Appendix 1 Detailed descriptions of the statistical methodology

LASSO and 10-fold cross-validation was used to select and sort the statistically significant MVI related features in the training cohort. A log partial likelihood minimization was carried out under the constraint of the sum of the absolute values of the parameters multiplied by a constant (44).

$$\hat{\beta} = \arg\min l(\beta),\ \ subject\ to \sum \left|\beta_j\right| \le t$$

where $\hat{\beta}$ is parameter obtained through LASSO algorithm, $l(\beta)$ denotes the log-partial likelihood in the logistic regression model, and t >0 represents a constant. The LASSO algorithm automatically selects variables and shrinks some coefficients and reduces others to exactly 0 via the absolute constraint. In this study, the constant t was set at 0.01, and 8 nonzero coefficients were selected through LASSO algorithm for the present model (45).

Appendix 2 Analysis of DCA

The DCA was conducted to evaluate the clinical utility of this nomogram. The clinical utility of different MVI prediction models mentioned in this manuscript were compared and assessed through DCA after analyzing the net benefits within the range of threshold probabilities (46). The theory and computational method of the DCA is illustrated with the following equation:

$$\frac{a-c}{d-b} = \frac{1-Pt}{Pt}$$

When comparing two models for predicting or diagnosing a disease, b indicates net benefit from treated patients based on the model and d indicates net benefit from treating all patients. *a–c* represents net benefit for the untreated, which also can be interpreted as number of avoidable treatments. *Pt* is the threshold probability.

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Table S1 Major packages of R software used in this study

Functions	R package
Data Cleansing	fastStat
LASSO regression	glmnet
Univariate logistic regression analysis	glm
ROC and AUC	pROC
For ROC analysis to determine optimal cutoff value	OptimalCutpoints
Plot calibration curves	rms
DCA	rmda
NRI and IDI	PredictABEL

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Table S2 Univariate Logistic Regression Analysis of MVI Presence in the Training Cohort

Variable	P Value	OR	(95% CI)
Age, y	0.001	0.977	0.964–0.991
Gender, male *vs.* female	0.076	1.445	0.962–2.17
TB, >20.4 *vs.* ≤20.4 μmol/L	0.899	0.967	0.58–1.615
DB, >6.8 *vs.* ≤6.8 μmol/L	0.683	1.077	0.754–1.54
ALB, >35–55 *vs.* ≤35–55 g/L	0.945	1.025	0.502–2.096
ALT, >50 *vs.* ≤50 U/L	0.75	1.069	0.71–1.61
AST, >40 *vs.* ≤40 U/L	0.004	1.774	1.198–2.627
ALP >125 *vs.* ≤125 U/L	0.001	4.435	2.502–7.861
GGT >60 *vs.* ≤60 U/L	0.001	1.641	1.212–2.222
TC, >5.2 *vs.* ≤5.2 mmol/L	0.063	1.518	0.978–2.355
TG, >60 *vs.* ≤60 U/L	0.012	1.772	1.135–2.767
ApoA1, >1.7 *vs.* ≤1.7 g/L	0.194	0.751	0.488–1.157
ApoB1, >1.55 *vs.* ≤1.55 g/L	0.023	4.505	1.229–16.511
ApoE, >53 *vs.* ≤53 mg/L	0.465	1.144	0.798–1.639
Cr, >115 *vs.* ≤115 μmol/L	0.274	0.521	0.162–1.676
Glu, >5.6 *vs.* ≤5.6 mmol/L	0.1	1.335	0.946–1.883
AFP, ng/ml			
20–400 *vs.* ≤20	0.003	1.725	1.2–2.481
≥400 *vs.* 20–400	0.001	4.257	2.886–6.279
CEA, >5*vs.* ≤5 ng/ml	0.171	0.718	0.446–1.154
CA199, >34 *vs.* ≤34 U/ml	0.214	1.274	0.869–1.868
PLT, ≤125 *vs.* >125 $10^{\wedge 9}$/L	0.351	0.863	0.633–1.176
PT, >13 *vs.* ≤13 seconds	0.651	1.14	0.647–2.009
PIVKA–II, mAU/ml			
40–400 *vs.* ≤400	0.001	2.179	1.537–3.088
≥400 *vs.* 20–400	0.001	5.301	3.417–8.223
HBV DNA load, IU/ml			
$>10^{\wedge 4}$ *vs.* $\leq 10^{\wedge 4}$	0.152	1.253	0.92–1.705
HCV, Yes *vs.* No	0.845	1.318	0.082–21.156
Child–Pugh class, A *vs.* B	0.623	1.542	0.234–2.223
No. of tumors, Solitary *vs.* Multiple	0.027	1.632	1.057–2.519
Pseudo–capsule			
Ill–defined *vs.* well–defined	0.004	0.645	0.476–0.873
Tumor diameter, cm	0.001	1.856	1.54–2.238
Cirrhosis, Yes *vs.* No	0.697	0.942	0.699–1.27
Tumor boundary			
non–smooth *vs.* smooth	0.247	0.827	0.6–1.141
tumor growth pattern			
irregular *vs.* regular	0.001	2.627	1.935–3.566
Intratumor inhomogeneous			
present *vs.* absent	0.001	2.501	1.718–3.641
Arterial enhancement			
hypo–/mild *vs.* hyper–	0.346	2.23	0.774–3.42
Washout, absent *vs.* present	0.127	1.02	0.33–1.26

