

Table S1. Univariate analysis of 36 potential predictors for ICU admission in training set.

Variables	Overall (n=1070)	Patients admitted ICU (n=778)	not into admitted ICU (n=292)	P value
CTD type				
Polymyositis / Dermatomyositis (%)	318 (29.7)	217 (27.9)	101 (34.6)	0.039
Sjogren syndrome (%)	174 (16.3)	148 (19.0)	26 (8.9)	<0.001
Comorbidities				
cancer (%)	43 (4.0)	25 (3.2)	18 (6.2)	0.044
congestive heart failure (%)	113 (10.6)	61 (7.8)	52 (17.8)	<0.001
cerebrovascular disease (%)	40 (3.7)	22 (2.8)	18 (6.2)	0.017
diabetes (%)	140 (13.1)	88 (11.3)	52 (17.8)	0.007
COPD (%)	107 (10.0)	52 (6.7)	55 (18.8)	<0.001
Vital signs				
confusion (%)	32 (3.0)	7 (0.9)	25 (8.6)	<0.001
Diastolic blood pressure (mmHg)	76 (68, 85)	77 (69, 85)	74 (66, 83)	0.006
Systolic blood pressure (mmHg)	120 (108, 133)	121 (109, 134)	116 (105, 130)	0.004
Respiratory rate (breath/min)	22 (20, 29)	21 (20, 28)	24 (20, 30)	<0.001
Heart rate (beat/min)	90 (80, 102)	89 (79, 100)	97 (85, 109)	<0.001
Temperature (°C)	36.9 (36.5, 38.6)	36.9 (36.5, 38.5)	37.0 (36.5, 38.8)	0.047
Laboratory examinations				
Positive G test (%)	229 (21.4)	109 (14.0)	120 (41.1)	<0.001
Positive GM test (%)	28 (2.6)	8 (1.0)	20 (6.8)	<0.001
pH	7.41 (7.38, 7.44)	7.41 (7.39, 7.44)	7.40 (7.36, 7.43)	<0.001
BUN (mmol/L)	6.9 (4.5, 10.7)	6.6 (4.5, 10.5)	7.8 (4.6, 11.1)	0.009
sodium (mmol/L)	137.5 (133.8, 140.4)	138.1 (135.2, 140.6)	134.3 (130.4, 139.0)	<0.001
glucose (mmol/L)	7.15 (4.70, 10.77)	5.84 (4.63, 10.70)	10.00 (5.58, 11.00)	<0.001
hematocrit (L/L)	0.36 (0.31, 0.40)	0.37 (0.33, 0.41)	0.33 (0.27, 0.37)	<0.001
PF ratio	206 (168, 280)	210 (174, 311)	203 (150, 240)	<0.001
hemoglobin (g/L)	115 (102, 127)	118 (105, 129)	107 (100, 118)	<0.001
platelet ( $\times 10^9$ /L)	182 (132, 244)	190 (144, 249)	162 (115, 218)	<0.001
neutrophil ( $\times 10^9$ /L)	7.47 (4.94, 11.00)	7.02 (4.80, 10.72)	10.08 (5.43, 11.64)	<0.001
lymphocyte ( $\times 10^9$ /L)	0.99 (0.60, 1.46)	1.09 (0.77, 1.56)	0.58 (0.30, 0.99)	<0.001
ALT (U/L)	23 (14, 50)	21 (13, 44)	27 (15, 109)	<0.001

AST (U/L)	24 (18, 47)	23 (17, 40)	31 (20, 108)	<0.001
albumin (g/L)	33.9 (28.6, 38.8)	35.0 (30.4, 39.4)	29.5 (25.6, 35.5)	<0.001
HDL C (mmol/L)	1.01 (0.74, 1.33)	1.06 (0.78, 1.37)	0.84 (0.55, 1.18)	<0.001
LDH (U/L)	247 (191, 363)	234 (184, 318)	321 (221, 550)	<0.001
NT-proBNP (ng/L)	398 (156, 917)	309 (131, 593)	1056 (357, 1537)	<0.001
CRP (mg/L)	30.00 (10.50, 88.75)	24.50 (8.99, 74.00)	51.85 (15.17, 121.00)	<0.001
D dimer (mg/L)	1.79 (0.75, 4.92)	1.54 (0.62, 3.74)	7.44 (1.07, 10.45)	<0.001
CD4+ T cell (cell/ $\mu$ L)	344 (198, 529)	428 (265, 583)	153 (72, 301)	<0.001
CD8+ T cell (cell/ $\mu$ L)	252 (132, 386)	270 (157, 403)	204 (100, 339)	<0.001
pleural effusion (%)	386 (36.1)	244 (31.4)	142 (48.6)	<0.001

