Supplementary material 1

Linear Mixed-Effect Model (LME):

The linear mixed effects model is an important analytical method for processing longitudinal data, which allows estimation of model parameters that describe the inter-subject and intra-subject variability of individual responses. Its basic form is as follows:

$$y_{ij} = m_i(t) + \varepsilon_{ij} = b_{0i} + b_{1i}t_{ij} + \sum_{k=1}^k b_k x_k + \varepsilon_{ij} = b_{00} + \mu_{0i} + (b_{10} + \mu_{0i})t_{ij} + \sum_{k=1}^k b_k x_k + \varepsilon_{ij}$$

 y_{ij} represents the observed value of subject i at the JTH follow-up visit, $m_i(t)$ is the true measurement approximate by y_{ij} , \mathcal{E}_{ij} is the random error, satisfying $\mathcal{E}_{ij} \sim N$ (0,o2), b_{0i} and b_{1i} are the outcome and slope of time t of subject i . b_{0i} can be decomposed into b_{00} and μ_{0i} , b_{00} is the average intercept of all subjects, μ_{0i} is the random effect of intercept, and can be expressed as the variation of intercept between individuals. b_{1i} can be decomposed into b_{10} and μ_{1i} , where b_{10} is the average slope of all subjects and μ_{1i} is the random effect of slope, representing the variation of slope among individual subjects. b_{00} and b_{10} are the fixed effects part of the model, μ_{0i} , μ_{1i} , and \mathcal{E}_{ij} represent the random effects part of the model, x_k represents the fixed covariates that do not change over time, such as gender, baseline age at enrollment, and b_k is its slope. The JM package in R is used to build a linear mixed effect model.

Joint modelling of longitudinal and survival data (JMLS):

The JMLS model is a Joint model that connects the LME model with the Cox model using the association coefficient, which allows the longitudinal repeated covariates and the event occurrence time data to be modeled together. It can analyze the impact of data measures at the subject's baseline on survival risk, and the impact of changes in longitudinal data measures over time on survival risk. Combining these two seed models, the basic form of the combined model is as follows:

$$\begin{cases} y_{ij} = m_i(t) + \varepsilon_{ij} = b_{0i} + b_{1i}t_{ij} + \sum_{k=1}^k b_k x_k + \varepsilon_{ij} = b_{00} + \mu_{0i} + (b_{10} + (b_{10} + \mu_{0i})t_{ij} + \sum_{k=1}^k b_k x_k + \varepsilon_{ij} \\ h_i[[t|M_i(t), x_i] = h_0(t)exp\left[\sum \beta_i x_i + \alpha m_i(t)\right] \end{cases}$$

 $h_0(t)$ represents the risk function under the subject's baseline state, that is, the risk probability of an individual subject having a intercept event at time t when all

independent variables x are 0, $\sum \beta_i x_i$ is the cumulative risk function. Represents the cumulative risk of an outcome event occurring until time t is terminated, and α is defined as the joint coefficient of the joint model, meaning the effect of changes in mi(t) on $h_i(t)$.

Supplementary material 2

Variables settings:

LME and JMLS models for the total population:

LME model uses the ratio as the dependent variable, with time, Cage, state, gender, liver cirrhosis, and their interactions (Time:cage, Time:state) as independent variables.

JMLS approach consists of two components: (1). The LME sub-model, which takes the ratio as the dependent variable and includes time, Cage, gender, state, liver cirrhosis, and their interactions (Time:cage) as independent variables. (2). The COX sub-model, which uses state and time as the dependent variables, with baseline ratio, Cage, Gender, and liver cirrhosis as independent variables.

LME and JMLS models for the males and females:

LME model uses the ratio as the dependent variable, with time, Cage, state, liver cirrhosis, and their interactions (Time:cage, Time:state) as independent variables.

