression of *STAT5A* ($P = 0.009$, HR=1.60, 95% CI=1.13–2.27), *STAT5B* ($P = 0.006$, HR=1.64, 95%

CI=1.15–2.33) and *STAT6* ($P = 0.007$, HR=1.61, 95% CI=1.14–2.29) were significantly associated with a significantly increased risk of death (Table 3). Cox regression model adjusted for prognostic-related characteristics in the GEO database showed that low expression of *STAT1* ($P = 0.047$, HR=1.55, 95% CI=1.01–2.38), *STAT5A* ($P = 0.011$, HR=1.76, 95% CI=1.14–2.72), *STAT5B*

Table 2 Clinical characteristics of 241 HCC patients in GEO database

Variables	Patients	Overall survival			Recurrence-free survival		
		MST (months)	HR (95% CI)	Log-rank P-value	MST (months)	HR (95% CI)	Log-rank P-value
Gender							
Male	191	NA	1.70 (0.82–3.52)	0.153	37.9	2.17 (1.13–4.14)	0.019*
Female	30	NA			NA		
Age							
≤60	181	NA	1.04 (0.59–1.81)	0.903	45.9	0.99 (0.63–1.58)	0.986
>60	40	NA			36.6		
HBV							
AVR-CC	56	51.6	0.91 (0.12–6.74)	0.929	28.8	1.39 (0.19–10.17)	0.744
CC+NO	162	NA			51.1		
Missing	3						
ALT							
≤50 U/L	130	NA	0.93 (0.60–1.42)	0.727	53.0	0.80 (0.56–1.15)	0.230
>50 U/L	91	NA			40.4		
Tumour size							
≤5 cm	140	47	0.51 (0.34–0.79)	0.003**	51.1	0.71 (0.49–1.03)	0.076
>5 cm	80	38			28.4		
Missing	1						
Multinodular							
Yes	45	23	1.59 (0.98–2.57)	0.057	28.7	1.19 (0.77–1.84)	0.428
No	176	62			48.0		
Cirrhosis							
Yes	203	NA	4.62 (1.14–18.8)	0.032*	37.9	2.18 (0.96–4.97)	0.062
No	18	NA			NA		
TNM							
I+II	170	NA		0.000***	51.6		0.000***
III+IV	49	18	3.52 (2.24–5.51)		17.8	2.26 (1.52–3.38)	
Missing	2						
BCLC							
0+A	199	NA		0.016*	NA		0.026*
B+C	20	NA	5.57 (1.37–22.7)		37.9	2.55 (1.12–5.79)	
Missing	2						
AFP							
≤300 ng/mL	118	NA	0.61 (0.40–0.95)	0.025*	49.1	0.80 (0.56–1.14)	0.230
>300 ng/mL	100	NA			30.9		
Missing	3						

Notes: * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$.

($P = 0.015$, HR = 1.71, 95% CI = 1.11–2.64) and *STAT6* ($P = 0.041$, HR = 1.57, 95% CI = 1.02–2.43) was significantly associated with OS (Table 4). In addition, Kaplan-Meier survival curves of STAT genes in the TCGA database are presented in Figure 4A–G, and survival curves of these genes in the GEO database are shown in Figure 4H–N.

Joint effects analysis of STAT5A, STAT5B and STAT6 genes

We further investigated the joint effects of *STAT5A*, *STAT5B* and *STAT6* in the prediction of HCC patient prognosis. In the TCGA database, joint effects analysis of the *STAT5A* and *STAT5B* combinations showed that group 1 (low *STAT5A* and

Table 3 Prognostic survival analysis of STATs genes and HCC patients in TCGA database

Genes	Events/total	MST (months)	Crude HR (95% CI)	P-value	Adjusted HR (95% CI)	Adjusted P-value
<i>STAT1</i> Low High	60/182 70/183	56.2 56.5	1.15 (0.81–1.62)	0.436	0.96 (0.65–1.42)	0.849
<i>STAT2</i> Low High	62/182 68/183	71.0 54.1	1.13 (0.80–1.59)	0.487	0.96 (0.66–1.39)	0.831
<i>STAT3</i> Low High	65/182 65/183	56.2 61.7	1.01 (0.72–1.43)	0.945	0.87 (0.61–1.24)	0.445
<i>STAT5A</i> Low High	59/182 71/183	81.9 47.4	1.34 (0.95–1.89)	0.101	1.39 (0.95–2.02)	0.088
<i>STAT5B</i> Low High	58/182 72/183	81.9 38.2	1.60 (1.13–2.27)	0.009**	1.44 (1.00–2.07)	0.048*
<i>STAT5B</i> Low High	53/182 77/183	81.9 42.4	1.64 (1.15–2.33)	0.006**	1.58 (1.10–2.28)	0.012*
<i>STAT6</i> Low High	75/182 55/183	41.0 81.9	1.61 (1.14–2.29)	0.007**	1.47 (1.02–2.13)	0.041*

Notes: * $P < 0.05$ and ** $P < 0.01$.

