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ORIGINAL RESEARCH

RETRACTED ARTICLE: Development and Validation of a Novel Nomogram to Predict the Impact of the Polymorphisms of the Variants of ICAM-1 Gene on the Prognosis of Ischemic Cardiomyopathy

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Object: This study investigated the correlation between polymorphis of the *ICAM-1* g and prognosis of Ischemic cardiomyopathy (ICM), and developed a prognostic model for predicting the prognosis ICM on the basis of *ICAM-1* gene variants.

Methods: The current study included totally 576 patients with ICM. All patients were randomly divided into training group with 399 patients and validation group with 177 patients. The prognostic model was construc d by using the data of training group. Univariable Cox-regression analysis was performed, including clinic l gene vari , then used the least absolute shrinkage and selection operator (LASSO) regression model to optimize feature se ction. rmore, multivariate Cox-regression was applied to build the prognostic nomogram model, which included clinical and ge atures chosen by the LASSO regression model. Following that, the receiver operating characteristic (ROC) curve -inde calibr on plot analyses and decision curve analysis (DCA) were carried out to evaluate the discrimination ability, con tency, a clinical lity of the prognostic model.

Results: Predicting factors rs281430 ventri lar arrhythmi treating by PCI or CABG, use of β-blockers, heart rate (HR), serum sodium level, left ventricular end-di stolic dian r (LVDD) were the risk factors of the prognosis of ICM, incorporated these factors into the prognostic nomogram ode The construc d nomogram performed well in discrimination ability, as observed by the ROC and C-index. Furthermore, as shown b calibration curves, our nomogram's predicted probabilities were highly consistent with measured values. With th eshold probabili DCA suggested that our nomogram could be useful in the clinic.

Conclusion: rs2814 mutatio (from AA genotype to AG or GG genotype) is a risk factor for ICM patients to have a higher survival probability; the surviv prob lity of ICM patients with the mutant genotype (AG or GG) is lower than those with the wild genotype (AA).

Keywords: g olymo ism, *ICAM-1* gene variants, ischemic cardiomyopathy, ICM, prognostic model, risk factors for prognosis of ICM

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Introd tion

Ischemic heart isease (IHD), also referred to as coronary heart disease, is associated with inadequate supply of blood to the myocardium. Patients are described as stable when symptoms are manageable with either medical or revascularization therapy.[1] Chronic coronary ischemia could cause significantly impaired left ventricular function, leading to ischemic cardiomyopathy (ICM).[2,3]

Ischemic cardiomyopathy (ICM) is a major cause of global prevalence and death,[4] in accordance with the global pandemic, around 26 million ICM cases have cardiac insufficiency, costing global health systems more than $30 billion.[5,6]

The initial cause of ICM is the development of atherosclerosis in multi-coronary arteries, particularly the diffusive lesions, and reduced or ceased myocardial blood flow that can generate severe myocardial dysfunction, resulting in heart muscle injury[7,8] and persisting injury. The content of intercellular adhesion molecule-1 (ICAM-1) in blood has previously

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been proposed as a marker for coronary heart disease (CHD),[4,9,10] *ICAM-1* is an immunoglobulin superfamily member and is highly denoted in leukocytes and endothelial cells, where it functions as a receptor for the leukocyte integrin lymphocyte function-related antigen-1 and Mac-1.[11,12] *ICAM-1* is an important factor in the pathogenesis of atherosclerosis, exerting critical effects on mononuclear cell recruitment in the vasculature basement membrane.[5,13] Therefore, ICAM-1 exerts a vital role in both atherosclerosis and the occurrence of ICM.

As previously reported, ICM refers to a disease featured with high morbidity and mortality, and it is costly to the global health system; thus, there is a need to investigate the causes of ICM, as well as predicting factors that have a prognostic value on the prognosis of ICM, and measures to be taken to reduce morbidity and mortality. Although the *ICAM-1* gene has been linked to ICM, there is no evidence linking it to long-term ICM prognosis. In our previous study, we analyzed the correlation between the relationship of the polymorphisms of several SNPs (rs112872667, rs12462944, rs2358581, rs281430, rs281434, rs3093030, rs3093032, rs5030348, rs5030377, rs5491, rs62130660, rs923366) of *ICAM-1* gene and p[illegible]is of ICM, the result indicate that the variation of rs112872667 is correlated with the prognosis of ICM prognosis, [illegible] we found except from rs112872667 the other SNPs in our previous research are close to have correlation with the pr[illegible]osis of ICM in initial statistical analysis, but the final result had not included these SNPs as the independent related factors on the prognosis of ICM. We consider the reason of this is the quantity of sample is small, and maybe the large quantity of sampl[illegible]ake the result accurately, for this purpose to optimize the result of previous research and make it mor[illegible]ac[illegible]ate[illegible] and persuasive we regarded the previous research as the screening process of the doubtable SNPs which may[illegible] related w[illegible] the pr[illegible]gnosis of ICM and on the basis of previous research we continued this research. In this research firstly we increase[illegible]e sample size, secondly removed the confounding factors which may be impact the accuracy of the result. Th[illegible]s112872667 which is demonstrated that it is definitely correlated with the prognosis of ICM and some SNPs had no signific[illegible]t difference in initial sitatistical analysis in previous research. Thus we regarded these SNPs with rs[illegible]12872667 a[illegible]he confounding factor and removed from this research. Therefore, we tested the most doubtable target SNPs (rs[illegible]2462944, rs[illegible]1430 and rs3093030) in all enrolled ICM patients, and analysed. The impact of the polymorphism of [illegible]ese SNPs o[illegible]he pr[illegible]nosis of ICM. And we also developed a new nomogram model for accurately predicting ICM prognosis [illegible]ased [illegible] *ICAM-1* gene polymorphisms.

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Materials and Methods

Subjects and Study Design

Participants were recruited from th[illegible]irst A[illegible]iated Hospital of Xinjiang Medical University, be hospitalized from January 2013 to December 2017 [illegible] participants [illegible]rovided written informed consent to participate in this research, in accordance with the Declaration of Hel[illegible]ki. The current work enrolled 639 subjects in total, with 576 of them meeting our study eligibility criteri[illegible] and divided in[illegible] training group with 399 patients and validation group 177 patients, using the data of training gro[illegible]p (inclu[illegible]ng 263 alieve and 136 dead) construct the model (Figure 1). All participants (training group and validation gr[illegible]e) i[illegible] the curr[illegible]nt study had previously received coronary angiography in the hospital or during their most recen[illegible]t[illegible]ital st[illegible] The f[illegible]llowing criteria were used to make the diagnosis of ICM: (1) coronary angiography revealed >50[illegible]% lumin[illegible] stenosi[illegible]n at least one coronary artery of the leading branch or a previous history of coronary artery bypa[illegible] graf[illegible]ng ([illegible]PG) or percutaneous coronary intervention (PCI), have a history of acute myocardial infarction (2) [illegible]erminal pro-B-type natriuretic peptide (NT-proBNP)>125ng/mL; (3) nitroglycerin or rest relieved divinable angina; ([illegible] symptoms including dyspnea, shortness of breath, and chest tightness relieved immediately after resting.

The following criteria was excluded from this study: Acute decompensated HF; the previous history of unstable hemodynamics; liver/kidney/blood/autoimmune diseases; cachexia; noncardiac disorder with a predicted lifespan of <1 year; and those unwilling to participate in this study.

