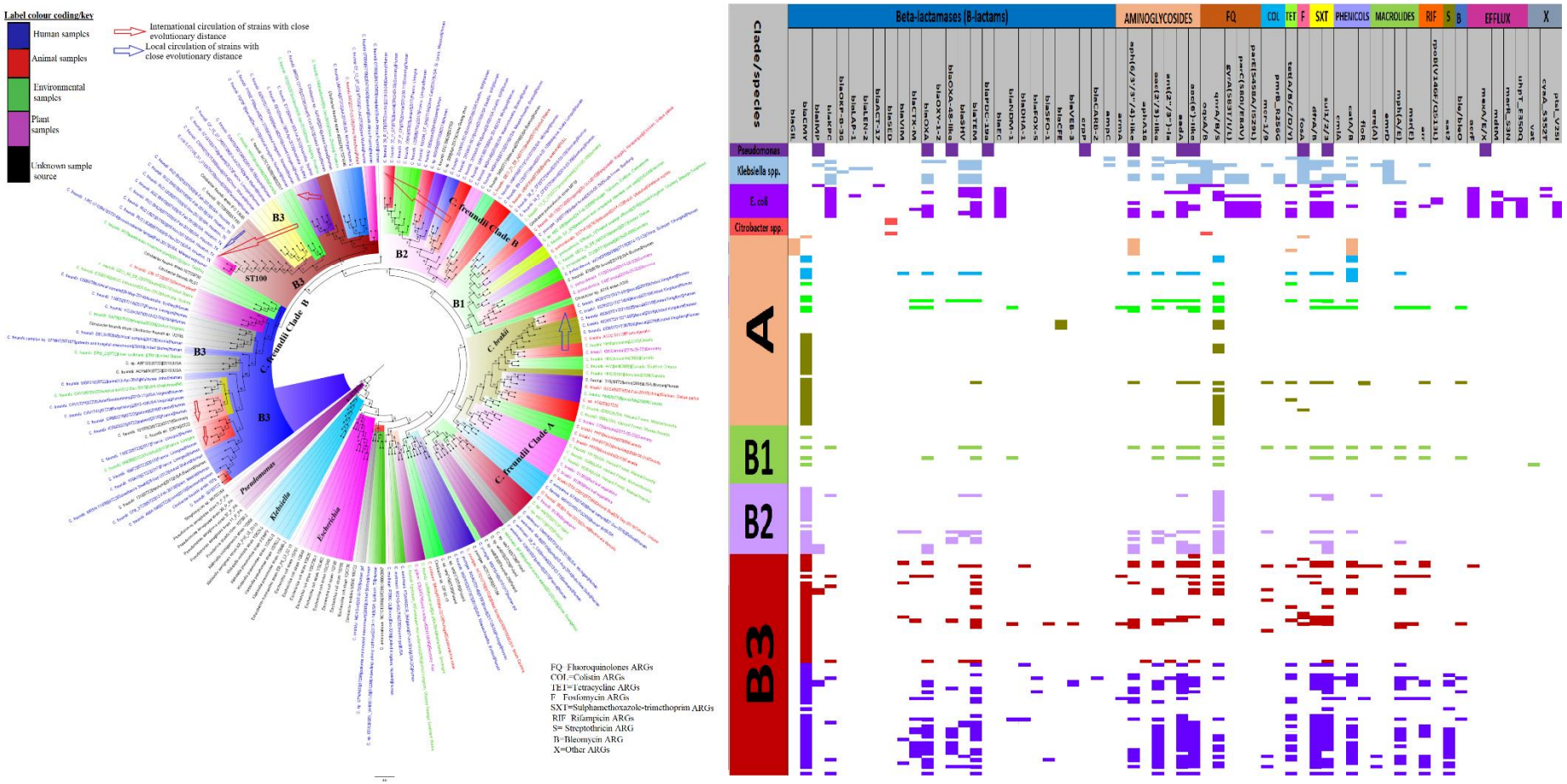
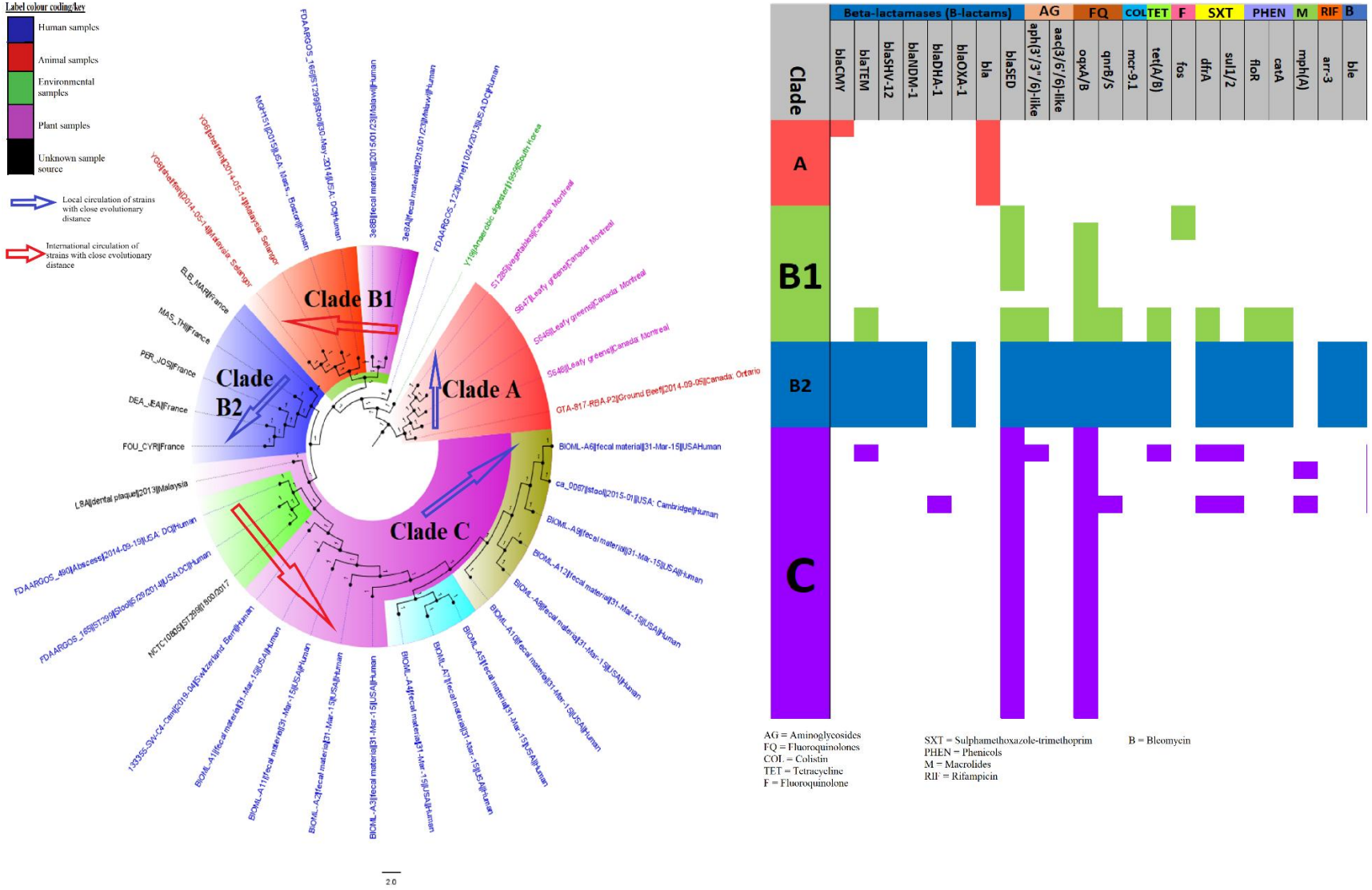
Supplementary figures