low *STAT5B* expression) and group 2 (low *STAT5A* and high *STAT5B* expression) were associated with a significantly increased risk of death in HCC compared to group 4 (high *STAT5A* and high *STAT5B* expression; Figure 5A). Meanwhile, analysis of the *STAT5A* and *STAT6* combinations showed that MST was best in group IV (high *STAT5A* and high *STAT6* expression; 81.9 months; $P = 0.001$; Figure 5B) and that of the *STAT5B* and *STAT6* combinations showed the poorest MST in group a (low *STAT5B* and low *STAT6* expression; 38.3 months; $P < 0.001$) and the best MST in group c (high *STAT5B* and low *STAT6* expression; 54.1 months; $P < 0.001$; Figure 5C). Finally, joint effects analysis of the *STAT5A*, *STAT5B*, and *STAT6* combinations showed that MST was poorest in group B (high *STAT5A*, low *STAT5B*, and low *STAT6* expression; low *STAT5A*, high *STAT5B*, and low *STAT6* expression; and low *STAT5A*, low *STAT5B*, and high *STAT6* expression; 27.9 months; $P < 0.001$) and best in group C (high *STAT5A*, high *STAT5B*, and low *STAT6* expression; high *STAT5A*, low *STAT5B*, and high *STAT6* expression; and low *STAT5A*, high *STAT5B*, and high *STAT6* expression; 82.9 months; $P < 0.001$; Figure 5D). Surprisingly, the MST

could not be determined for group D, which contained the best factors for patients, possibly due to the sample size in our study was relatively small. In addition, similar results were obtained in the GEO database (Figure 5E–H). Our joint effects analysis of three STAT genes as prognostic markers suggested that the prognosis difference for any marker combination was more significant than that for any individual marker.

Construction of a prognostic gene signature based on *STAT5A*, *STAT5B* and *STAT6* genes

A prognostic gene signature model was constructed based on *STAT5A*, *STAT5B* and *STAT6*, which contained risk score ranking, survival status and heat maps of gene expressions (Figure 6A). Time-dependent ROC and Kaplan–Meier curve were used to assess the prognostic values of the model. The AUCs (Area under the ROC curve) for 1-year, 3-year, and 5-year OS were 0.586, 0.671, 0.697, respectively (Figure 6B). Patients in the

Table 4 Prognostic survival analysis of STATs genes and HCC patients in GEO database

Genes	Patients (n=146)	Overall survival				Recurrence-free survival			
		Crude HR (95% CI)	Crude P-value	Adjusted HR (95% CI)	Adjusted P-value	Crude HR (95% CI)	Crude P-value	Adjusted HR (95% CI)	Adjusted P-value
STAT1 Low High	49/111 36/110	1.55 (1.01–2.38)	0.047*	1.49 (0.92–2.40)	0.103	1.29 (0.90–1.85)	0.162	1.22 (0.83–1.80)	0.310
STAT2 Low High	46/111 39/110	1.29 (0.84–1.97)	0.248	1.08 (0.68–1.70)	0.741	1.12 (0.79–1.6)	0.527	1.08 (0.74–1.58)	0.689
STAT3 Low High	39/111 46/110	0.88 (0.57–1.35)	0.556	0.77 (0.49–1.19)	0.239	0.89 (0.62–1.27)	0.520	0.84 (0.58–1.22)	0.351
STAT4 Low High	48/111 37/110	1.34 (0.87–2.05)	0.185	1.11 (0.69–1.77)	0.678	1.17 (0.82–1.67)	0.392	1.07 (0.72–1.57)	0.749
STAT5A Low High	52/73 33/73	1.76 (1.14–2.72)	0.011*	1.52 (0.96–2.40)	0.071	1.41 (0.98–2.02)	0.061	1.34 (0.93–1.95)	0.121
STAT5B Low High	50/111 35/110	1.71 (1.11–2.64)	0.015*	1.62 (1.02–2.55)	0.040*	1.31 (0.92–1.88)	0.134	1.33 (0.91–1.95)	0.142
STAT6 Low High	51/111 34/110	1.57 (1.02–2.43)	0.041*	1.36 (0.86–2.17)	0.188	1.04 (0.73–1.48)	0.847	0.91 (0.62–1.34)	0.650

Note: * $P < 0.05$.

high-risk group shown significantly poorer OS than patients in the low-risk group ($P = 0.001$) (Figure 6C). To validate the predictive value of the model, we calculated risk score with the same formula for patients in GSE14520 (Figure 6D). Consistent with the results in the TCGA cohort, patients in the high-risk group shown significantly poorer OS than patients in the low-risk group ($P = 0.009$; Figure 6E). The AUCs for 1-year, 3-year, and 5-year OS were 0.678, 0.643, and 0.633, respectively (Figure 6F). Collectively, our results indicated a good performance of the prognostic gene signature for HCC survival prediction.

Construction of a predictive nomogram based on STAT5A, STAT5B and STAT6 genes

We then built a nomogram to predict 3-year, and 5-year OS for HCC patients. The prognostic nomograms were developed based on *STAT5A*, *STAT5B*, *STAT6*, and

independent prognostic factors in the TCGA database and GEO database, respectively (Figure 7A–B). The C-index of TCGA database and GEO database were 0.65 (95% CI, 0.59–0.71) and 0.71 (95% CI, 0.65–0.76), respectively. The calibration plot for the probability of survival at 3 and 5 years showed good agreement between the prediction by nomogram and actual observations (Figure 7C–F). These findings demonstrated that the nomogram based on STAT genes is a good nomogram for predicting survival for HCC patients.

