Supplementary Materials

Table S1. Relative abundance of the faecal microbiota composition at different levels in 210 samples.

Table S2. Variations of faecal bacterial functional pathways by LEfSe analysis and Welch's t-test between Death and Survival groups, *p_correct* <0.05.

Table S3. Relative abundance of 9891 antibiotic resistance genes in 210 samples.

Table S4. The ARG types and abundances in both groups.

Table S5. The ARG subtypes and abundances in both groups.

Figure Legends

Figure S1. Variations in the composition of the faecal microbiota and abundance correlation analysis between the Death and Survival groups. The top 10 abundance stacking maps at (A) the genus level, (B) the species level. Correlation analysis of top 10 genus in (C) the Death group, (D) the Survival group.

Figure S2. Comparison of α-diversity between the Death and Survival groups using the Shannon index. (A) At the family level; (B) at the genus level; (C) at the species level; (D) at the functional pathway level.

Figure S3. Comparison of β-diversity using principal coordinate analysis between the Death and Survival groups based on the Bray-Curtis matrix. (A) At the family level; (B) at the genus level; (C) at the species level; (D) at the functional pathway level.

Figure S4. Pathway differences between Death and Survival groups. (A) LEfSe analysis (LDA > 2.5, $p < 0.05$); (B) STAMP analysis ($p\_corrected < 0.05$).

Figure S5. Variations in the composition of the faecal microbiota between the Death and Survival groups, according to Welch's *t*-test $p < 0.05$. (A) At the family level, (B) at the genus level and (C) at the species level. Blue indicates the enriched flora in the Death group, and orange indicates the enriched flora in the Survival group.

Figure S6. Variations in the composition of the faecal microbiota in a more age-homogeneous subset (age from 30 to 70 years old, $p > 0.05$) with both groups using STAMP analysis. (A) At the family level, (B) at the genus level and (C) at the species level. Blue indicates the enriched flora in the Death group, and orange indicates the enriched flora in the Survival group.

Figure S7. Composition of ARGs and regulator genes in both groups. (A) The relative abundance of ARGs types; (B) resistance mechanism in Death Group; (C) resistance mechanism in Survival Group.

Figure S8. Differential comparison of antibiotic resistance genes (ARGs) between the Death and Survival groups. (A) α-diversity (Shannon index); (B) β-diversity (PCoA), $p = 0.001$.

Figure S9. Correlated analysis of enriched ARG types. (A) The Death Group; (B) The Survival Group.

Figure S10. Box plots show the relative abundances of ARG subtypes that showed significant differences between the two groups.

Figure S11. Diagnostic potential of gut microbial markers with the separate pre-filter process for each group. (A) The top 13 species in terms of importance; (B) ROC curve of species.

Figure S12. Confusion matrix as the additional performance metrics for random forest analysis. (A) The pre-filter process for all samples in both groups; (B) The separate pre-filter process for each group.

Figure S1

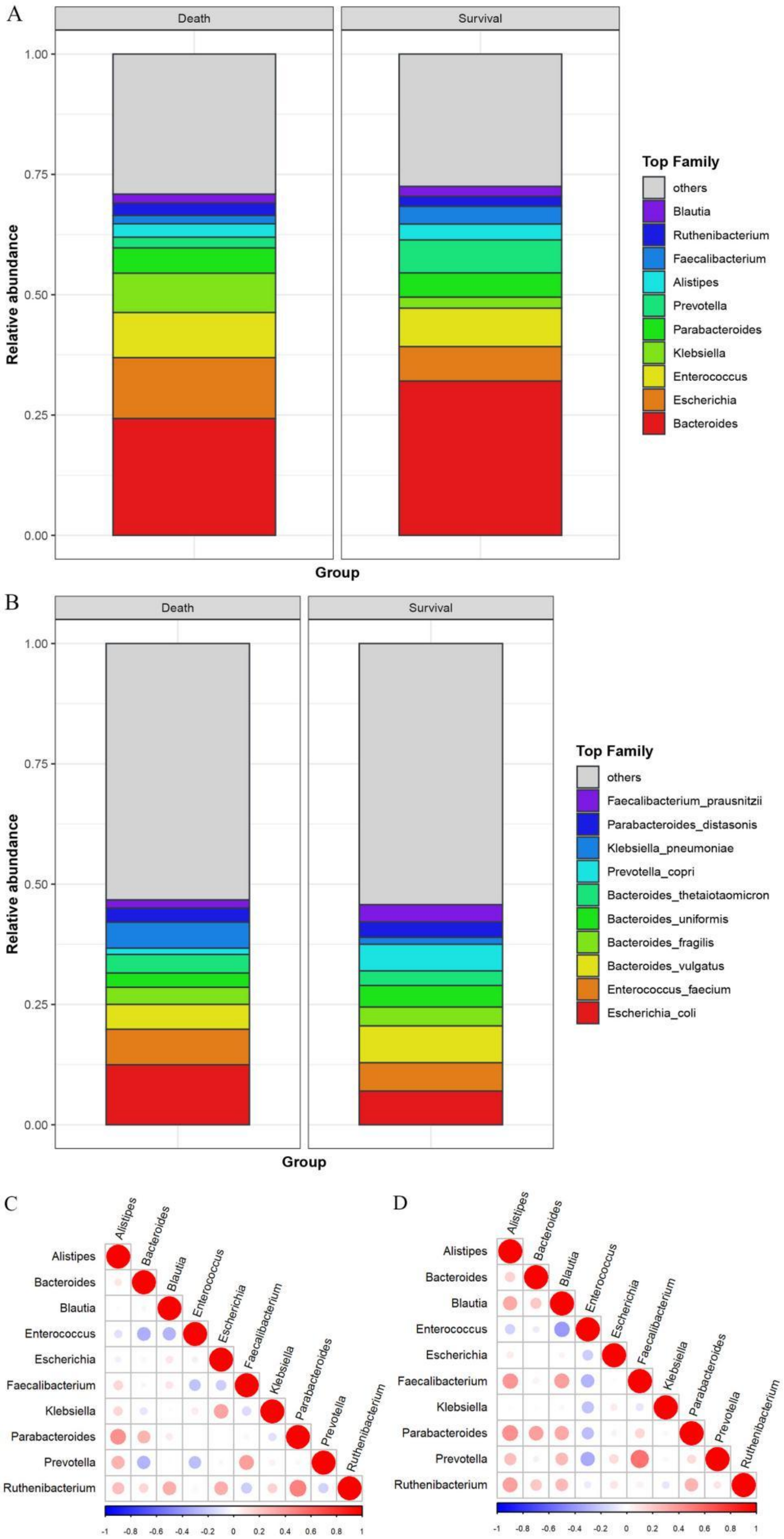

A
Death
Survival
1.00
0.75
0.50
0.25
0.00
Relative abundance
Group
Top Family
others
Blautia
Ruthenibacterium
Faecalibacterium
Alistipes
Prevotella
Parabacteroides
Klebsiella
Enterococcus
Escherichia
Bacteroides
B
Death
Survival
Relative abundance
Group
Top Family
others
Faecalibacterium_prausnitzii
Parabacteroides_distasonis
Klebsiella_pneumoniae
Prevotella_copri
Bacteroides_thetaiotaomicron
Bacteroides_uniformis
Bacteroides_fragilis
Bacteroides_vulgatus
Enterococcus_faecium
Escherichia_coli
C
D
Alistipes
Bacteroides
Blautia
Enterococcus
Escherichia
Faecalibacterium
Klebsiella
Parabacteroides
Prevotella
Ruthenibacterium
-1
-0.8
-0.6
-0.4
-0.2
0
0.2
0.4
0.6
0.8
1

