

Supplementary Materials

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Table S1. Disease codes and their corresponding disease names included in the study.

ICD	Disease names
ICD9	
410	Acute myocardial infarction
411	Other acute and subacute forms of ischemic heart disease
413	Angina pectoris
414	Other forms of chronic ischemic heart disease
ICD10	
I20.0	Unstable angina
I20.1	Angina pectoris with documented spasm
I20.8	Other forms of angina pectoris
I20.9	Angina pectoris, unspecified
I21.0	Acute transmural myocardial infarction of anterior wall
I21.01, I21.02, I21.09	Other subtypes of anterior wall myocardial infarction
I21.11, I21.19	Acute myocardial infarction of inferior wall
I21.21, I21.29	Acute myocardial infarction of other sites
I21.3	Acute myocardial infarction, unspecified site
I21.4	Acute subendocardial myocardial infarction
I21.9	Acute myocardial infarction, unspecified
I21.A1, I21.A9	Other types of myocardial infarction
I22.0, I22.1, I22.2, I22.8, I22.9	Subsequent myocardial infarction
I23.0-I23.8	Current complications following acute myocardial infarction
I24.0	Acute coronary thrombosis not resulting in myocardial infarction
I24.1	Dressler's syndrome
I24.8, I24.9	Other forms of acute ischemic heart disease
I25.5	Ischemic cardiomyopathy
I25.10, I25.110-I25.119	Atherosclerotic heart disease
I25.810, I25.82-I25.84:	Other forms of chronic ischemic heart disease
ICD, International Classification of Diseases.	

Table S2. Missing values of each variable included in this study.

Characteristics	Overall	Number of missing values	Proportion
n	1595	0	0.0%
Gender	1595	0	0.0%
Age	1595	0	0.0%
Height	1145	450	28.2%
Weight	1555	40	2.5%
Smoker	1595	0	0.0%
AKI	1595	0	0.0%
Sepsis	1595	0	0.0%
Congestive heart failure	1595	0	0.0%
Cerebrovascular disease	1595	0	0.0%
Dementia	1595	0	0.0%
Chronic pulmonary disease	1595	0	0.0%
Invasive ventilation	1595	0	0.0%
Statins	1595	0	0.0%
Aspirin	1595	0	0.0%
Anti-hypertensives	1595	0	0.0%
Glucocorticoids	1595	0	0.0%
Albumin	1201	394	24.7%
Total bilirubin	1388	207	13.0%
WBC	1595	0	0.0%
RDW	1595	0	0.0%
Platelet	1595	0	0.0%
RBC	1595	0	0.0%
Creatinine	1595	0	0.0%
BUN	1595	0	0.0%
Total calcium	1489	106	6.6%
INR	1557	38	2.4%
Glucose	1595	0	0.0%
Potassium	1595	0	0.0%
Sodium	1595	0	0.0%
Hemoglobin	1595	0	0.0%
HbA1c	1595	0	0.0%
SHR	1595	0	0.0%
SD, Standard Deviation; AKI, Acute Kidney Injury; WBC, White Blood Cell; RDW, Red Cell Distribution Width; RBC, Red Blood Cell count; BUN, Blood Urea Nitrogen; INR, International Normalized Ratio; HbA1c, Hemoglobin A1c; SHR, Stress Hyperglycemia Ratio.			

Table S3. Identification of model feature using LASSO method.	
Characteristics	Value
Intercept	-2.221
Gender	-
Age	0.018
Height	-
Weight	-
Smoker	-
AKI	-
Sepsis	0.151
Congestive heart failure	-
Cerebrovascular disease	0.708
Dementia	-
Chronic pulmonary disease	-
Invasive ventilation	0.144
Statins	-
Aspirin	0.052
Anti-hypertensives	0.742
Glucocorticoids	-
Albumin	-0.479
Total bilirubin	0.055
WBC	0.012
RDW	0.001
Platelet	-
RBC	-0.041
Creatinine	-
BUN	0.016
Total calcium	-
INR	0.027
Glucose	-
Potassium	0.083
Sodium	-
Hemoglobin	-
HbA1c	-
SHR	-
LASSO, Least Absolute Shrinkage and Selection Operator; AKI, Acute Kidney Injury; WBC, White Blood Cell; RDW, Red Cell Distribution Width; RBC, Red Blood Cell count; BUN, Blood Urea Nitrogen; INR, International Normalized Ratio; HbA1c, Hemoglobin A1c; SHR, Stress Hyperglycemia Ratio.	

Table S4. Spearman correlation analysis between model features.														
Model features	Age	Sepsis	CVD	IV	Aspirin	Anti-HTN	Albumin	Total bilirubin	WBC	RDW	RBC	BUN	INR	Potassium
Age	1.000	0.028	0.128	-0.004	0.017	0.015	-0.020	0.043	-0.067	0.087	-0.166	0.087	0.066	-0.009
Sepsis	0.028	1.000	0.014	0.170	-0.019	-0.040	-0.141	0.059	0.091	0.074	-0.112	0.193	0.077	0.084
CVD	0.128	0.014	1.000	-0.061	-0.017	-0.048	-0.135	0.064	0.074	-0.001	-0.036	-0.053	-0.007	-0.054
IV	-0.004	0.170	-0.061	1.000	0.139	0.106	0.029	-0.012	-0.036	-0.044	0.043	-0.074	-0.017	0.000
Aspirin	0.017	-0.019	-0.017	0.139	1.000	0.152	0.134	-0.117	-0.144	-0.103	0.092	-0.046	-0.027	0.006
Anti-HTN	0.015	-0.040	-0.048	0.106	0.152	1.000	0.082	-0.041	-0.033	-0.074	0.105	-0.129	-0.021	-0.067
Albumin	-0.020	-0.141	-0.135	0.029	0.134	0.082	1.000	-0.059	-0.163	-0.216	0.336	-0.215	-0.164	-0.020
Total bilirubin	0.043	0.059	0.064	-0.012	-0.117	-0.041	-0.059	1.000	0.068	0.107	0.055	0.025	0.237	-0.076
WBC	-0.067	0.091	0.074	-0.036	-0.144	-0.033	-0.163	0.068	1.000	0.069	0.017	0.056	0.085	0.002
RDW	0.087	0.074	-0.001	-0.044	-0.103	-0.074	-0.216	0.107	0.069	1.000	-0.258	0.254	0.203	0.066
RBC	-0.166	-0.112	-0.036	0.043	0.092	0.105	0.336	0.055	0.017	-0.258	1.000	-0.358	-0.114	-0.116
BUN	0.087	0.193	-0.053	-0.074	-0.046	-0.129	-0.215	0.025	0.056	0.254	-0.358	1.000	0.221	0.380
INR	0.066	0.077	-0.007	-0.017	-0.027	-0.021	-0.164	0.237	0.085	0.203	-0.114	0.221	1.000	0.059
Potassium	-0.009	0.084	-0.054	0.000	0.006	-0.067	-0.020	-0.076	0.002	0.066	-0.116	0.380	0.059	1.000
CVD, Cardiovascular disease; IV, Invasive Ventilation; Anti-HTN, Anti-hypertensives; WBC, White Blood Cell; RDW, Red Cell Distribution Width; RBC, Red Blood Cell; BUN, Blood Urea Nitrogen; INR, International Normalized Ratio.														

Table S5. Machine learning algorithms and their best-performing hyperparameters.

Algorithms	Hyperparameters
LR	C=1, random_state=42
SVM	'C': 0.010832308858067883, 'gamma': 0.23338144662398996, 'kernel': 'linear'
RF	'max_depth': 99, 'max_features': 'log2', 'min_samples_leaf': 38, 'min_samples_split': 25, 'n_estimators': 29
ANN	Best: 0.813957130908966 using {'batch_size': 20, 'epochs': 100, 'optimizer': 'rmsprop'
DT	'ccp_alpha': 0.010361382450402823, 'criterion': 'gini', 'max_depth': 17, 'max_features': None, 'max_leaf_nodes': 41, 'min_impurity_decrease': 0.004689646779121992, 'min_samples_leaf': 8, 'min_samples_split': 40, 'splitter': 'random'
XGBoost	'learning_rate': 0.22118274109743927, 'max_depth': 24, 'min_child_weight': 5, 'n_estimators': 20
Ensemble	VotingClassifier(estimators=[('lr', LogisticRegression(C=1, random_state=42)), ('dt', DecisionTreeClassifier(ccp_alpha=0.010361382450402823, max_depth=17, max_leaf_nodes=41, min_impurity_decrease=0.004689646779121992, min_samples_leaf=8, min_samples_split=40, random_state=42, splitter='random'))], ('xgbm', XGBClassifier(base_score=None, booster=None, callbacks=None, importance_type=None, interaction_constraints=None, learning_rate=0.22118274109743927, max_bin=None, max_cat_threshold=None, max_cat_to_onehot=None, max_delta_step=None, max_depth=24, max_leaves=None, min_child_weight=5, missing=nan, monotone_constraints=None, multi_strategy=None, n_estimators=20, n_jobs=None, num_parallel_tree=None, random_state=42, ...)]), voting='soft')
LR, Logistic Regression; SVM, Support Vector Machine; RF, Random Forest; ANN, Artificial Neural Network; DT, Decision Tree; XGBoost, eXtreme Gradient Boosting Machine	

Table S6. The ranking of prediction performance for each machine learning model.

Metrics	Model					
	LR	SVM	RF	ANN	DT	XGBoost
Accuracy	4	3	2	1	6	5
Precision	3	1	4	2	5	6
Recall	4	5	1	2	6	3
F1 score	4	3	1	2	6	5
AUC	4	3	2	1	5	6
Brier score	4	3	2	1	5	6
Log loss	4	3	2	1	5	6
Intercept-in-large	6	5	3	1	4	2
Calibration slope	4	5	2	1	3	6
Discrimination slope	3	2	1	5	4	6
Sum	40	33	20	17	49	51

LR, Logistic Regression; SVM, Support Vector Machine; RF, Random Forest; ANN, Artificial Neural Network; DT, Decision Tree; XGBoost, eXtreme Gradient Boosting Machine; AUC, Area Under the Curve.

Table S7. Feature importance in each machine learning model.						
Feature	Model					
	ANN	DT	LR	RF	SVM	XGBoost
Age	0.110	0.000	0.703	0.003	0.543	0.072
Albumin	0.034	0.000	0.371	0.108	0.203	0.050
Anti-HTN	0.070	0.277	1.583	0.119	1.275	0.210
Aspirin	0.063	0.323	1.442	0.098	1.247	0.149
Bilirubin	0.013	0.000	0.176	0.054	0.140	0.047
BUN	0.093	0.233	0.472	0.131	0.373	0.068
CVD	0.043	0.000	0.267	0.006	0.158	0.025
INR	0.047	0.000	0.162	0.160	0.180	0.173
IV	0.053	0.167	0.434	0.028	0.270	0.035
Potassium	0.056	0.000	0.194	0.047	0.216	0.034
RBC	0.133	0.000	0.229	0.078	0.264	0.035
RDW	0.041	0.000	0.034	0.053	0.033	0.034
Sepsis	0.032	0.000	0.425	0.001	0.361	0.023
WBC	0.065	0.000	0.513	0.113	0.572	0.045
LR, Logistic Regression; SVM, Support Vector Machine; RF, Random Forest; ANN, Artificial Neural Network; DT, Decision Tree; XGBoost, eXtreme Gradient Boosting Machine; HTN, Hypertension; BUN, Blood Urea Nitrogen; WBC, White Blood Cell; RBC, Red Blood Cell; INR, International Normalized Ratio; IV, Invasive Ventilation; CVD, Cardiovascular disease; RDW, Red Cell Distribution Width.						

Table S8. Ranking for model features in each machine learning model.

Features	Models						Sum
	LR	SVM	RF	ANN	DT	XGBoost	
Anti-HTN	1	1	3	4	2	1	12
Aspirin	2	2	6	6	1	3	20
BUN	5	5	2	3	3	5	23
WBC	4	3	4	5	5	8	29
Age	3	4	13	2	5	4	31
RBC	10	8	7	1	5	9	40
INR	13	11	1	9	5	2	41
Albumin	8	10	5	12	5	6	46
IV	6	7	11	8	4	10	46
Potassium	11	9	10	7	5	11	53
Bilirubin	12	13	8	14	5	7	59
Sepsis	7	6	14	13	5	14	59
CVD	9	12	12	10	5	13	61
RDW	14	14	9	11	5	12	65

LR, Logistic Regression; SVM, Support Vector Machine; RF, Random Forest; ANN, Artificial Neural Network; DT, Decision Tree; XGBoost, eXtreme Gradient Boosting Machine; HTN, Hypertension; BUN, Blood Urea Nitrogen; WBC, White Blood Cell; RBC, Red Blood Cell; INR, International Normalized Ratio; IV, Invasive Ventilation; CVD, Cardiovascular disease; RDW, Red Cell Distribution Width.

Table S9. Prediction performance for the ensemble model and its base estimators.

Metrics	Models			
	LR	DT	XGBoost	Ensemble
Accuracy	0.760	0.807	0.785	0.845
Precision	0.770	0.777	0.876	0.849
Recall	0.742	0.862	0.665	0.840
F1 score	0.756	0.817	0.756	0.845
AUC	0.848	0.858	0.903	0.912
Brier score	0.162	0.150	0.146	0.130
Log loss	0.490	0.471	0.445	0.420
Intercept-in-large	0.009	-0.200	0.877	0.144
Calibration slope	1.114	1.380	1.048	1.904
Discrimination slope	0.334	0.346	0.460	0.380
LR, Logistic Regression; DT, Decision Tree; XGBoost, eXtreme Gradient Boosting Machine; AUC, Area Under the Curve.				

Table S10. The ranking of prediction performance for the ensemble model and its base estimators.

Metrics	Models			
	LR	DT	XGBoost	Ensemble
Accuracy	1	3	2	4
Precision	1	2	4	3
Recall	2	4	1	3
F1 score	2	3	1	4
AUC	1	2	3	4
Brier score	1	2	3	4
Log loss	1	2	3	4
Intercept-in-large	4	3	1	2
Calibration slope	3	2	4	1
Discrimination slope	1	2	4	3
Sum	17	25	26	32
LR, Logistic Regression; SVM, Support Vector Machine; RF, Random Forest; ANN, Artificial Neural Network; DT, Decision Tree; XGBoost, eXtreme Gradient Boosting Machine; AUC, Area Under the Curve.				