Figure S1A-B Evolutionary epidemiology and resistome of global *Citrobacter freundii*, *brakii*, *portucalensis*, and *amalonaticus* isolates. S1A shows *Citrobacter sp*., *particularly freundii*, *portucalensis* and *brakii* clustering into clades A, B1, B2 and B3 whilst S1B shows *C. amalonaticus* strains clustering into clades A (red highlight), B1 (green highlight), B2 (blue highlight) and C (mauve highlight); clade B2 had very rich resistome repertoire and were all from France, but the other clades had very few resistance genes. Strains from humans (blue labels), animals (red labels), plants (purple/mauve labels) and the environment (green labels) were found in the same clade/cluster. Included in S1A are *Pseudomonas*, *Klebsiella*, and *Escherichia coli* species that were originally classified as *C. freundii* but later reclassified into their actual species using ANI; their clustering away from the *Citrobacter* species confirms the ANI results that they were initially misclassified. Bla_{SED} and *oqxAB* were almost conserved in these genomes. Branches with bootstrap support values of ≥50 were defined as belonging to the same clade. The branch lengths also show the evolutionary distance between the isolates. Blue and red arrows show the direction of evolution as well as local and international dissemination of strains of the same clone/clade through different hosts.

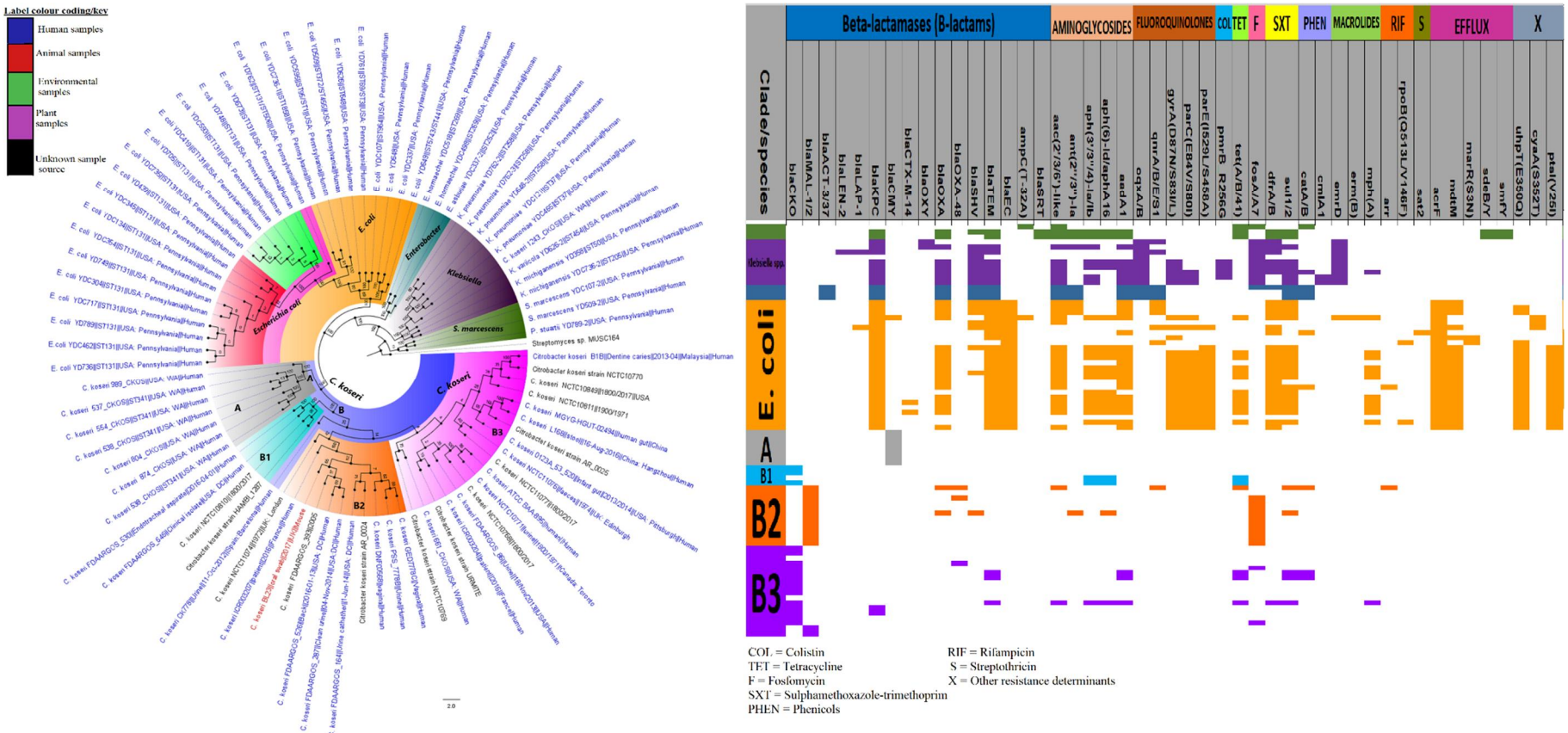

Label colour coding/key
Human samples
Animal samples
Environmental samples
Plant samples
Unknown sample source
International circulation of strains with close evolutionary distance
Local circulation of strains with close evolutionary distance
C. freundii Clade B
C. freundii Clade A
C. braakii
ST100
B1
B2
B3
Pseudomonas
Klebsiella
Escherichia
FQ- Fluoroquinolones ARGs
COL=Colistin ARGs
TE1=Tetracycline ARGs
F- Fosfomycin ARGs
SXT=Sulphamethoxazole-trimethoprim ARGs
RIF- Rifampicin ARGs
S= Streptothricin ARG
B=Bleomycin ARG
X=Other ARGs
Clade/species
Beta-lactamases (B-lactams)
AMINOGLYCOSIDES
FQ
COL
TET
F
SXT
PHENICOLS
MACROLIDES
RIF
S
B
EFFLUX
X
Pseudomonas
Klebsiella spp.
E.coli
Citrobacter spp.
A
B1
B2
B3

