Additional file 1: Supplementary Tables

Table S1. Complete distribution of bacterial isolates by specimen source and MDR status

Bacteria	Total (n = 191)	MDR (n = 125)	Non-MDR (n = 66)	χ^2	*P* value
Gram-positive bacteria	80 (41.9%)	58 (46.4%)	22 (33.3%)	3.030	0.082
Enterococcus faecium	32 (16.8%)	28 (22.4%)	4 (6.1%)	8.269	0.004
Staphylococcus hominis	7 (3.7%)	5 (4.0%)	2 (3.0%)	0.000	1.000
Staphylococcus aureus	6 (3.1%)	4 (3.2%)	2 (3.0%)	0.000	1.000
Staphylococcus haemolyticus	5 (2.6%)	3 (2.4%)	2 (3.0%)	0.000	1.000
MRSA	5 (2.6%)	5 (4.0%)	0 (0.0%)	1.369	0.242
MRSE	4 (2.1%)	2 (1.6%)	2 (3.0%)	0.016	0.900
Corynebacterium species	3 (1.6%)	2 (1.6%)	1 (1.5%)	0.000	1.000
Bacillus cereus	2 (1.0%)	1 (0.8%)	1 (1.5%)	-	0.545
Micrococcus luteus	2 (1.0%)	0 (0.0%)	2 (3.0%)	-	0.118
Enterococcus faecalis	2 (1.0%)	2 (1.6%)	0 (0.0%)	-	0.545
Enterococcus casseliflavus	2 (1.0%)	1 (0.8%)	1 (1.5%)	-	0.545
Clostridium species	1 (0.5%)	0 (0.0%)	1 (1.5%)	-	0.346
Enterococcus gallinarum	1 (0.5%)	1 (0.8%)	0 (0.0%)	-	1.000
Staphylococcus epidermidis	1 (0.5%)	0 (0.0%)	1 (1.5%)	-	0.346
Bacillus subtilis	1 (0.5%)	0 (0.0%)	1 (1.5%)	-	0.346
Streptococcus mitis group	1 (0.5%)	1 (0.8%)	0 (0.0%)	-	1.000
Streptococcus bovis	1 (0.5%)	1 (0.8%)	0 (0.0%)	-	1.000
Weissella species	1 (0.5%)	1 (0.8%)	0 (0.0%)	-	1.000
Streptococcus pneumoniae	1 (0.5%)	1 (0.8%)	0 (0.0%)	-	1.000
Micrococcus species	1 (0.5%)	0 (0.0%)	1 (1.5%)	-	0.346
Nocardia species	1 (0.5%)	0 (0.0%)	1 (1.5%)	-	0.346
Gram-negative bacteria	111 (58.1%)	67 (53.6%)	44 (66.7%)	3.030	0.082
Escherichia coli	39 (20.4%)	33 (26.4%)	6 (9.1%)	7.964	0.005
Klebsiella pneumoniae	31 (16.2%)	16 (12.8%)	15 (22.7%)	3.131	0.077
Acinetobacter baumannii	10 (5.2%)	9 (7.2%)	1 (1.5%)	1.784	0.182
Stenotrophomonas maltophilia	8 (4.2%)	0 (0.0%)	8 (12.1%)	12.938	<0.001
Haemophilus influenzae	7 (3.7%)	2 (1.6%)	5 (7.6%)	2.840	0.092
Enterobacter cloacae	3 (1.6%)	1 (0.8%)	2 (3.0%)	0.322	0.571
Bacteroides fragilis	2 (1.0%)	0 (0.0%)	2 (3.0%)	-	0.118
Pseudomonas aeruginosa	2 (1.0%)	1 (0.8%)	1 (1.5%)	-	0.545
Salmonella dublin	1 (0.5%)	1 (0.8%)	0 (0.0%)	-	1.000
Burkholderia pickettii	1 (0.5%)	0 (0.0%)	1 (1.5%)	-	0.346
Acinetobacter lwoffii	1 (0.5%)	0 (0.0%)	1 (1.5%)	-	0.346
Morganella species	1 (0.5%)	1 (0.8%)	0 (0.0%)	-	1.000
Serratia marcescens	1 (0.5%)	1 (0.8%)	0 (0.0%)	-	1.000
Aeromonas hydrophila	1 (0.5%)	0 (0.0%)	1 (1.5%)	-	0.346