GSEA investigation of STAT genes in HCC

To further explore the potential mechanism of *STAT5A*, *STAT5B* and *STAT6* in HCC, we also developed a single-gene GSEA to investigate potential biological processes and pathways. The enrichment of c5 suggested that high expression of *STAT5A* may be involved in biologic

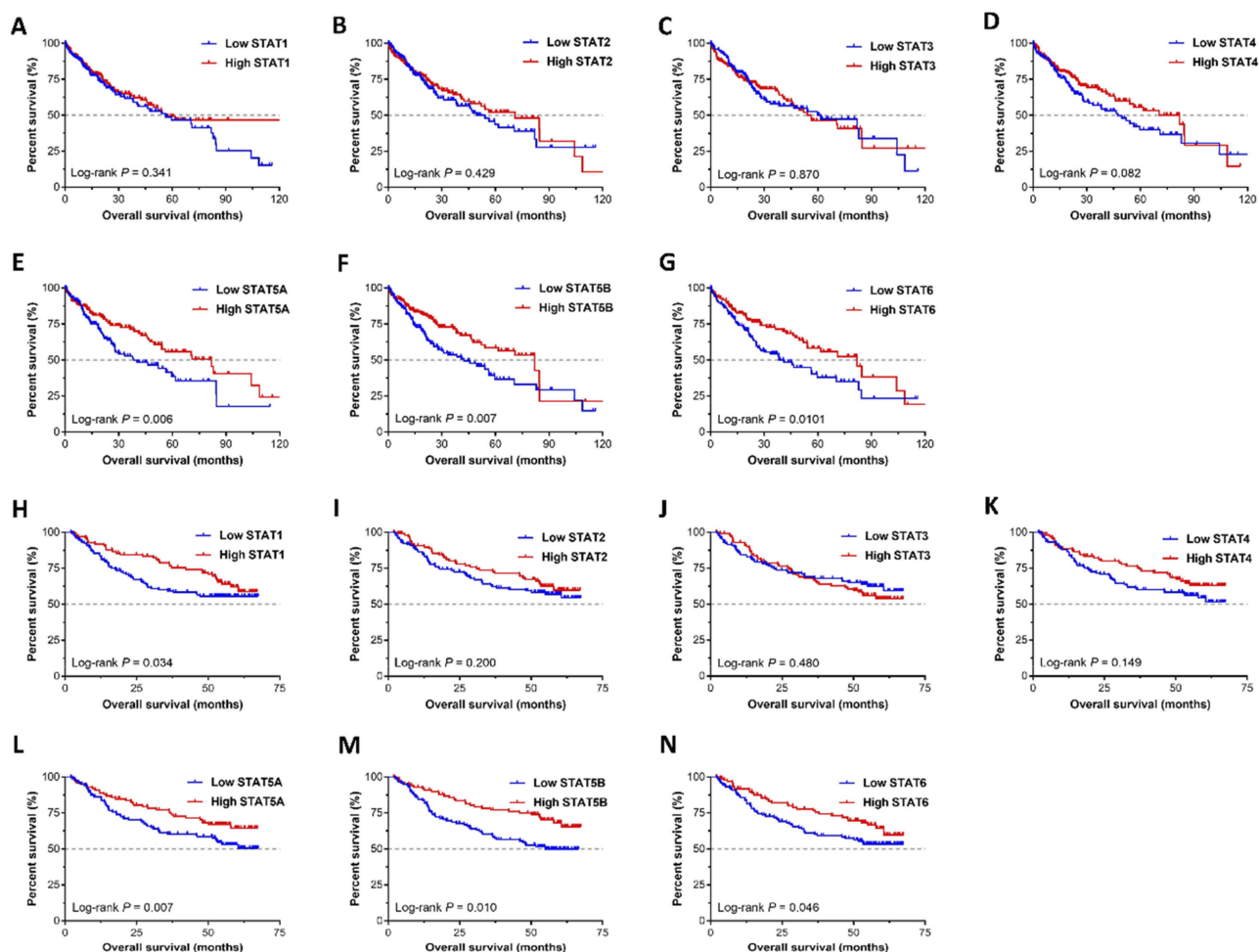


Figure 4 Survival analysis of STAT genes in HCC. (A–G) Kaplan-Meier survival curves of the *STAT1*, *STAT2*, *STAT3*, *STAT4*, *STAT5A*, *STAT5B*, and *STAT6* in the TCGA database; (H–N) Kaplan-Meier survival curves of the *STAT1*, *STAT2*, *STAT3*, *STAT4*, *STAT5A*, *STAT5B*, and *STAT6* in the GEO database.