Figure S2

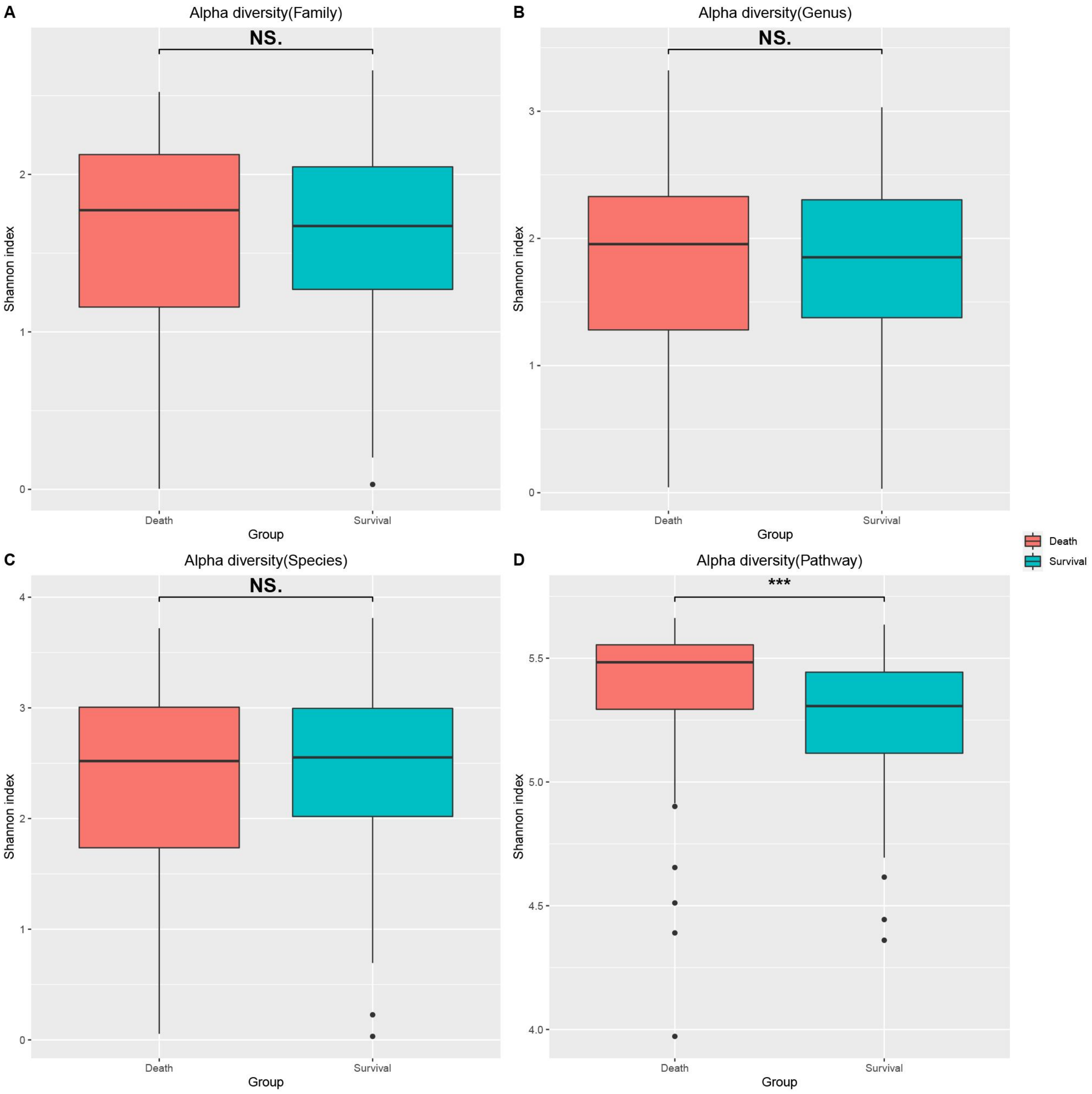

A
Alpha diversity(Family)
NS.
Shannon index
0
1
2
Death
Survival
Group
B
Alpha diversity(Genus)
NS.
Shannon index
0
1
2
3
Death
Survival
Group
Death
Survival
C
Alpha diversity(Species)
NS.
Shannon index
0
1
2
3
4
Death
Survival
Group
D
Alpha diversity(Pathway)
***
Shannon index
4.0
4.5
5.0
5.5
Death
Survival
Group