JMLS approach consists of two components: (1). The LME sub-model, which takes the ratio as the dependent variable and includes time, Cage, state, liver cirrhosis, and their interactions (time:Cage) as independent variables. (2). The COX sub-model, which uses state and time as the dependent variables, with baseline ratio, Cage, gender, and liver cirrhosis as independent variables

Variables	Description			
Id	Number			
	Interval between each detection time and the first detection			
Time	time,(year)			
Etime	Time interval between last test and first test, (year)			
Care	Baseline age after centralization			
Cage	(Cage= Baseline age-Median age of subjects)			

Supplementary Table 1 fundamental descriptions of the variables in the model

Liver cirrhosis	1(cirrhosis at baseline),			
Liver cirritosis	0 (no cirrhosis at baseline)			
Gender	1(male),2(female)			
State	1(HCC),0(non-HCC)			
Ratio	Ln(10APR)			

Supplementary Table 2 Model equations for all models

	LME models
LME ₁	$ln (10APR) = \beta_0 + \beta_1 (Liver cirrhosis)_{ij} + \beta_2 gender_{ij} + \beta_3 Cage_{ij} + \beta_4 state_{ij} + \beta_5 (time: Cage)_{ij} + \beta_6 (time: state)_{ij} + \varepsilon_{ij}$
LME ₂	$ln (10APR) = \beta_0 + \beta_1 (Liver cirrhosis)_{ij} + \beta_2 Cage_{ij} + \beta_3 state_{ij} + \beta_4 (time: Cage)_{ij} + \beta_5 (time: state)_{ij} + \varepsilon_{ij}$
LME ₃	$ln (10APR) = \beta_0 + \beta_1 (Liver cirrhosis)_{ij} + \beta_2 Cage_{ij} + \beta_3 state_{ij} + \beta_4 (time: Cage)_{ij} + \beta_5 (time: state)_{ij} + \varepsilon_{ij}$
	JMLS Models
JMLS ₁	$\begin{cases} \ln (10\text{APR}) = \beta_0 + \beta_1 (Liver \ cirrhosis)_{ij} + \beta_2 gender_{ij} + \beta_3 \text{Cage}_{ij} + \beta_4 \text{state}_{ij} \\ + \beta_5 (\text{time: Cage})_{ij} + \beta_6 (\text{time: state})_{ij} + \varepsilon_{ij} \\ h_i [[t M_i(t), x_i] = h_0(t)exp[\beta_0 \ln (10\text{APR}) + \beta_1 (Liver \ cirrhosis)_{ij} + \beta_2 gender_{ij} + \beta_3 \text{C} \text{C} \\ \end{pmatrix}$
JMLS ₂	$\begin{cases} \ln (10\text{APR}) = \beta_0 + \beta_1 (Liver \ cirrhosis)_{ij} + \beta_2 \text{Cage}_{ij} + \beta_3 \text{state}_{ij} \\ + \beta_4 (\text{time: Cage})_{ij} + \beta_5 (\text{time: state})_{ij} + \varepsilon_{ij} \\ h_i [[t M_i(t), x_i] = h_0(t) exp[\beta_0 \ln (10\text{APR}) + \beta_1 (Liver \ cirrhosis)_{ij} + \beta_2 gender_{ij} + \beta_3 \text{C} \end{cases}$
JMLS ₃	$\begin{cases} \ln (10\text{APR}) = \beta_0 + \beta_1 (Liver \ cirrhosis)_{ij} + \beta_2 \text{Cage}_{ij} + \beta_3 \text{state}_{ij} \\ + \beta_4 (\text{time: Cage})_{ij} + \beta_5 (\text{time: state})_{ij} + \varepsilon_{ij} \\ h_i [[t M_i(t), x_i] = h_0(t) exp[\beta_0 \ln (10\text{APR}) + \beta_1 (Liver \ cirrhosis)_{ij} + \beta_2 gender_{ij} + \beta_3 \text{C} \end{cases}$
ТМЕ	Linear Mixed Effect Mode: IME1: Linear Mixed Effect Mode for the everall