Table S11. Prediction performance for the ensemble model and its base estimators with and without incorporating the variable of SHR.				
Metrics	Models			
	LR	DT	XGBoost	Ensemble
Without incorporating SHR				
Accuracy	0.760	0.807	0.785	0.845
Precision	0.770	0.777	0.876	0.849
Recall	0.742	0.862	0.665	0.840
F1 score	0.756	0.817	0.756	0.845
AUC	0.848	0.858	0.903	0.912
Brier score	0.162	0.150	0.146	0.130
Log loss	0.490	0.471	0.445	0.420
Intercept-in-large	0.009	-0.200	0.877	0.144
Calibration slope	1.114	1.380	1.048	1.904
Discrimination slope	0.334	0.346	0.460	0.380
With incorporating SHR				
Accuracy	0.765	0.707	0.771	0.762
Precision	0.774	0.754	0.878	0.816
Recall	0.749	0.615	0.629	0.676
F1 score	0.762	0.677	0.733	0.740
AUC	0.840	0.730	0.894	0.880
Brier score	0.165	0.205	0.156	0.153
Log loss	0.499	0.607	0.473	0.473
Intercept-in-large	0.049	0.072	0.961	0.257
Calibration slope	1.036	0.831	0.960	1.536
Discrimination slope	0.332	0.206	0.450	0.329
SHR, Stress Hyperglycemia Ratio; LR, Logistic Regression; DT, Decision Tree; XGBoost, eXtreme Gradient Boosting Machine; AUC, Area Under the Curve.				

Supplementary Table 12. Baseline characteristics in the external validation cohort.

Characteristics	Overall
n	307
Gender (male/female, %)	186/121 (60.6/39.4)
Age (years, mean (SD))	66.02 (12.22)
Height (cm, mean (SD))	170.67 (7.76)
Weight (kg, mean (SD))	85.95 (16.23)
Smoker (no/yes, %)	278/29 (90.6/9.4)
AKI (no/yes, %)	29/278 (9.4/90.6)
Sepsis (no/yes, %)	187/120 (60.9/39.1)
Congestive heart failure (no/yes, %)	125/182 (40.7/59.3)
Cerebrovascular disease (no/yes, %)	245/62 (79.8/20.2)
Dementia (no/yes, %)	302/5 (98.4/1.6)
Chronic pulmonary disease (no/yes, %)	271/36 (88.3/11.7)
Hypertension (no/yes, %)	197/110 (64.2/35.8)
Invasive ventilation (no/yes, %)	137/170 (44.6/55.4)
Statins (no/yes, %)	267/40 (87.0/13.0)
Aspirin (no/yes, %)	27/280 (8.8/91.2)
Glucocorticoids (no/yes, %)	286/21 (93.2/6.8)
Albumin (g/dL, mean (SD))	3.57 (0.48)
Total bilirubin (mg/dL, mean (SD))	0.61 (0.39)
WBC ($\times 10^{12}$ /L, mean (SD))	10.47 (5.01)
RDW (% , mean (SD))	14.45 (2.23)
Platelet ($\times 10^9$ /L, mean (SD))	231.73 (73.48)
RBC ($\times 10^{12}$ /L, mean (SD))	3.97 (0.76)
Creatinine (mg/dL, mean (SD))	1.73 (1.32)
BUN (mg/dL, mean (SD))	27.73 (17.01)
Total calcium (mg/dL, mean (SD))	8.77 (0.53)
INR (mean (SD))	1.27 (0.41)
Glucose (mg/dL, mean (SD))	201.98 (87.47)
Potassium (mEq/L, mean (SD))	4.28 (0.89)
Sodium (mEq/L, mean (SD))	137.31 (3.12)
Hemoglobin (g/dL, mean (SD))	11.78 (1.91)
HbA1c (% , mean (SD))	7.84 (1.61)
SHR (mean (SD))	1.20 (0.46)
30-day mortality (no/yes, %)	277/30 (90.2/9.8)
SD, Standard Deviation; AKI, Acute Kidney Injury; WBC, White Blood Cell; RDW, Red Cell Distribution Width; RBC, Red Blood Cell count; BUN, Blood Urea Nitrogen; INR, International Normalized Ratio; HbA1c, Hemoglobin A1c; SHR, Stress Hyperglycemia Ratio.	

Supplementary Figures

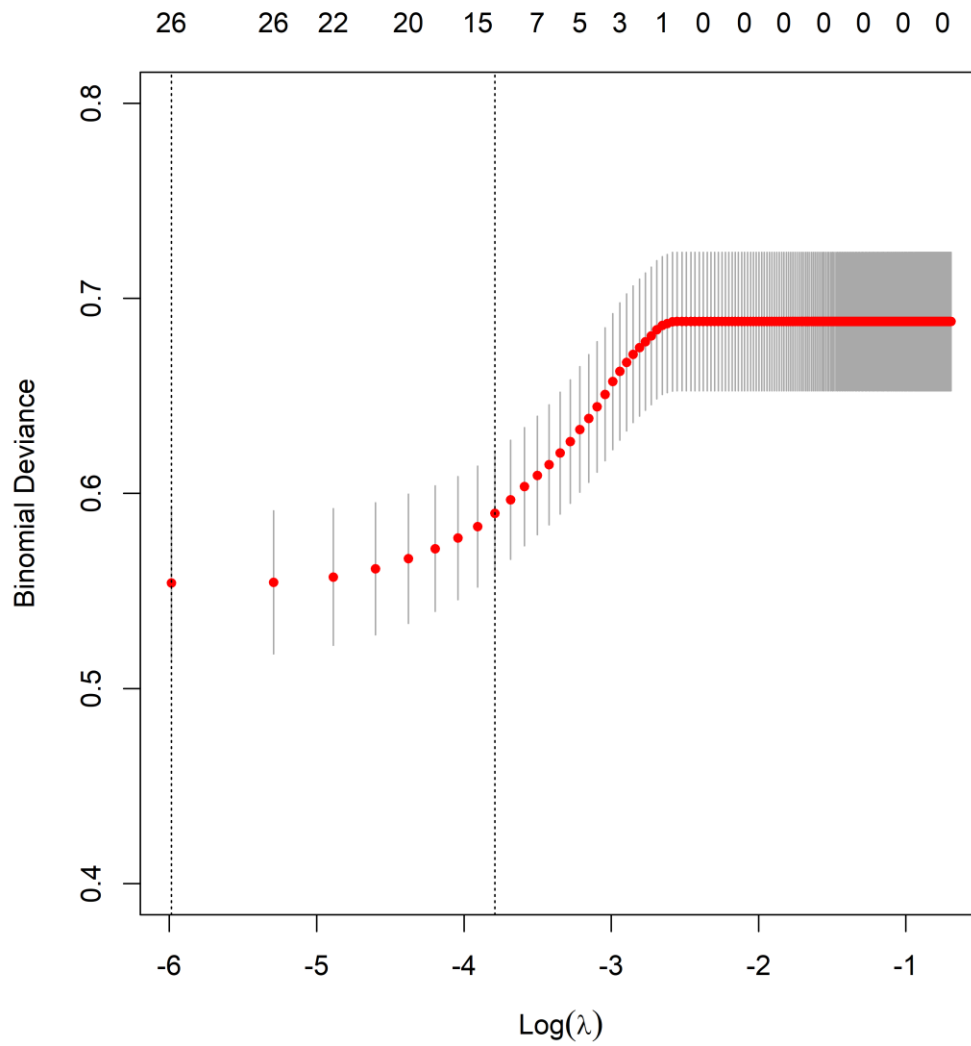


Figure S1. LASSO regression coefficient profiles for feature selection. Trajectory of coefficients as lambda (regularization parameter) varies, with vertical line indicating optimal lambda selection.

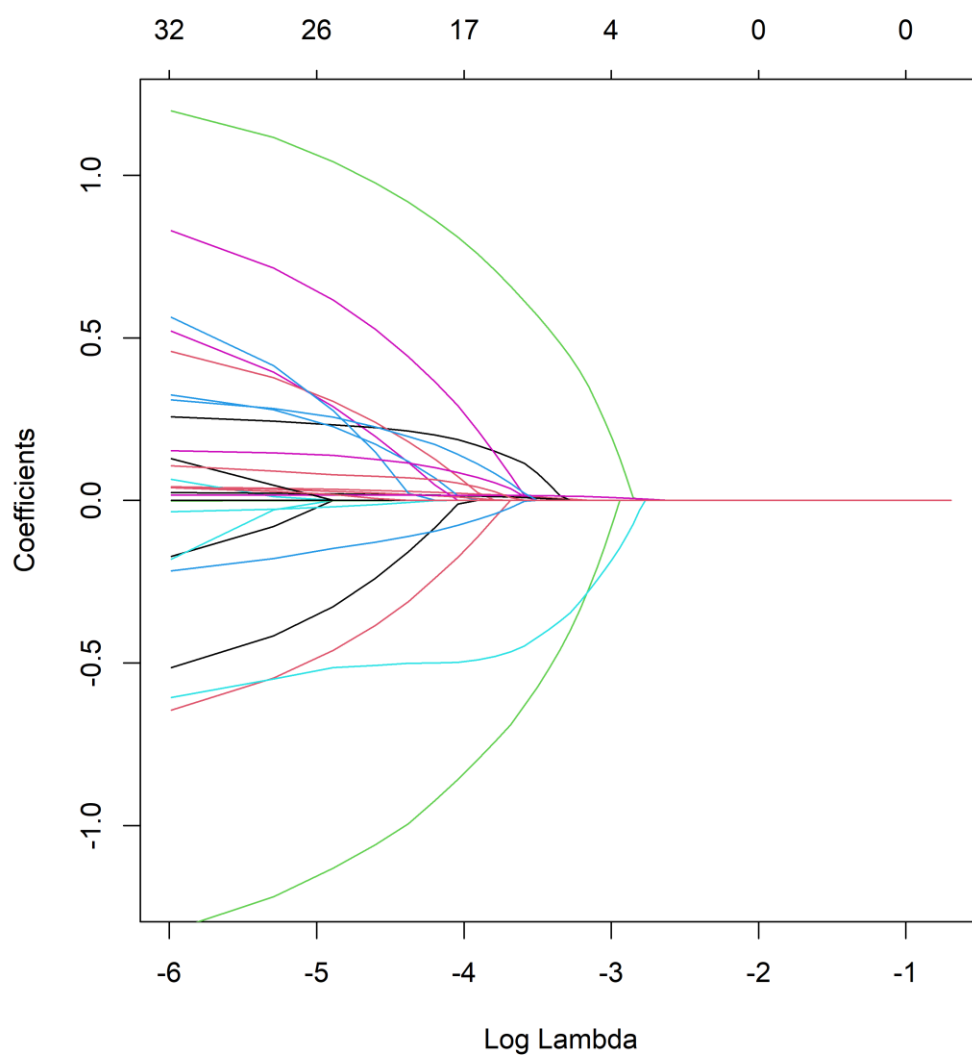


Figure S2. LASSO-selected features with non-zero coefficients. The final 14 variables retained for model development, including age, sepsis, BUN, and anti-hypertensives.

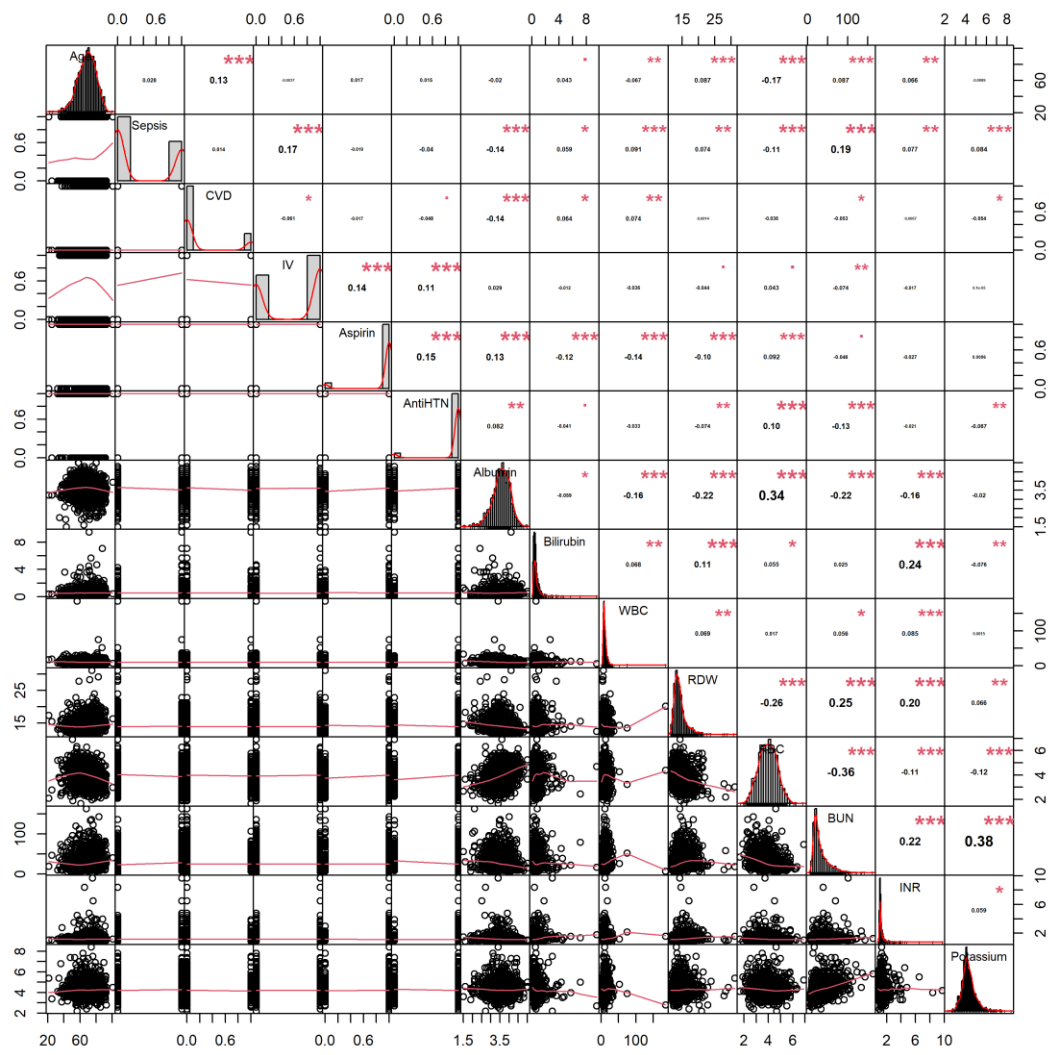


Figure S3. Correlation matrix of selected features. All pairwise correlations were ≤ 0.38 , confirming no multicollinearity.