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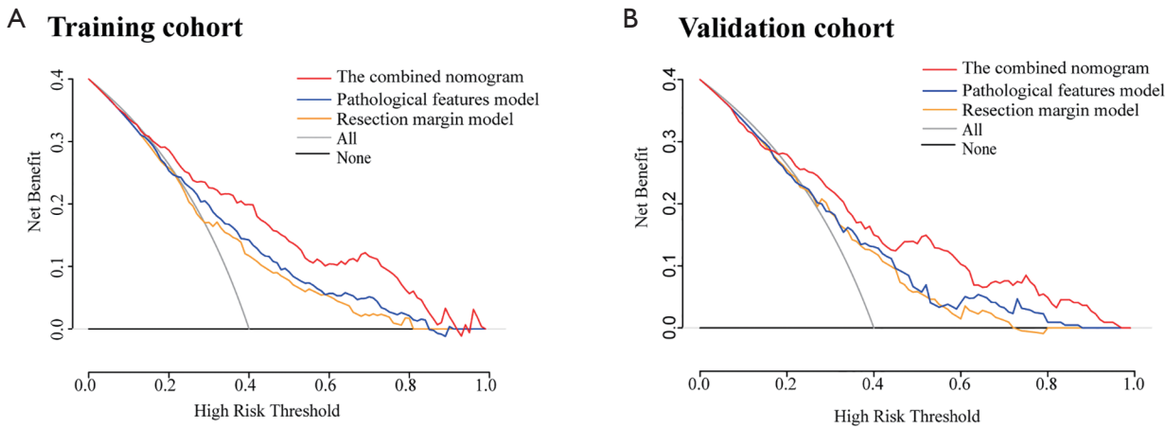

Figure S1 The DCA analysis of the nomogram, pathological features model, resection margin model in recurrence prediction of HCC in the training (A) and validation cohort (B). The DCA shows that present nomogram derived from this study (red curve) predicting recurrence of HCC provides a greater benefit than the pathological features model (green curve) and resection margin model alone (orange curve) in previous studies within 0 to 0.8 threshold probability.

Table S3 Evaluation of the models with respect to NRI and IDI

Characteristic	Training cohort			Validation cohort		
	Categorical NRI (95% CI)	Continuous NRI (95% CI)	IDI (95% CI)	Categorical NRI (95% CI)	Continuous NRI (95% CI)	IDI (95% CI)
The combined model, *vs.*						
Hematological test model	0.379 (0.284 –0.474)	0.7954 (0.633–0.958)	0.152 (0.119–0.184)	0.28 (0.13–0.43)	0.64 (0.381–0.898)	0.103 (0.06–0.146)
Resection margin model	0.337 (0.239–0.435)	0.719 (0.553–0.884)	0.125 (0.096–0.155)	0.367 (0.205–0.529)	0.817 (0.568–1.067)	0.0.214 (0.157–0.27)
P value	P<0.001*** (both)	P<0.001*** (both)	P<0.001*** (both)	P=0.001***, (both)	P<0.001*** (both)	P<0.001*** (both)

*: P<0.05; **: P<0.01; ***: P<0.001

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