Proteus mirabilis	1 (0.5%)	1 (0.8%)	0 (0.0%)	-	1.000
Alcaligenes species	1 (0.5%)	0 (0.0%)	1 (1.5%)	-	0.346
Citrobacter freundii	1 (0.5%)	1 (0.8%)	0 (0.0%)	-	1.000

Data are presented as n (%). MDR, multidrug-resistant; MRSA, methicillin-resistant Staphylococcus aureus; MRSE, methicillin-resistant Staphylococcus epidermidis; χ^2, chi-square test. Categorical variables were compared using the chi-square test with Yates' continuity correction for 2×2 tables, or Fisher's exact test when expected frequencies were < 5. "-" indicates that the chi-square test was not applicable.

Table S2. Complete antimicrobial susceptibility and resistance profiles of MDR and non-MDR isolates

Table S2 (A). Overall bacteria (n = 191)

Antimicrobial agent	Overall (n = 191)	MDR (n = 125)	Non-MDR (n = 66)	χ^2	*P* value
Ampicillin	137 (71.7%)	101 (80.8%)	36 (54.5%)	13.424	<0.001
Ciprofloxacin	105 (55.0%)	99 (79.2%)	6 (9.1%)	82.963	<0.001
Trimethoprim/sulfamethoxazole	91 (47.6%)	89 (71.2%)	2 (3.0%)	77.765	<0.001
Levofloxacin	91 (47.6%)	86 (68.8%)	5 (7.6%)	62.484	<0.001
Gentamicin	86 (45.0%)	77 (61.6%)	9 (13.6%)	40.144	<0.001
Erythromycin	64 (33.5%)	55 (44.0%)	9 (13.6%)	17.874	<0.001
Cefazolin	62 (32.5%)	50 (40.0%)	12 (18.2%)	9.379	0.002
Ceftriaxone	60 (31.4%)	49 (39.2%)	11 (16.7%)	10.179	0.001
Ampicillin/sulbactam	55 (28.8%)	41 (32.8%)	14 (21.2%)	2.292	0.130
Cefepime	54 (28.3%)	50 (40.0%)	4 (6.1%)	24.535	<0.001
Penicillin	51 (26.7%)	45 (36.0%)	6 (9.1%)	15.980	<0.001
Ceftazidime	50 (26.2%)	36 (28.8%)	14 (21.2%)	1.287	0.257
Tetracycline	49 (25.7%)	49 (39.2%)	0 (0.0%)	34.800	<0.001
Cefotaxime	47 (24.6%)	31 (24.8%)	16 (24.2%)	0.007	0.932
Clindamycin	41 (21.5%)	39 (31.2%)	2 (3.0%)	18.686	<0.001
Amoxicillin/clavulanic acid	40 (20.9%)	29 (23.2%)	11 (16.7%)	1.114	0.291
Piperacillin	35 (18.3%)	33 (26.4%)	2 (3.0%)	15.762	<0.001
Tobramycin	33 (17.3%)	24 (19.2%)	9 (13.6%)	0.935	0.333
Aztreonam	33 (17.3%)	22 (17.6%)	11 (16.7%)	0.026	0.871
Cefuroxime	27 (14.1%)	22 (17.6%)	5 (7.6%)	3.576	0.059
Cefoxitin	26 (13.6%)	22 (17.6%)	4 (6.1%)	4.891	0.027
Imipenem	26 (13.6%)	14 (11.2%)	12 (18.2%)	1.246	0.264
Rifampicin	25 (13.1%)	25 (20.0%)	0 (0.0%)	15.188	<0.001
Amikacin	23 (12.0%)	11 (8.8%)	12 (18.2%)	3.589	0.058
Meropenem	21 (11.0%)	12 (9.6%)	9 (13.6%)	0.719	0.396
Oxacillin	19 (9.9%)	15 (12.0%)	4 (6.1%)	1.102	0.294
Moxifloxacin	17 (8.9%)	15 (12.0%)	2 (3.0%)	4.286	0.038
Streptomycin	16 (8.4%)	16 (12.8%)	0 (0.0%)	9.220	0.002
Ertapenem	16 (8.4%)	8 (6.4%)	8 (12.1%)	1.842	0.175
Quinupristin/dalfopristin	9 (4.7%)	9 (7.2%)	0 (0.0%)	-	0.031
Gatifloxacin	8 (4.2%)	8 (6.4%)	0 (0.0%)	2.958	0.085
Ticarcillin/clavulanic acid	7 (3.7%)	7 (5.6%)	0 (0.0%)	2.414	0.120
Chloramphenicol	5 (2.6%)	5 (4.0%)	0 (0.0%)	1.369	0.242
Piperacillin/tazobactam	5 (2.6%)	5 (4.0%)	0 (0.0%)	1.369	0.242
Vancomycin	4 (2.1%)	3 (2.4%)	1 (1.5%)	0.016	0.900
Nitrofurantoin	4 (2.1%)	4 (3.2%)	0 (0.0%)	0.879	0.349
Lomefloxacin	3 (1.6%)	3 (2.4%)	0 (0.0%)	0.431	0.511