Blood Sampling and Laboratory Tests

On the first day of admission, blood was drawn from each ICM patient and analyzed at the Laboratory of the First Affiliated Hospital of Xinjiang Medical University. White blood cell (WBC), hemoglobin, creatinine (CR), platelet

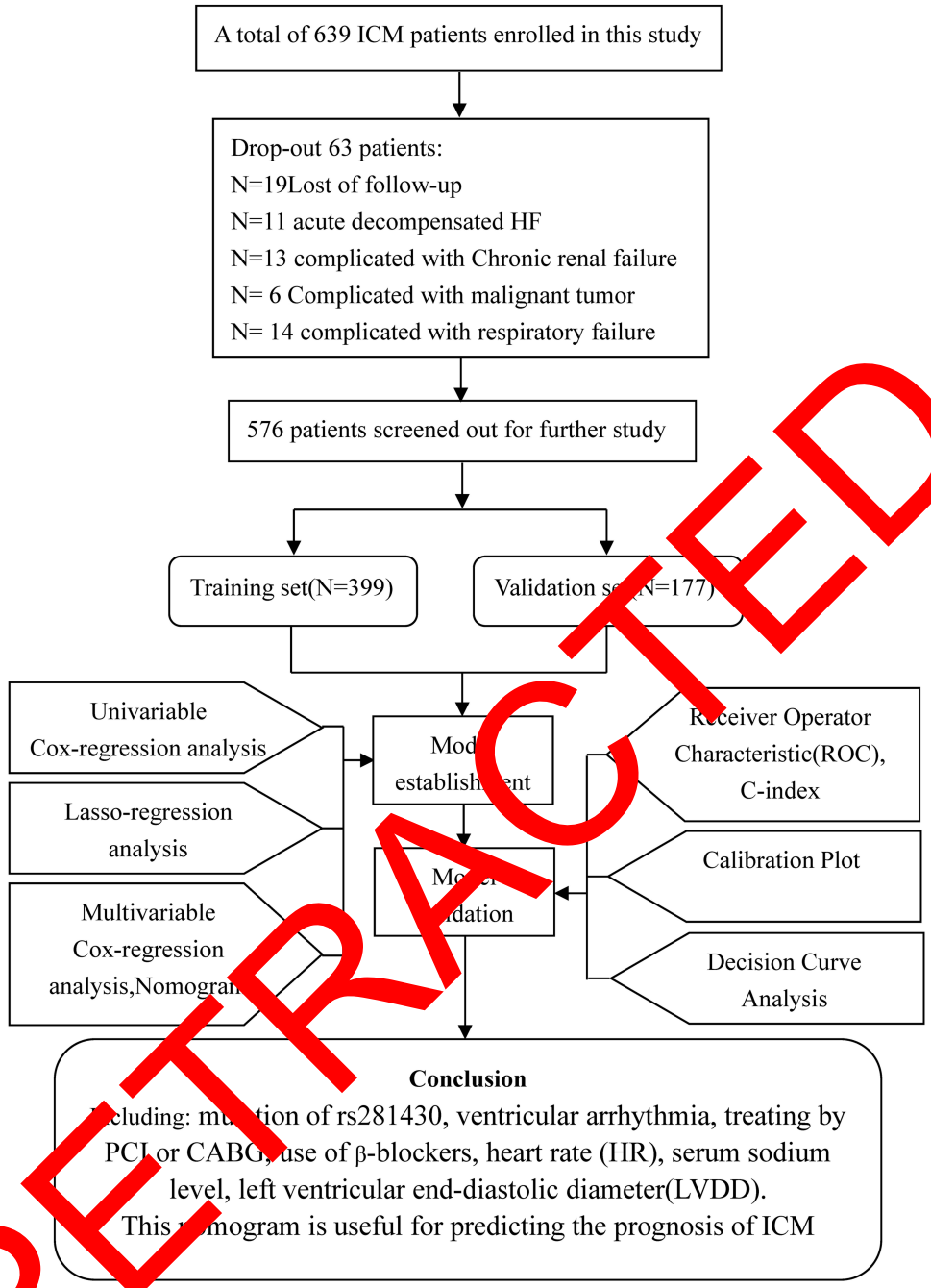

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Figure 1 Flowchart showing subject selection, establishment and validation of the model.

(PLT), high/low-density lipoprotein-cholesterol (HDL-C/LDL-C), blood urea nitrogen (BUN), total cholesterol (TC). In addition, triglyceride levels were all measured (TG).

Isolation of DNA

Following laboratory tests, this work isolated DNA from venous blood. First, blood samples were centrifuged for 10 min at 1500rpm with the Eppendorf high-speed centrifuge using the anticoagulant ethylene diamine tetra acetic acid (EDTA) to separate blood cells and plasma. After that, DNA was extracted from peripheral leukocytes with the use of a whole-

blood genome extraction kit (Xiamen Kaishuo Biotechnology Corporation, China) and related protocols. Finally, the extracted DNA sample was stored at 80 C before genotyping.

Genotyping of the *ICAM-1* Gene

Of extracted DNA, 1 μL was collected for DNA preparation using specific protocols. Following the detailed instructions, the amplified samples were subjected to SNP genotyping using the SNaPshot multiplex SNP genotyping kit (Application Binary Interface Company, USA).

Determination of Cardiovascular Risk Factors

Through dividing body weight (kg) by body height squared (m), body mass index (BMI) was calculated. In this study, smokers were defined as those who had smoked for more than 6 months or within the previous 6 months. Drinkers were those who consumed 100 g of alcohol weekly in the previous month. According to the 2018 European Society of Cardiology (ESC)/European Society of Hypertension (EHS) Guidelines,[14] hypertension was defined as diastolic blood pressure (DBP)≥90 mmHg, systolic blood pressure (SBP)≥140 mmHg, or use of antihypertensive drugs in the previous two weeks. Diabetes mellitus (DM) was diagnosed based on glucose levels ≥11.1 mmol/L (200 mg/dL) at 2-h after administration of 75 g oral glucose load, fasting plasma glucose levels ≥7.0 mmol/L (126 mg/dL), diabetes or antidiabetic drug use history, and diabetes or antidiabetic drug use history. Atrial tachycardia (AT), atrial premature beat (APB), atrial fibrillation (AF), and atrial flutter were the four types of atrial arrhythmia (AEA). Based on the American College of Cardiology/American Heart Association Task Force on Clinical Practice Guidelines and the Heart Rhythm Society,[15] ventricular arrhythmia (VA) is referred to as a spectrum that includes ventricular tachycardia (VT), premature ventricular complex (PVC), ventricular fibrillation (VF), and ventricular flutter (VF).

Study Endpoints in Follow-Up

The study's endpoint was cardiogenic death during the hospital stay and after discharge, and we recorded the time length from the first diagnosis of ICM to cardiogenic death as the survival time. The patients and their families were contacted by phone and confirmed strictly whether the cause of death is cardiogenic. Data, including the dead cases, were obtained through telephone interviews with family members of the deceased patients or through hospital records. Telephone calls were made three, six, twelve, twenty-four, and sixty months after the initial diagnosis of ICM. Follow-up work was done by trained investigators, and data entry was done by three experienced researchers to ensure data quality. Clinicians trained in systemic data acquisition and event confirmation were in charge of follow-up.

Statistical Analysis

SPSS25.0 and R 4.2.1 software were used for statistical analysis. Data of training group were classified into two groups: survival (n = 263) and cardiogenic death (n = 136). Using COX-univariable logistic regression analysis, $P<0.05$ was adopted for detecting statistical significance. Following that, the best predicting factors were chosen using the least absolute shrinkage and selection operator (LASSO) algorithm and adjusted for the decreased high-dimensional data, by enrolling significant factors ($P<0.1$) from COX-univariable regression to LASSO regression,[16] features with non-zero coefficients were chosen. Following that, COX-multivariate regression was used to develop the prognostic model by incorporating variables chosen from LASSO regression. In addition, the following features were chosen: SE, β, Hazard ratio (HR), associated 95% confidence interval (CI), and *P*-value.