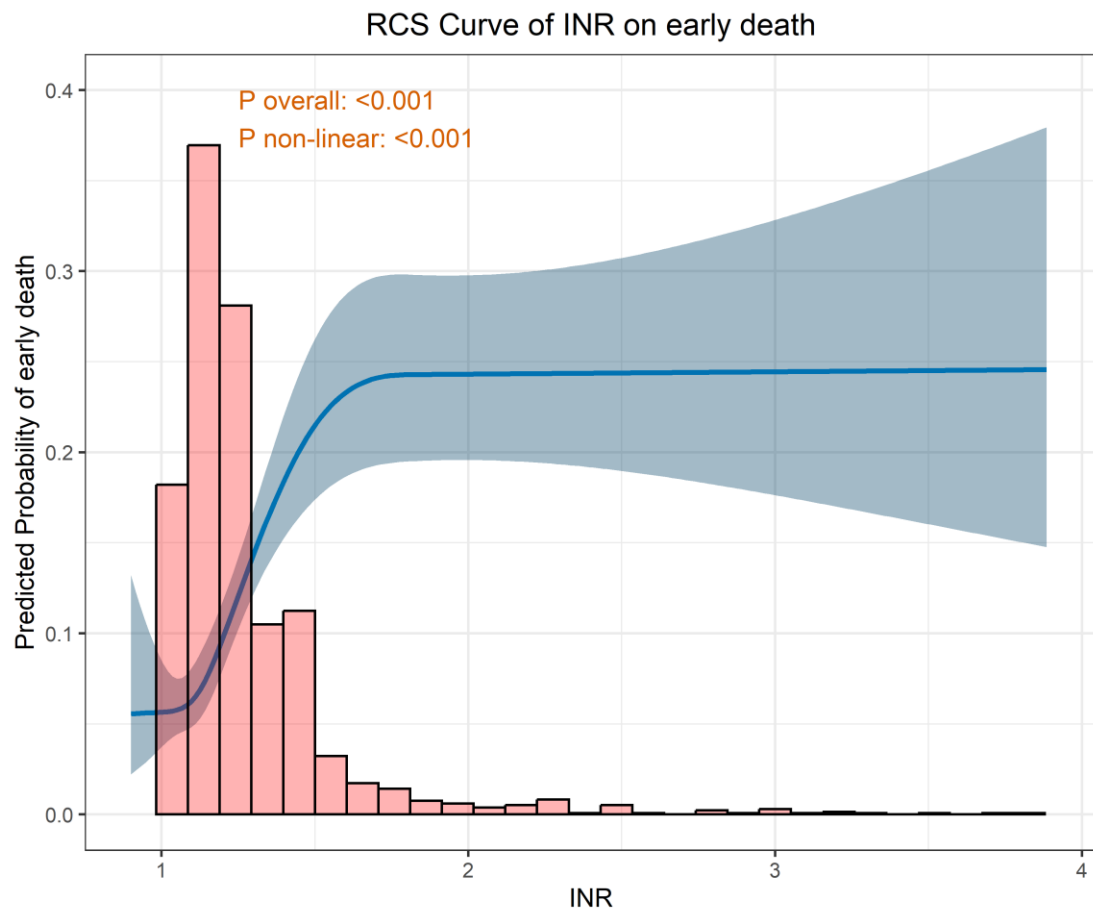


Figure S4. RCS analysis of INR's nonlinear association with mortality. Risk plateaued at higher INR values.

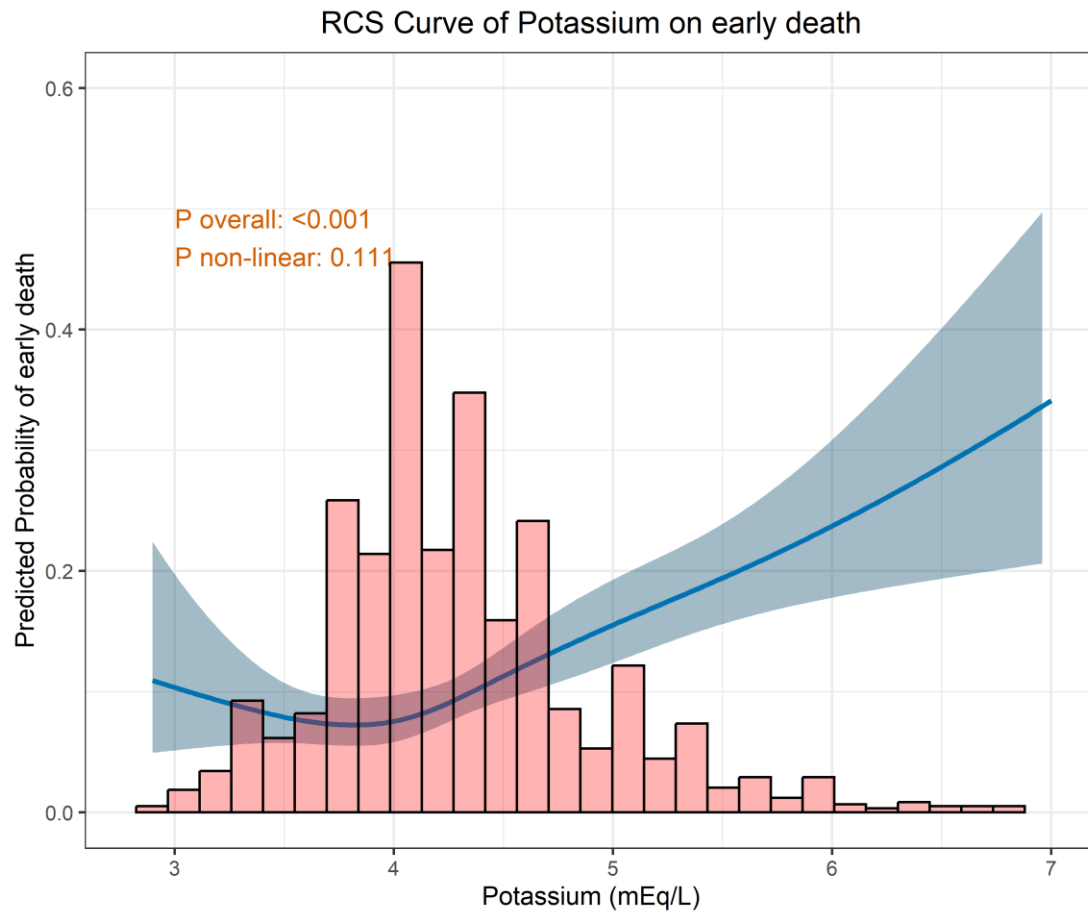


Figure S5. RCS analysis of potassium's linear association with mortality. Positive correlation with mortality risk.

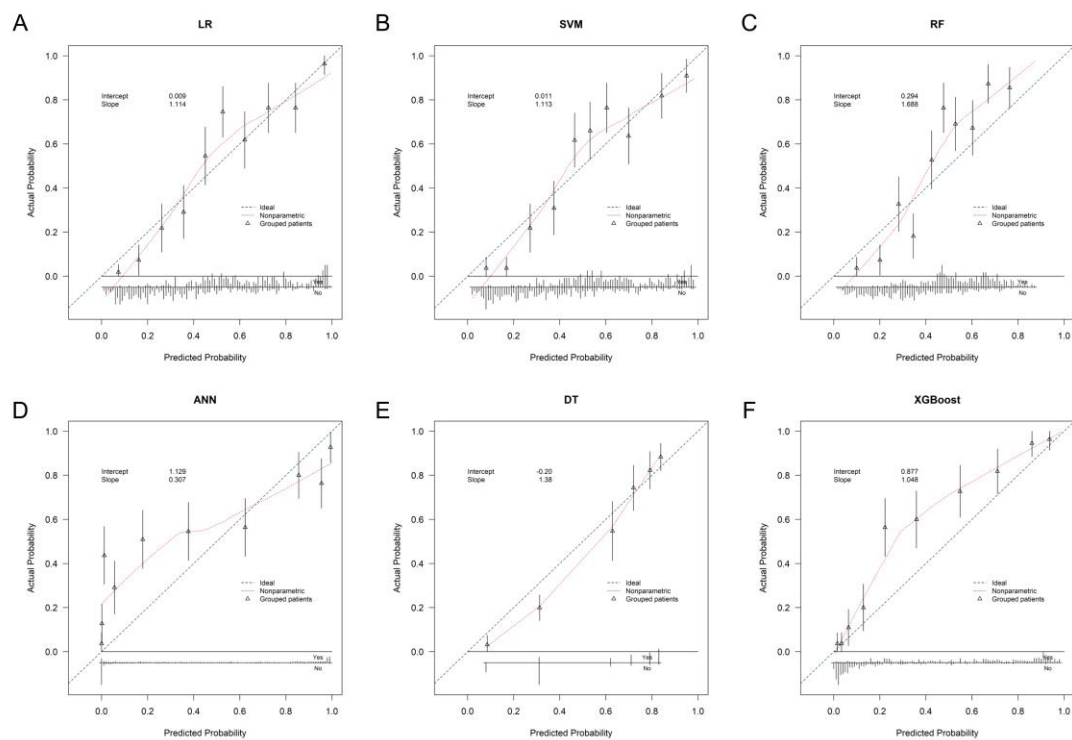


Figure S6. Calibration curves for ML models. (A) LR; (B) SVM; (C) RF; (D) ANN; (E) DT; (F) XGBoost.

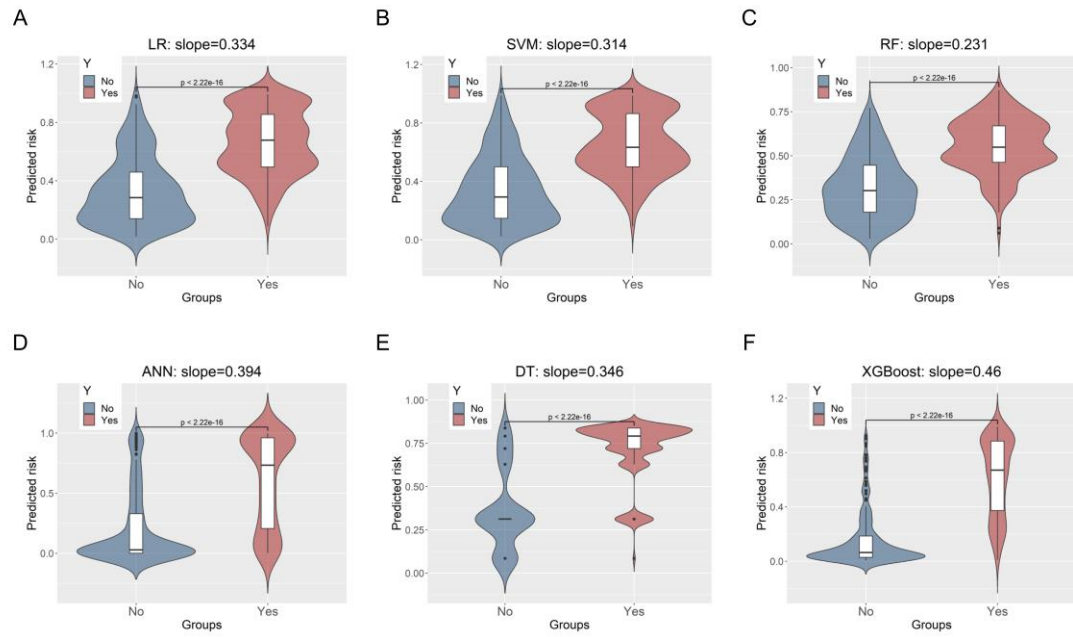


Figure S7. Discrimination slopes of ML models. (A) LR; (B) SVM; (C) RF; (D) ANN; (E) DT; (F) XGBoost.

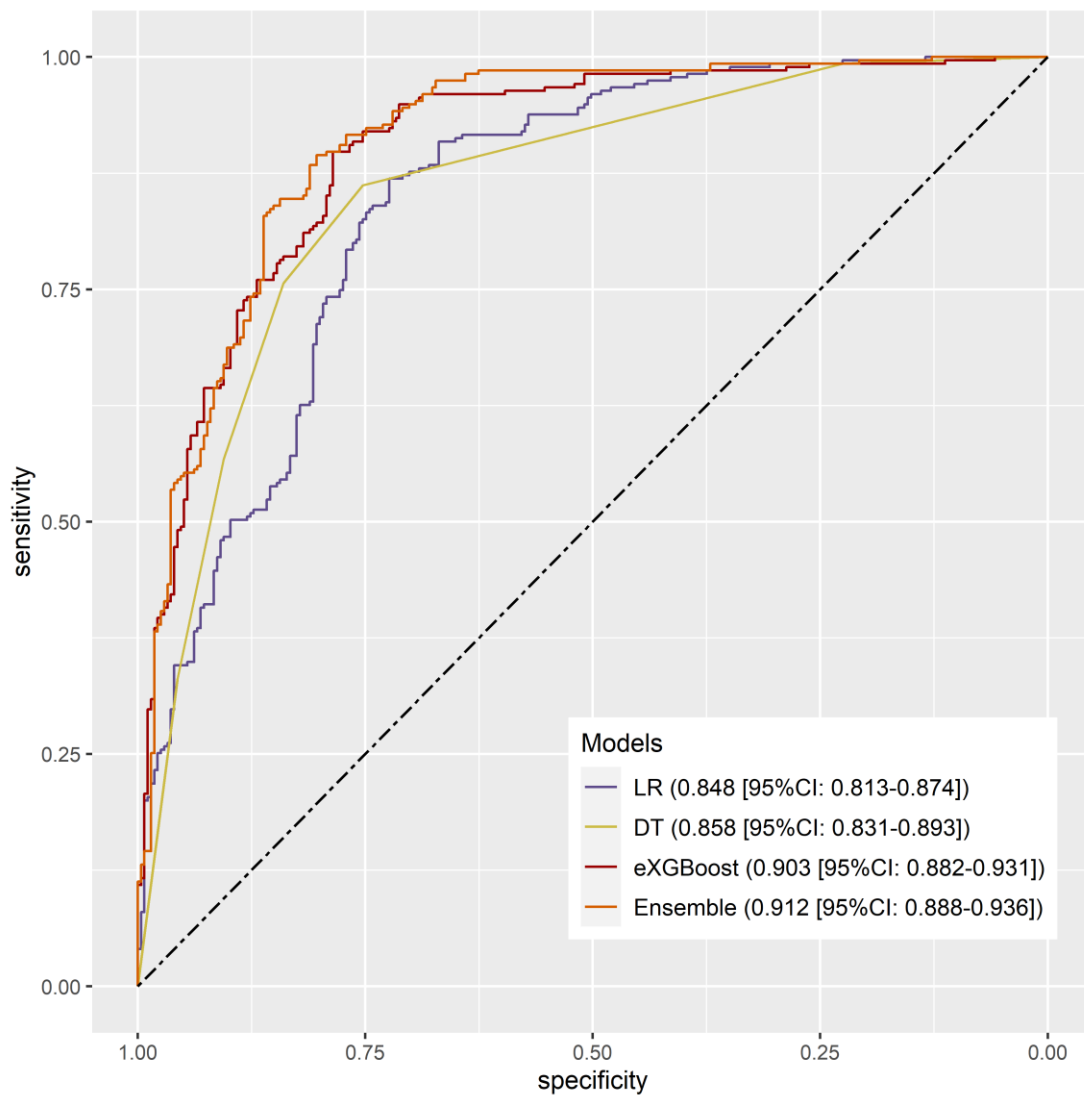


Figure S8. ROC curve of the ensemble model versus base estimators. Ensemble achieved superior AUC (0.912) compared to LR, DT, and XGBoost.