S1A


Label colour coding/key
Human samples
Animal samples
Environmental samples
Plant samples
Unknown sample source
Local circulation of strains with close evolutionary distance
International circulation of strains with close evolutionary distance
Clade B1
Clade B2
Clade A
Clade C
Clade
A
B1
B2
C
Beta-lactamases (B-lactams)
AG
FQ
COLTET
F
SXT
PHEN
M
RIF
B
blaCMY
blaTEM
blaSHV-12
blaNDM-1
blaDHA-1
blaOXA-1
bla
blaSED
aph(3')(3")(6)-like
aac(3/6')(6)-like
oqxA/B
qnrB/S
mcr-9.1
tet(A/B)
fos
dfrA
sul1/2
floR
catA
mph(A)
arr-3
ble
AG = Aminoglycosides
FQ = Fluoroquinolones
COL = Colistin
TET = Tetracycline
F = Fluoroquinolone
SXT = Sulphamethoxazole-trimethoprim
PHEN = Phenicols
M = Macrolides
RIF = Rifampicin
B = Bleomycin

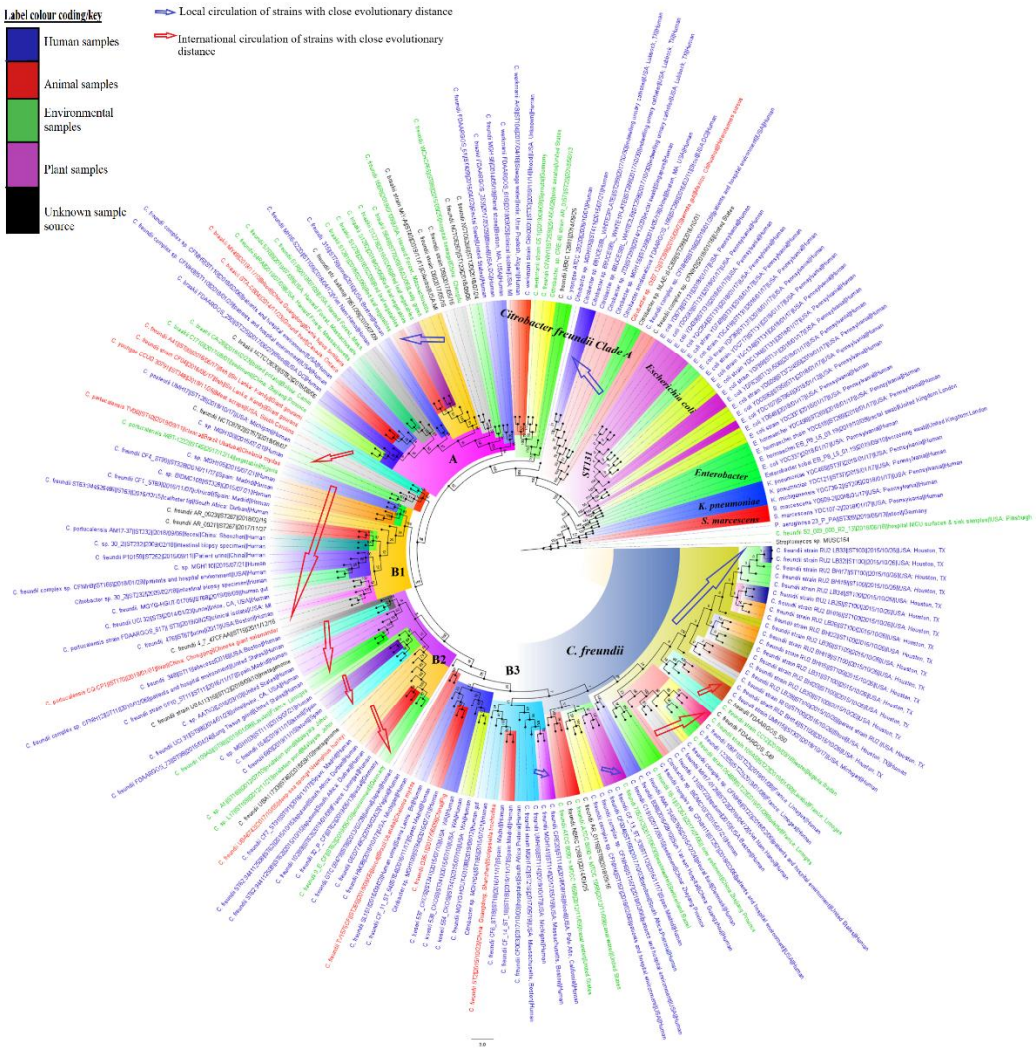
S1B

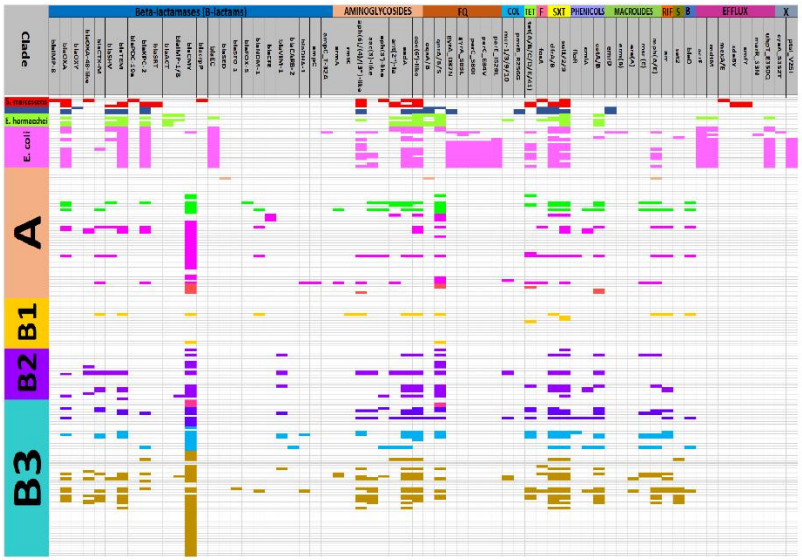
Fig. S1C. Evolutionary epidemiology and resistome of global *Citrobacter koseri* isolates. *C. koseri* strains clustered into clades A (grey highlight), B1 (light blue highlight), B2 (orange highlight) and B3 (mauve highlight). Strains from humans (blue labels) and animals (red labels) were found in the same clade/cluster. *Bla*$_{CKO}$ and *bla*$_{MAL}$ were almost conserved in these genomes. Included in S1C are *Serratia marcescens*, *Klebsiella*, *Enterobacter* and *Escherichia coli* species that were originally classified as *C. koseri* but later reclassified into their actual species using ANI; their clustering away from *Citrobacter koseri* confirms the ANI results that they were initially misclassified. Branches with bootstrap support values of ≥50 were defined as belonging to the same clade. The branch lengths also show the evolutionary distance between the isolates. Blue and red arrows show the direction of evolution as well as local and international dissemination of strains of the same clone/clade through different hosts.


Label colour coding/key
Human samples
Animal samples
Environmental samples
Plant samples
Unknown sample source
E. coli
Enterobacter
Klebsiella
S. marcescens
C. koseri
Escherichia coli
A
B
B1
B2
B3
Clade/species
Beta-lactamases (B-lactams)
AMINOGLYCOSIDES
FLUOROQUINOLONES
COL
TET
F
SXT
PHEN
MACROLIDES
RIF
S
EFFLUX
X
blaCKO
blaMAL-1/2
blaACT-3/37
blaLEN-2
blaLAP-1
blaKPC
blaCMY
blaCTX-M-14
blaOXY
blaOXA
blaOXA-48
blaTEM
blaSHV
blaEC
ampC(T-32A)
blaSRT
aac(2')/3(6')-like
ant(2'')/3''-la
aph(3'')/4)-Ia/Ib
aph(6)-Id/aphA16
aadA1
cqsA/B
qnrA/B/E/S1
gyrA(D87N/S83I/L)
parC(E84V/S80I)
parE(I529L/S458A)
pmrB_R256G
tet(A/B/41)
fosA/A7
dfrA/B
sul1/2
catA/B
cmlA1
emrD
erm(B)
mph(A)
arr
rpoB(G513L/V146F)
sat2
acrF
mdtM
marR(S3N)
sdeB/Y
smfY
uhpT(E350Q)
cyaA(S352T)
ptsI(V25I)
Klebsiella spp.
E. coli
A
B1
B2
B3
COL = Colistin
TET = Tetracycline
F = Fosfomycin
SXT = Sulphamethoxazole-trimethoprim
PHEN = Phenicols
RIF = Rifampicin
S = Streptothricin
X = Other resistance determinants

S1C

Fig. S1D. Evolutionary epidemiology and resistome of global *Citrobacter spp*, isolates, A and B. This tree shows information for additional *Citrobacter freundii* and *Citrobacter sp*. that were not featured figures 1, and S1A–C above. Included in S1D are *Serratia marcescens*, *Klebsiella*, *Enterobacter* and *Escherichia coli* species that were originally classified as *C. freundii*, but later reclassified into their actual species using ANI; their clustering away from *C. freundii* confirms the ANI results that they were initially misclassified. *C. freundii* clustered into four main clades (A, B1, B2 and B3), highlighted with distinct colours. Clade B3 had the most resistome abundance and diversity. Strains from humans (blue labels), animals (red labels), plants (purple/mauve labels) and the environment (green labels) were found in the same clade/cluster. Bla_{CMY} was conserved in these genomes. Branches with bootstrap support values of ≥50 were defined as belonging to the same clade. The branch lengths also show the evolutionary distance between the isolates. Blue and red arrows show the direction of evolution as well as local and international dissemination of strains of the same clone/clade through different hosts.