The intersection point was the cutoff value of the total point, and all patients were classified into high- or low-risk groups, and a scatter plot for the corresponding survival time in different samples was plotted.

The survival curves of high- and low-risk group patients, as well as the survival curves of wild genotype (AA) and mutant genotype (AG+GG) patients, were plotted using the Kaplan–Meier (KM) method and calculated the *P*-value, and the Hazard-Ratio (HR) was calculated using Cox-regression, and we presented the baseline characteristics of all patients as well as patients who carried different genotype (AA an AG+GG), the continues variables present as Mean+standard deviation if conformed to normal contribution, or presented as median and interquartile if not conformed to normal contribution. Categorical variables were presented as frequency and percentage.

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Validation of the Model

Internal validation was carried out in this study. We evaluate the model by discrimination ability, consistency, and clinical usefulness. First: We confirmed nomogram discrimination ability by receiver operating characteristic (ROC) curves and C-index, a value close to 1 indicates improved model performance.[17] Second, Calibration plots[18] is a tool to evaluate calibration ability. In this work, to determine the consistency of predicted and observed values, calibration plots were created. Furthermore, the 45° diagonal line in the curve suggested that the model performed well in predicting disease incidence. Third, decision curve analysis (DCA)[19] was adopted for determining the model's clinical utility on the basis of the net benefits under different threshold probabilities. Furthermore, this study subtracted the proportion of false-positive cases from the proportion of true-positive cases to calculate the net benefit. Then, we weighed the risk of discontinuing interventions against the negative outcomes of unnecessary interventions.

Results

The current study included 576 ICM patients according to the eligibility criteria, of which 382 survived the 60-month follow-up study and 194 died from cardiogenic causes. All patients randomly divided into training set with 399 patients (263 survival patients and 136 dead patients) and validation set with 177 patients (119 survival patients and 58 dead patients). Patients in training set were categorized into two groups on the basis of 60-month follow-up outcome: survival (n = 263) and cardiogenic death (n = 163). Univariable Cox-regression analysis was performed on basic clinical features and genotypes in the survival and death groups. Therefore, there were obvious differences in Ventricular arrhythmia (P<0.05), Heart rate (P<0.001), serum sodium level (P<0.001), serum chlorine (P<0.05), ejection fraction (P<0.05), LVEDD (P<0.001), treating by PCI or CABG (P<0.05), using β-Blockers (P<0.001), mutation of rs281430 (P<0.001). Meanwhile, in Age, Gender, BMI, Smoking, Drinking, Hypertension, Diabetes, Atrial arrhythmia, SBP, DBP, Serum potassium, Serum calcium, Serum chlorine, WBC, PLT, Hemoglobin, AST, ALT, CR, BUN, TC, TG, HDL-C, LDL-C, NT-proBNP, using ACEI/ARB, Spironolactone, Furosemide, Antiplatelet aggregation, Statins, mutation of rs12462944 and mutation of rs3093030 are not significantly differenced (P<0.05) (Table 1).

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Table 1 Univariate Cox-Regression Analysis of the Clinical Data and SNPs in the *ICAM-1* Gene

Variable	*β*	*SE*	*HR*(95% *CI*)	*P*-value
Age (years)	0.006	0.007	1.006(0.994–1.019)	0.329
Gender				
Male			1.000	
Female	−0.366	0.191	0.694(0.477–1.009)	0.056
BMI (kg/m²)	0.006	0.021	1.006(0.965–1.049)	0.773
Smoking	0.243	0.172	1.276(0.911–1.786)	0.156
Drinking	0.269	0.243	1.309(0.813–2.107)	0.268
Hypertension	−0.022	0.172	0.978(0.698–1.372)	0.898
Diabetes	0.038	0.184	1.038(0.723–1.491)	0.838
Atrial arrhythmia	0.028	0.175	1.029(0.730–1.45)0	0.871
Ventricular arrhythmia	0.774	0.184	2.168(1.513–3.107)	< 0.001
SBP (mmHg)	0.010	0.006	1.01(0.999–1.022)	0.067
DBP (mmHg)	0.011	0.008	1.011(0.995–1.027)	0.168
Heart rate (beats/min)	0.094	0.011	1.099(1.074–1.124)	< 0.001
Serum sodium (mmol/L)	−0.061	0.012	0.941(0.919–0.964)	< 0.001
Serum potassium (mmol/L)	0.056	0.228	1.058(0.676–1.654)	0.806
Serum calcium (mmol/L)	−0.572	0.379	0.564(0.269–1.186)	0.131
Serum chlorine (mmol/L)	−0.041	0.016	0.960(0.930–0.991)	0.013
WBC (10^9/L)	0.050	0.045	1.052(0.963–1.149)	0.263
PLT (10^9/L)	−0.002	0.001	0.998(0.996–1.000)	0.107

(*Continued*)

Table 1 (Continued).

Variable	*β*	*SE*	*HR*(95% *CI*)	*P*-value
Hemoglobin (g/L)	0.007	0.005	1.007(0.997–1.016)	0.170
AST (μg/L)	0.000	0.003	1.000(0.995–1.005)	0.998
ALT (μg/L)	−0.001	0.002	0.999(0.995–1.003)	0.562
CR (umol/L)	0.000	0.001	1.000(0.998–1.002)	0.752
BUN (mmol/L)	−0.004	0.002	0.996(0.992–1.001)	0.086
TC (mmol/L)	0.002	0.053	1.002(0.903–1.110)	0.977
TG (mmol/L)	0.224	0.124	1.251(0.982–1.594)	0.070
HDL-C (mmol/L)	−0.346	0.245	0.707(0.438–1.143)	0.157
LDL-C (mmol/L)	0.133	0.093	1.142(0.951–1.371)	0.155
NT-proBNP (ng/L)	0.048	0.029	1.049(0.992–1.11)	0.092
Ejection fraction (%)	−0.027	0.012	0.973(0.951–0.996)	0.0
LVED (mm)	0.059	0.010	1.061(1.040–1.082)	< 0.0
Treating by PCI or CABG	−0.398	0.177	0.671(0.475–0.949)	0.024
Using ACEI/ARB	−0.363	0.260	0.696(0.418–1.15	0.16
β-Blockers	−1.488	0.173	0.226(0.161–0.3	< .001
Spironolactone	−0.251	0.185	0.778(0.54 .117)	0.173
Furosemide	0.263	0.172	1.301(0 9–1.822)	.126
Antiplatelet aggregation	0.155	0.233	1. (0.7 843)	0.
Statins	−0.031	0.226	0.969(0.623–1.)	0.890
rs12462944				
Genotype				
GG			1.0	
GC	−0.286	0.196	0.751(0.5 –1.102)	0.143
CC	−0.140	0.235	0.87(49–1.378)	0.552
Dominant model				
GG			1.000	
GC+CC		.180	0.787(0.553–1.121)	0.184
rs281430				
Genotype				
AA			1.000	
AG	955	0.211	2.598(1.717–3.933)	< 0.001
GG	1.6	0.308	5.191(2.840–9.488)	< 0.001
Dominant model				
AA			1.000	
+GG	0.998	0.205	2.712(1.815–4.052)	< 0.001
rs 93030				
Geno				
CC			1.000	
CT	−0.400	0.187	0.670(0.465–0.967)	0.032
	−0.110	0.270	0.896(0.527–1.521)	0.683
Dominant model				
CC			1.000	
CT+TT	−0.332	0.172	0.718(0.512–1.005)	0.053

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Clinical Features

Based on the univariable Cox-regression analysis on clinical and gene polymorphism data, 15 features of $P<0.1$ were contained into LASSO regression analysis, and SNP variables were incorporated based on *P*-values obtained from the dominant model. By analyzing the 399 study participants, fifteen variables were reduced to seven variables (Figure 2A and B). Furthermore, non-zero coefficients were added to the LASSO model.