LME: Linear Mixed-Effect Mode; LME1: Linear Mixed-Effect Mode for the overall population; LME2: Linear Mixed-Effect Mode for males; LME3: Linear Mixed-Effect Mode for females; JMLS: Joint Modelling of Longitudinal and Survival data for the overall population; JMLS2: Joint Modelling of Longitudinal and Survival data for males; JMLS3: Joint Modelling of Longitudinal and Survival data for males; JMLS3: Joint Modelling of Longitudinal and Survival data for males; JMLS3: Joint Modelling of Longitudinal and Survival data for males; JMLS3: Joint Modelling of Longitudinal and Survival data for males; JMLS3: Joint Modelling of Longitudinal and Survival data for males; JMLS3: Joint Modelling of Longitudinal and Survival data for males; JMLS3: Joint Modelling of Longitudinal and Survival data for males; JMLS3: Joint Modelling of Longitudinal and Survival data for males; JMLS3: Joint Modelling of Longitudinal and Survival data for males; JMLS3: Joint Modelling of Longitudinal and Survival data for males; JMLS3: Joint Modelling of Longitudinal and Survival data for males; JMLS3: Joint Modelling of Longitudinal and Survival data for males; JMLS3: Joint Modelling of Longitudinal and Survival data for females.

Abbreviation	Full name in English			
СНВ	Chronic Hepatitis B			
НСС	Hepatocellular carcinoma			
non-HCC	non-Hepatocellular carcinoma			
ALP	Alkaline phosphatase			
PA	Prealbumin			
	Alkaline phosphatase to prealbumin			
APR	ratio			
PLT	Thrombocyte			
WBC	white blood cell			
RBC	Red blood cells			
Hb	Hemoglobin			
NE	Neutrophil			
LYM	lymphocyte			
ALT	Alanine aminotransferase			
AST	Aspartate aminotransferase			
TbIL	Total bilirubin			
DbIL	Direct Bilirubin			
GGT	Gamma-glutamyltransferase			
РҮ	Person-year			

Supplementary Table 3 Abbreviations in English

Supplementary Table 4 Baseline comparison of the effectively cohort with the baseline cohort

Variable	Effectively cohort (<i>n</i> = 4843)	Original cohort (<i>n</i> = 5143)	P value
Male (%)	63.74	63.80	0.96
Liver cirrhosis (%)	35.13	34.51	0.52
Age	48.83	48.85	0.93

	(48.83±11.58)	(48.85±11.63)		
	148.93	149.82	- 	
PLT(g/L)	(148.93±69.26)	(149.82±69.26)	0.55	
WDC(1000/1)	4.86	4.88	0.74	
WBC(10^9/L)	(4.87±1.87)	(4.88±1.88)	0.74	
RBC(10^12/L)	4.54	4.60	0.70	
KDC(10 ⁻¹ 2/L)	(4.54±0.68)	(4.53±0.68)	0.70	
$Hb(\alpha/I)$	140.04	139. 90	0.75	
Hb(g/L)	(140.04 ± 21.91)	(139.9±21.95)	0.75	
NE(10^9/L)	2.73	2.74	0.75	
NE(10 9/ L)	(2.73±1.42)	(2.74±1.43)	0.75	
LYM(g/L)	1.66	1.66	0.97	
L I WI(g/L)	(1.66 ± 0.73)	(1.66 ± 0.73)	0.77	
ALT(U/L)	84.06	87.59	0.33	
$\operatorname{MLI}(\mathbb{O}/\mathbb{L})$	(84.06±177.18)	(87.62±184.13)	0.00	
AST(U/L)	74.44	75.49	0.67	
101(0/1)	(74.44±124.11)	(75.49±123.75)	0.07	
TbIL(umol/L)	22.17	23.30	0.07	
	(22.17±29.13)	(23.29 ± 32.11)	0.07	
DbIL(umol/L)	11.28	12.27	0.04	
	(11.28±22.52)	(12.27±25.34)	0.04	
GGT(U/L)	83.96	85.37	0.56	
	(83.96±119.63)	(48.9±11.69)	0.00	
ALP(U/L)	81.95	82.56	0.53	
	(81.95±48.03)	(82.56±47.96)	0.00	
PA(ma/I)	178.09	177.51	0.33	
PA(mg/L)	(178.09±81.61)	(177.51±82.82)	0.33	