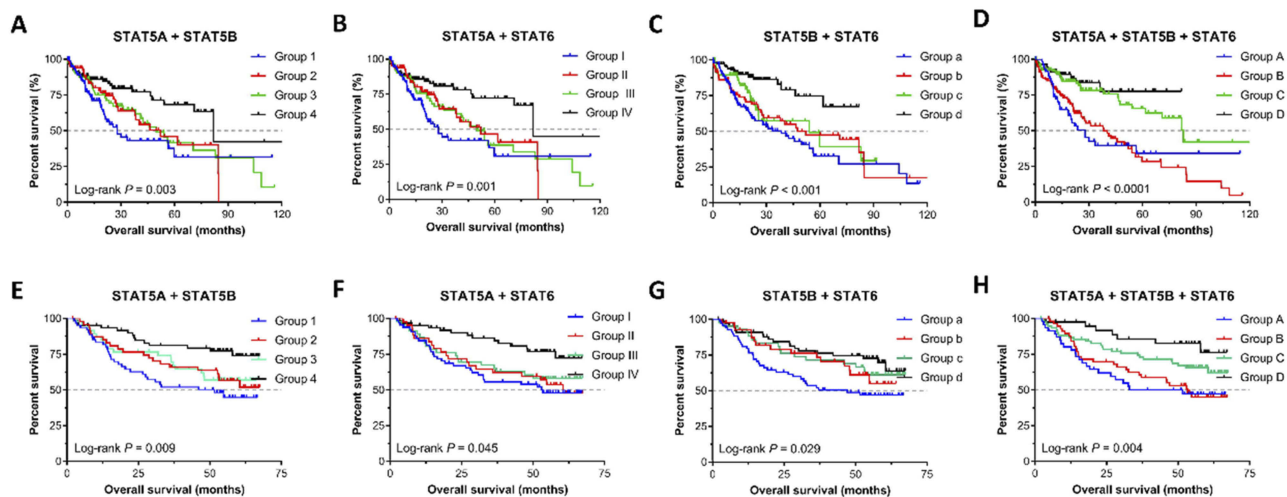


Figure 5 Kaplan-Meier survival curves for joint effects analysis among *STAT5A*, *STAT5B*, and *STAT6* in HCC. (A–D) Joint effects analysis of *STAT5A*, *STAT5B*, and *STAT6* in the TCGA database; (E–H) Joint effects analysis of *STAT5A*, *STAT5B*, and *STAT6* in the GEO database.

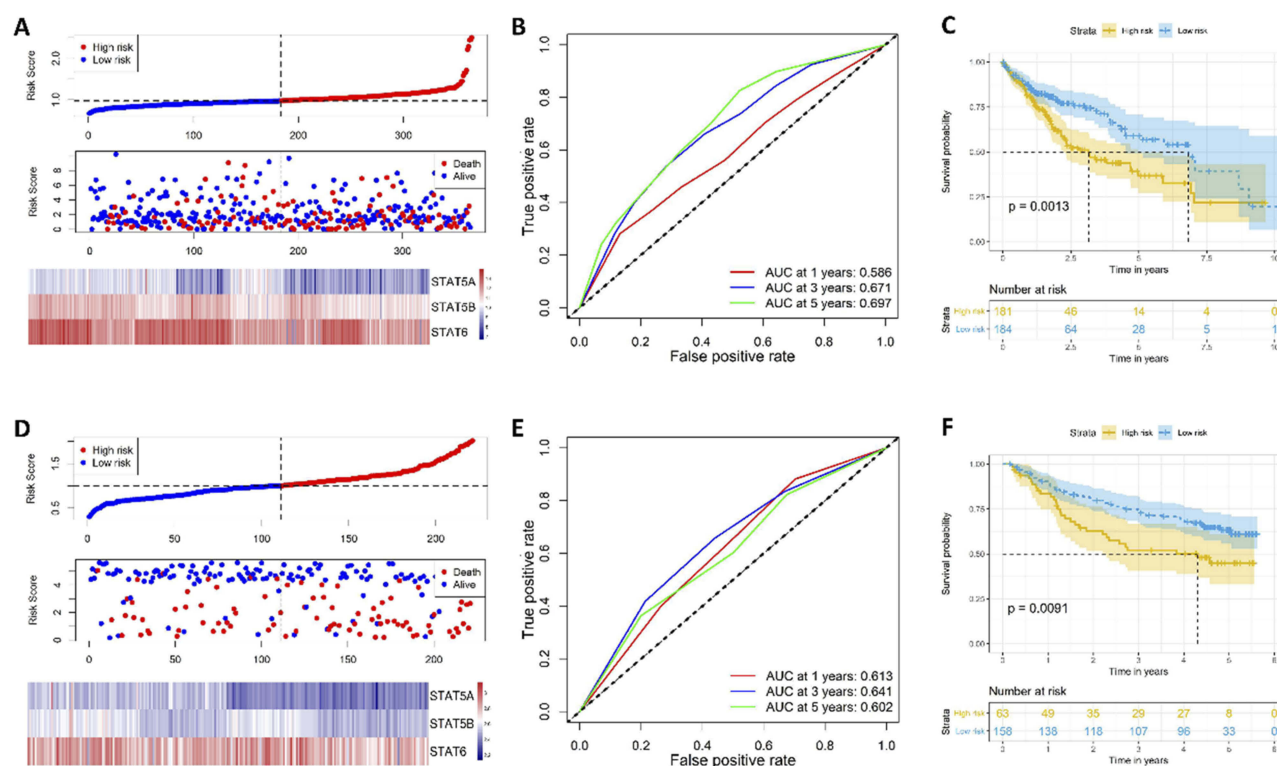


Figure 6 Risk score model, time-dependent ROC analysis, and survival analysis for the *STAT5A*, *STAT5B* and *STAT6* signature in HCC. (A–C) Risk score model, time-dependent ROC analysis, and survival analysis in the TCGA database, respectively. (D–F) Risk score model, time-dependent ROC analysis, and survival analysis in GSE14520 cohort, respectively.

processes, such as activation immune response, immune effector process, and lymphocyte activation (Figure 8A–C), whereas the enrichment of c2 indicated that high expression of *STAT5A* may participate in the chemokine signalling pathway, natural killer cell mediated cytotoxicity, and T cell receptor signalling pathways (Figure 8D–F). The enrichment of c5 suggested that high expression of *STAT5B* may be involved in biologic processes, such as drug metabolic process, bile acid metabolic process, and viral life cycle (Figure 9A–C), whereas the enrichment of c2 indicated that high expression of *STAT5B* may participate in the drug metabolism cytochrome P450, TGF-beta signalling pathway, and JAK-STAT signalling pathways (Figure 9D–F). The enrichment of c5 suggested that high expression of *STAT6* may be involved in response to biologic processes, such as type I interferon, drug metabolic process, and defence response to virus (Figure 10A–C), whereas the enrichment of c2 indicated that high expression of *STAT6* may participate in the JAK-STAT signalling pathway, drug metabolism cytochrome P450, and PPAR signalling pathways (Figure 10D–F).