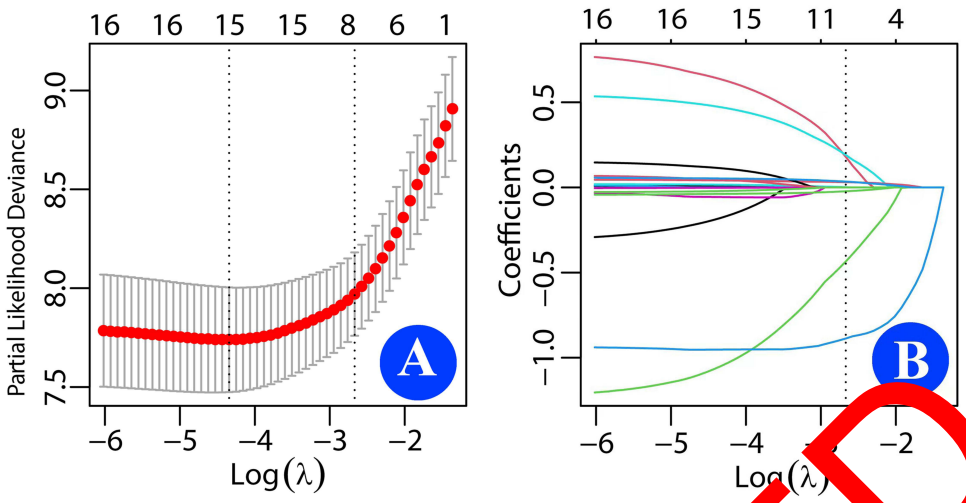

Figure 2 Selected features based on the LASSO model. (**A**) 10-fold cross-validation was carried out to select the tuning parameter (λ) based on the LASSO model based on the minimum criteria. The C-index was plotted versus log(λ). Dotted vertical lines were drawn at the optimal values by using the minimum criteria and the 1 standard error of the minimum criteria (1-SE criteria). A λ value of 0.069 was chosen according to the 10-fold cross-validation. (**B**) LASSO coefficient profiles of the 7 features, a coefficient profile plot was produced against the log(λ) sequence. Vertical line was drawn at the value selected using 10-fold cross-validation, where optimal λ resulted in nonzero coefficients.

Individualized Prognostic Model Establishment

First and foremost, by performing the multivariable Cox-regression analysis on seven variables screened out from the LASSO regression analysis, we established the prognostic model (Table 2).

The result of the model indicated that: having Ventricular arrhythmia, not treating by PCI or CABG, not using βblockers, having fast heart rate, lower serum sodium level, larger LVEDD and mutation of rs281430 are the risk factors of having higher survival rate of ICM patients. ICM patients who carried the mutant genotype (AG+GG) have higher cardiogenic death rate than ICM patients who carried the wild genotype (AA) (P<0.05; HR:1.581; CI:1.025–2.439). And we developed the nomogram incorporated these risk factors (Figure 3).

Nomogram Validation

Based on the discrimination ability, consistency of predicted probability and actual statues, and clinical usefulness, we validated this nomogram.

According to the AUC of the ROC, this nomogram has higher discrimination ability both in training set and validation set (Figure 4).

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Table 2 Multi-variableCox-Regression Analysis of the Clinical Data and SNPs in the ICAM-1 Gene

Variable	*β*	*SE*	*HR*(95% *CI*)	*P*-value
Ventricular arrhythmia	0.753	0.201	2.123(1.432–3.147)	<0.001
Treating by PCI or CABG	−1.045	0.237	0.352(0.221–0.559)	<0.001
β-Blockers	−0.894	0.204	0.409(0.274–0.611)	<0.001
Heart rate (beats/min)	0.040	0.015	1.041(1.010–1.072)	0.009
Serum sodium (mmol/L)	−0.044	0.013	0.957(0.933–0.982)	0.001
LVED(mm)	0.075	0.013	1.078(1.051–1.106)	<0.001
rs281430				
AA			1.000	
AG+GG	0.458	0.221	1.581(1.025–2.439)	0.038

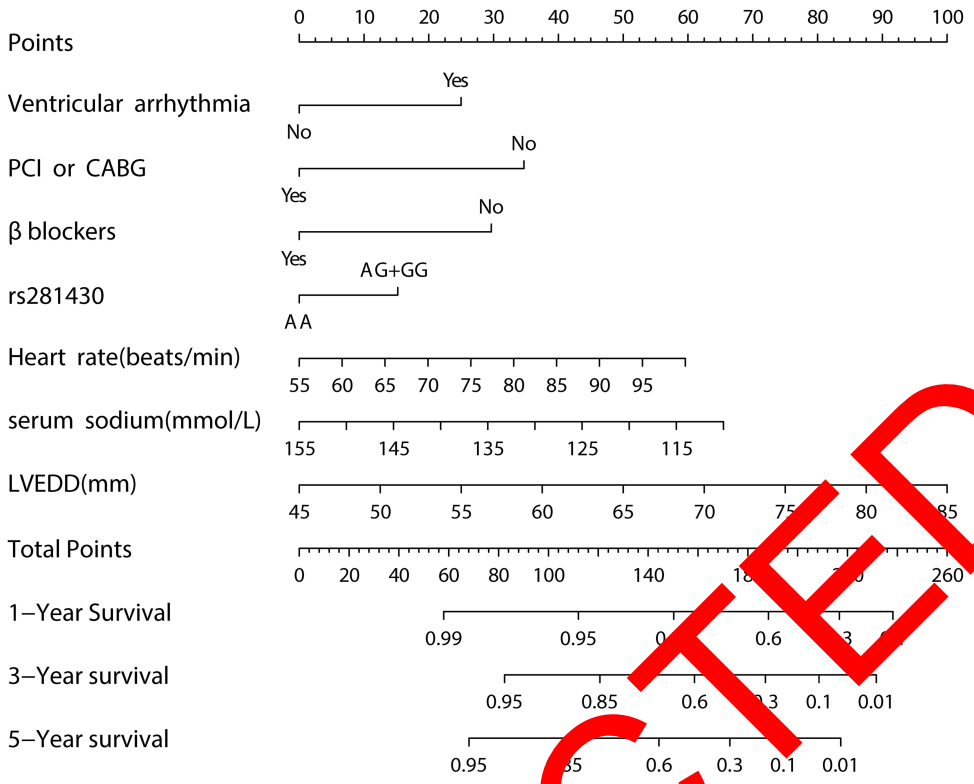

Figure 3 Nomogram for evaluating the survival rate of ICM. The nomogram was developed using several clinical and genomic variables, including complicated ventricular arrhythmia, treating by PCI or CABG, using of β-blockers, polymorphism of rs281430, heart rate, Serum sodium, Left ventricular end diastolic diameter (LVEDD).