Figure S3

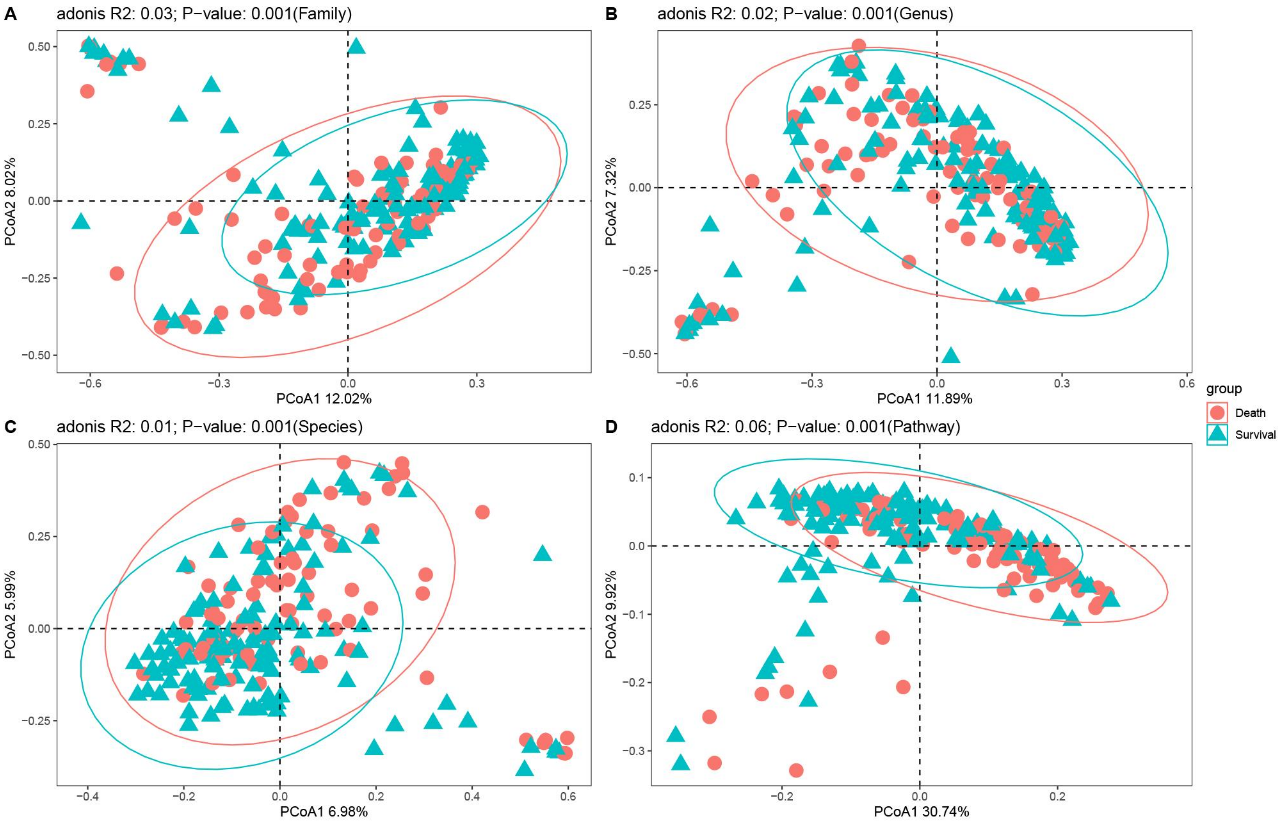

A
adonis R2: 0.03; P−value: 0.001(Family)
PCoA2 8.02%
PCoA1 12.02%
0.50
0.25
0.00
−0.25
−0.50
−0.6
−0.3
0.0
0.3
B
adonis R2: 0.02; P−value: 0.001(Genus)
PCoA2 7.32%
PCoA1 11.89%
0.25
0.00
−0.25
−0.50
−0.6
−0.3
0.0
0.3
0.6
C
adonis R2: 0.01; P−value: 0.001(Species)
PCoA2 5.99%
PCoA1 6.98%
0.50
0.25
0.00
−0.25
−0.4
−0.2
0.0
0.2
0.4
0.6
D
adonis R2: 0.06; P−value: 0.001(Pathway)
PCoA2 9.92%
PCoA1 30.74%
0.1
0.0
−0.1
−0.2
−0.3
−0.2
0.0
0.2
group
Death
Survival

Figure S4

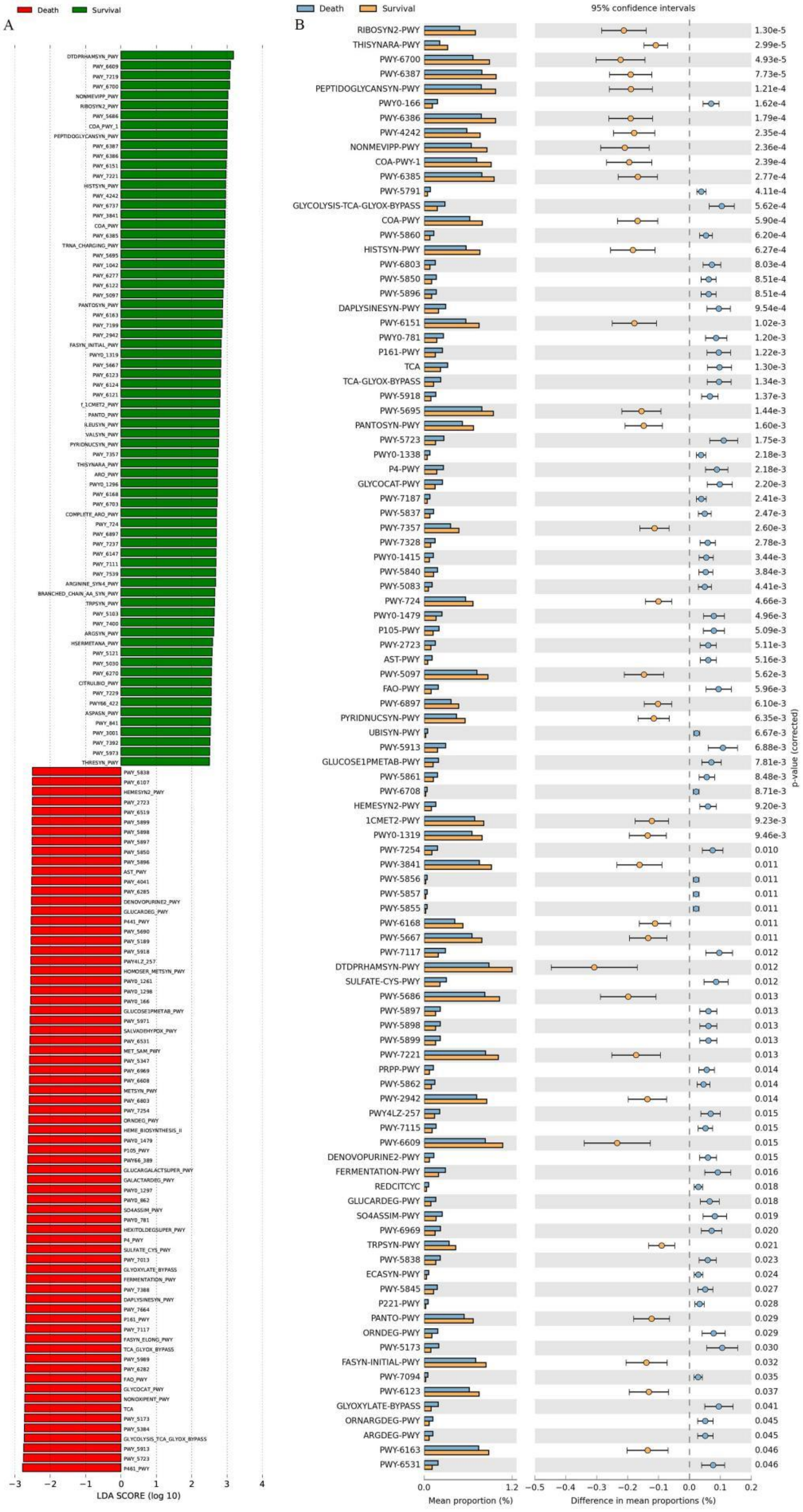
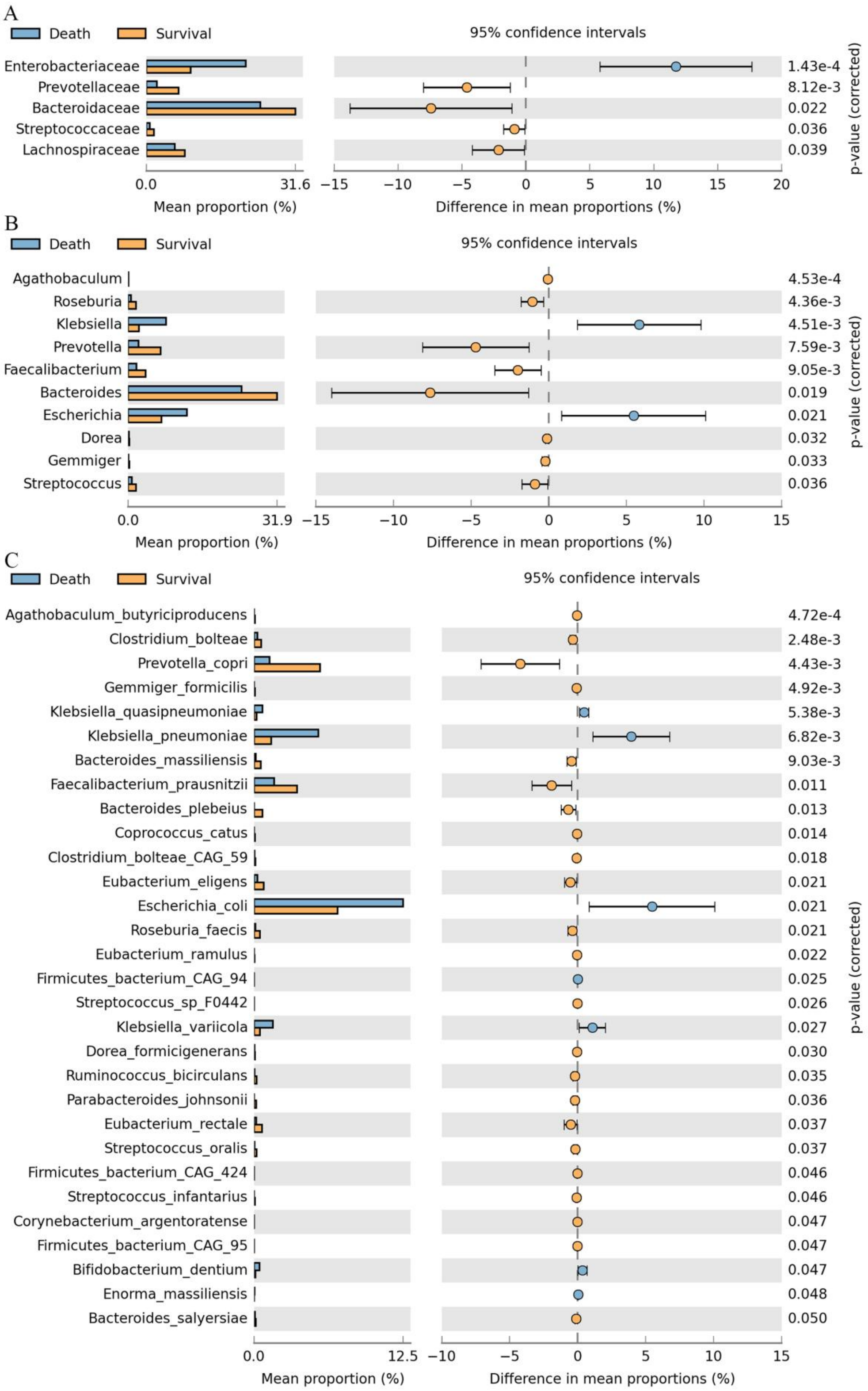