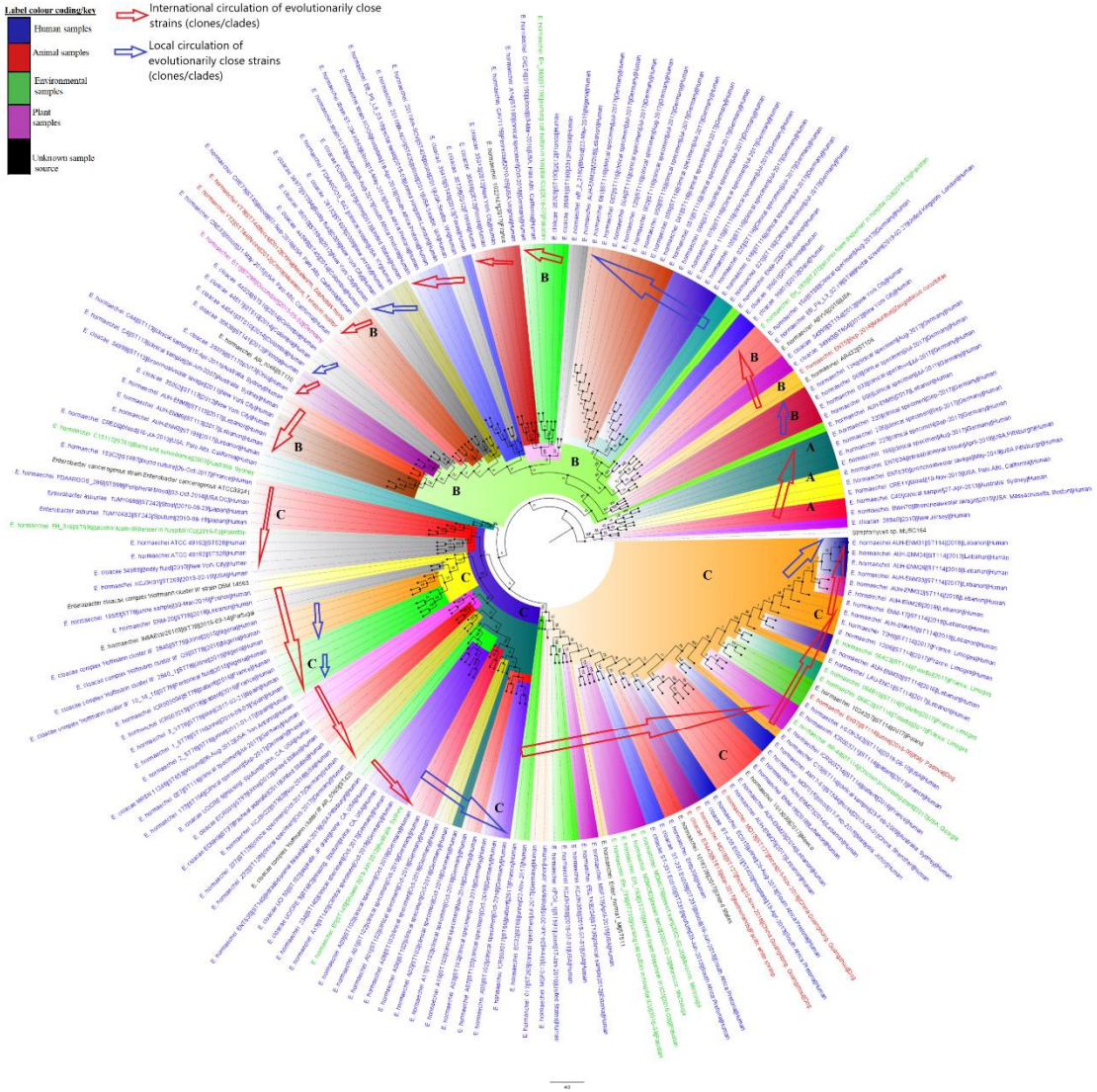


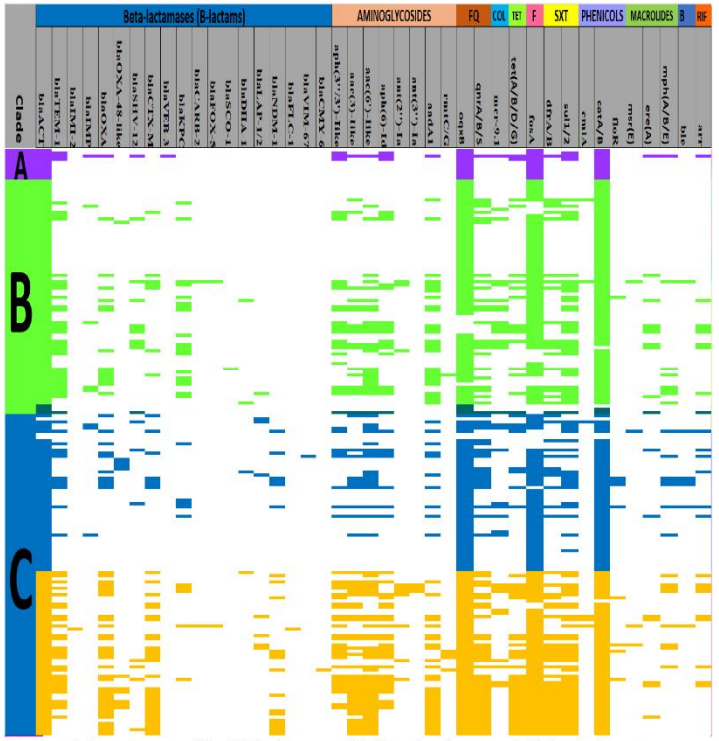
FQ=Fluoroquinolones ARGs
COL=Colistin ARGs
TET=Tetracycline ARGs
F= Fosfomycin ARGs
SXT Sulphamethoxazole-trimethoprim ARGs
RIF=Rifampicin ARGs
S= Streptothricin ARG

B Bleomycin
X=Other ARGs

S1D

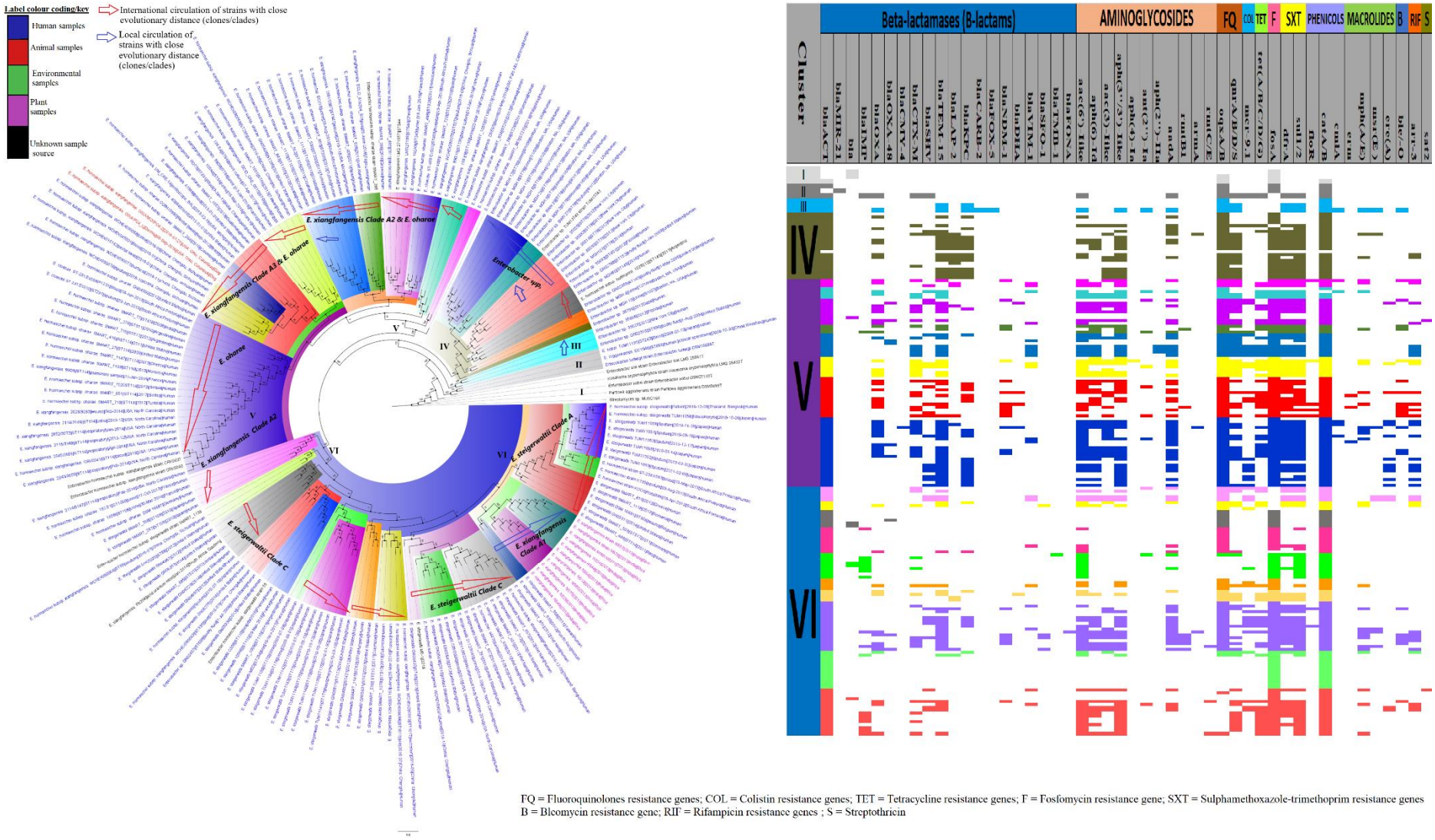
Figs S2A-B. Evolutionary epidemiology and resistome of global *Enterobacter hormaechei subsp*. Hormaechei, Xiangfangensis, Oharae, and Steigerwaltii, isolates. S2A is strictly *E. hormaechei subsp*. Hormaechei and is an addition to Figure 4 whilst S2B is an addition to Figures 3-4 above as additional genomes of *E. hormaechei subsp*. Xiangfangensis, Oharae, and Steigerwaltii; these could not be added to Figures 3-4 and are shown here in Fig. S2B. The *E. hormaechei* isolates in S2A clustered into three main clades A, B and C (with distinct highlights) that contained strains distributed globally from humans (blue labels), and animals (red labels), plants (purple/mauve labels) and the environment (green labels). Clades B and C contained diverse and rich resistome repertoire. bla_{ACT} was conserved in these genomes. S2B contains *E. hormaechei subsp*.Xiangfangensis, Oharae, and Steigerwaltii isolates clustering into 6 branches (I-VI); genomes of the same subsp. clustered closely together. Branches with bootstrap support values of ≥50 were defined as belonging to the same clade. The branch lengths also show the evolutionary distance between the isolates. Blue and red arrows show the direction of evolution as well as local and international dissemination of strains of the same clone/clade through different hosts.