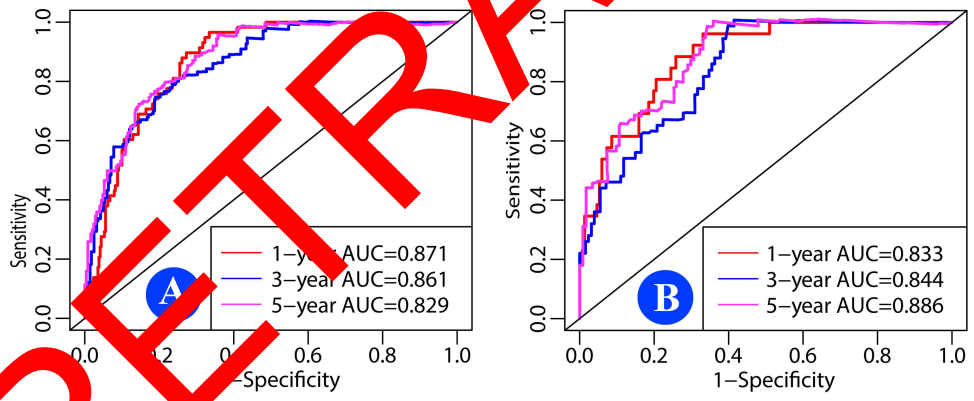

Figure 4 Receiver operating characteristic curves for 1-year, 2-year, 3-year in the training set (**A**) and validation set (**B**).

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The AUC of ROC in training set 0.871, 0.861, 0.829 for 1-year, 2-year, 3-year respectively. In the validation set it is 0.833, 0.844, 0.886 for 1-year, 2-year, 3-year respectively.

The C-index value of the model in training set is 0.822 (0.792–0.852) and 0.833 (0.788–0.878) in validation set.

Developed calibration plot, using the bootstrap method, both in training set and validation set for 1-year, 3-year, 5-year respectively, revealed a high degree of consistency in predicted and measured probabilities (Figure 5).

As demonstrated in DCA both in training set and validation set, using our constructed nomogram to predict long-term survival probability yielded a greater net benefit than the "treat none" or "treat all" strategies, demonstrating favorable nomogram clinical utility (Figure 6).

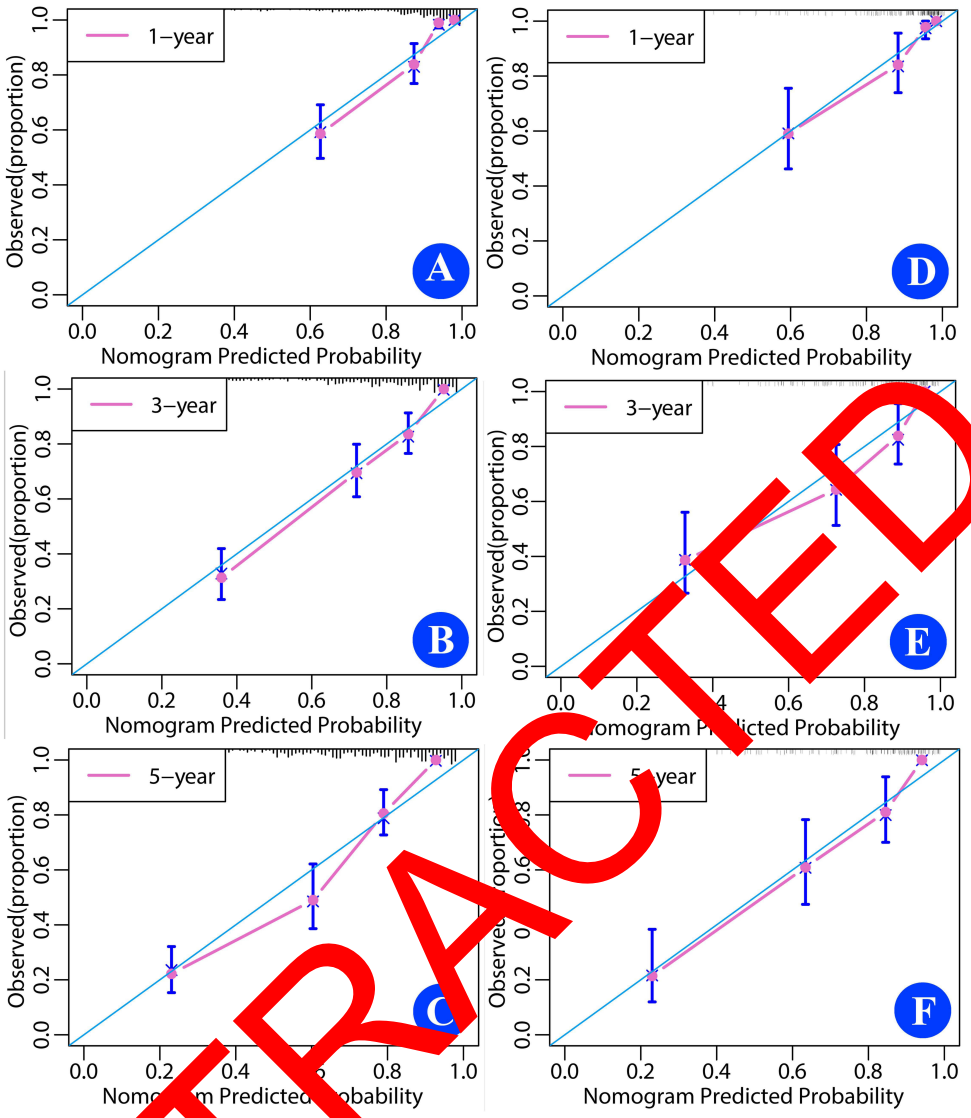

Figure 5 Calibration plot for the nomogram. (**A–C**) Calibration plot for the 1-year survival (**A**), 3-year survival (**B**) and 5-year survival (**C**) in the training set. (**D–F**): Calibration plot for the 1-year survival (**D**), 3-year survival (**E**) and 5-year survival (**F**) in the validation set. The diagonal blue line represents a perfect prediction by an ideal model. The pink line represents the performance of the nomogram conducted by bootstrap method, of which a closer fit to the diagonal blue line represents a better prediction.

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Follow-Up Study of the Patients

Using the optimal value of total points 121.786, as the intersection point, all patients were categorized into high- and low-risk groups (Figure 7A), model sensitivity was 95.86, specificity was 64.27%, positive/negative predictive values (PPV/NPV) were 61.8% and 96.23%, respectively, accuracy was 76.18%, and displayed survival status distribution between high- and low-risk groups (Figure 7B).

We developed a Kaplan–Meier survival curve in high- and low-risk groups (Figure 8), and the survival status was notably different in two groups (P<0.001; HR = 19.217; 95%, CI: 8.971–41.164).

We discovered that the rs281430 mutation is a novel factor related with the prognosis of ICM patients. All patients were classified into two groups based on wild genotype (AA) and mutant genotype (AG+GG). After that, we presented the baseline characteristics of all patients and patients who carried different genotype (AA and AG+GG), all the continues variables were not conformed to normal contribution, thus we presented them as median and interquartile (Table 3).