Death
Survival
A
DTDPRHAMSYN_PWY
PWY_6609
PWY_7219
PWY_6700
NONMEVIPP_PWY
RIBOSYN2_PWY
PWY_5686
COA_PWY_1
PEPTIDOGLYCANSYN_PWY
PWY_6387
PWY_6386
PWY_6151
PWY_7221
HISTSYN_PWY
PWY_4242
PWY_6737
PWY_3841
COA_PWY
PWY_6385
TRNA_CHARGING_PWY
PWY_5695
PWY_1042
PWY_6277
PWY_6122
PWY_5097
PANTOSYN_PWY
PWY_6163
PWY_7199
PWY_2942
FASYN_INITIAL_PWY
PWY0_1319
PWY_5667
PWY_6123
PWY_6124
PWY_6121
f_1CMET2_PWY
PANTO_PWY
ILEUSYN_PWY
VALSYN_PWY
PYRIDNUCSYN_PWY
PWY_7357
THISYNARA_PWY
ARO_PWY
PWY0_1296
PWY_6168
PWY_6703
COMPLETE_ARO_PWY
PWY_724
PWY_6897
PWY_7237
PWY_6147
PWY_7111
PWY_7539
ARGININE_SYN4_PWY
BRANCHED_CHAIN_AA_SYN_PWY
TRPSYN_PWY
PWY_5103
PWY_7400
ARGSYN_PWY
HSERMETANA_PWY
PWY_5121
PWY_5030
PWY_6270
CITRULBIO_PWY
PWY_7229
PWY66_422
ASPASN_PWY
PWY_841
PWY_3001
PWY_7392
PWY_5973
THRESYN_PWY
PWY_5838
PWY_6107
HEMESYN2_PWY
PWY_2723
PWY_6519
PWY_5899
PWY_5898
PWY_5897
PWY_5850
PWY_5896
AST_PWY
PWY_4041
PWY_6285
DENOVOPURINE2_PWY
GLUCARDEG_PWY
P441_PWY
PWY_5690
PWY_5189
PWY_5918
PWY4LZ_257
HOMOSER_METSYN_PWY
PWY0_1261
PWY0_1298
PWY0_166
GLUCOSE1PMETAB_PWY
PWY_5971
SALVADEHYPOX_PWY
PWY_6531
MET_SAM_PWY
PWY_5347
PWY_6969
PWY_6608
METSYN_PWY
PWY_6803
PWY_7254
ORNDEG_PWY
HEME_BIOSYNTHESIS_II
PWY0_1479
P105_PWY
PWY66_389
GLUCARGALACTSUPER_PWY
GALACTARDEG_PWY
PWY0_1297
PWY0_862
SO4ASSIM_PWY
PWY0_781
HEXITOLDEGSUPER_PWY
P4_PWY
SULFATE_CYS_PWY
PWY_7013
GLYOXYLATE_BYPASS
FERMENTATION_PWY
PWY_7388
DAPLYSINESYN_PWY
PWY_7664
P161_PWY
PWY_7117
FASYN_ELONG_PWY
TCA_GLYOX_BYPASS
PWY_5989
PWY_6282
FAO_PWY
GLYCOCAT_PWY
NONOXIPENT_PWY
TCA
PWY_5173
PWY_5384
GLYCOLYSIS_TCA_GLYOX_BYPASS
PWY_5913
PWY_5723
P461_PWY
−3
−2
−1
0
1
2
3
4
LDA SCORE (log 10)
B
Death
Survival
95% confidence intervals
RIBOSYN2-PWY 1.30e-5
THISYNARA-PWY 2.99e-5
PWY-6700 4.93e-5
PWY-6387 7.73e-5
PEPTIDOGLYCANSYN-PWY 1.21e-4
PWY0-166 1.62e-4
PWY-6386 1.79e-4
PWY-4242 2.35e-4
NONMEVIPP-PWY 2.36e-4
COA-PWY-1 2.39e-4
PWY-6385 2.77e-4
PWY-5791 4.11e-4
GLYCOLYSIS-TCA-GLYOX-BYPASS 5.62e-4
COA-PWY 5.90e-4
PWY-5860 6.20e-4
HISTSYN-PWY 6.27e-4
PWY-6803 8.03e-4
PWY-5850 8.51e-4
PWY-5896 8.51e-4
DAPLYSINESYN-PWY 9.54e-4
PWY-6151 1.02e-3
PWY0-781 1.20e-3
P161-PWY 1.22e-3
TCA 1.30e-3
TCA-GLYOX-BYPASS 1.34e-3
PWY-5918 1.37e-3
PWY-5695 1.44e-3
PANTOSYN-PWY 1.60e-3
PWY-5723 1.75e-3
PWY0-1338 2.18e-3
P4-PWY 2.18e-3
GLYCOCAT-PWY 2.20e-3
PWY-7187 2.41e-3
PWY-5837 2.47e-3
PWY-7357 2.60e-3
PWY-7328 2.78e-3
PWY0-1415 3.44e-3
PWY-5840 3.84e-3
PWY-5083 4.41e-3
PWY-724 4.66e-3
PWY0-1479 4.96e-3
P105-PWY 5.09e-3
PWY-2723 5.11e-3
AST-PWY 5.16e-3
PWY-5097 5.62e-3
FAO-PWY 5.96e-3
PWY-6897 6.10e-3
PYRIDNUCSYN-PWY 6.35e-3
UBISYN-PWY 6.67e-3
PWY-5913 6.88e-3
GLUCOSE1PMETAB-PWY 7.81e-3
PWY-5861 8.48e-3
PWY-6708 8.71e-3
HEMESYN2-PWY 9.20e-3
1CMET2-PWY 9.23e-3
PWY0-1319 9.46e-3
PWY-7254 0.010
PWY-3841 0.011
PWY-5856 0.011
PWY-5857 0.011
PWY-5855 0.011
PWY-6168 0.011
PWY-5667 0.011
PWY-7117 0.012
DTDPRHAMSYN-PWY 0.012
SULFATE-CYS-PWY 0.012
PWY-5686 0.013
PWY-5897 0.013
PWY-5898 0.013
PWY-5899 0.013
PWY-7221 0.013
PRPP-PWY 0.014
PWY-5862 0.014
PWY-2942 0.014
PWY4LZ-257 0.015
PWY-7115 0.015
PWY-6609 0.015
DENOVOPURINE2-PWY 0.015
FERMENTATION-PWY 0.016
REDCITCYC 0.018
GLUCARDEG-PWY 0.018
SO4ASSIM-PWY 0.019
PWY-6969 0.020
TRPSYN-PWY 0.021
PWY-5838 0.023
ECASYN-PWY 0.024
PWY-5845 0.027
P221-PWY 0.028
PANTO-PWY 0.029
ORNDEG-PWY 0.029
PWY-5173 0.030
FASYN-INITIAL-PWY 0.032
PWY-7094 0.035
PWY-6123 0.037
GLYOXYLATE-BYPASS 0.041
ORNARGDEG-PWY 0.045
ARGDEG-PWY 0.045
PWY-6163 0.046
PWY-6531 0.046
0.0
1.2
Mean proportion (%)
−0.5
−0.4
−0.3
−0.2
−0.1
0.0
0.1
0.2
Difference in mean proportions (%)
p-value (corrected)