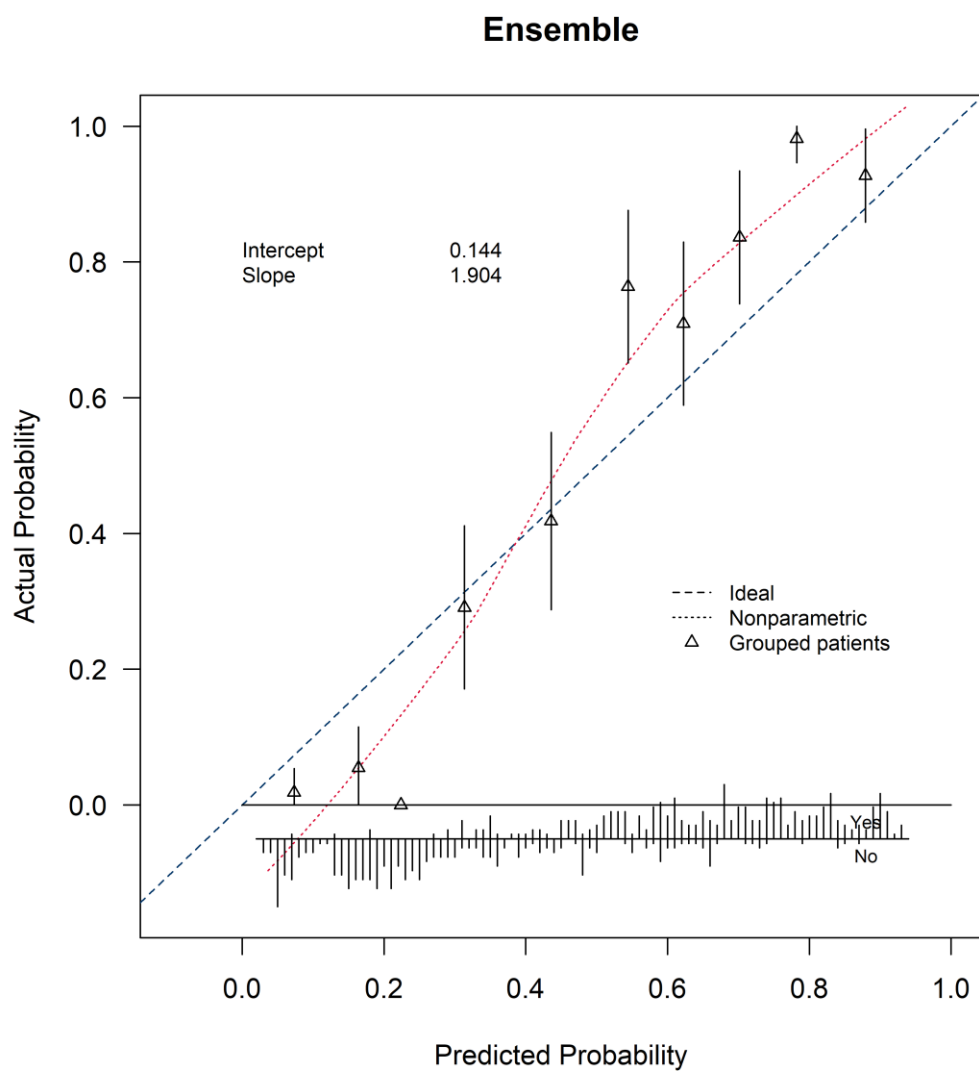


Figure S9. Calibration curve of the ensemble model.

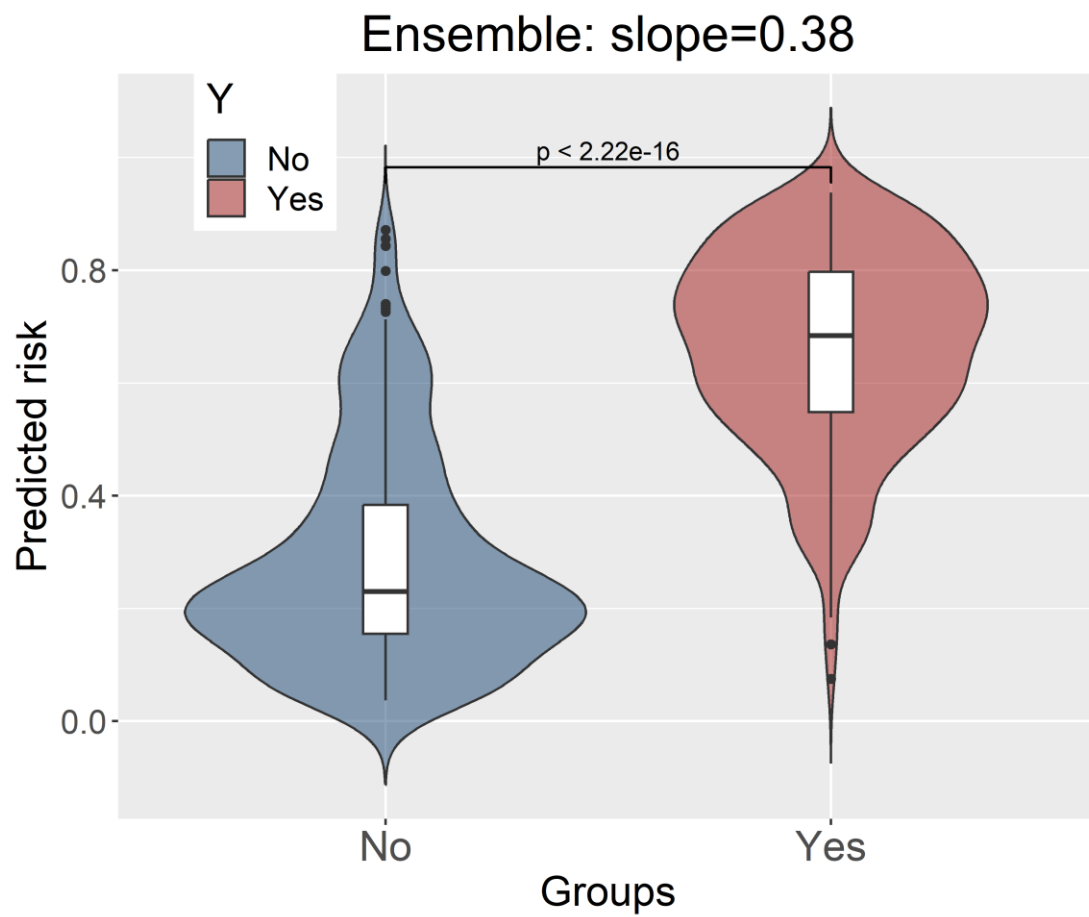


Figure S10. Discrimination slope of the ensemble model.

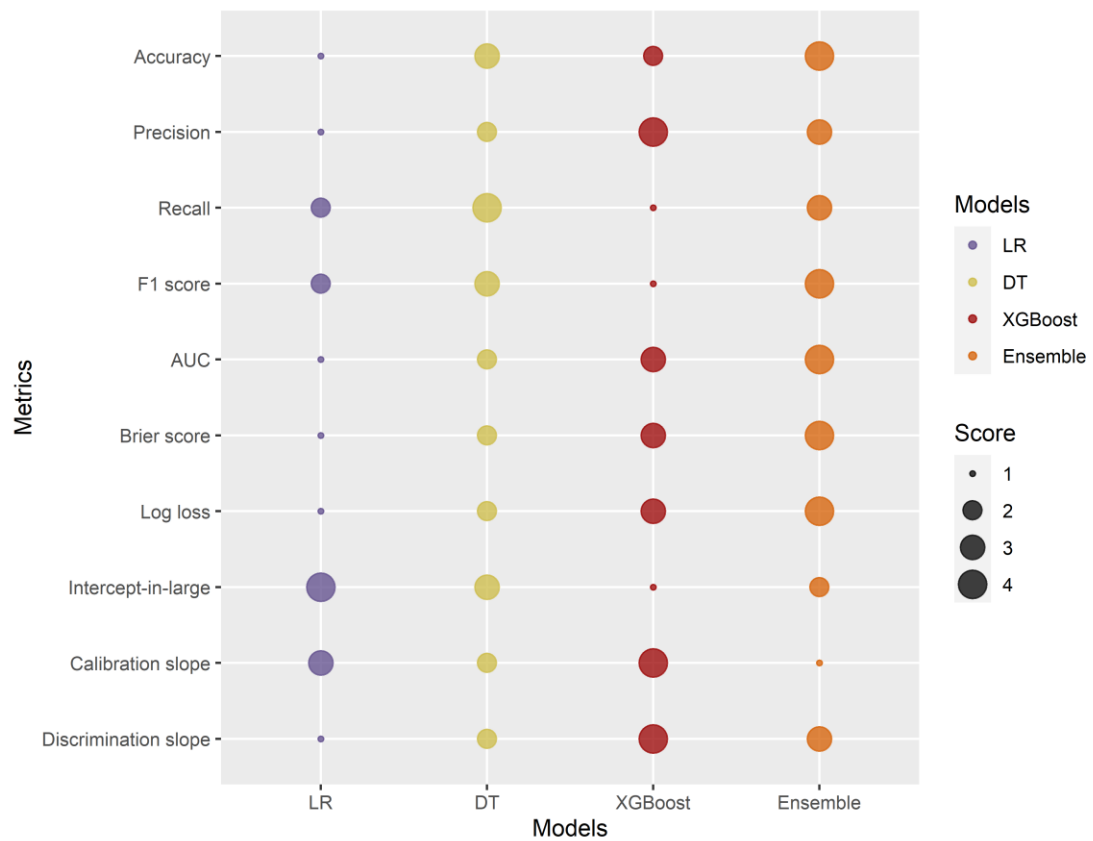


Figure S11. Sum score comparison of the ensemble model versus base models.

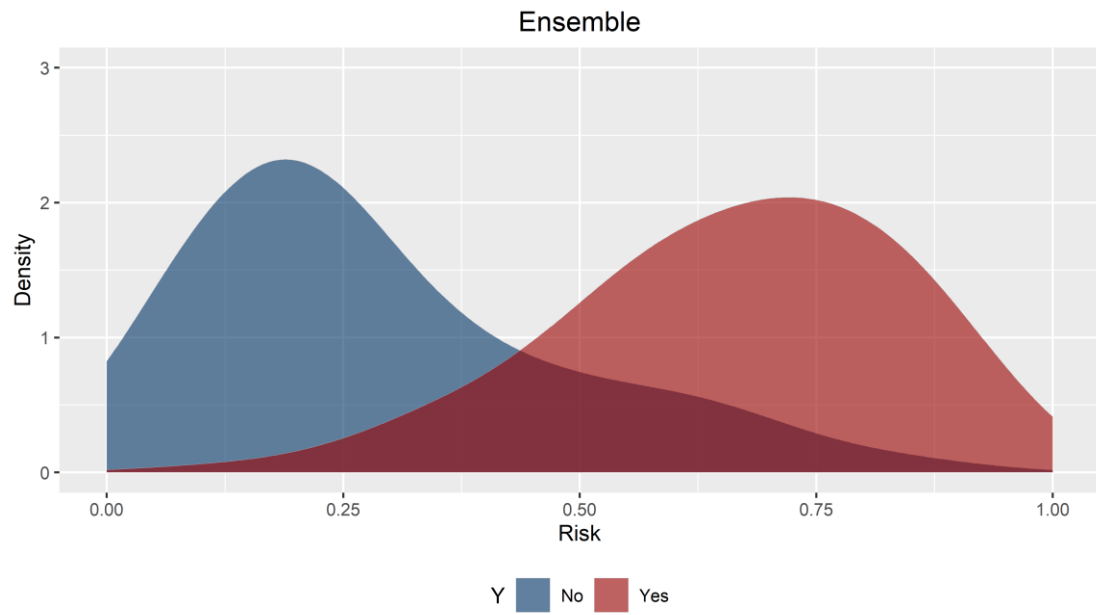


Figure S12. Probability density curves of the ensemble model. Clear bimodal separation between mortality and survival classes.