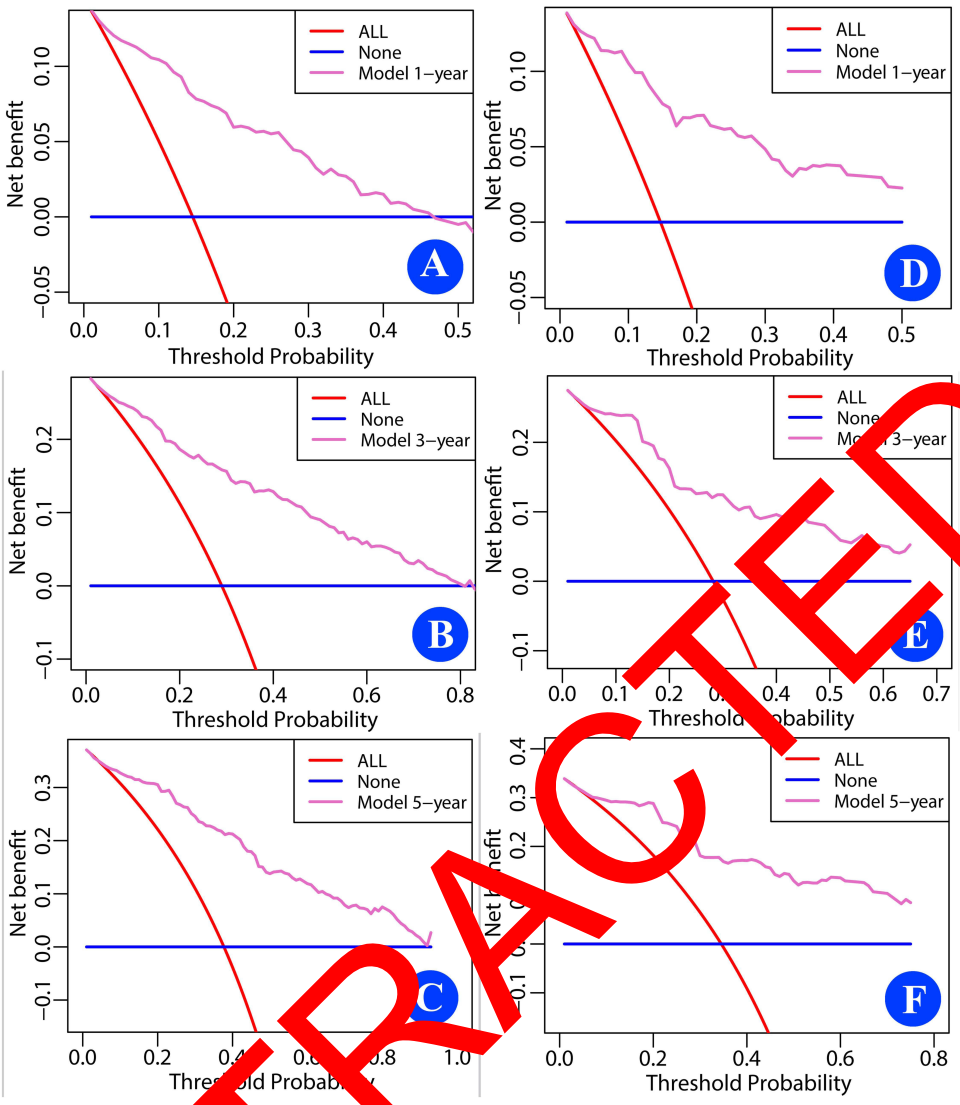

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Figure 6 Decision curve analysis of the nomogram. (**A**–**C**) Decision curve analysis of the nomogram for 1-year (**A**), 3-year (**B**) and for 5-year (**C**) in the training set. (**D**–**F**): Decision curve analysis of the nomogram for 1-year (**D**), 3-year (**E**) and for 5-year (**F**) in the validation set. Obviously, the threshold probability is shown by the x-axis. The threshold probability is the value where the expected benefit of treatment can be equivalent to that of avoiding treatment. The y-axis measures the net benefit computed by subtracting the rate of all patients who are false positive from the proportion of those who are true positive and weighting by the relative risk of forgoing treatment in comparison with the negative consequences of the unnecessary treatment.

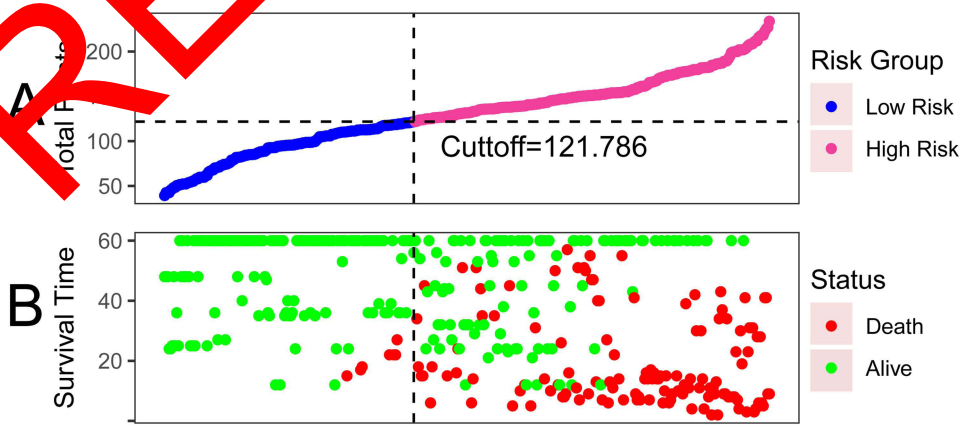

Figure 7 Division and distribution of patients according the risk and statues. (**A**) Division of high and low risk group according to the cutoff value of total point of nomoscore. (**B**) Distribution of survival status of high and low risk patients.

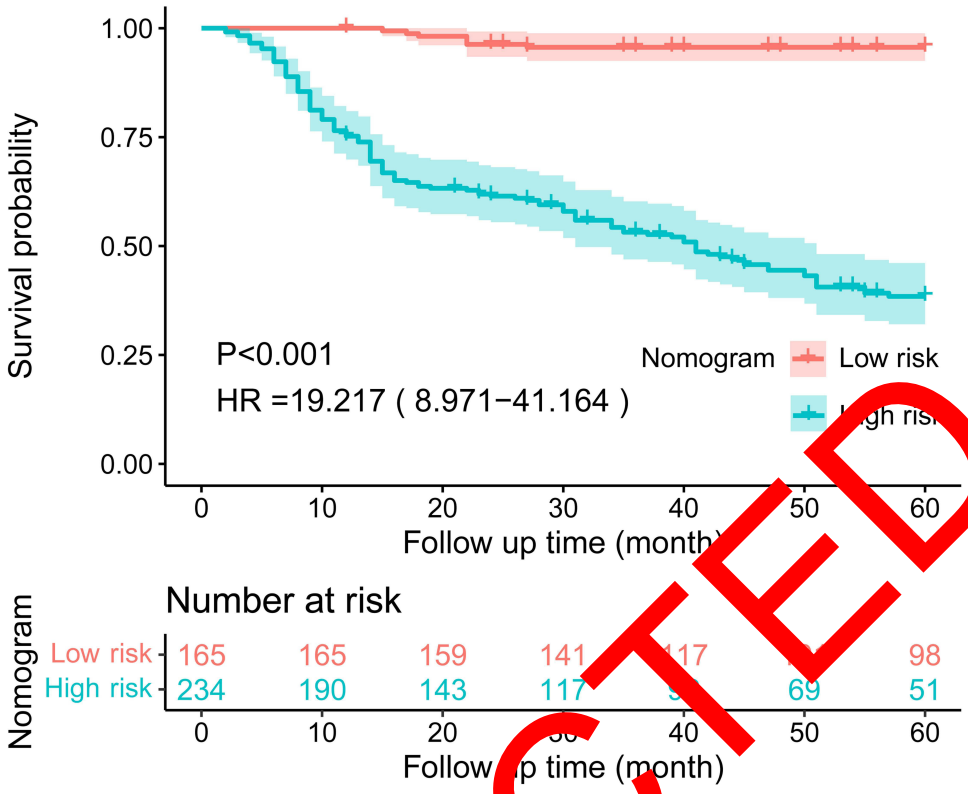

Figure 8 Survival curve showing high- and low-risk group patients of ICM.