NOTES: The numbers in the table are mean (mean \pm SD).

Supplementary Table 5 Alkaline phosphatase to prealbumin ratio levels in

Follow-up	Male		Female		
years	НСС	non-HCC	НСС	non-HCC	
0	0.69	0.37	0.74	0.39	
0	(0.37, 1.35)	(0.25, 0.68)	(0.49, 1.42)	(0.27, 0.64)	
1	0.56	0.30	0.72	0.35	
1	(0.34, 1.07)	(0.22, 0.46)	(0.45, 1.21)	(0.25, 0.51)	
2	0.44	0.28	0.56	0.32	
2	(0.29, 0.94)	(0.21, 0.39)	(0.41, 1.06)	(0.24, 0.45)	
3	0.41	0.27	0.55	0.31	
3	(0.28, 0.71)	(0.21, 0.37)	(0.42, 1.02)	(0.24, 0.44)	
Λ	0.45	0.27	0.50	0.31	
4	(0.30, 0.68)	[0.20, 0.38]	(0.41, 1.16)	(0.24, 0.44)	
5	0.37	0.26	0.48	0.31	
5	(0.27, 0.58)	(0.20, 0.35)	(0.35, 0.94)	(0.23, 0.42)	
>6	0.43	0.26	0.56	0.30	
≧6	(0.29, 0.69)	(0.20, 0.36)	(0.38, 0.84)	(0.22, 0.42)	

hepatocellular carcinoma and non-hepatocellular carcinoma groups during follow-up

The numbers in the Table are median [P25, P75]

Supplementary Table 6 Linear Mixed-Effect Mode for the overall population Results

Variable	β	SE	t-value	<i>P</i> value
Intercept	1.147	0.025	46.787	<i>P</i> < 0.01
Liver cirrhosis	0.455	0.017	26.506	<i>P</i> < 0.01
Gender	0.085	0.016	5.261	<i>P</i> < 0.01
Time	-0.093	0.002	-38.908	<i>P</i> < 0.01
Cage	-0.002	0.001	-3.106	P < 0.01

State	0.314	0.037	8.583	<i>P</i> < 0.01
Time:cage	0.003	0.002	17.336	<i>P</i> < 0.01
Time:state	0.006	0.009	0.657	0.511

Intercept: The average intercept of all subjects; Liver cirrhosis: Whether cirrhosis had occurred at baseline; Time: Interval between each detection time and the first detection time(year); Cage: Baseline age after centralization; State: Outcome state; Time:Cage: The interaction of time and Cage; Time:State: The interaction of time and state; β : Fixed-effect regression coefficient.

Variable	β	SE	t-value	P value
Intercept	1.234	0.015	83.421	<i>P</i> <0.01
Liver cirrhosis	0.446	0.022	20.173	<i>P</i> <0.01
Time	-0.093	0.003	-29.938	<i>P</i> <0.01
Cage	0.006	0.001	-6.526	<i>P</i> <0.01
State	0.325	0.045	7.172	<i>P</i> <0.01
Time:Cage	0.004	0.000	16.075	<i>P</i> <0.01
Time:state	0.006	0.011	0.554	0.580

Supplementary Table 7 Linear Mixed-Effect Mode for male Results

Intercept: The average intercept of all subjects; Liver cirrhosis: Whether cirrhosis had occurred at baseline; Time: Interval between each detection time and the first detection time(year); Cage: Baseline age after centralization; State: Outcome state; Time:Cage: The interaction of time and Cage; Time:State: The interaction of time and state; β : Fixed-effect regression coefficient.