FQ = Fluoroquinolones resistance genes; COL = Colistin resistance genes; TET = Tetracycline resistance genes; F = Fosfomycin resistance gene; B = Bleomycin resistance gene; RIF = Rifampicin resistance genes SXT = Sulphamethoxazole-trimethoprim resistance genes

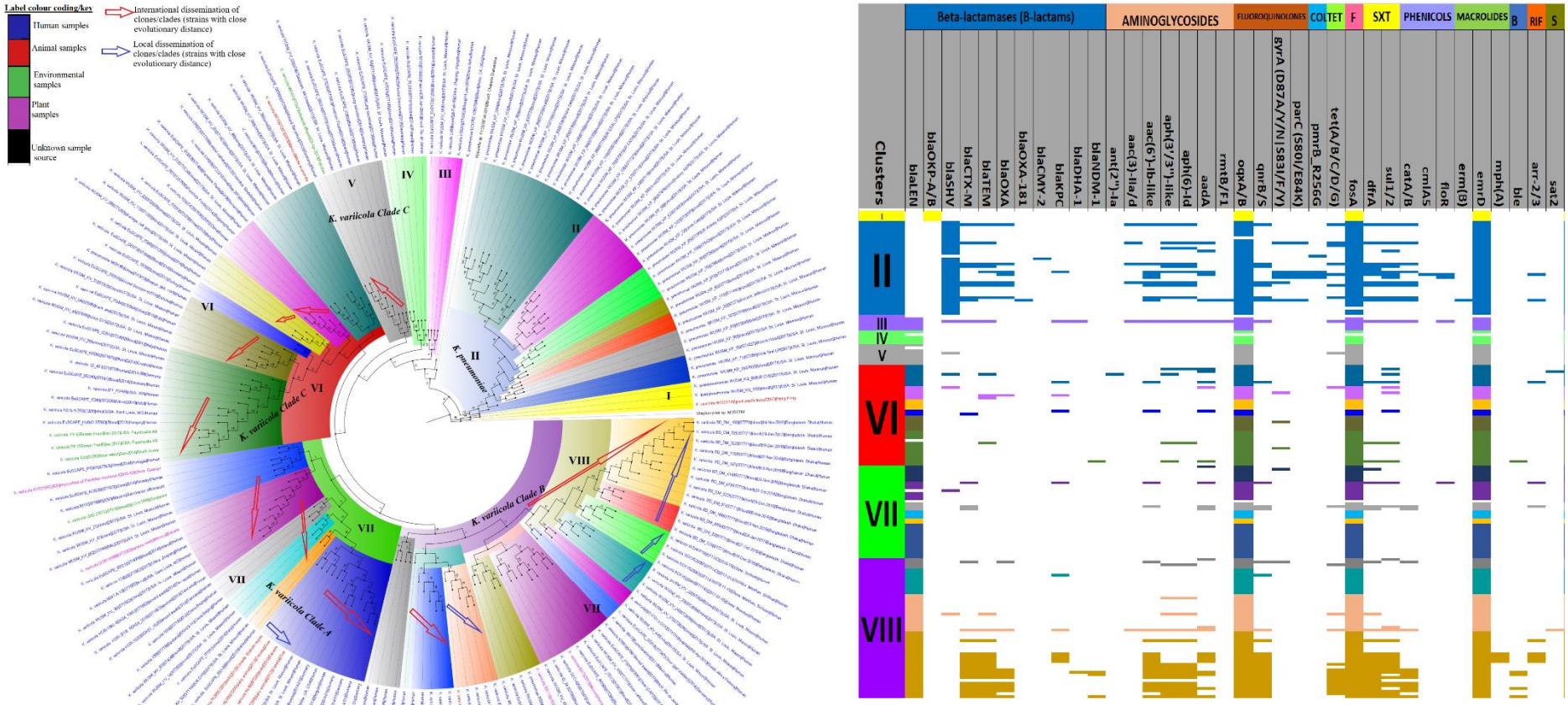
S2A



FQ = Fluoroquinolones resistance genes; COL = Colistin resistance genes; TET = Tetracycline resistance genes; F = Fosfomycin resistance gene; SXT = Sulphamethoxazole-trimethoprim resistance genes
B = Bleomycin resistance gene; RIF = Rifampicin resistance genes ; S = Streptothricin