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Based on the K-M curve and Cox regression analyses, the group with wild genotype AA had a higher survival rate during follow-up compared to mutant genotype (AG or GG) ($P< 0.001$, HR = 2.726; 95% CI: 1.825–4.074) (Figure 9).

Table 3 Baseline Characteristics of All Patients and Patients Who Carried Different Genotype in rs281430

	Genotype		Total
	AA	AG+GG	
Number	232(40.3)	344(59.7)	576
Age, M(Q_L, Q_U)	65(56, 71)	63(53, 69.8)	63.5(55, 71)
Gender			
Male	151(65.1)	222(64.5)	373(64.8)
Female	81(34.9)	122(35.5)	203(35.2)
BMI, M	27(24.2, 29.2)	25.5(23.1, 28.7)	26.3(23.3, 28.9)
Smoking	98(42.2)	150(43.6)	248(43.1)
Drinking	42(18.1)	38(11)	80(13.9)
Hypertension	129(55.6)	197(57.3)	326(56.6)
Diabetes	70(30.2)	113(32.8)	183(31.8)
Atrial arrhythmia	67(28.9)	143(41.6)	210(36.5)
Ventricular arrhythmia	107(46.1)	190(55.2)	297(51.6)
SBP (mmHg), M(Q_L, Q_U)	120(107.3, 130.8)	123(114, 134)	122(112, 133)
DBP (mmHg), M(Q_L, Q_U)	71(61, 78)	74(68, 79)	73(66, 78)
HR (beats/min), M(Q_L, Q_U)	70(66, 71)	69(64, 72)	69(65, 72)
Serum sodium (mmol/L), M(Q_L, Q_U)	141.4(138.1, 144.7)	141.4(137.4, 143.9)	141.4(137.6, 144)

(*Continued*)

Table 3 (Continued).

	Genotype		Total
	AA	AG+GG	
Serum potassium (mmol/L), M(Q_L, Q_U)	4.1(3.8, 4.3)	3.9(3.7, 4.3)	3.9(3.8, 4.3)
Serum calcium (mmol/L), M(Q_L, Q_U)	2.2(2.1, 2.3)	2.2(2.1, 2.3)	2.2(2.1, 2.3)
Serum chlorine (mmol/L), M(Q_L, Q_U)	106.4(103, 108.2)	105(102.2, 107)	105.3(102.5, 107.5)
WBC (10^9/L), M(Q_L, Q_U)	6.1(5.3, 7.8)	6.4(5.3, 8)	6.3(5.3, 8)
PLT (10^9/L), M(Q_L, Q_U)	208(193, 222)	197(155, 267)	205(170.5, 253.8)
Hemoglobin (g/L), M(Q_L, Q_U)	134(122, 150)	133(117.3, 142)	134(120, 144)
AST (μg/L), M(Q_L, Q_U)	18.2(14.5, 26.3)	19.4(14.3, 31)	19.4(14.5, 27)
ALT (μg/L), M(Q_L, Q_U)	18(14.4, 30)	17.4(10.8, 30)	17.4(11.6
CR (μmol/L), M(Q_L, Q_U)	75(65, 89)	78(62, 96.4)	77(, 96)
BUN (mmol/L), M(Q_L, Q_U)	6.3(4.9, 8.1)	6.5(5, 10.4)	6. .9, 8.7)
TC (mmol/L), M(Q_L, Q_U)	3.1(2.5, 4)	2.9(2.4, 3.9)	3.1(2. .9)
TG (mmol/L), M(Q_L, Q_U)	1.1(0.9, 1.5)	1.3(0.9, 1.8)	1.2(0.9,
HDL-C (mmol/L), M(Q_L, Q_U)	1(0.8, 1.2)	1(0.7, 1.2)	.8, 1.2)
LDL-C (mmol/L), M(Q_L, Q_U)	1.9(1.5, 2.6)	1.9(1.5, 2.)	1.9(1.5, 2.)
NT-proBNP (×10^3, ng/L), M(Q_L, Q_U)	2(0.3, 3.7)	2.3(0.3 .9)	2(0.3 .8)
Ejection fraction (%), M(Q_L, Q_U)	38(32, 41)	38)	3 4, 42)
LVED (mm), M(Q_L, Q_U)	61.5(56, 67)	6 (56, 66.	62(56, 67)
Treating by PCI or CABG	142(61.2)	113(32.8)	255(44.3)
Using ACEI/ARB	198(85.3)	310(90.1)	508(88.2)
β-Blockers	204(87.9)	250(7)	454(78.8)
Spironolactone	187(80.6)	256( )	443(76.9)
Furosemide	107(46.1)	174(6)	281(48.8)
Antiplatelet aggregation	18	(82.3)	466(80.9)
Statins	200(2)	279(81.1)	479(83.2)

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Discussion

ICM is a complex disease that resulte from bus reasons, and the prognosis of ICM correlated with multiple factors. The current single-center follow study dev oped a clinically useful new nomogram tool for predicting ICM prognosis; the variables listed below this nomogram were identified as related factors of ICM patient prognosis: complicated with Ventricula arrhythmia, treating by PCI or CABG, not using βblockers, having fast heart rate, lower serum sodium level, lar LVEDD and mutation of rs281430 are the risk factors of having higher survival rate of ICM patients, patients havi these atures have lower survival rate than patients not having these features. ICM patients who carried the wild g type A) have igher survival rate than ICM patients who carried the mutant genotype (AG+GG) (P<0.05; HR: 581; 1.025 .4).

Nomog ms are nly used as effective tools in medicine today. Nomograms rely on user-friendly digital interfaces to achieve en d accuracy and to simplify understanding prognosis for better predicting clinical prognosis in CVDs. The current study reated a nomogram for predicting ICM prognosis.

We validated this predictive nomogram using AUC of ROC and C-index value, calibration plot, and DCA plot. Based on AUC values and the C-index value, our constructed nomogram demonstrated favorable discrimination capacity both in training set and validation set, as displayed in Figure 4A and B. Later, the nomogram's calibration curves (Figure 5A–F), drawn both in training and validation set, indicating good consistency between predicted and real values. DCA is a novel test for evaluating a nomogram.[20] According to Figure 6A–F, the DCA demonstrated that using this nomogram to predict the probability of survival rate provides additional benefits over the "treat-none" and "treat-all" strategies, as well as has good clinical utility.