Linezolid	2 (1.0%)	2 (1.6%)	0 (0.0%)	-	0.545
Latamoxef	2 (1.0%)	2 (1.6%)	0 (0.0%)	-	0.545
Minocycline	2 (1.0%)	2 (1.6%)	0 (0.0%)	-	0.545
Cefoperazone/sulbactam	2 (1.0%)	2 (1.6%)	0 (0.0%)	-	0.545
Fusidic acid	2 (1.0%)	2 (1.6%)	0 (0.0%)	-	0.545
Trimethoprim	2 (1.0%)	2 (1.6%)	0 (0.0%)	-	0.545

Table S2 (B). Gram-positive bacteria (n = 80)

Antimicrobial agent	Overall (n = 80)	MDR (n = 58)	Non-MDR (n = 22)	χ^2	*P* value
Erythromycin	64 (80.0%)	55 (94.8%)	9 (40.9%)	25.709	<0.001
Ampicillin	50 (62.5%)	45 (77.6%)	5 (22.7%)	18.207	<0.001
Penicillin	49 (61.3%)	45 (77.6%)	4 (18.2%)	23.715	<0.001
Ciprofloxacin	45 (56.3%)	43 (74.1%)	2 (9.1%)	27.423	<0.001
Clindamycin	41 (51.3%)	39 (67.2%)	2 (9.1%)	19.317	<0.001
Levofloxacin	39 (48.8%)	37 (63.8%)	2 (9.1%)	16.971	<0.001
Gentamicin	36 (45.0%)	36 (62.1%)	0 (0.0%)	24.828	<0.001
Trimethoprim/sulfamethoxazole	32 (40.0%)	30 (51.7%)	2 (9.1%)	10.336	0.001
Ceftriaxone	31 (38.8%)	29 (50.0%)	2 (9.1%)	11.247	<0.001
Rifampicin	25 (31.3%)	25 (43.1%)	0 (0.0%)	13.793	<0.001
Tetracycline	20 (25.0%)	20 (34.5%)	0 (0.0%)	10.115	0.001
Amoxicillin/clavulanic acid	20 (25.0%)	15 (25.9%)	5 (22.7%)	0.084	0.772
Oxacillin	19 (23.8%)	15 (25.9%)	4 (18.2%)	0.182	0.670
Streptomycin	16 (20.0%)	16 (27.6%)	0 (0.0%)	5.960	0.015
Ampicillin/sulbactam	10 (12.5%)	8 (13.8%)	2 (9.1%)	0.036	0.850
Quinupristin/dalfopristin	9 (11.3%)	9 (15.5%)	0 (0.0%)	-	0.098
Cefoxitin	7 (8.8%)	6 (10.3%)	1 (4.5%)	0.142	0.706
Cefazolin	6 (7.5%)	3 (5.2%)	3 (13.6%)	0.653	0.419
Cefotaxime	5 (6.3%)	3 (5.2%)	2 (9.1%)	0.017	0.897
Moxifloxacin	5 (6.3%)	5 (8.6%)	0 (0.0%)	0.819	0.365
Imipenem	5 (6.3%)	3 (5.2%)	2 (9.1%)	-	0.613
Amikacin	4 (5.0%)	3 (5.2%)	1 (4.5%)	0.211	0.646
Tobramycin	4 (5.0%)	4 (6.9%)	0 (0.0%)	0.475	0.491
Vancomycin	4 (5.0%)	3 (5.2%)	1 (4.5%)	0.211	0.646
Nitrofurantoin	3 (3.8%)	3 (5.2%)	0 (0.0%)	-	0.557
Chloramphenicol	2 (2.5%)	2 (3.4%)	0 (0.0%)	-	1.000
Linezolid	2 (2.5%)	2 (3.4%)	0 (0.0%)	-	1.000
Fusidic acid	2 (2.5%)	2 (3.4%)	0 (0.0%)	-	1.000
Trimethoprim	2 (2.5%)	2 (3.4%)	0 (0.0%)	-	1.000
Meropenem	1 (1.3%)	1 (1.7%)	0 (0.0%)	-	1.000
Ciprofloxacin	1 (1.3%)	1 (1.7%)	0 (0.0%)	-	1.000