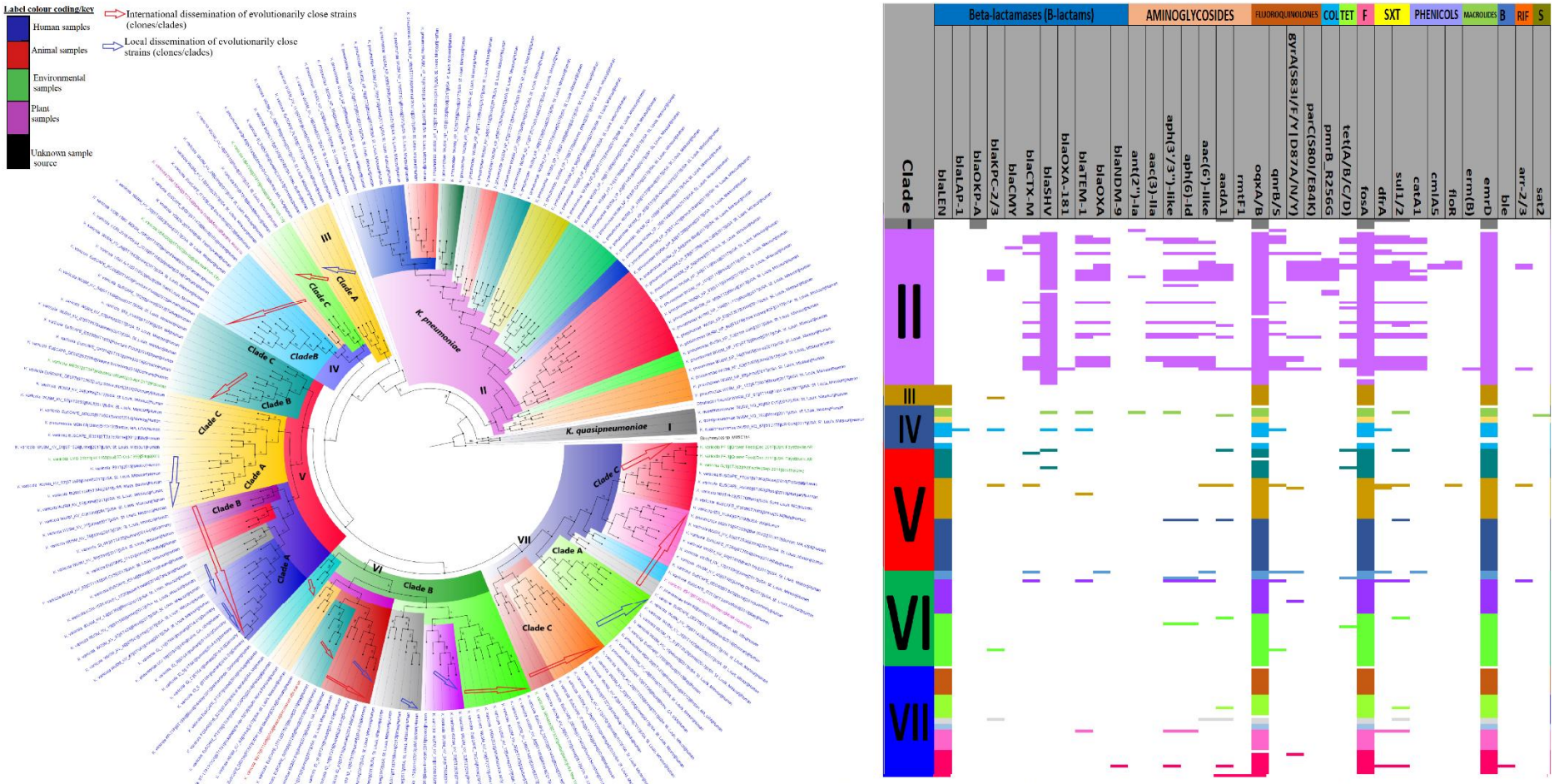
S2B

Fig. S3A-B. Evolutionary epidemiology and resistome of global *Klebsiella variicola* isolates. S3A-B are additional trees to Figure 5 and show additional *K. variicola* genomes that could not be added to Figure 5; in all, Figures 5 and S3A-B show 600 *K. variicola* genomes. S3A and S3B trees are composed of different *K. variicola* genomes, which is reflected in the differences in the resistomes and tree topologies. Included in S3A and S3B are *K. pneumoniae* and *K. pneumoniae* and *quasipneumoniae* species respectively, that were originally classified as *K. variicola*, but later reclassified into their actual species using ANI; their clustering away from *K. variicola* confirms the ANI results that they were initially misclassified. The *K. variicola* strains clustered into eight (S3A) and seven (S3B) clades I-VIII and I-VII respectively, which were highlighted with distinct colours and were isolated from countries around the globe. The clades contained strains distributed globally from humans (blue labels), animals (red labels), plants (purple/mauve labels) and the environment (green labels). Besides a few strains in clade B2, the other strains contained very few resistance genes. bla_{LEN} was conserved in these genomes. Branches with bootstrap support values of ≥50 were defined as belonging to the same clade. The branch lengths also show the evolutionary distance between the isolates. Blue and red arrows show the direction of evolution as well as local and international dissemination of strains of the same clone/clade through different hosts.