Discussion

The STAT gene family is an intracellular transcription factor that mediates many biological processes, such as cellular immunity, proliferation, apoptosis, and differentiation.¹⁴ Extensive studies have shown that dysregulation of STAT1-6 family proteins can be observed in a variety of cancer types and indicate that STAT1-6 may play an important role in cancer progression.^{15,16} In this study, the association between STAT family genes and HCC was investigated in both the TCGA and GEO databases. The results showed that low expression levels of *STAT5A*, *STAT5B*, and *STAT6* were associated with a poor prognosis of HCC patients in both the TCGA and GEO databases. Moreover, the combination of *STAT5A*, *STAT5B*, and *STAT6* had good prediction values for HCC patients. Thus, our findings imply that the combination of *STAT5A*, *STAT5B*, and *STAT6* may serve as a potential prognostic biomarker for HCC.

It is well known that STAT signalling can be activated by diverse cytokines that are involved in many biological processes, such as immunity, cell division, cell death, and

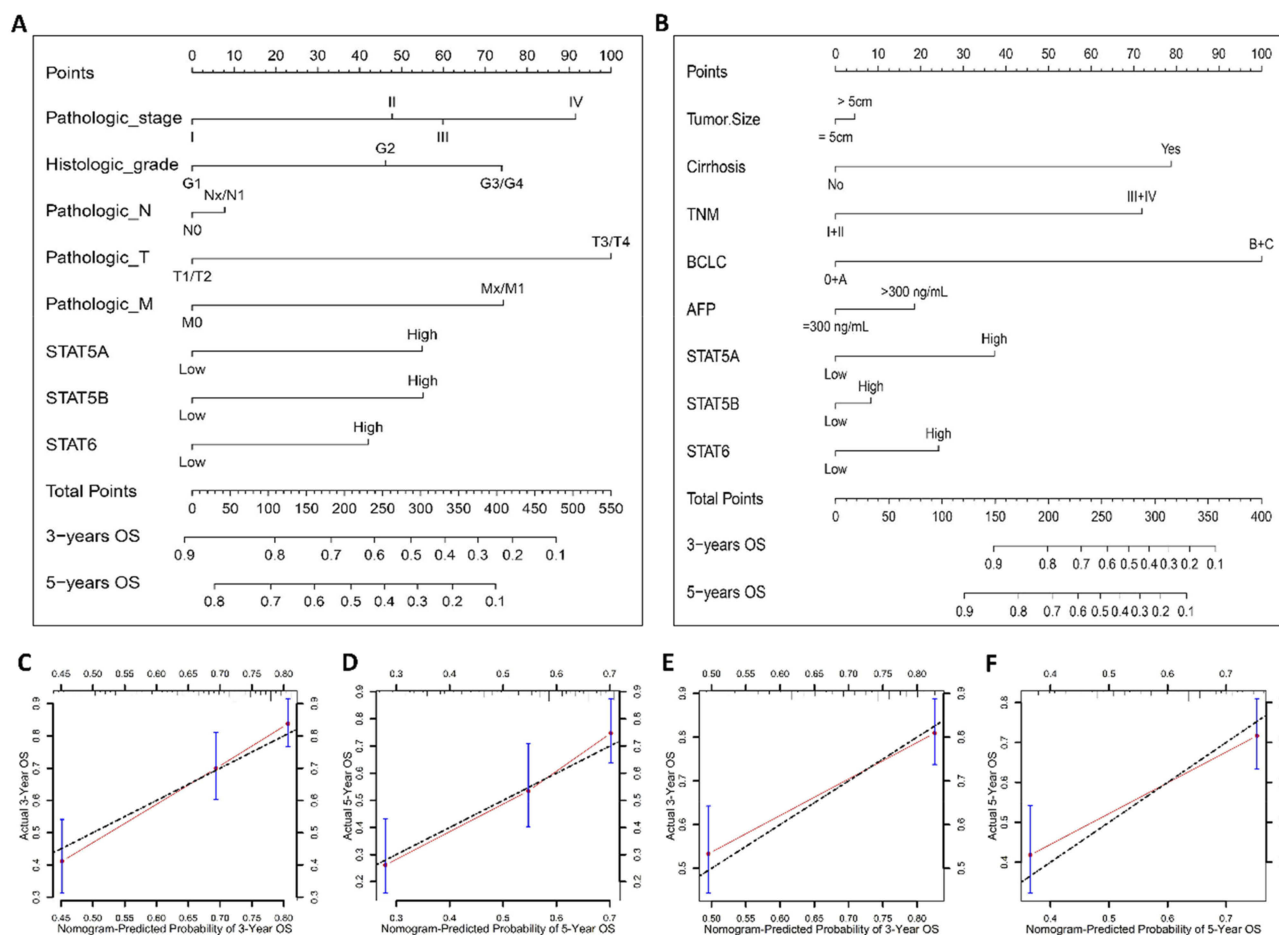


Figure 7 Nomogram for predicting HCC patient overall survival with *STAT5A*, *STAT5B* and *STAT6* and clinical information. (A–B) Nomogram to predict the 3-, and 5-year overall survival in the TCGA database and GSE14520 cohort, respectively. (C–F) The calibration curve of overall survival at 3, and 5 years for HCC patient in the TCGA database and GSE14520 cohort, respectively.