As the environment, life habits, customs and treating are only a small part of mechanisms correlated with the prognosis of ICM, the impact of the genetic factors on the prognosis of ICM is not fully addressed. Finding of genetic

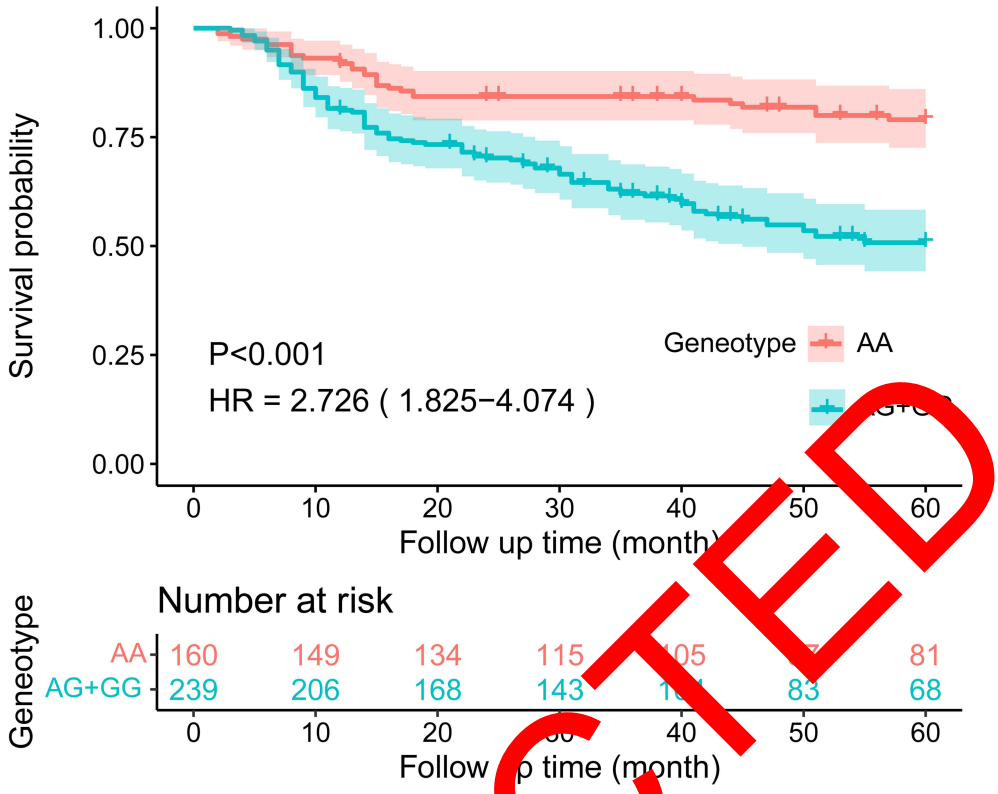

Figure 9 Survival curve for ICM patients of AA and AG+GG genotypes with in SNP rs281430.

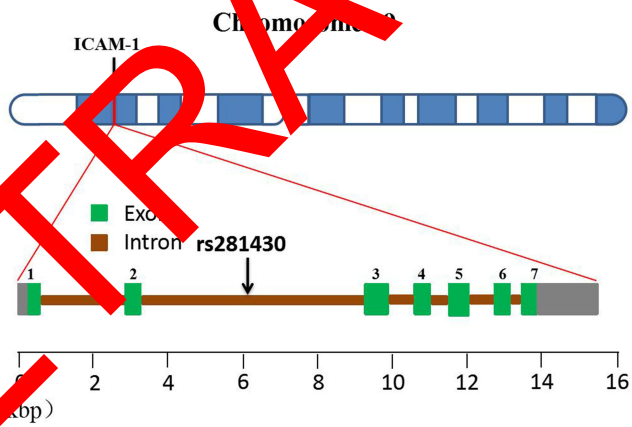

Figure 1 Location of the ICAM-1 gene on the chromosome and location of rs281430 on the ICAM-1 gene.

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risk factors is of great interest in clinic, and will help predicting and improving the management of ICM. In the present study, we discovered a new predictor factor, can predict the prognosis of ICM and has not been reported in previous studies, that variation of rs281430 in the *ICAM-1* gene correlated with ICM prognosis, mutation of rs281430 (from AA to AG+GG) is the risk factor of ICM patients on having higher survival probability, AG+GG genotype of ICM patients have higher cardiogenic death probability than those patients with AA genotype.

Although soluble *ICAM-1* (s*ICAM-1*) level has previously been linked to ICM and atherosclerosis severity,[21] inhibiting *ICAM-1* level can delay atherosclerosis development in apolipoprotein E knockout mice, the relationship of *ICAM-1* gene polymorphism with ICM patient prognosis remains unknown. Therefore, our findings are novel and will significantly impact on accurately predicting the prognosis of ICM patients.

Single nucleotide polymorphism is a type of DNA variation that occurs in an individual.[22] It is the cause of a wide range of individuals, including differences in facial expression and complexity in diseases including coronary artery disease and other disorders.

The SNP may occur in the coding region and play the role of synthetic other kind of amino acid. If mutations occur in noncoding regions, they may perform various functions such as regulating the expression of various genes and proteins. Thus, understanding gene variation and its role can help us understand the mechanism of disease and the relationship between gene variation and disease, as well as with the prognosis of disease, allowing us to take effective measures to prevent disease progression or treat disease early.

ICAM-1 gene can be found on chromosome 19 (Chr19:10,271,120-10,286,615;15.495 kbp) (Figure 10), and it contains 7 exons separated by 6 introns,[23] and rs281430 SNP is found in *ICAM-1* gene(intron2).

The rs281430 SNP has A and G allele gene and AA wild-type gene; the allele gene A and G frequencies are 0.57033 and 0.42967, respectively, globally, while they are 0.742 and 0.258, respectively, in Asian populations. Mutations to AG and GG genotypes are possible in the AA genotype.

According to previous research, 50% of SNPs occur within noncoding regions.[24] rs281430 SNP is also located in noncoding regions of *ICAM-1* gene(intron2), and it shows association with the prognosis of ICM patients, but the mechanism of how the mutation of rs281430 play a role on the prognosis of ICM is unclear. Human body is the best complete system, and the original state of the SNP is the best situation and it has corresponding functions in human body. If there is a mutation on SNP, it is clear that the functional situation of this SNP is not the best, it cannot play the normal function in body, and maybe resulted various kinds of disease or make an aggravation on disease and shorten the life-span.

Regardless of how the mechanism is, the mutation rs281430 is associated with the prognosis of ICM. Based on Cox-regression and K-M survival analyses of 60-month follow-up data, ICM cases carrying the AG or GG genotype had an elevated risk of cardiogenic death compared to cases carrying the AA genotype (Figure 9). Perhaps it influences the function of other related genes. This implies that the pathological mechanisms underlying this correlation should be clarified in future research.

Such findings provide a foundation for developing more effective SNP markers in medical tests, the prediction of personalized prognosis of ICM patients, and providing safe personalized treatment. This will provide the medical field with a new tool.

This work does, however, have some limitations. At first, this is a unicentric study; thus, there is a need to verify the result of the cohorts from other places are or not with the result of this research. Second, while our model underwent internal validation, its generalizability (external validity) remains unknown. Third, in addition to rs281430, multiple variables were identified as being related factors for the prognosis of ICM patients; these variables may be confounding factors for the accurate description of the relevant degree of rs281430 with ICM prognosis. This was the first study to establish a link between the rs281430 polymorphism and ICM prognosis, thus further research is needed to control additional variables by matching those between survival and death groups and to describe the relevance degree more accurately than this.

To summarize, this study discovered that the rs281430 polymorphism of the *ICAM-1* gene was related to the prognosis of ICM patients. The rs281430 mutation is a risk factor for having a high survival probability of ICM. The ICM patients carrying the mutant genotype (AG+GG) have lower survival probability the wild genotype (AA). Although the contribution of rs281430 mutation on estimating the prognosis of ICM in small but it is the novel predictor to evaluate the prognosis of ICM. We created a prognostic model that included *ICAM-1* polymorphism and clinical variables; our model was useful in identifying high- and low-risk patients on the prognosis of ICM patients, and it assisted in managing and treating ICM cases individually to improve the prognosis and reduce mortality.

Ethics Statement

The present work gained approval from Ethics Committee of the First Affiliated Hospital of Xinjiang Medical University (Approval No. 2021D01D17). Individuals who participated in the present work provided written informed consent to participate in this research, in accordance with the Declaration of Helsinki.

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Disclosure

All authors report no conflicts of interest in this work.

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