Lomefloxacin	1 (1.3%)	1 (1.7%)	0 (0.0%)	-	1.000

Table S2(C). Gram-negative bacteria (n = 111)

Antimicrobial agent	Overall (n = 111)	MDR (n = 67)	Non-MDR (n = 44)	χ^2	*P* value
Ampicillin	87 (78.4%)	56 (83.6%)	31 (70.5%)	1.981	0.159
Ciprofloxacin	59 (53.2%)	55 (82.1%)	4 (9.1%)	53.942	<0.001
Trimethoprim/sulfamethoxazole	59 (53.2%)	59 (88.1%)	0 (0.0%)	-	<0.001
Cefazolin	56 (50.5%)	47 (70.1%)	9 (20.5%)	26.237	<0.001
Cefepime	54 (48.6%)	50 (74.6%)	4 (9.1%)	45.661	<0.001
Levofloxacin	52 (46.8%)	49 (73.1%)	3 (6.8%)	44.229	<0.001
Ceftazidime	50 (45.0%)	36 (53.7%)	14 (31.8%)	5.152	0.023
Gentamicin	50 (45.0%)	41 (61.2%)	9 (20.5%)	17.807	<0.001
Ampicillin/sulbactam	45 (40.5%)	33 (49.3%)	12 (27.3%)	4.443	0.035
Cefotaxime	42 (37.8%)	28 (41.8%)	14 (31.8%)	1.123	0.289
Piperacillin	35 (31.5%)	33 (49.3%)	2 (4.5%)	24.589	<0.001
Aztreonam	33 (29.7%)	22 (32.8%)	11 (25.0%)	0.781	0.377
Ceftriaxone	29 (26.1%)	20 (29.9%)	9 (20.5%)	1.215	0.270
Tetracycline	29 (26.1%)	29 (43.3%)	0 (0.0%)	25.780	<0.001
Tobramycin	29 (26.1%)	20 (29.9%)	9 (20.5%)	1.215	0.270
Cefuroxime	27 (24.3%)	22 (32.8%)	5 (11.4%)	6.652	0.010
Imipenem	21 (18.9%)	11 (16.4%)	10 (22.7%)	0.689	0.406
Meropenem	20 (18.0%)	11 (16.4%)	9 (20.5%)	0.293	0.588
Amoxicillin/clavulanic acid	20 (18.0%)	14 (20.9%)	6 (13.6%)	0.947	0.330
Amikacin	19 (17.1%)	8 (11.9%)	11 (25.0%)	3.193	0.074
Cefoxitin	19 (17.1%)	16 (23.9%)	3 (6.8%)	5.450	0.020
Ertapenem	16 (14.4%)	8 (11.9%)	8 (18.2%)	0.839	0.360
Moxifloxacin	12 (10.8%)	10 (14.9%)	2 (4.5%)	1.989	0.158
Gatifloxacin	8 (7.2%)	8 (11.9%)	0 (0.0%)	4.017	0.045
Ticarcillin/clavulanic acid	7 (6.3%)	7 (10.4%)	0 (0.0%)	3.298	0.069
Piperacillin/tazobactam	5 (4.5%)	5 (7.5%)	0 (0.0%)	1.922	0.166
Chloramphenicol	3 (2.7%)	3 (4.5%)	0 (0.0%)	0.680	0.410
Penicillin	2 (1.8%)	0 (0.0%)	2 (4.5%)	-	0.155
Lomefloxacin	2 (1.8%)	2 (3.0%)	0 (0.0%)	-	0.517
Latamoxef	2 (1.8%)	2 (3.0%)	0 (0.0%)	-	0.517
Minocycline	2 (1.8%)	2 (3.0%)	0 (0.0%)	-	0.517
Cefoperazone/sulbactam	2 (1.8%)	2 (3.0%)	0 (0.0%)	-	0.517
Nitrofurantoin	1 (0.9%)	1 (1.5%)	0 (0.0%)	-	1.000

Data are presented as *n* (%). MDR, multidrug-resistant; χ^2, chi-square test. Categorical variables were compared using the Pearson chi-square test; for 2×2 tables, Yates' continuity correction was applied. Fisher's exact test was used when expected frequencies were < 5. "-" indicates that the chi-square test was not applicable.