cancer development.¹⁷ Previous studies have shown that *STAT1* acts as a tumour suppressor via multiple mechanisms, including the downregulation of caspases, Fas, FasL, TRAIL, and p21.^{18,19} However, polymorphisms of the *STAT1* gene at rs867637, rs3771300, and rs2280235 are significantly associated with the risk of HCC patients with viral hepatitis.¹⁹ *STAT3* protein expression and phosphorylation are elevated in human HCC tissues compared with normal healthy liver tissues.²⁰ Importantly, inhibition of *STAT3* activation by *STAT3* inhibitors could suppress HCC growth in vitro and in vivo, while activation of *STAT3* by HBX or HCV core protein promoted HCC development.^{21,22} Therefore, *STAT3* acts as an oncogenic factor that promotes tumourigenesis and is a potential target for HCC targeted therapy. Recent studies have shown that high *STAT5A* expression is a better prognostic indicator in patients with HCC after hepatectomy.^{23,24} Many studies have suggested that *STAT5* acts as a tumour suppressor in

liver tumourigenesis via its anti-steatogenic and hepatoprotective effects and through the upregulation of cell cycle inhibitors *Cdkn2b* and *Cdkn1a*.²⁵ These results suggest that *STAT1-6* play an important role in the development and progression of HCC.

Despite numerous reports on the role of the *STAT* gene family in the development of HCC, the prognostic value of *STAT* genes has rarely been investigated. Previous studies indicated that *STAT5A* might act as a potential prognostic marker for HCC patients, and lower expression of *STAT5A* may be associated with worse survival.^{23,26} In the current study, our results demonstrate that *STAT5A*, *STAT5B*, and *STAT6* were expressed at low levels in HCC tissues, which was associated with an unfavourable prognosis. We constructed a prognostic gene signature model based on *STAT5A*, *STAT5B*, and *STAT6*, and time-dependent ROC and Kaplan–Meier curve indicated a good performance of this model for HCC survival prediction. In addition, we

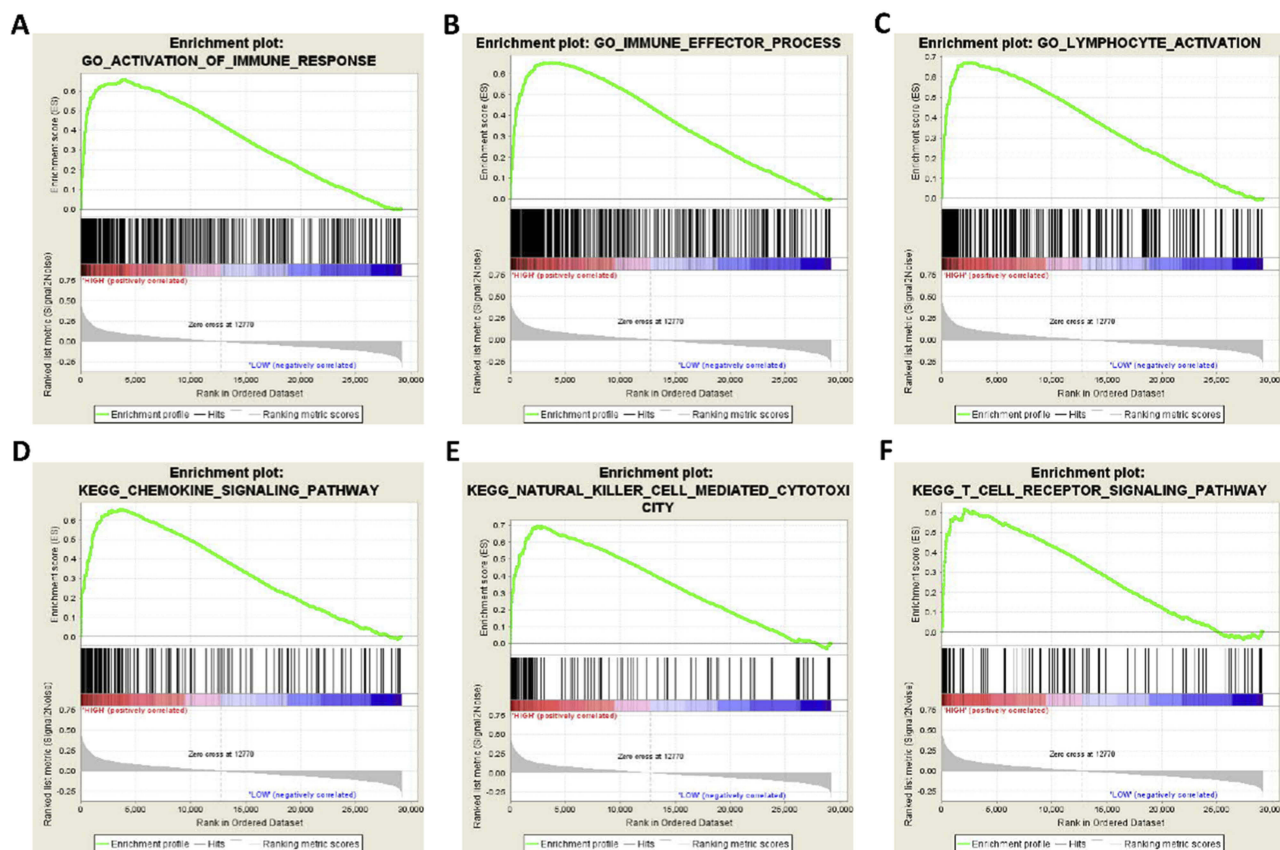


Figure 8 GSEA results of *STAT5A* expressed in HCC patients. (A–C) GSEA results of c5 reference gene sets for high *STAT5A* expression groups; (D–F) GSEA results of c2 reference gene sets for high *STAT5A* expression groups.

also constructed a nomogram based on clinical parameters and *STAT5A*, *STAT5B* and *STAT6* mRNA expression levels. The calibration plots indicated that actual survival corresponded closely with predicted survival, suggesting that the predictive performance of the nomogram was good and indicating that the combination of *STAT5A*, *STAT5B*, and *STAT6* may be an independent prognostic indicator for HCC.