Figure S5



A
Death
Survival
95% confidence intervals
Enterobacteriaceae
Prevotellaceae
Bacteroidaceae
Streptococcaceae
Lachnospiraceae
1.43e-4
8.12e-3
0.022
0.036
0.039
p-value (corrected)
0.0
31.6
Mean proportion (%)
−15
−10
−5
0
5
10
15
20
Difference in mean proportions (%)
B
Death
Survival
95% confidence intervals
Agathobaculum
Roseburia
Klebsiella
Prevotella
Faecalibacterium
Bacteroides
Escherichia
Dorea
Gemmiger
Streptococcus
4.53e-4
4.36e-3
4.51e-3
7.59e-3
9.05e-3
0.019
0.021
0.032
0.033
0.036
p-value (corrected)
0.0
31.9
Mean proportion (%)
−15
−10
−5
0
5
10
15
Difference in mean proportions (%)
C
Death
Survival
95% confidence intervals
Agathobaculum_butyriciproducens
Clostridium_bolteae
Prevotella_copri
Gemmiger_formicilis
Klebsiella_quasipneumoniae
Klebsiella_pneumoniae
Bacteroides_massiliensis
Faecalibacterium_prausnitzii
Bacteroides_plebeius
Coprococcus_catus
Clostridium_bolteae_CAG_59
Eubacterium_eligens
Escherichia_coli
Roseburia_faecis
Eubacterium_ramulus
Firmicutes_bacterium_CAG_94
Streptococcus_sp_F0442
Klebsiella_variicola
Dorea_formicigenerans
Ruminococcus_bicirculans
Parabacteroides_johnsonii
Eubacterium_rectale
Streptococcus_oralis
Firmicutes_bacterium_CAG_424
Streptococcus_infantarius
Corynebacterium_argentoratense
Firmicutes_bacterium_CAG_95
Bifidobacterium_dentium
Enorma_massiliensis
Bacteroides_salyersiae
4.72e-4
2.48e-3
4.43e-3
4.92e-3
5.38e-3
6.82e-3
9.03e-3
0.011
0.013
0.014
0.018
0.021
0.021
0.021
0.022
0.025
0.026
0.027
0.030
0.035
0.036
0.037
0.037
0.046
0.046
0.047
0.047
0.047
0.048
0.050
p-value (corrected)
0.0
12.5
Mean proportion (%)
−10
−5
0
5
10
15
Difference in mean proportions (%)