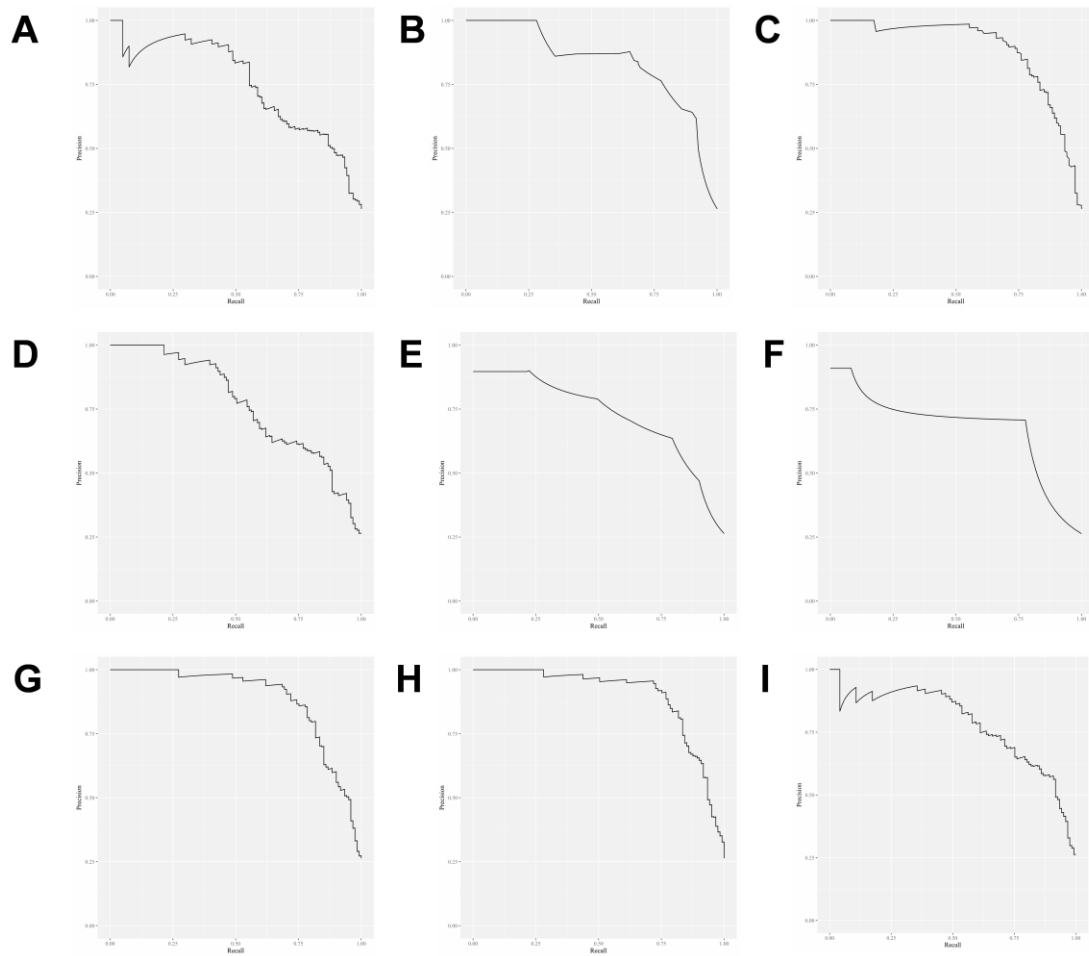
Data are shown as median with interquartile range (IQR) for continuous variables and number with percentage for categorical variables.

ICU: intensive care unit; CTD: connective tissue disease; COPD: chronic obstructive pulmonary disease; G test: serum (1,3)- $\beta$ -D-glucan test; GM test: serum Aspergillus galactomannan test; BUN: blood urea nitrogen; PF ratio: the ratio of arterial oxygen partial pressure (mmHg) to fractional inspired oxygen; ALT: alanine aminotransferase; AST: aspartate aminotransferase; HDL-C: High density lipoprotein cholesterol; LDH: lactate dehydrogenase; NT-proBNP: N-terminal pro-B-type natriuretic peptide; CRP: C-reactive protein;

Table S2. the predictors identified by Lasso regression and Boruta algorithm.

Feature selection methods	Features
Lasso regression	NT-proBNP, CD4+T cell, lymphocyte, CRP, positive G test, sodium, PF ratio, neutrophil, Heart rate, COPD, glucose, pH, HDL-C, albumin, platelet, confusion, PaCO <sub>2</sub> , monocyte, LDL-C, potassium, AT III, globulin, Sjogren syndrome, cancer, cerebrovascular disease, pleural effusion, Respiratory rate, Hemoglobin, Procalcitonin, Mixed connective tissue disease, congestive heart failure, Diastolic blood pressure, PT
Boruta algorithm	NT-proBNP, CD4+T cell, lymphocyte, CRP, positive G test, sodium, PF ratio, neutrophil, HR, COPD, glucose, pH, HDL-C, albumin, platelet, confusion, PaCO <sub>2</sub> , monocyte, LDL.C, potassium, AT III, globulin, positive GM test, hematocrit, bilirubin, ALT, AST, LDH, myoglobin, APTT, fibrinogen, D-dimer