Finally, GSEA analysis was performed to investigate the potential mechanism of STAT genes in HCC prognosis. The results showed that *STAT5A*, *STAT5B* and *STAT6* were involved in immune-related biological processes, such as JAK-STAT, PPAR and P450-related signalling pathways. The JAK-STAT signalling pathway can be activated by many cytokines, growth factors, and hormones, which play a critical role in HCC.²⁴ Recent studies have demonstrated that liver-specific STAT5 knockout mice were more susceptible to chronic CCl₄-induced liver fibrosis and HCC development.²⁷ PPARs are ligand-activated transcription factors that belong to the nuclear hormone receptor superfamily,

which play a role in the regulation of cancer cell growth.^{28,29} Indeed, PPAR γ -null mice displayed a higher susceptibility to the development of HCC induced by the carcinogen diethylnitrosamine (DEN).³⁰ The administration of PPAR γ agonists (rosiglitazone) also reduced HCC development induced by DEN in rats or by hepatoma cell xenografts in mice.³¹ In contrast to PPAR γ , activation of PPAR α in the liver leads to carcinogenesis in rodents. P450 enzymes also play a key role in cancer formation and cancer treatment and mediate the metabolic activation of anticancer drugs and precarcinogens, as well as anticancer drug inactivation.³² Based on GSEA results, we deduced that the potential mechanism of STAT genes in HCC prognosis may be involvement in multiple biological processes and signalling pathways that are related to HCC development, immune response, and survival.

There were some limitations to our study that need to be recognized. First, the sample size in our study was relatively small, and larger sample sizes are needed to increase the reliability of our findings. Second, the clinical

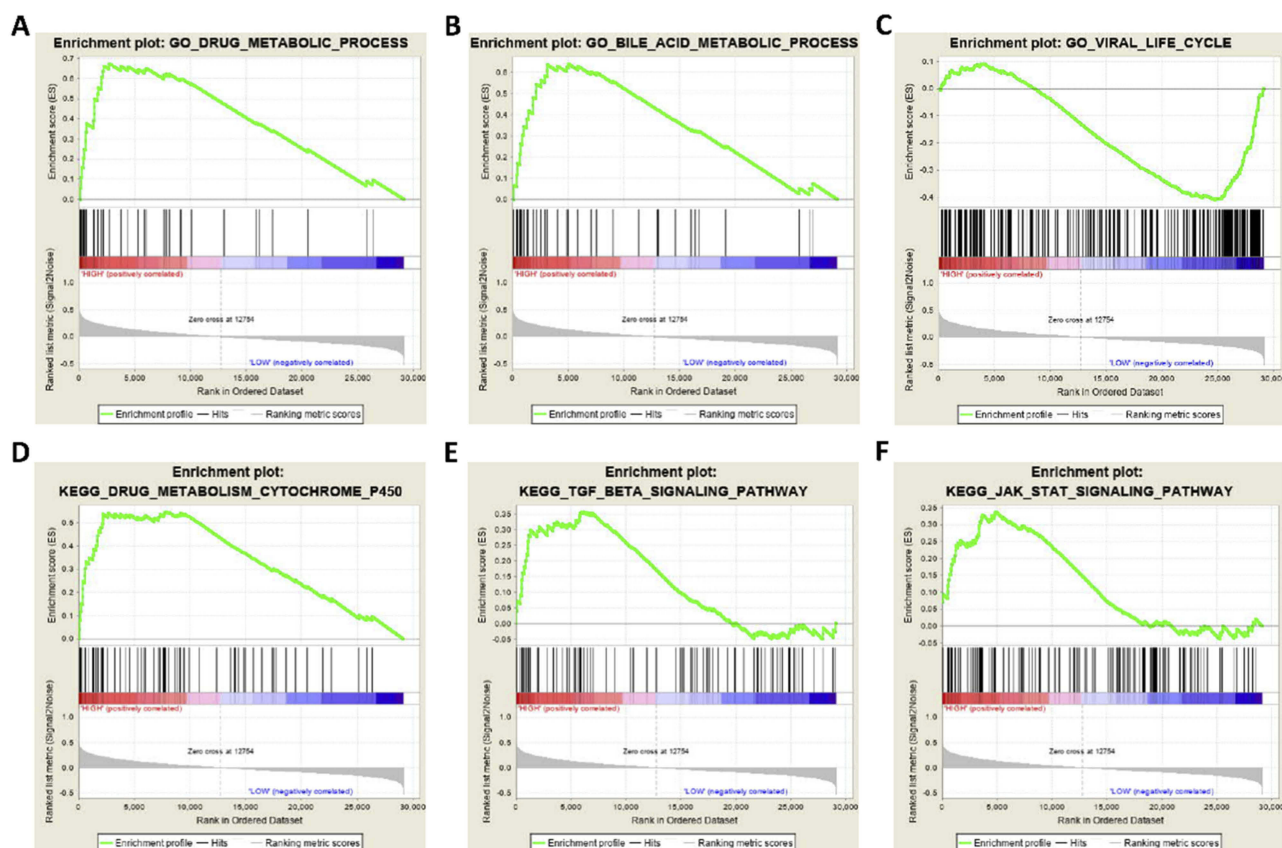


Figure 9 GSEA results of *STAT5B* expressed in HCC patients. (A–C) GSEA results of c5 reference gene sets for high *STAT5B* expression groups; (D–F) GSEA results of c2 reference gene sets for high *STAT5B* expression groups.

information from the TCGA database was not comprehensive, and more clinical data concerning tumour progression and prognosis, such as smoking and drinking status, Child–Pugh scoring, presence of cirrhosis, transarterial chemoembolization, antitherapy status, radical resection status, pathological differentiation diagnosis, main tumour size, number of tumours, status of tumour capsules, regional invasion, intrahepatic metastasis, and vascular invasion, should be included to better evaluate the relationship between the STAT family genes and HCC. Third, our current study based on the public databases to analyse the prognosis prediction of the mRNA expression level of STAT genes lacks verification at the protein level. Therefore, future research is still needed to address these issues. Due to the small sample size and incomplete clinical information in the current study, further well-designed and larger sample size studies are necessary to validate our results.