Figure S6

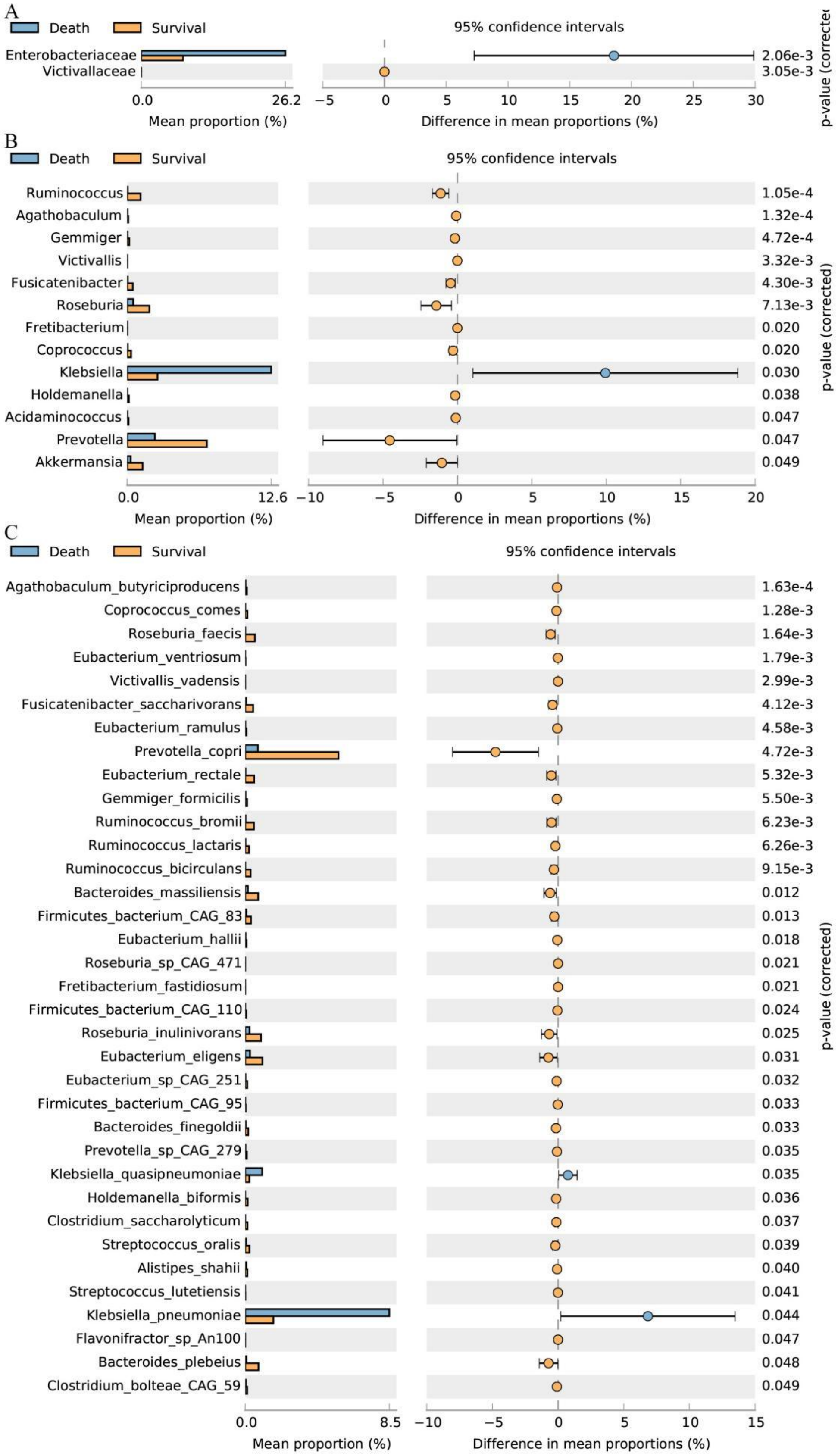

A
Death
Survival
95% confidence intervals
Enterobacteriaceae
Victivallaceae
2.06e-3
3.05e-3
p-value (correcte
0.0
26.2
−5
0
5
10
15
20
25
30
Mean proportion (%)
Difference in mean proportions (%)
B
Death
Survival
95% confidence intervals
Ruminococcus
Agathobaculum
Gemmiger
Victivallis
Fusicatenibacter
Roseburia
Fretibacterium
Coprococcus
Klebsiella
Holdemanella
Acidaminococcus
Prevotella
Akkermansia
1.05e-4
1.32e-4
4.72e-4
3.32e-3
4.30e-3
7.13e-3
0.020
0.020
0.030
0.038
0.047
0.047
0.049
p-value (corrected)
0.0
12.6
−10
−5
0
5
10
15
20
Mean proportion (%)
Difference in mean proportions (%)
C
Death
Survival
95% confidence intervals
Agathobaculum_butyriciproducens
Coprococcus_comes
Roseburia_faecis
Eubacterium_ventriosum
Victivallis_vadensis
Fusicatenibacter_saccharivorans
Eubacterium_ramulus
Prevotella_copri
Eubacterium_rectale
Gemmiger_formicilis
Ruminococcus_bromii
Ruminococcus_lactaris
Ruminococcus_bicirculans
Bacteroides_massiliensis
Firmicutes_bacterium_CAG_83
Eubacterium_hallii
Roseburia_sp_CAG_471
Fretibacterium_fastidiosum
Firmicutes_bacterium_CAG_110
Roseburia_inulinivorans
Eubacterium_eligens
Eubacterium_sp_CAG_251
Firmicutes_bacterium_CAG_95
Bacteroides_finegoldii
Prevotella_sp_CAG_279
Klebsiella_quasipneumoniae
Holdemanella_biformis
Clostridium_saccharolyticum
Streptococcus_oralis
Alistipes_shahii
Streptococcus_lutetiensis
Klebsiella_pneumoniae
Flavonifractor_sp_An100
Bacteroides_plebeius
Clostridium_bolteae_CAG_59
1.63e-4
1.28e-3
1.64e-3
1.79e-3
2.99e-3
4.12e-3
4.58e-3
4.72e-3
5.32e-3
5.50e-3
6.23e-3
6.26e-3
9.15e-3
0.012
0.013
0.018
0.021
0.021
0.024
0.025
0.031
0.032
0.033
0.033
0.035
0.035
0.036
0.037
0.039
0.040
0.041
0.044
0.047
0.048
0.049
p-value (corrected)
0.0
8.5
−10
−5
0
5
10
15
Mean proportion (%)
Difference in mean proportions (%)

