

Supplementary Table 1 Comparison of microorganisms causing species between groups of survivors and non-survivors in training group.

Variable [n (%)]	Total (n=284)	Survivors (n=177)	Non-survivors (n=107)	P value
Gram positive	159 (55.99)	100 (56.50)	59 (55.14)	0.82
Staphylococcus	102 (35.92)	66 (37.29)	36 (33.64)	0.54
Staphylococcus aureus	34 (11.97)	18 (10.17)	16 (14.95)	0.23
Methicillin-resistant staphylococcus	20 (7.04)	12 (6.78)	8 (7.48)	0.82
Coagulase negative staphylococcus	74 (26.06)	50 (28.25)	24 (22.43)	0.28
Staphylococcus epidermidis	29 (10.21)	18 (10.17)	11 (10.28)	0.98
Staphylococcus hominis	24 (8.45)	18 (10.17)	6 (5.61)	0.18
Staphylococcus capitis	12 (4.23)	9 (5.08)	3 (2.80)	0.53
Other coagulase negative staphylococci	19 (6.69)	10 (5.65)	9 (8.41)	0.37
Enterococcus	54 (19.01)	27 (15.25)	27 (25.23)	0.04
Enterococcus faecalis	16 (5.63)	9 (5.08)	7 (6.54)	0.61
Enterococcus faecium	35 (12.32)	16 (9.04)	19 (17.76)	0.03
Other enterococcus	4 (1.41)	3 (1.69)	1 (0.93)	0.99
Streptococcus	23 (8.10)	18 (10.17)	5 (4.67)	0.10
Corynebacterium	12 (4.23)	7 (3.95)	5 (4.67)	>0.99
Other Gram positive	5 (1.76)	4 (2.26)	1 (0.93)	0.72
Gram negative	177 (62.32)	110 (62.15)	67 (62.62)	0.94
Enterobacteriaceae	133 (46.83)	87 (49.15)	46 (42.99)	0.31
Escherichia coli	68 (23.94)	52 (29.38)	16 (14.95)	0.006
Klebsiella	69 (24.30)	37 (20.90)	32 (29.91)	0.09
Klebsiella pneumoniae	64 (22.54)	34 (19.21)	30 (28.04)	0.08
Other Klebsiella	9 (3.17)	5 (2.82)	4 (3.74)	0.94
Other Enterobacteriaceae	13 (4.58)	8 (4.52)	5 (4.67)	1.00
Proteus	11 (3.87)	7 (3.95)	4 (3.74)	1.00
pseudomonas aeruginosa	43 (15.14)	19 (10.73)	24 (22.43)	0.008
Stenotrophomonas maltophilia	57 (20.07)	23 (12.99)	34 (31.78)	<0.001
Acinetobacter baumannii	22 (7.75)	8 (4.52)	14 (13.08)	0.009
Burkholderia cepacia	18 (6.34)	8 (4.52)	10 (9.35)	0.11
Haemophilus influenzae	8 (2.82)	5 (2.82)	3 (2.80)	1.00
Vibrio	6 (2.11)	6 (3.39)	0 (0.00)	0.13
Other Gram negative	28 (9.86)	17 (9.60)	11 (10.28)	0.85
virus	22 (7.75)	13 (7.34)	9 (8.41)	0.75
Fungus	100 (35.21)	57 (32.20)	43 (40.19)	0.17
Candida albicans	72 (25.35)	44 (24.86)	28 (26.17)	0.81
Non-candida albicans	48 (16.90)	22 (12.43)	26 (24.30)	0.01
Mixed infection (≥ 2) ^a	134 (47.18)	76 (42.94)	58 (54.21)	0.07
Mixed infection (≥ 3) ^b	101 (35.56)	53 (29.94)	48 (44.86)	0.01

Pathogenic bacteria resistant to initial antibiotics	52 (18.31)	25 (14.12)	27 (25.23)	0.02
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Notes: The time point for the biological indicators was on day of sepsis diagnosis. Bold, indicates $p < 0.05$.

^a Mixed infection refers to the presence of ≥ 2 different pathogens during the same hospitalization.

^b Mixed infection refers to the presence of ≥ 3 different pathogens during the same hospitalization.

Supplementary Table 2 Comparison of clinical outcomes between Survived and Non-Survived.

Outcomes	Total (n = 407)	Survivors (n = 255)	Non-survivors (n = 152)	p-value
ICU stay duration, days (IQR)	7.00 (3.00, 16.75)	6.00 (3.00, 12.00)	9.00 (3.00, 24.25)	0.03
Hospital stay duration, days (IQR)	16.00 (9.00, 30.00)	17.00 (11.00, 28.50)	12.00 (3.75, 35.00)	0.006
Survival time, days (IQR)	123.00 (17.00, 427.00)	326.00 (148.50, 715.50)	10.00 (3.00, 28.25)	<0.001
Total hospitalization costs (IQR)	47124.38 (23535.36, 120155.35)	39695.66 (22538.85, 86195.68)	82583.67 (26791.85, 175694.80)	<0.001
Average hospitalization costs (IQR)	3046.38 (2110.98, 5350.63)	2373.78 (1833.10, 3233.37)	5746.19 (3863.17, 9196.96)	<0.001
ICU stay after sepsis, days (IQR)	7.50 (3.00, 17.00)	7.00 (3.00, 12.75)	9.00 (3.00, 26.00)	0.02
Hospital stay after sepsis, days (IQR)	15.00 (8.00, 28.00)	16.00 (11.00, 27.00)	10.50 (3.00, 29.00)	<0.001

Notes: Bold, indicates $p < 0.05$.

ICU, Intensive Care Unit; IQR, Interquartile Range.

Supplementary Figure 1 LASSO regression for feature selection and model tuning. (A) LASSO coefficient profiles for each predictor as a function of the logarithm of the regularization parameter ($\log(\lambda)$). As λ increases, the coefficients of less important features progressively shrink toward zero and are ultimately excluded from the model, illustrating the feature selection mechanism of LASSO. (B) Ten-fold cross-validation curve used to select the optimal λ for the LASSO model. The vertical axis represents binomial deviance, and the horizontal axis displays $\log(\lambda)$. The dotted red line indicates $\lambda_{\min}$, corresponding to the minimum mean binomial deviance (optimal model fit), while the dotted blue line shows λ_{1se} , representing the most regularized model within one standard error of the minimum. LASSO, least absolute shrinkage and selection operator; λ , regularization parameter; $\lambda_{\min}$, minimum lambda; λ_{1se} , lambda at one standard error.