Table S3. Univariate logistic regression analysis of candidate variables for MDR infection

Variable	β	OR	95% CI	*P* value
Length of hospital stay (days)	0.088	1.092	1.055–1.136	<0.001
CRP (mg/L)	0.037	1.038	1.023–1.056	<0.001
PCT (ng/mL)	0.445	1.560	1.307–2.035	<0.001
Lac (mmol/L)	0.332	1.394	1.187–1.688	<0.001
Age (years)	0.040	1.040	1.017–1.066	<0.001
i-MELD	0.063	1.065	1.027–1.108	0.001
PT (s)	0.050	1.051	1.019–1.090	0.003
INR	0.530	1.699	1.220–2.508	0.004
PTA (%)	-0.026	0.974	0.956–0.991	0.005
Monocyte count (×10⁹/L)	1.123	3.075	1.427–7.170	0.006
TT (s)	0.096	1.101	1.026–1.190	0.011
IL-6 (pg/mL)	0.007	1.007	1.003–1.013	0.012
APTT (s)	0.019	1.019	1.004–1.037	0.022
HE grade	0.203	1.225	1.032–1.465	0.023
Ammonia (μmol/L)	0.007	1.007	1.001–1.014	0.024
MELD	0.059	1.061	1.009–1.120	0.025
Child-Pugh score	0.148	1.159	1.019–1.323	0.026
MELD-Na	0.059	1.061	1.008–1.121	0.027
ALT (U/L)	0.000	1.000	1.000–1.001	0.049
AST (U/L)	0.001	1.001	1.000–1.001	0.054
TC (mmol/L)	-0.238	0.788	0.606–0.997	0.058
Fib (g/L)	-0.327	0.721	0.503–1.000	0.059
HCT (%)	0.039	1.040	0.998–1.086	0.066
HGB (g/L)	0.011	1.011	0.999–1.023	0.068
TG (mmol/L)	-0.268	0.765	0.556–1.040	0.090
WBC (×10⁹/L)	0.039	1.040	0.978–1.116	0.241
Neutrophil count (×10⁹/L)	0.036	1.037	0.972–1.118	0.304

Dependent variable: MDR infection (1 = yes, 0 = no). Total sample: n = 191; MDR group: n = 125; Non-MDR group: n = 66. Continuous variables were analyzed per 1-unit increase to calculate the OR; the ordinal variable (HE grade) was also analyzed per 1-grade increase.

MDR, multidrug-resistant; OR, odds ratio; CI, confidence interval; β, beta coefficient; CRP, C-reactive protein; PCT, procalcitonin; Lac, lactate; i-MELD, integrated model for end-stage liver disease; PT, prothrombin time; INR, international normalized ratio; PTA, prothrombin activity; TT, thrombin time; IL-6, interleukin-6; APTT, activated partial thromboplastin time; HE, hepatic encephalopathy; MELD, model for end-stage liver disease; MELD-Na, MELD combined with serum sodium; ALT, alanine aminotransferase; AST, aspartate aminotransferase; TC, total cholesterol; Fib, fibrinogen; HCT, hematocrit; HGB, hemoglobin; TG, triglycerides; WBC, white blood cell.

Table S4. Ten-fold cross-validation AUC of the 4-variable prediction model

Fold	AUC
1	0.948
2	0.782
3	0.967
4	0.845
5	0.817
6	0.852
7	0.897
8	0.850
9	0.964
10	0.910
Mean ± SD	0.883 ± 0.064

AUC, area under the receiver operating characteristic curve; SD, standard deviation.

Figure S1



Supplementary Figure S1. Complete distribution of all 38 bacterial species by specimen source (*n* = 191). Bubble size represents the number of isolates. Colors indicate Gram stain: red for Gram-positive bacteria, and blue for Gram-negative bacteria. Species are ordered by total isolate count.