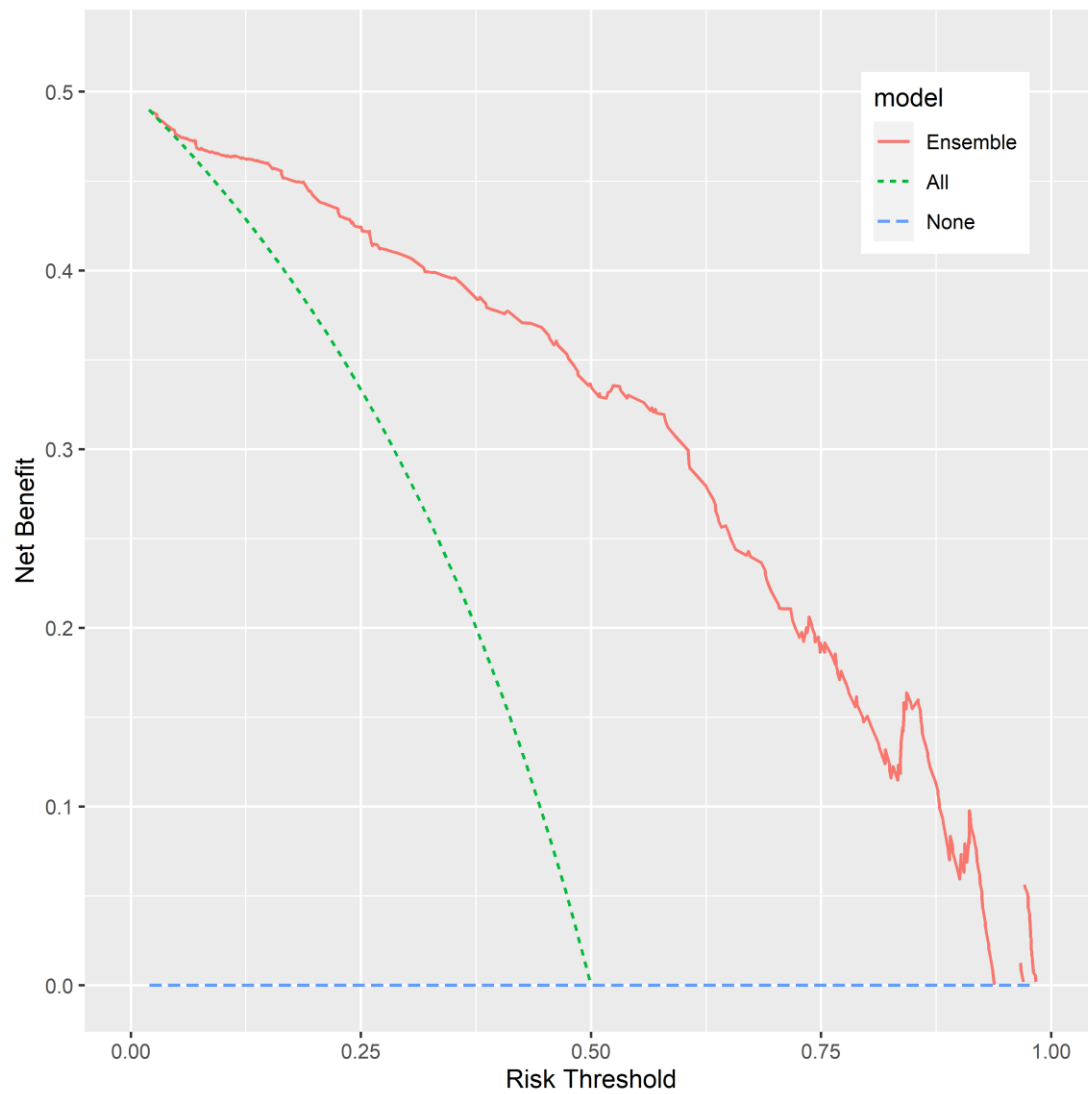


Figure S13. Decision curve analysis of the ensemble model.

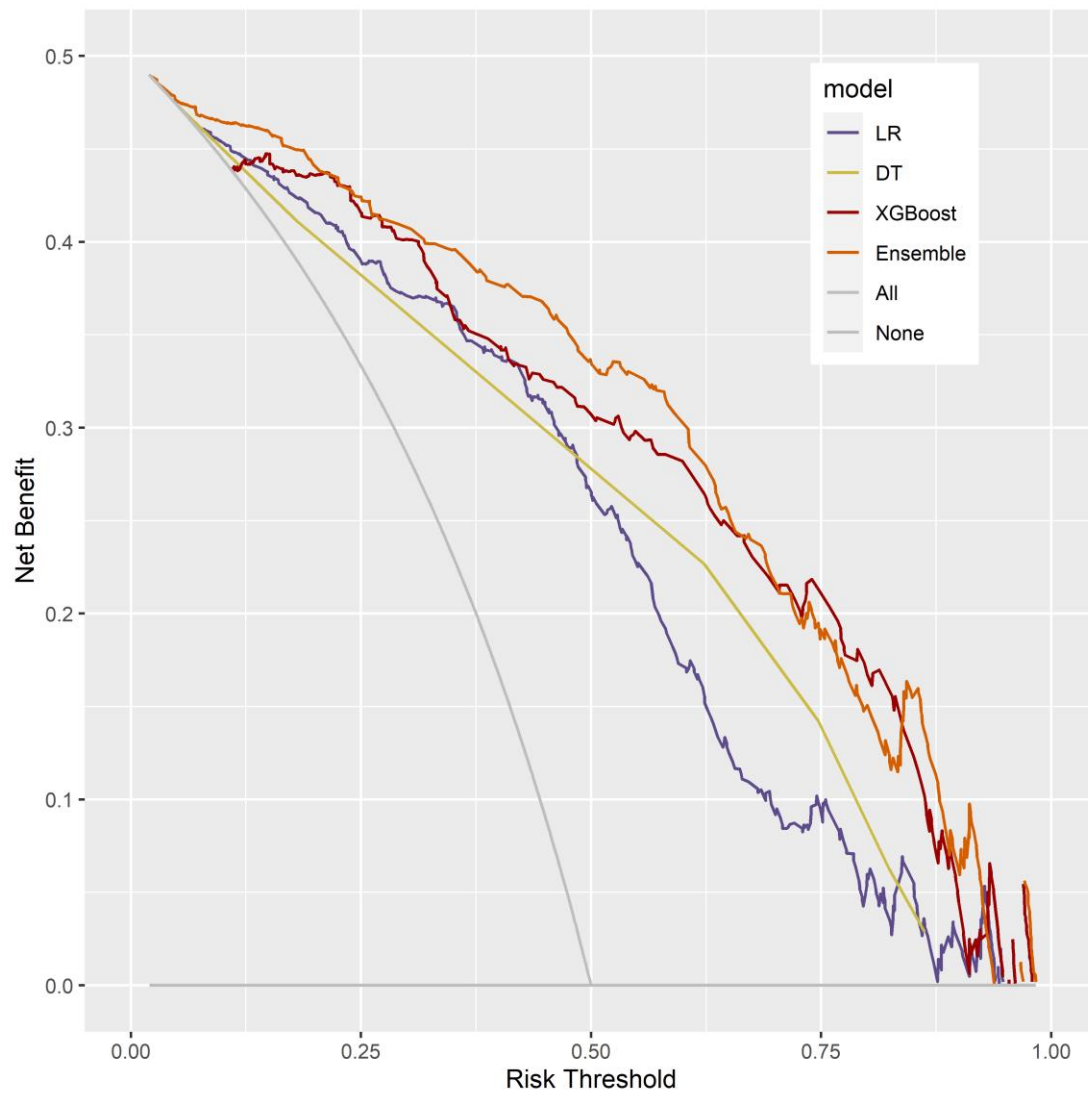


Figure S14. Decision curve analysis of the ensemble model versus base models.

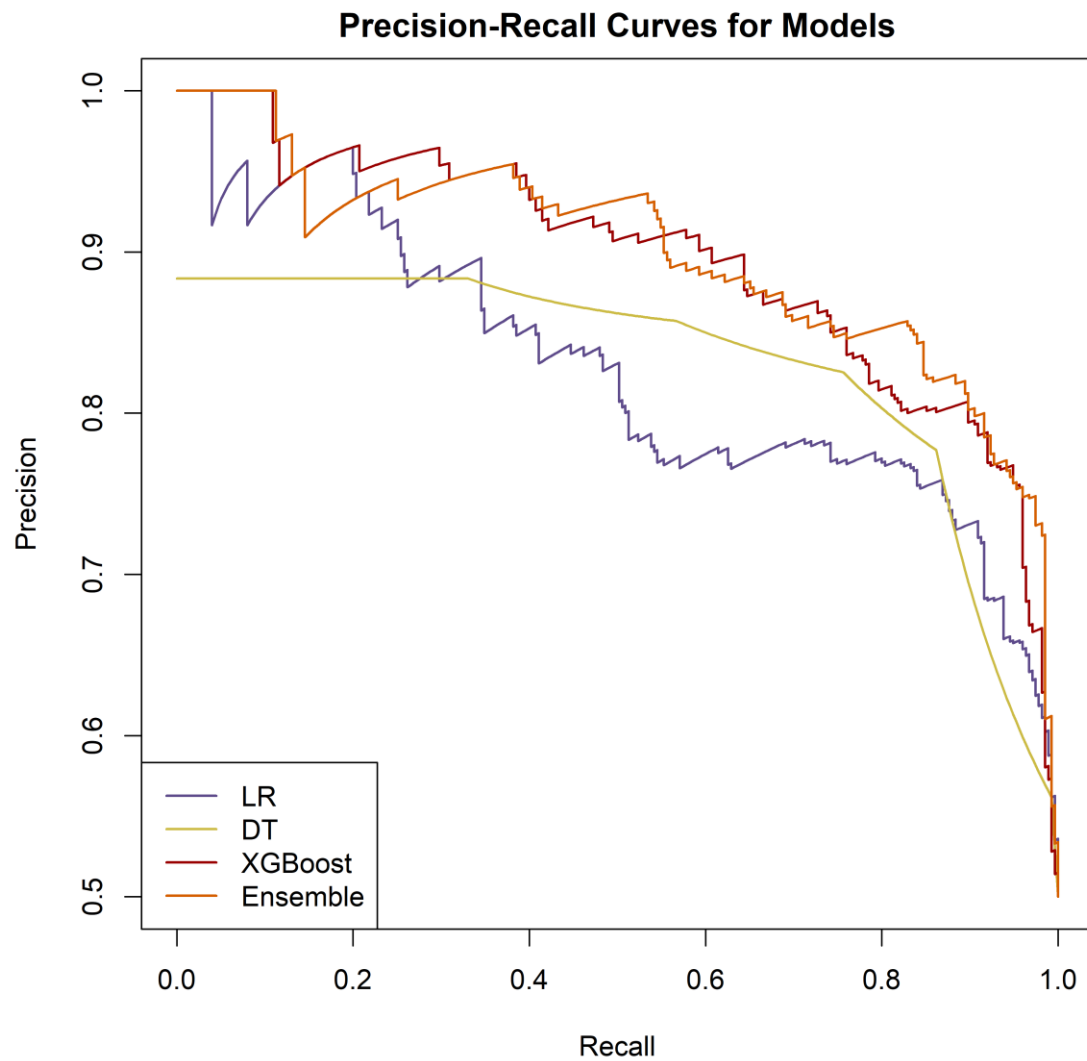


Figure S15. Precision-recall curve of the ensemble model.

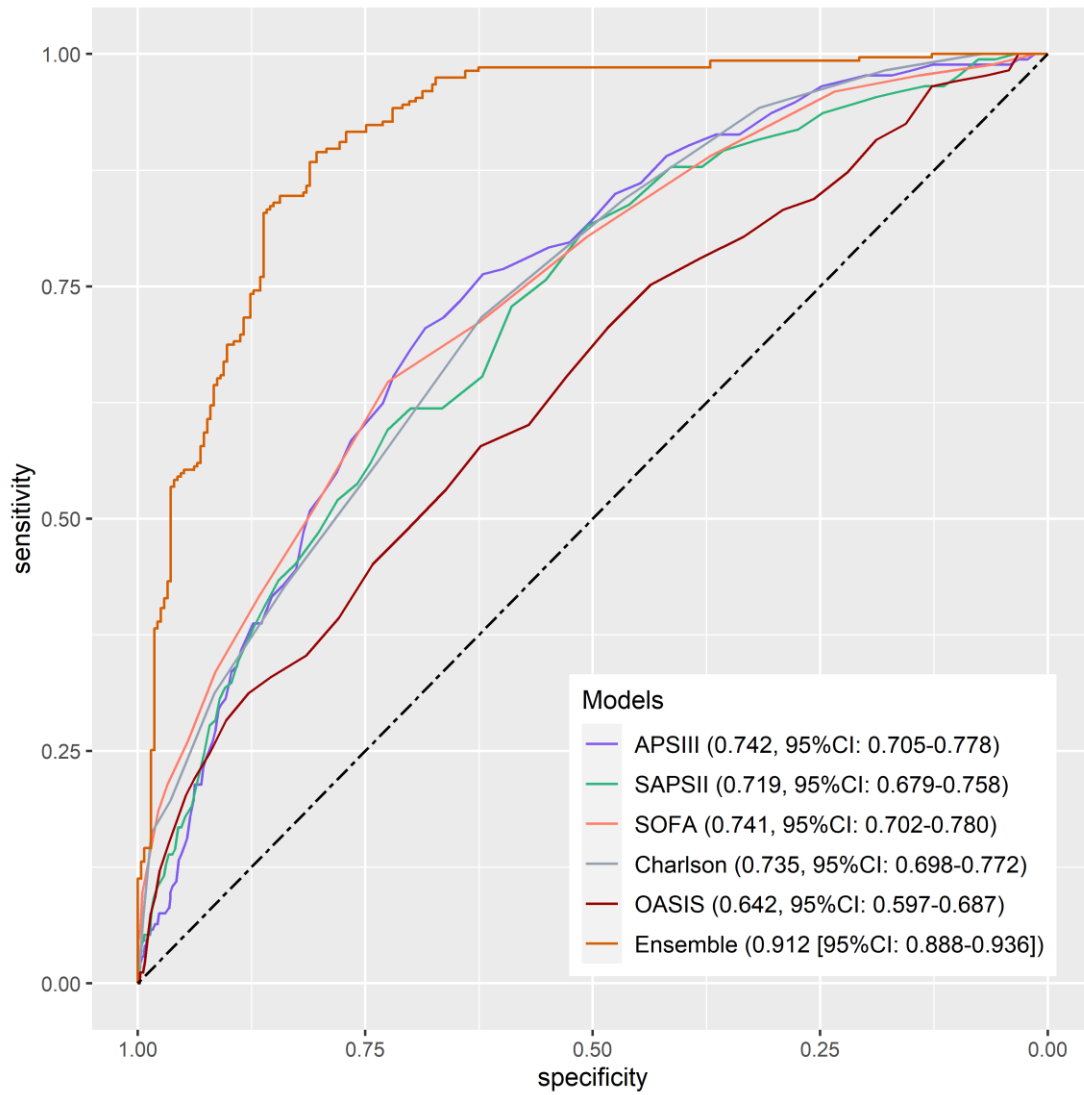


Figure S16. ROC curves comparing the ensemble model to traditional scores. Ensemble (AUC: 0.912) surpassed all conventional scores (AUCs ≤ 0.742 ; $P < 0.001$, Delong tests)