NT-proBNP: N-terminal pro-B-type natriuretic peptide; CRP: C-reactive protein; G test: serum (1,3)- $\beta$ -D-glucan test; PF ratio: the ratio of arterial oxygen partial pressure (mmHg) to fractional inspired oxygen; COPD: chronic obstructive pulmonary disease; HDL-C: High density lipoprotein cholesterol; AT III: antithrombin III; PT: prothrombin time; GM test: serum *Aspergillus* galactomannan test; ALT: alanine aminotransferase; AST: aspartate aminotransferase; LDH: lactate dehydrogenase; APTT: activated partial thromboplastin time;

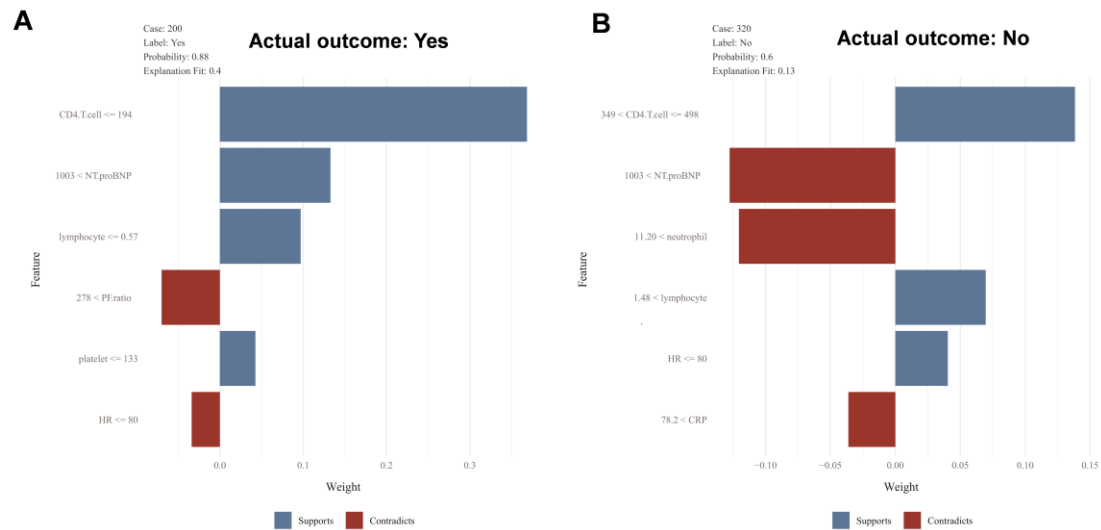


**Figure S1. The precision-recall (PR) curves and the areas under the curves of nine models. A.** LR model (0.751). **B.** CART model (0.834). **C.** RF model (0.887). **D.** SVM model (0.766). **E.** KNN model (0.726). **F.** DT model (0.676). **G.** GBM model (0.885). **H.** XGBoost model (0.897). **I.** NB model (0.783). LR: logistic regression; CART: classification and regression tree; RF: random forest; SVM: support vector machine; KNN: k-nearest neighbors; DT: decision tree; GBM: gradient boosting machine; XGBoost: eXtreme gradient boosting; NB: naive bayes.

Table S3. Comparison of AUCs for machine learning-based models in the testing set using up-sampling, down-sampling and SMOTE.

Model	Original AUC	AUC of down-sampling model	AUC of up-sampling model	AUC of SMOTE model
LR	0.871	0.870	0.871	0.871
CART	0.911	0.879	0.876	0.864
RF	0.934	0.929	0.935	0.932
SVM	0.868	0.887	0.884	0.887
KNN	0.865	0.848	0.834	0.852
DT	0.834	0.834	0.821	0.828
GBM	0.931	0.920	0.935	0.922
XGBoost	0.941	0.922	0.921	0.937
NB	0.896	0.844	0.911	0.900

AUC: area under the receiver operating characteristic curve; SMOTE: synthetic minority oversampling technique; LR: logistic regression; CART: classification and regression tree; RF: random forest; SVM: support vector machine; KNN: k-nearest neighbors; DT: decision tree; GBM: gradient boosting machine; XGBoost: eXtreme gradient boosting; NB: naive bayes;



**Figure S2. LIME algorithm for explaining individual's prediction results.** **A.** a case of patient actually admitted into ICU (the expected probability of ICU admission was 88% according to the XGBoost model). **B.** a case of patient actually not admitted into ICU (The expected probability of no ICU admission was 60% according to prediction model). It showed the top 6 variables that had the greatest impact on outcomes. The length of the bar for each feature is related to the weight of that feature in the prediction. A longer bar represents a characteristic that contributes more to predict results.