Figure S7

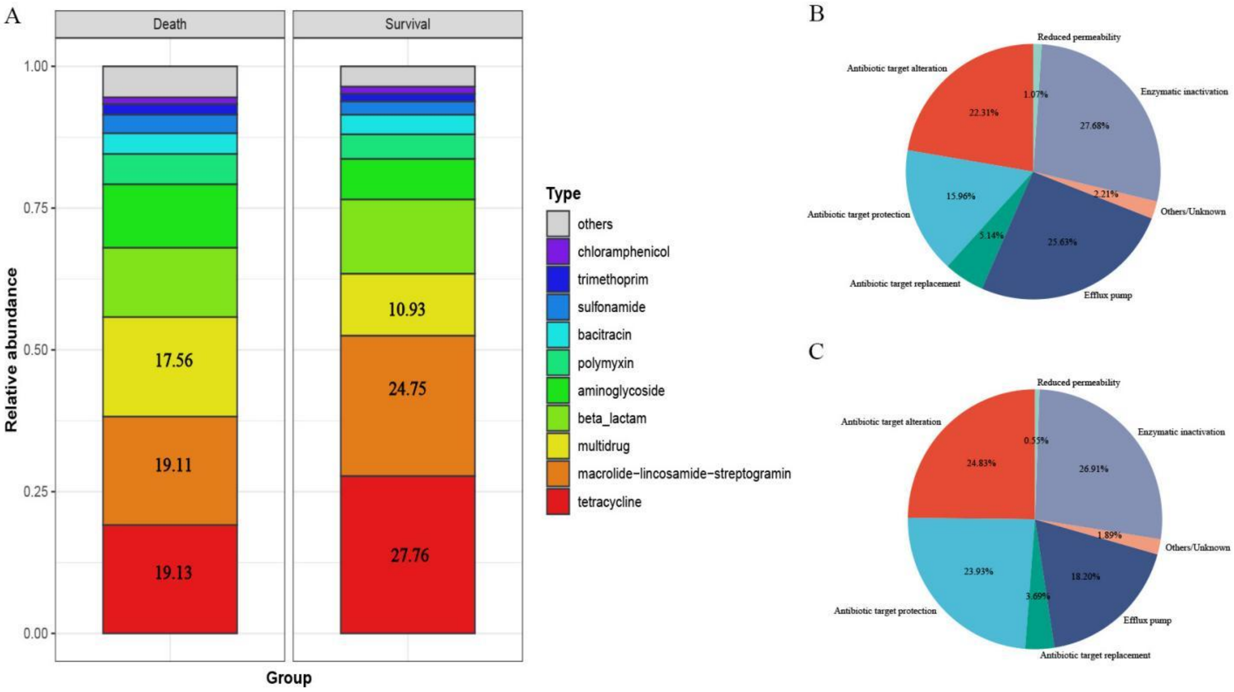


Figure S8

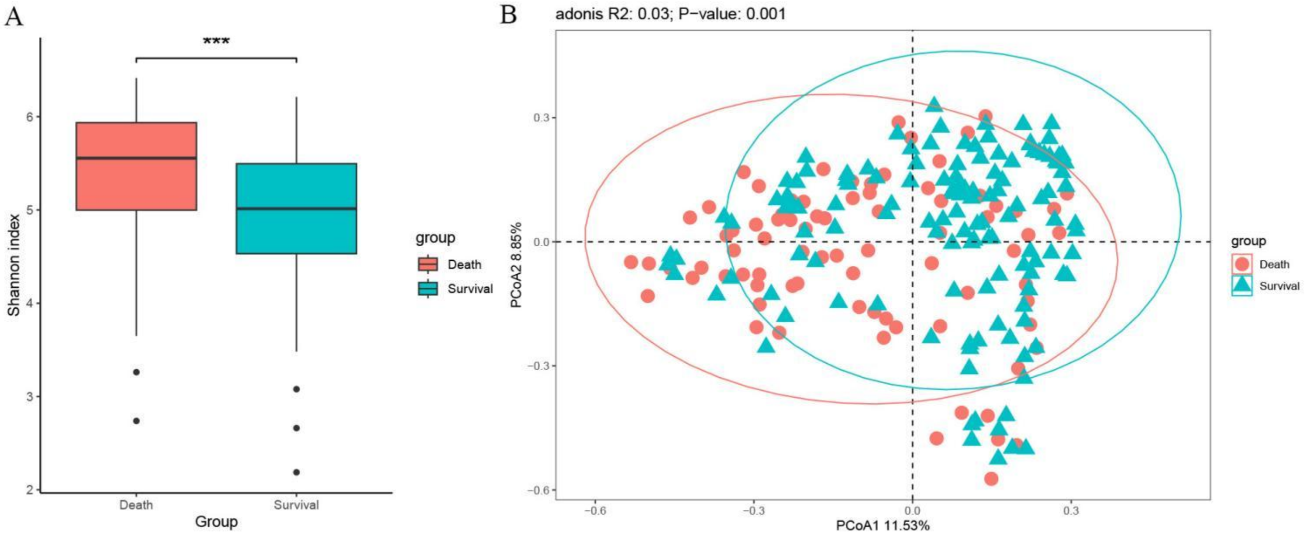


Figure S9

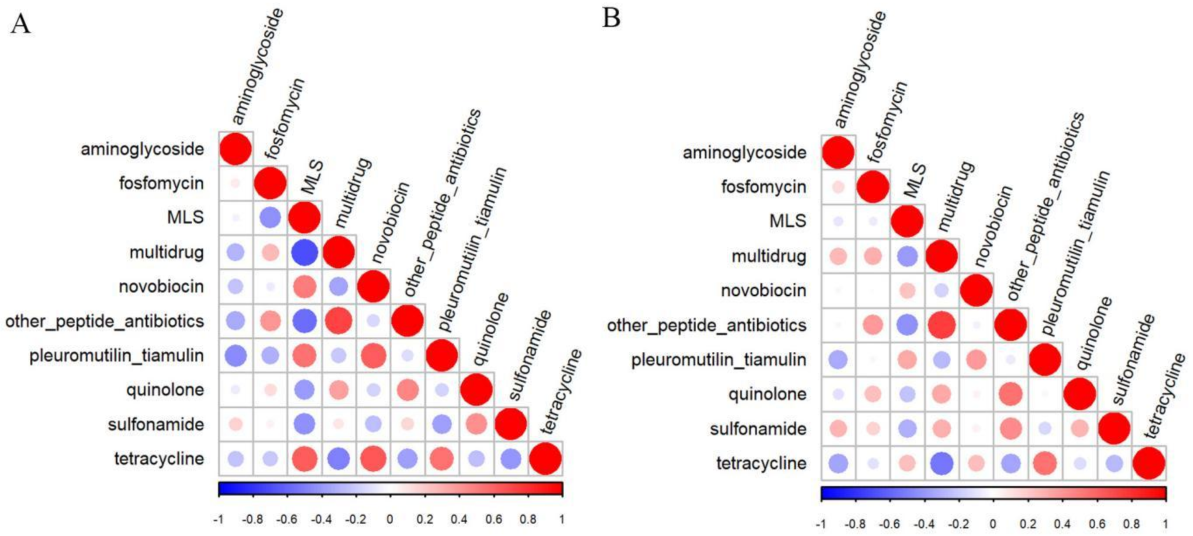

A
B
aminoglycoside
fosfomycin
MLS
multidrug
novobiocin
other_peptide_antibiotics
pleuromutilin_tiamulin
quinolone
sulfonamide
tetracycline
-1
-0.8
-0.6
-0.4
-0.2
0
0.2
0.4
0.6
0.8
1