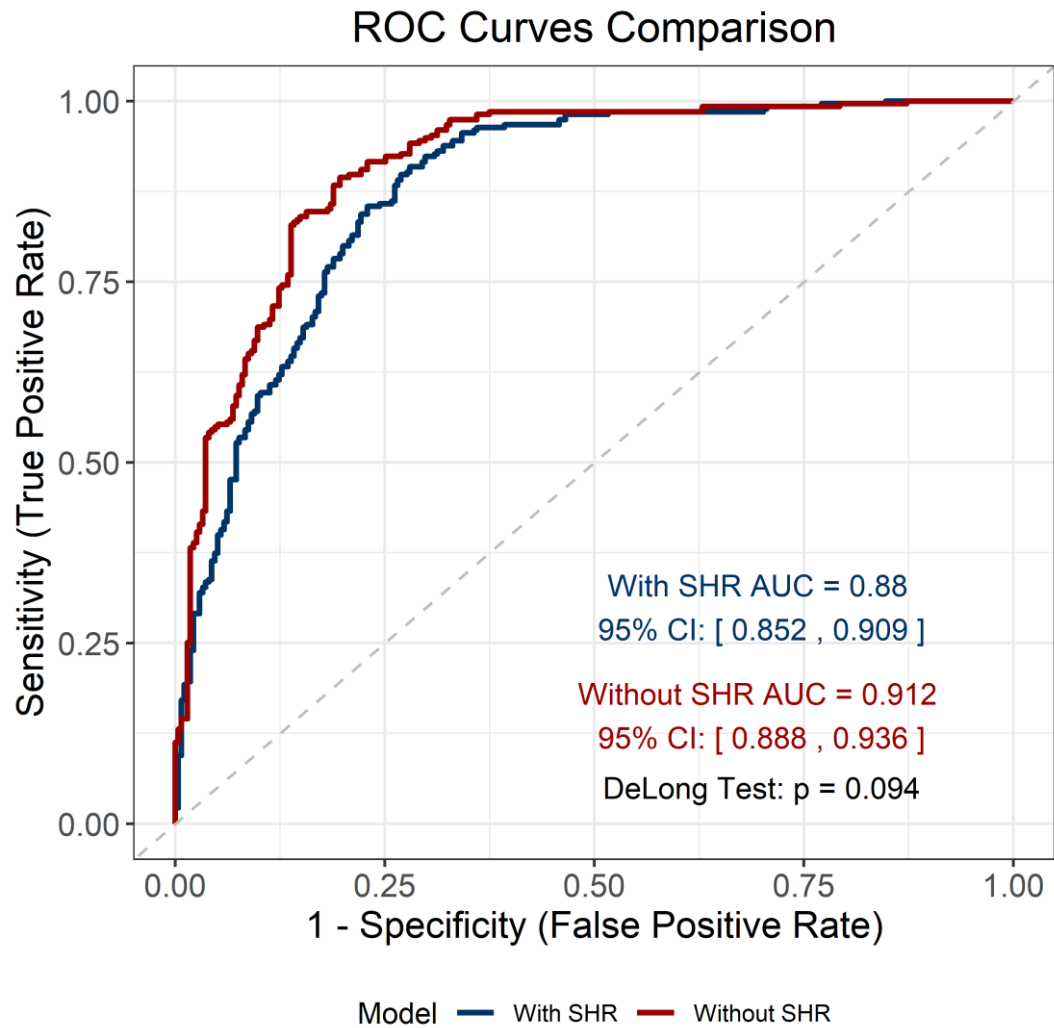


Figure S17. ROC curves of ensemble with/without SHR. No significant AUC difference ($\Delta\text{AUC} = -0.032$, $P = 0.094$).

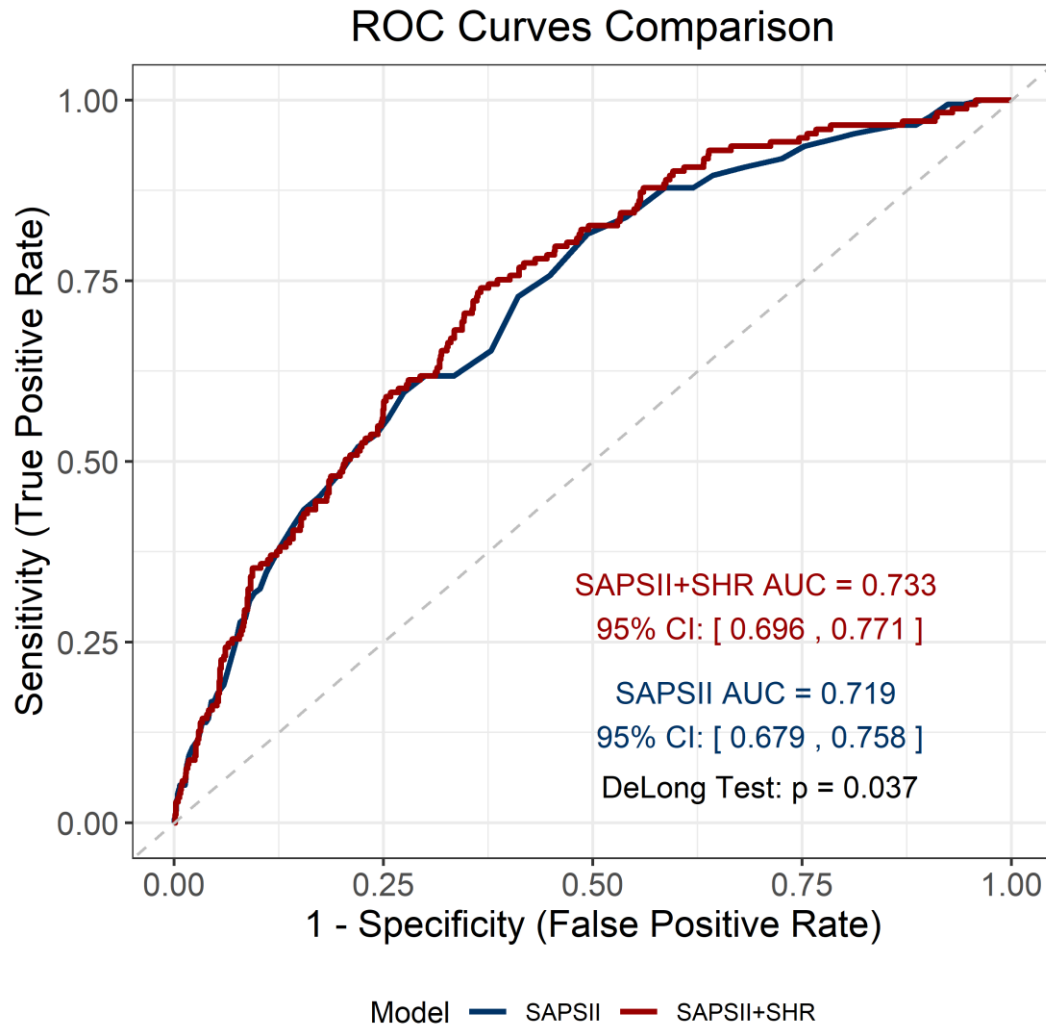


Figure S18. ROC curves of SAPS II with/without SHR. SHR improved SAPS II (AUC: 0.719→0.733, $P = 0.037$).

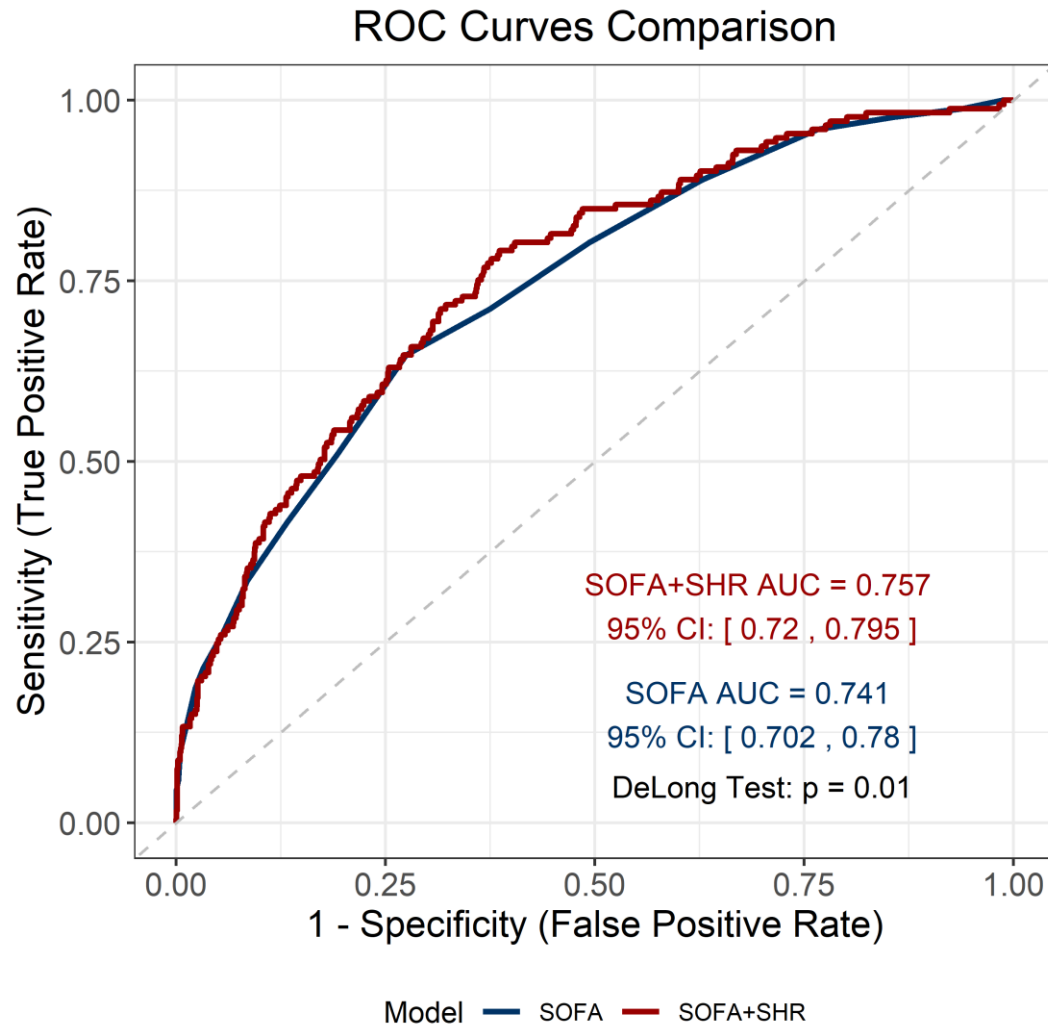


Figure S19. ROC curves of SOFA with/without SHR. SHR improved SOFA (AUC: 0.741→0.757, $P = 0.010$).

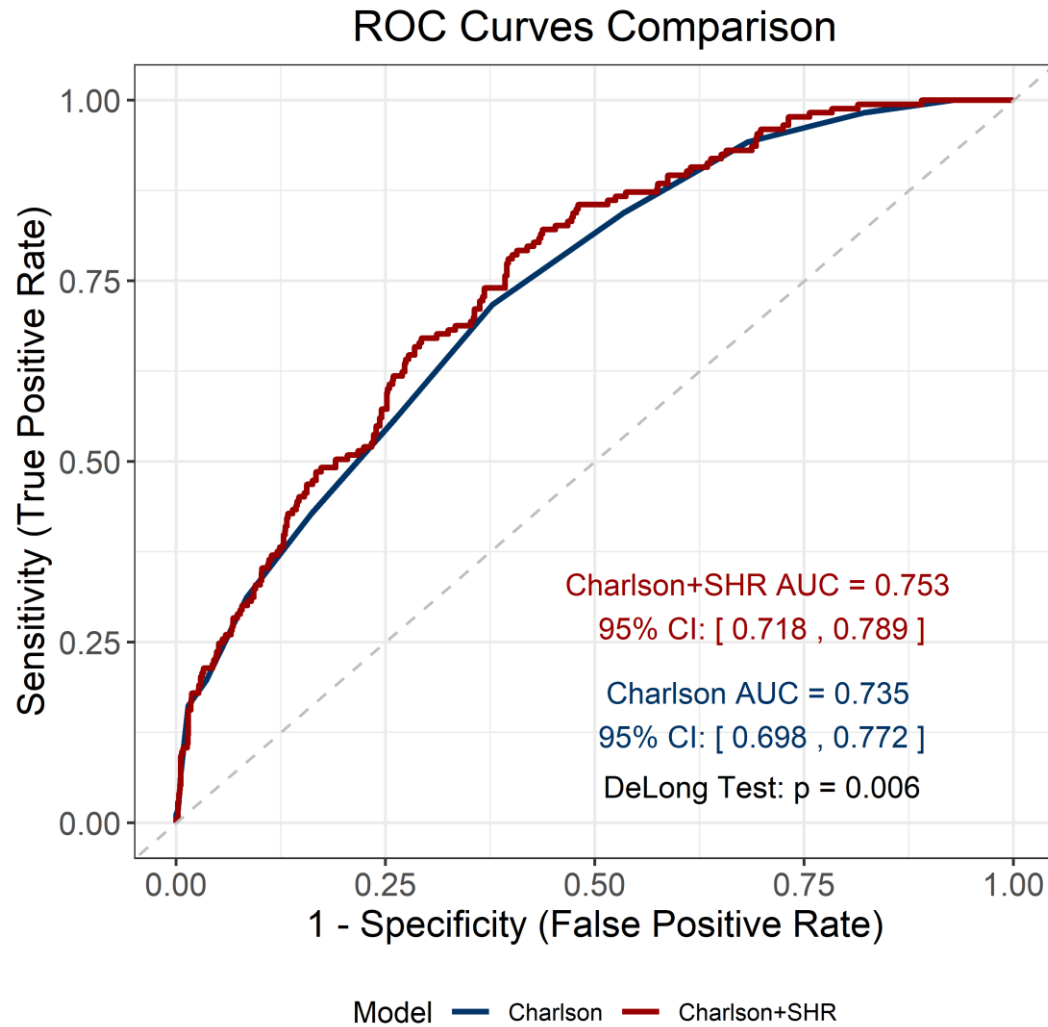


Figure S20. ROC curves of Charlson Index with/without SHR. SHR improved Charlson (AUC: 0.735→0.753, $P = 0.006$).