	-			
Variable	β	SE	t value	<i>P</i> value
Intercept	1.292	0.016	81.834	<i>P</i> <0.01
Liver cirrhosis	0.458	0.027	16.987	<i>P</i> <0.01
Time	-0.089	0.004	-23.770	P<0.01
Cage	0.005	0.004	4.693	P<0.01
State	0.317	0.006	5.092	P<0.01
Time:Cage	0.002	0.000	6.863	P<0.01
Time:state	-0.002	0.016	-0.130	0.897

Supplementary Table 8 Linear Mixed-Effect Mode for female model Results

Intercept: The average intercept of all subjects; Liver cirrhosis: Whether cirrhosis had occurred at baseline; Time: Interval between each detection time and the first detection time(year); Cage: Baseline age after centralization; State: Outcome state; Time:Cage: The interaction of time and Cage; Time:State: The interaction of time and state; β : Fixed-effect regression coefficient.

Supplementary Table 9 Joint Modelling of Longitudinal and Survival data for the overall population model results

Variable	β	SE	Z value	P value	HR	HR 95%CI
Longitudinal sub-model						
fixed effects						
Intercept	1.187	0.018	65.996	<i>P</i> <0.01		

Liver cirrhosis	0.531	0.012	45.583	<i>P</i> <0.01		
Gender	0.053	0.013	4.191	P<0.01		
Time	-0.091	0.002	-37.784	P<0.01		
Cage	-0.002	0.001	-2.619	P<0.01		
Time:cage	0.003	0.000	17.841	P<0.01		
Random effe	octs					
∂b_{00}	0.603					
∂b_{10}	0.114					
3	0.358					
Survival sub	-model					
Ratio	0.058	0.070	0.819	0.413	1.069	(0.923-1.216)
Cage	0.067	0.006	11.648	P<0.01	1.069	(1.057-1.216)
Gender	-0.735	0.122	-6.007	<i>P</i> <0.01	0.480	(0.377-0.610)
Liver cirrhosis	1.519	0.155	9.836	P<0.01		(1.749-2.439)
a	0.725	0.085	8.537	P<0.01	1.069	(0.923-1.216)

Intercept: The average intercept of all subjects; Liver cirrhosis: Whether cirrhosis had occurred at baseline; Time: Interval between each detection time and the first detection time(year); Cage: Baseline age after centralization; State: Outcome state; Time:Cage: The interaction of time and Cage; Time:State: The interaction of time and state; β : Fixed-effect regression coefficient.

Supplementary Table 10 Joint Modelling of Longitudinal and Survival data (JMLS₂) for

male model	Results
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Variable	β	SE	Z value	P value	HR	HR 95%CI
Longitudina	l sub-model					
fixed effects						
Intercept	1.124	0.012	107.562	<i>P</i> <0.01		
Liver cirrhosis	0.489	0.014	35.412	<i>P</i> <0.01		
Time	-0.091	0.003	-28.211	<i>P</i> <0.01		
Cage	-0.005	0.001	-6.371	<i>P</i> <0.01		
time:Cage	0.004	0.000	16.667	P<0.01		
Random effe	ects					
∂b_{00}	0.640					
∂b_{10}	0.122					
3	0.371					
Survival sub	-model					
Ratio	0.038	0.081	0.416	0.677	1.034	(0.882-1.213)
Cage	0.066	0.006	10.190	<i>P</i> <0.01	1.068	(1.055,1.082)
Liver cirrhosis	1.589	0.182	8.732	P<0.01	4.896	(3.428,6.994)
a	0.695	0.098	7.068	<i>P</i> <0.01	2.005	(1.653-2.431)