In this study, we investigated the association between the expression of individual STAT genes and overall survival in HCC patients. Furthermore, we studied the

joint effects of three STAT genes and constructed a nomogram for the prediction of HCC patient prognosis. In addition, we also investigated the potential mechanism of STAT genes in HCC patient prognostics using the GSEA approach. These results provide insight into STAT genes for cancer clinical outcomes, and these genes may serve as biomarkers for the prediction of HCC patient prognosis.

Conclusion

Our data suggest that *STAT5A*, *STAT5B*, and *STAT6* may be potential prognostic biomarkers of HCC, and their combination showed a strong interaction and better predictive value for HCC prognosis. The potential mechanism of these three STAT genes in HCC prognosis may be through participating in the biologic processes and pathways of immune-related biological processes, JAK-STAT, PPAR and P450-related signaling pathways. However, these results still need further validation and investigation in the future.

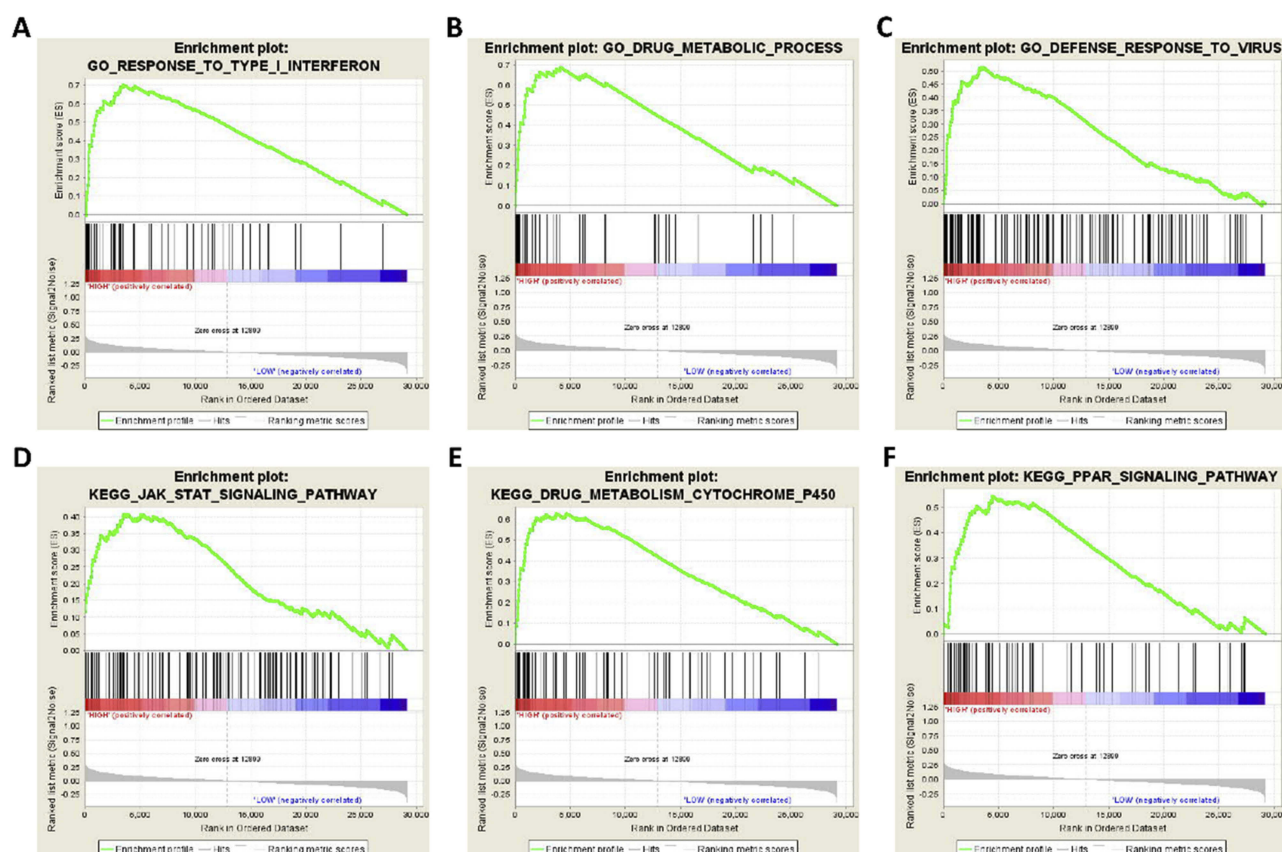


Figure 10 GSEA results of *STAT6* expressed in HCC patients. (A–C) GSEA results of c5 reference gene sets for high *STAT6* expression groups; (D–F) GSEA results of c2 reference gene sets for high *STAT6* expression groups.

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Disclosure

The authors declare that there are no conflicts of interest regarding the publication of this article.

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