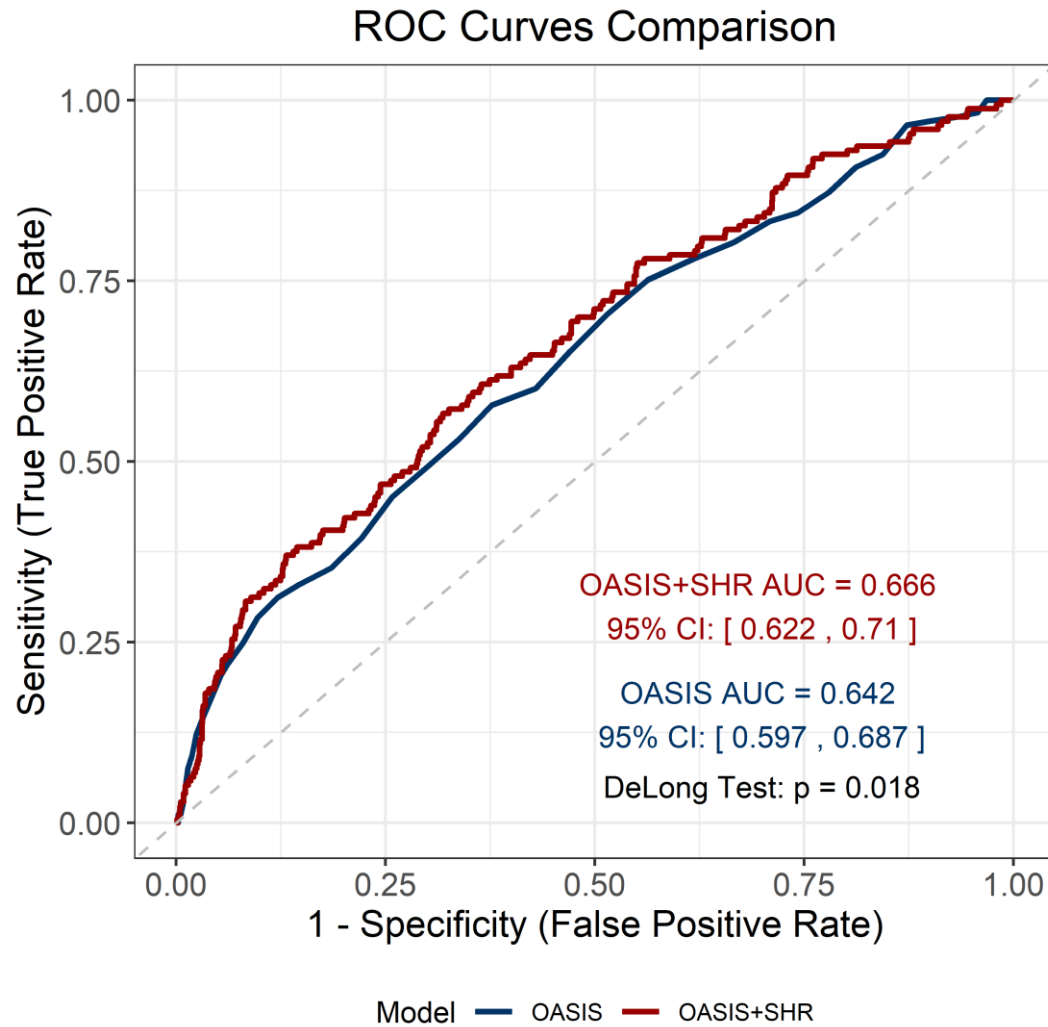


Figure S21. ROC curves of OASIS with/without SHR. SHR improved OASIS (AUC: 0.642→0.666, $P = 0.018$).

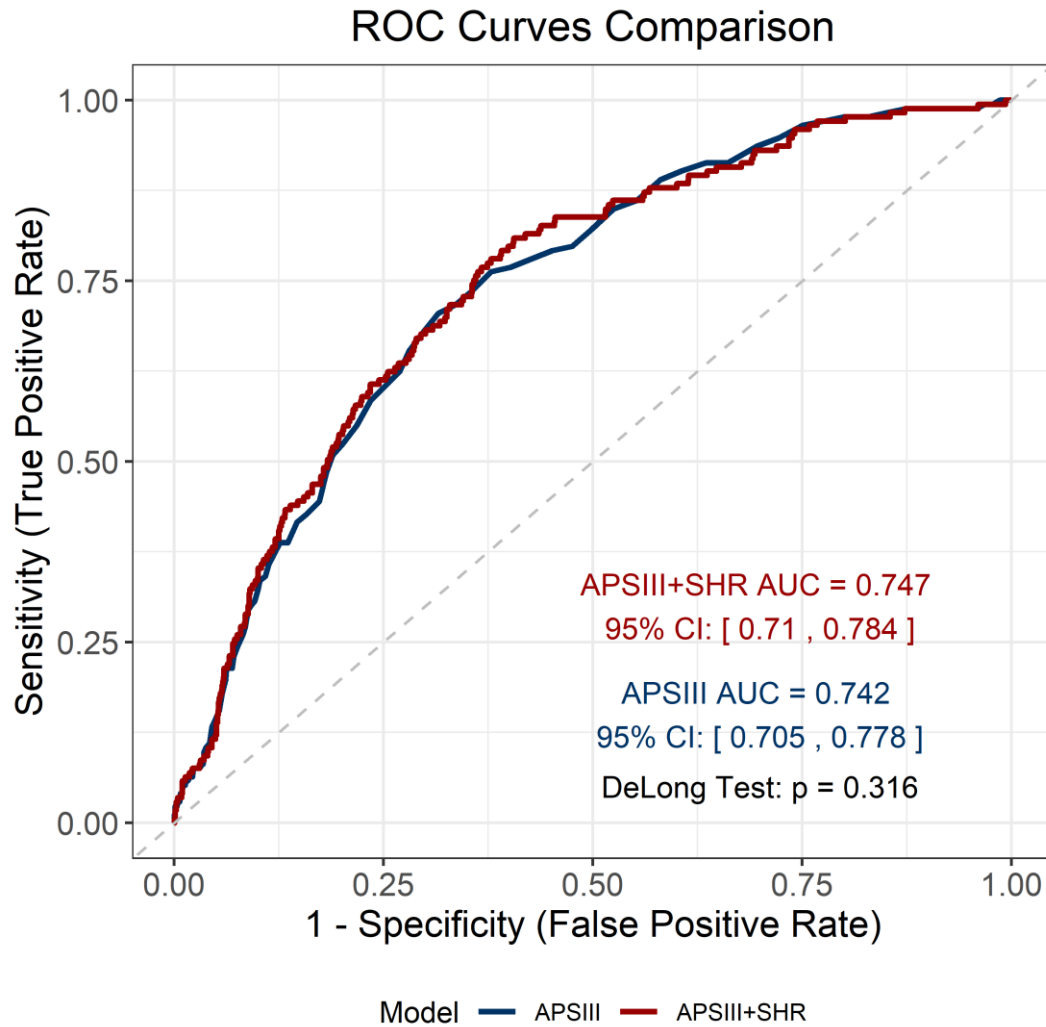


Figure S22. ROC curves of APS III with/without SHR. No significant improvement (AUC: 0.742→0.747, $P = 0.316$).

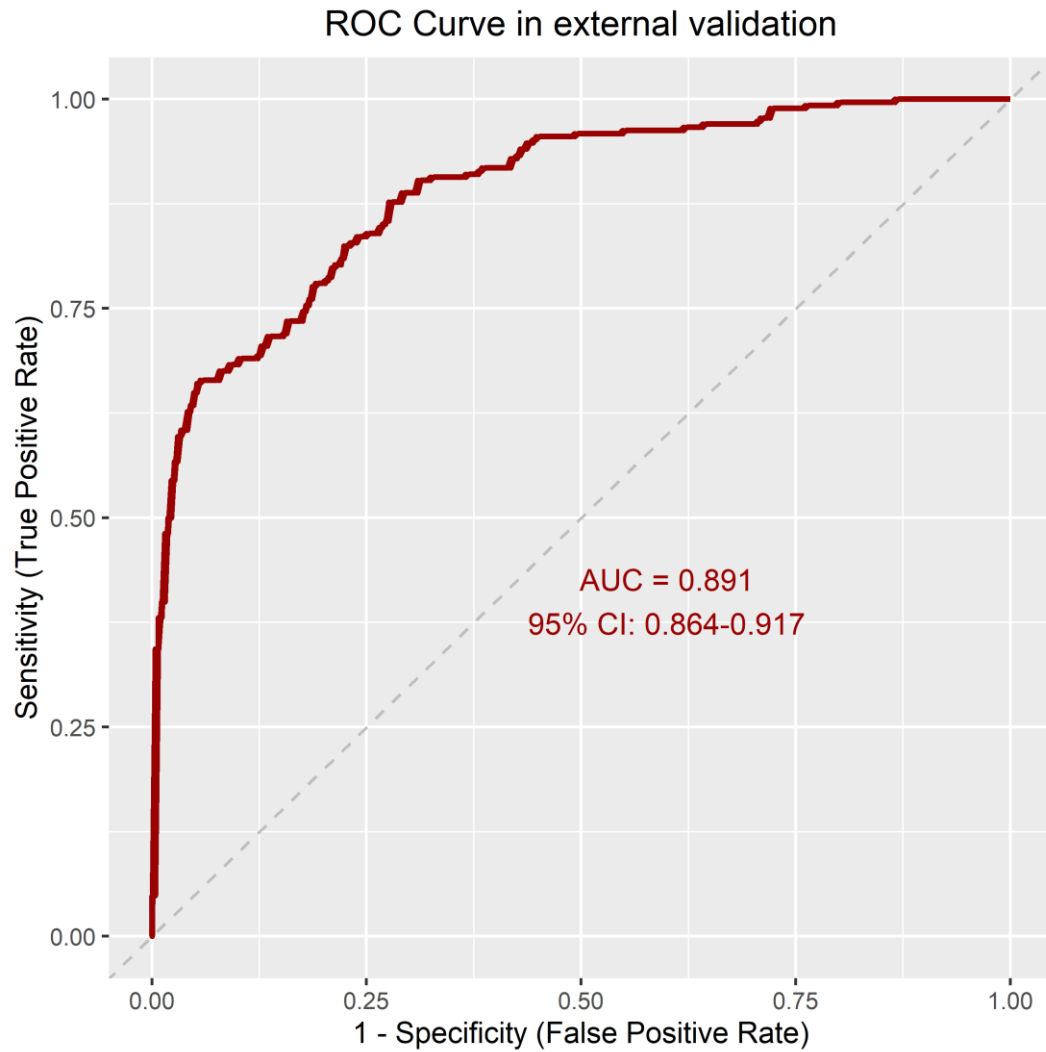


Figure S23. External validation ROC curve of the ensemble model. AUC of 0.891 (95% CI: 0.864–0.917).

Ensemble in external validation: slope=0.363

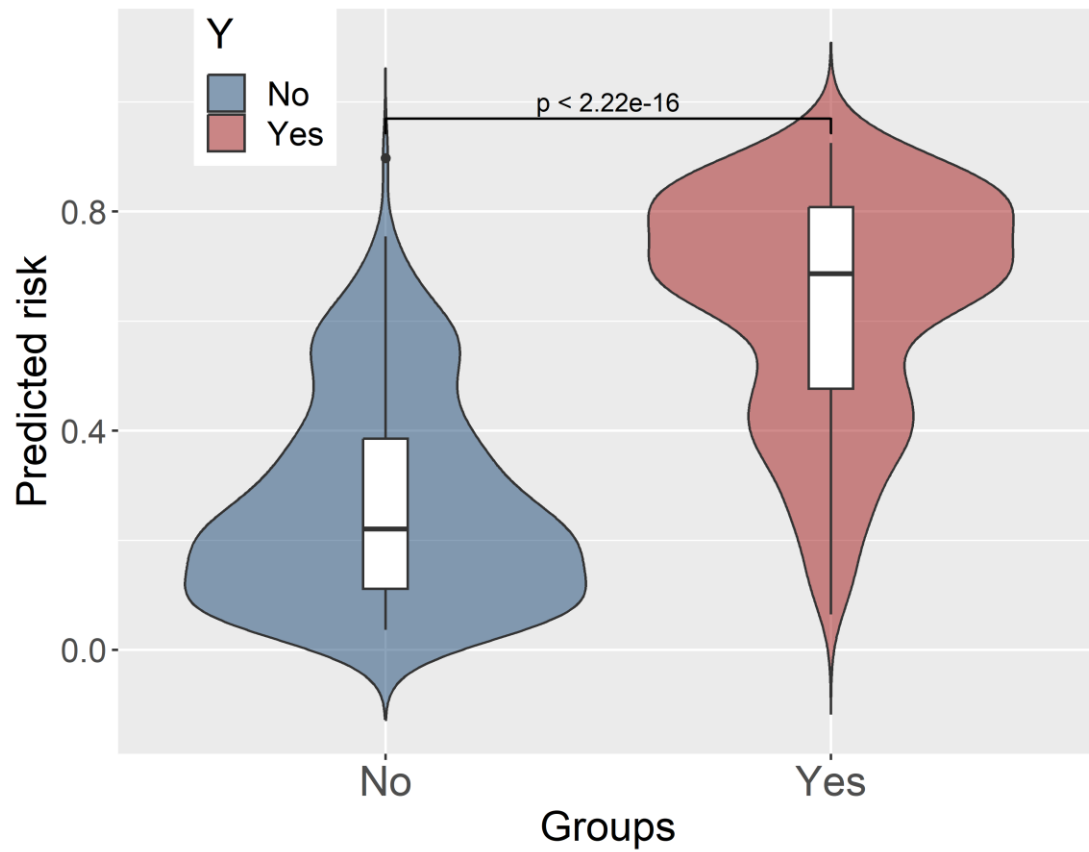


Figure S24. Discrimination slope in external validation. Slope of 0.363, consistent with derivation cohort.