Intercept: The average intercept of all subjects; Liver cirrhosis: Whether cirrhosis had occurred at baseline; Time: Interval between each detection time and the first detection time(year); Cage: Baseline age after centralization; State: Outcome state; Time:Cage: The interaction of time and Cage; Time:State: The interaction of time and state; β : Fixed-effect

Temale I	nodel Kesu	lits				
Variable	β	SE	Z value	P value	HR	HR 95%CI
Longitudina	ıl sub-mode	21				
fixed effects						
Intercept	1.287	0.013	100.722	<i>P</i> <0.01		
Liver cirrhosis	0.533	0.014	37.920	<i>P</i> <0.01		
Time	-0.093	0.003	-27.907	P<0.01		
Cage	-0.007	0.001	-7.723	P<0.01		
Time:cage	0.002	0.000	7.564	P<0.01		
Random effe	ects					
∂b_{00}	0.537					
∂b_{10}	0.101					
3	0.371					
Survival sub	o-model					
Ratio	0.139	0.145	0.958	0.338	1.149	(0.865-1.526)
Cage	0.068	0.012	5.549	<i>P</i> <0.01	1.071	(1.045-1.098)
Liver cirrhosis	1.589	0.182	4.446	P<0.01	3.690	(2.075-6.561)
α	0.695	0.098	4.748	<i>P</i> <0.01	2.273	(1.620-3.190)

Supplementary Table 11 Joint Modelling of Longitudinal and Survival data (JMLS₂) for female model Results

Intercept: The average intercept of all subjects; Liver cirrhosis: Whether cirrhosis had

occurred at baseline; Time: Interval between each detection time and the first detection time(year); Cage: Baseline age after centralization; State: Outcome state; Time:Cage: The interaction of time and Cage; Time:State: The interaction of time and state; β : Fixed-effect regression coefficient.

Times	Mean	Median	Lower	Upper
7.88	1.00	1.00	1.00	1.00
8.00	0.98	0.98	0.96	0.99
9.00	0.83	0.84	0.72	0.91
10.00	0.72	0.72	0.54	0.85

Supplementary Table 12 Survival function in a male patient

Supplementary Table 13 Survival function in a female patient

Times	Mean	Median	Lower	Upper
7.15	1.00	1.00	1.000	1.00
8.00	0.98	0.98	0.96	0.99
9.00	0.96	0.97	0.91	0.99
10.00	0.95	0.95	0.87	0.98

Supplementary Table 14 Summary of Studies on Inflammatory Indices and Fibrosis Progression in chronic hepatitis B