Figure S10

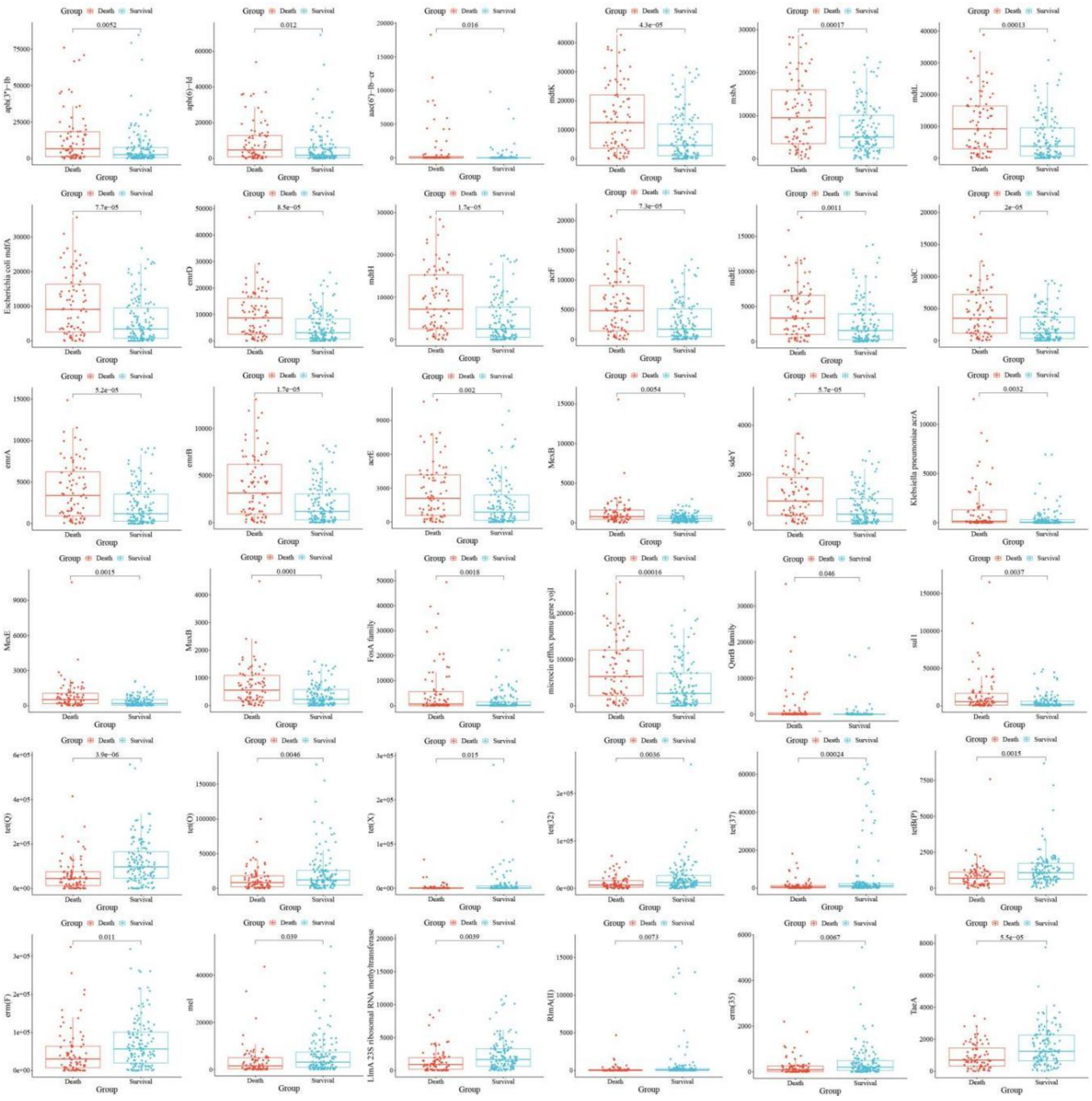

Group
Death
Survival
aph(3'')-Ib
0.0052
aph(6)-Id
0.012
aac(6')-Ib-cr
0.016
mdtK
4.3e-05
msbA
0.00017
mdtL
0.00013
Escherichia coli mdfA
7.7e-05
emrD
8.5e-05
mdtH
1.7e-05
acrF
7.3e-05
mdtE
0.0011
tolC
2e-05
emrA
5.2e-05
emrB
1.7e-05
acrE
0.002
MexB
0.0054
sdeY
5.7e-05
Klebsiella pneumoniae acrA
0.0032
MexE
0.0015
MuxB
0.0001
FosA family
0.0018
microcin efflux pump gene yojI
0.00016
QnrB family
0.046
sul1
0.0037
tet(Q)
3.9e-06
tet(O)
0.0046
tet(X)
0.015
tet(32)
0.0036
tet(37)
0.00024
tetB(P)
0.0015
erm(F)
0.011
mel
0.039
LlmA 23S ribosomal RNA methyltransferase
0.0039
RlmA(II)
0.0073
erm(35)
0.0067
TaeA
5.5e-05

Figure S11

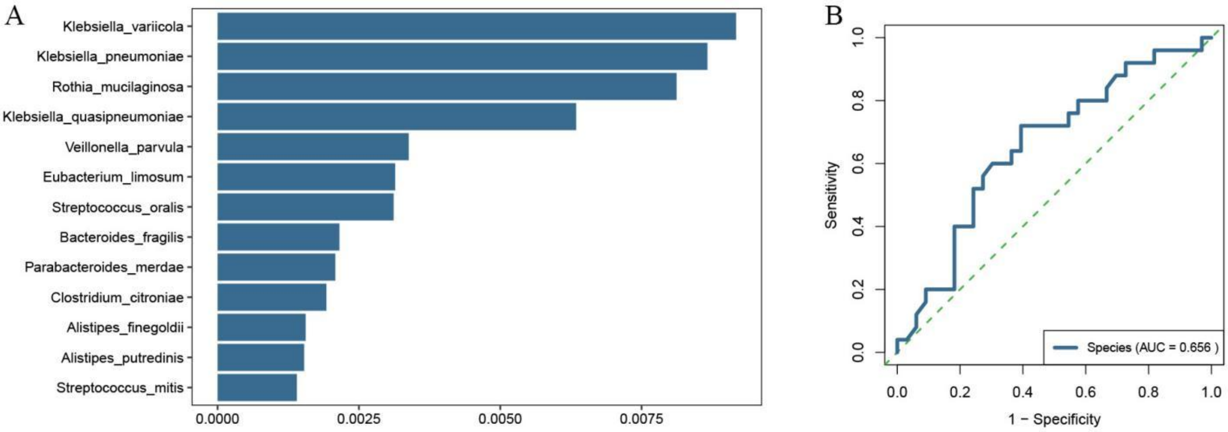
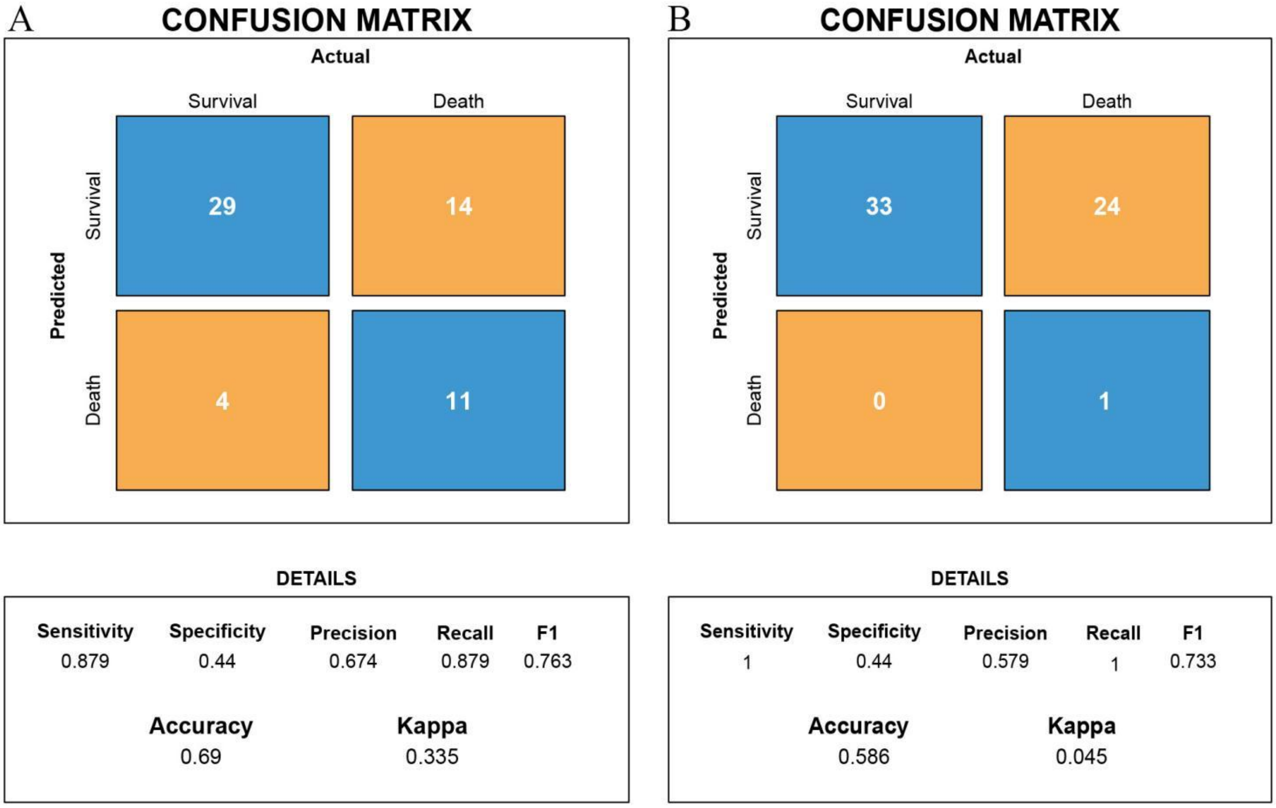


Figure S12



A

CONFUSION MATRIX

		Actual	
		Survival	Death
Predicted	Survival	29	14
	Death	4	11

DETAILS

Sensitivity	Specificity	Precision	Recall	F1
0.879	0.44	0.674	0.879	0.763

Accuracy	Kappa
0.69	0.335

B

CONFUSION MATRIX

		Actual	
		Survival	Death
Predicted	Survival	33	24
	Death	0	1

DETAILS

Sensitivity	Specificity	Precision	Recall	F1
1	0.44	0.579	1	0.733

Accuracy	Kappa
0.586	0.045