Ensemble in external validation

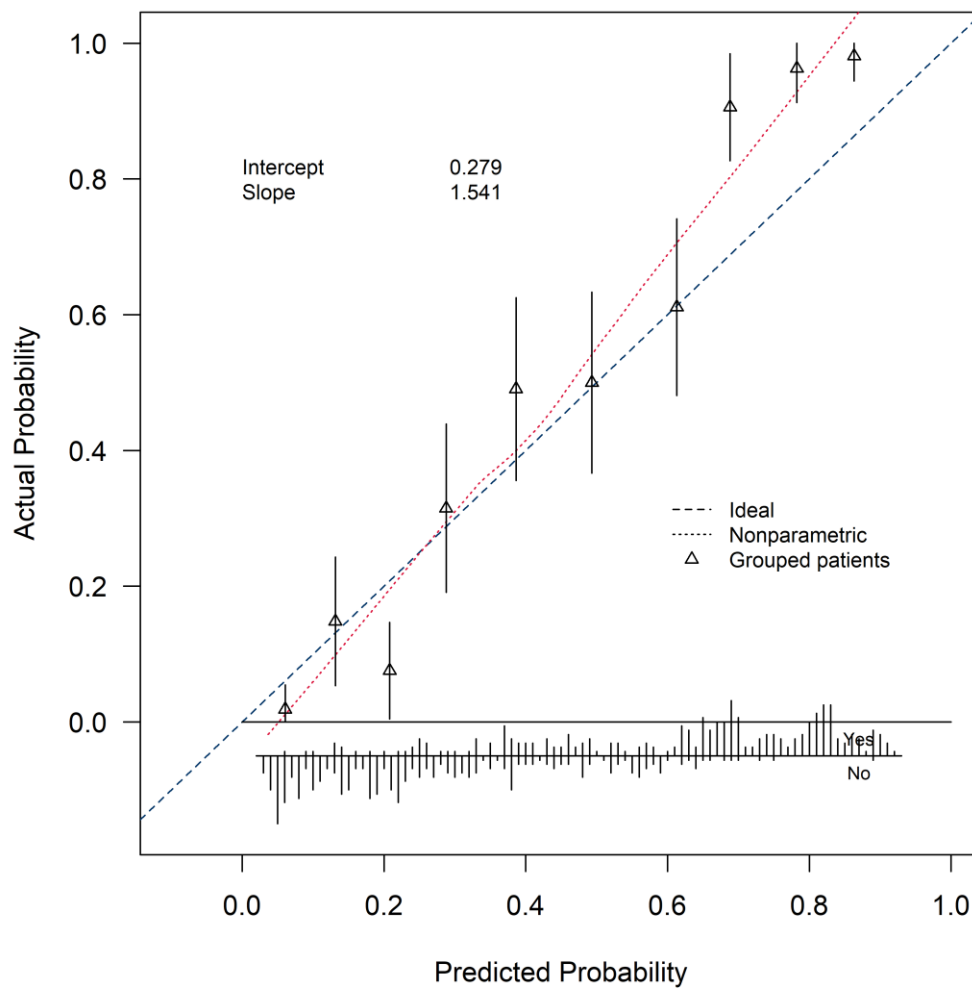


Figure S25. Calibration curve in external validation (Slope = 1.541, intercept = 0.279).

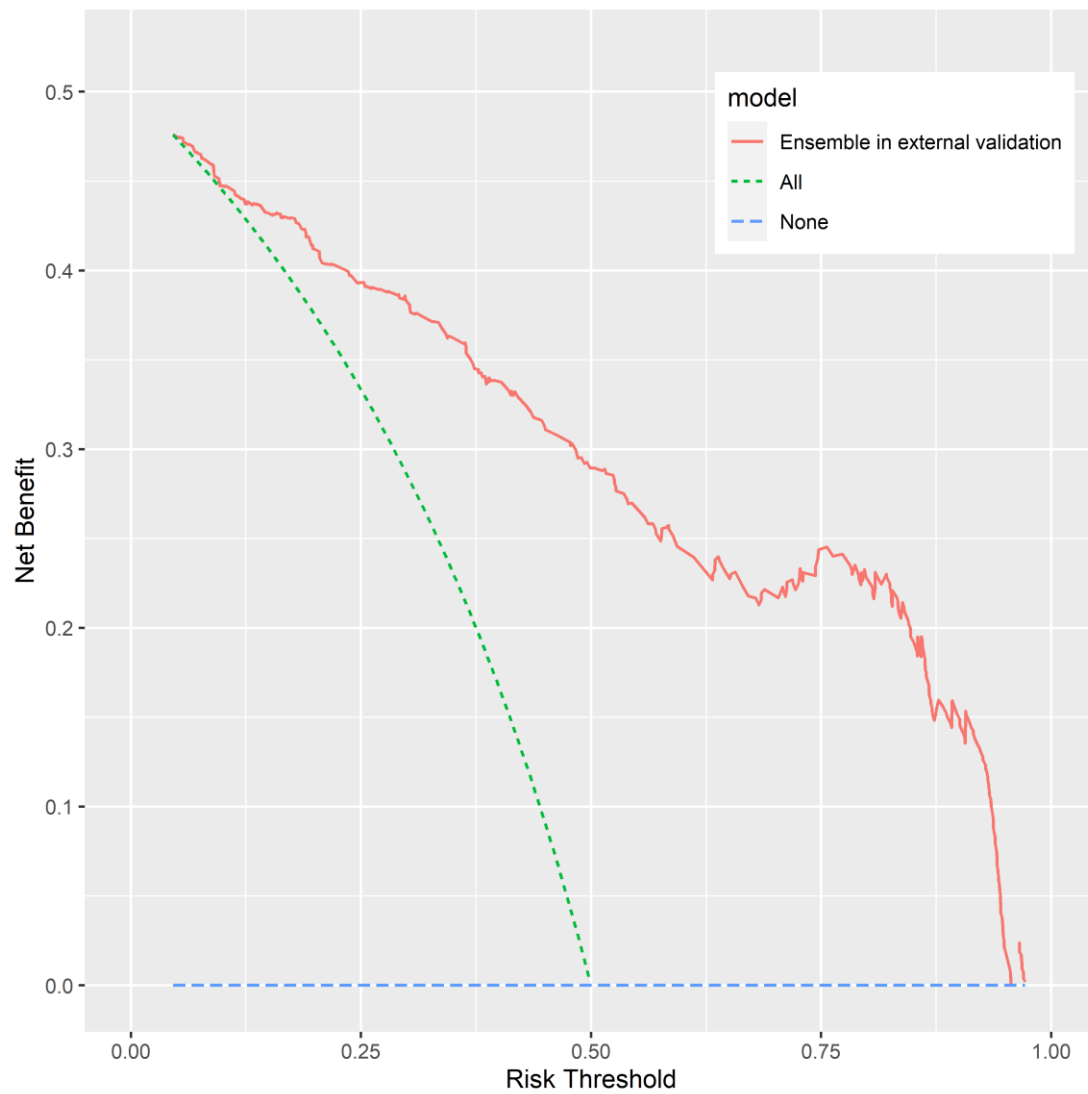


Figure S26. Decision curve analysis in external validation. Net benefit sustained across thresholds.

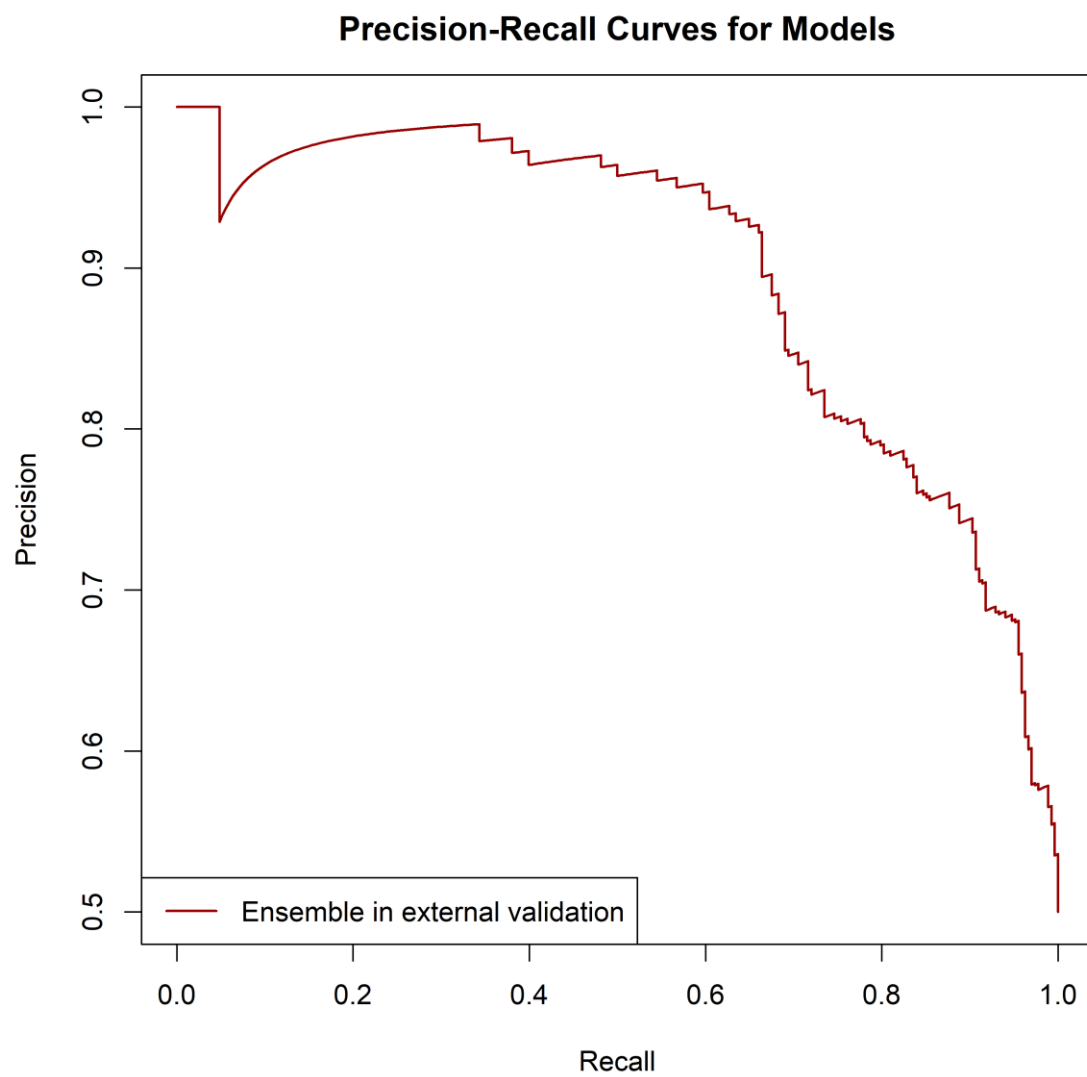


Figure S27. Precision-recall curve in external validation.

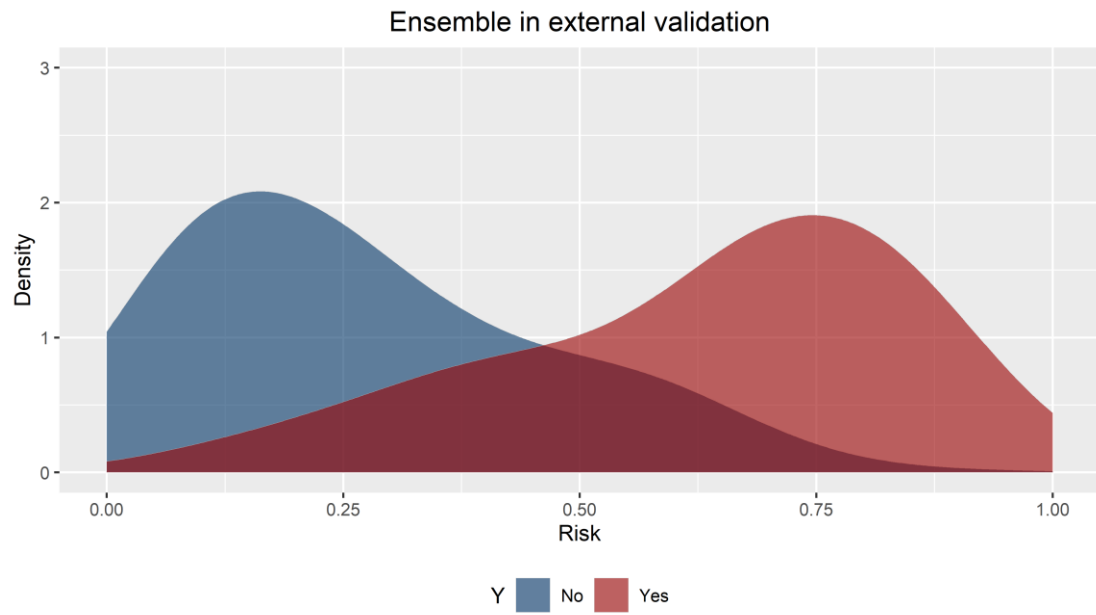


Figure S28. Probability density curves in external validation. Clear separation between outcome classes.

The formulas presented in this manuscript and their corresponding numbering

SHR was computed as:

$$SHR = \frac{\text{Admission blood glucose (mg/dL)}}{\text{Estimated average glucose (eAG) derived from HbA1c}} \quad (1)$$

where eAG was determined using the following formula:

$$eAG(\text{mg/dL}) = 28.7 \times \text{HbA1c}(\%) - 46.7 \quad (2)$$

The formulas for Brier score and log loss are outlined as follows:

$$\text{Brier Score} = \frac{1}{N} \sum_{i=1}^N (p_i - y_i)^2 \quad (3)$$

$$\text{Log loss} = -\frac{1}{N} \sum_{i=1}^N [y_i \log(p_i) + (1 - y_i) \log(1 - p_i)] \quad (4)$$

where N = Total number of samples, p_i = Predicted probability of the i -th sample belonging to the positive class ($0 \leq p_i \leq 1$), and y_i = True label of the i -th sample ($y_i \in \{0, 1\}$, where 0 = negative class and 1 = positive class). To avoid numerical instability when $p_i = 0$ or $p_i = 1$, apply probability smoothing (e.g., clip to $[\epsilon, 1-\epsilon]$).

In the ensemble model, particularly in the context of a Voting Classifier, the

formulation of the ensemble model can be expressed as follows:

$$\hat{y}_{ensemble} = \underset{c}{argmax} \sum_{i=1}^n w_i \hat{y}_{i,c} \quad (5)$$

where $\hat{y}_{ensemble}$ is the final prediction outcome of the ensemble model, c represents the class label, n is the number of base models participating in the voting process, w_i is the weight of the i -th base model (in the case of soft voting, the weights can be the probability predictions of the models), $\hat{y}_{i,c}$ denotes the predicted probability of the i -th base model for class c .

The SHAP value (ϕ_i) for the feature i is calculated as follows:

$$\phi_i = \sum_{S \subseteq F \setminus \{i\}} \frac{|S|! (|F| - |S| - 1)!}{|F|!} (f(S \cup \{i\}) - f(S)) \quad (6)$$

In this equation, F represents the complete set of features, while S denotes any subset of features that does not include i . The term $f(S)$ indicates the model's prediction based solely on the features in subset S , and $|S|$ indicates the factorial of the size of subset size, ensuring equitable treatment of permutations in weight assignments.