Ref. Target	Main Fings	Conclusion
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		Reviews the clinical utility of	HCC biomarkers may have an
Piñero et		HCC biomarkers for	increased clinical role in the near
al[1], 2020	HCC	surveillance, diagnosis,	future, particularly for prognostic
<i>m</i> [1] <i>)</i> 202 0		prognosis, and post-treatment	and predictive purposes.
		assessment.	
		Investigates whether serum	Serum anti-HBc may be a strong
		anti-HBc could serve as a	indicator for assessing the hepatic
Zhou et al[2],	CHB	biomarker for liver	inflammatory degree and used for
2017	Patients	inflammation in CHB patients,	antiviral treatment decisions in
		especially those with normal	CHB patients with normal ALT
		ALT levels.	levels.
		Investigated the association	The study identified several
۸··· /	CLID	between immunologic markers	immunologic markers associated
0	CHB	and cirrhosis in individuals	with the development of cirrhosis,
al[3], 2021	Patients	with chronic hepatitis B.	which showed high accuracy in
			predicting cirrhosis.
			1 0
		Compared the inflammatory	Patients with chronic hepatitis B
	СНВ		
Valiente <i>et</i>	CHB Patients,		Patients with chronic hepatitis B had a broader and stronger
Valiente <i>et</i> <i>al</i> [4], 2022		cytokine profiles of patients with chronic hepatitis B to	Patients with chronic hepatitis B had a broader and stronger
	Patients,	cytokine profiles of patients with chronic hepatitis B to	Patients with chronic hepatitis B had a broader and stronger inflammatory signature,
	Patients, AHB	cytokine profiles of patients with chronic hepatitis B to	Patients with chronic hepatitis B had a broader and stronger inflammatory signature, indicating a more extensive
	Patients, AHB	cytokine profiles of patients with chronic hepatitis B to those with acute hepatitis B	Patients with chronic hepatitis B had a broader and stronger inflammatory signature, indicating a more extensive immune activation in chronic
	Patients, AHB	cytokine profiles of patients with chronic hepatitis B to those with acute hepatitis B The study found that the	Patients with chronic hepatitis B had a broader and stronger inflammatory signature, indicating a more extensive immune activation in chronic hepatitis B.
	Patients, AHB	cytokine profiles of patients with chronic hepatitis B to those with acute hepatitis B The study found that the Hepatic Inflammation Model	Patients with chronic hepatitis B had a broader and stronger inflammatory signature, indicating a more extensive immune activation in chronic hepatitis B. The HIM, including GP73, AST,
	Patients, AHB Patients	cytokine profiles of patients with chronic hepatitis B to those with acute hepatitis B The study found that the Hepatic Inflammation Model (HIM), combining GP73, AST,	Patients with chronic hepatitis B had a broader and stronger inflammatory signature, indicating a more extensive immune activation in chronic hepatitis B. The HIM, including GP73, AST, and GGT, is a promising
al[4], 2022	Patients, AHB Patients	cytokine profiles of patients with chronic hepatitis B to those with acute hepatitis B The study found that the Hepatic Inflammation Model (HIM), combining GP73, AST, and GGT, significantly	Patients with chronic hepatitis B had a broader and stronger inflammatory signature, indicating a more extensive immune activation in chronic hepatitis B. The HIM, including GP73, AST, and GGT, is a promising non-invasive index for identifying
al[4], 2022 Yao <i>et al</i> [5],	Patients, AHB Patients CHB	cytokine profiles of patients with chronic hepatitis B to those with acute hepatitis B The study found that the Hepatic Inflammation Model (HIM), combining GP73, AST, and GGT, significantly improves diagnostic accuracy	Patients with chronic hepatitis B had a broader and stronger inflammatory signature, indicating a more extensive immune activation in chronic hepatitis B. The HIM, including GP73, AST, and GGT, is a promising non-invasive index for identifying patients with chronic hepatitis B
al[4], 2022 Yao <i>et al</i> [5],	Patients, AHB Patients CHB	cytokine profiles of patients with chronic hepatitis B to those with acute hepatitis B The study found that the Hepatic Inflammation Model (HIM), combining GP73, AST, and GGT, significantly improves diagnostic accuracy	Patients with chronic hepatitis B had a broader and stronger inflammatory signature, indicating a more extensive immune activation in chronic hepatitis B. The HIM, including GP73, AST, and GGT, is a promising non-invasive index for identifying patients with chronic hepatitis B who have moderate to severe liver necroinflammation, particularly
al[4], 2022 Yao et al[5],	Patients, AHB Patients CHB	cytokine profiles of patients with chronic hepatitis B to those with acute hepatitis B The study found that the Hepatic Inflammation Model (HIM), combining GP73, AST, and GGT, significantly improves diagnostic accuracy for liver necroinflammation,	Patients with chronic hepatitis B had a broader and stronger inflammatory signature, indicating a more extensive immune activation in chronic hepatitis B. The HIM, including GP73, AST, and GGT, is a promising non-invasive index for identifying patients with chronic hepatitis B who have moderate to severe liver necroinflammation, particularly

CHB: Chronic hepatitis B; HCC: Hepatocellular carcinoma.

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