COL = Colistin resistance genes; TET = Tetracycline resistance genes; F = Fosfomycin resistance gene; SXT = Sulphamethoxazole-trimethoprim resistance genes; B = Bleomycin resistance gene; RIF = Rifampicin resistance gene; S = Streptothricin resistance gene

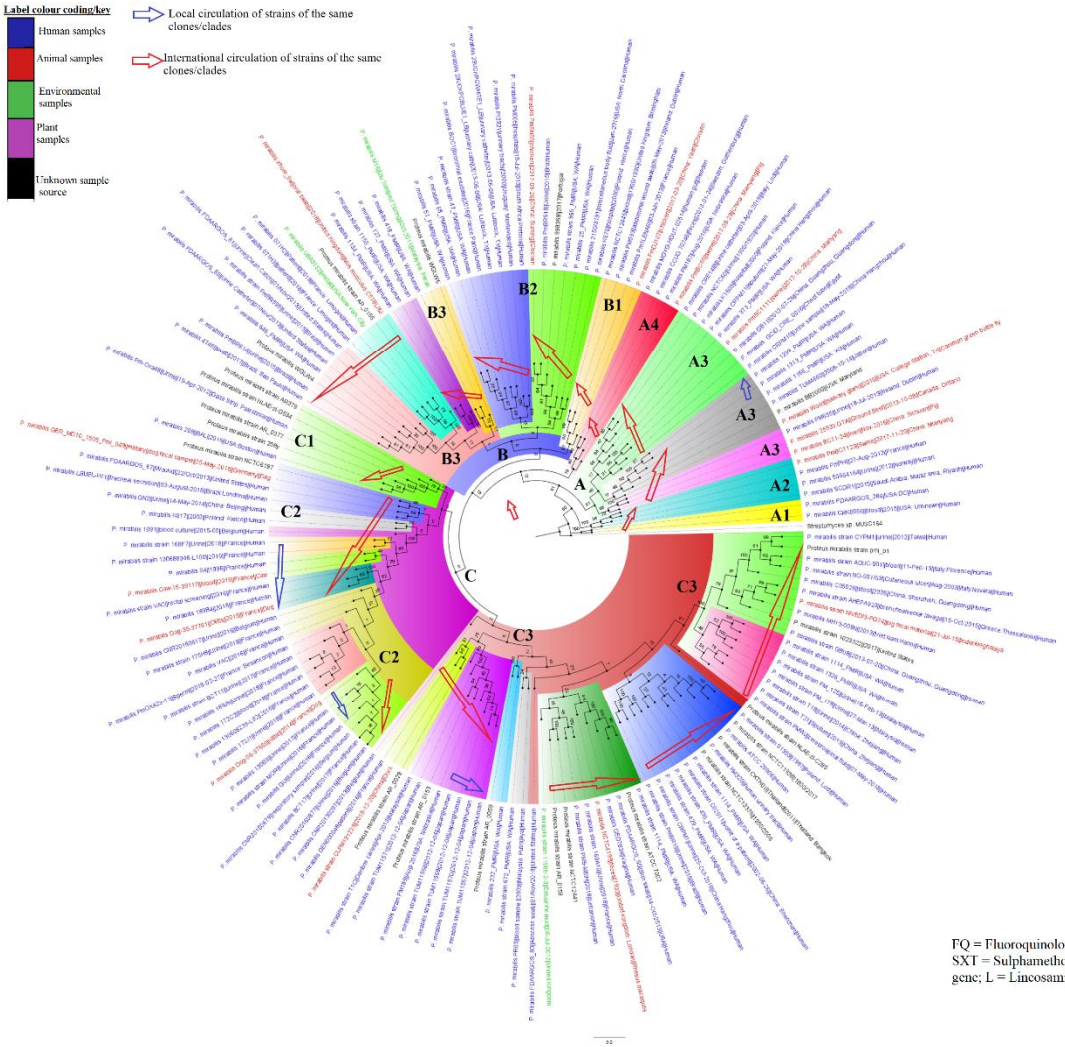
S3A

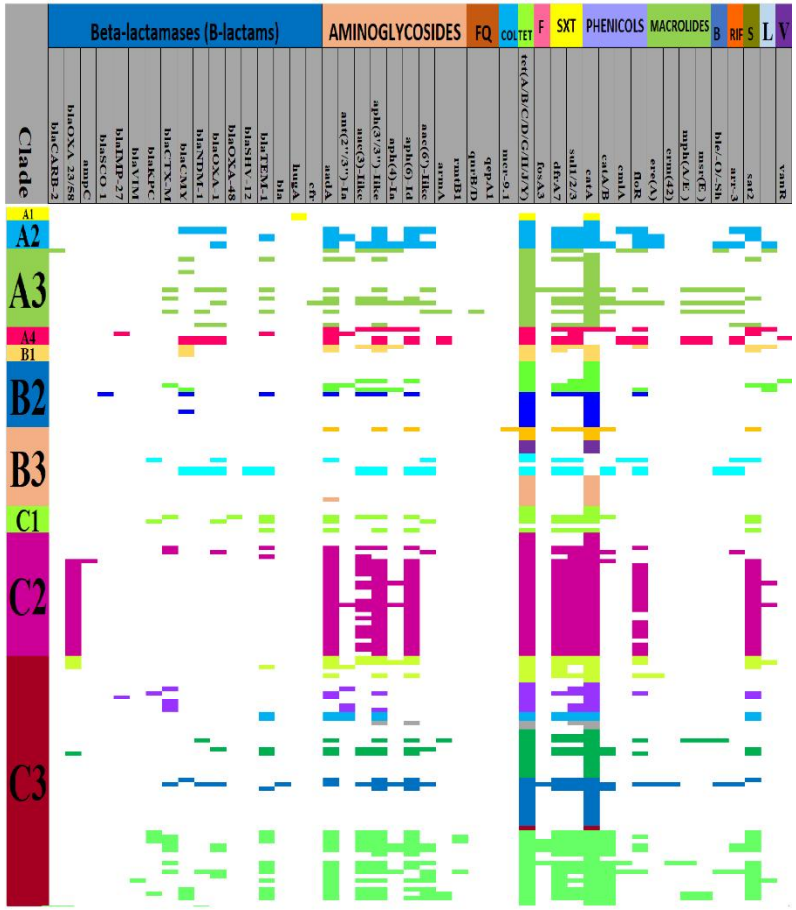


COL = Colistin resistance genes; TET = Tetracycline resistance genes; F = Fosfomycin resistance gene; SXT = Sulphamethoxazole-trimethoprim resistance genes; B = Bleomycin resistance gene; RIF = Rifampicin resistance gene; S = Streptothricin resistance gene

S3B

Fig. S4. Evolutionary epidemiology and resistome of global *Proteus mirabilis* isolates. The *P. mirabilis* isolates clustered into 10 clades, A-A3, B1-B3, and C1-C3 (shown with different highlights), which contained diverse and abundant resistomes with conserved *catA* and *tet* genes. The clades contained strains distributed globally from humans (blue labels), animals (red labels), plants (purple/mauve labels) and the environment (green labels). Branches with bootstrap support values of ≥50 were defined as belonging to the same clade. The branch lengths also show the evolutionary distance between the isolates. Blue and red arrows show the direction of evolution as well as local and international dissemination of strains of the same clone/clade through different hosts.

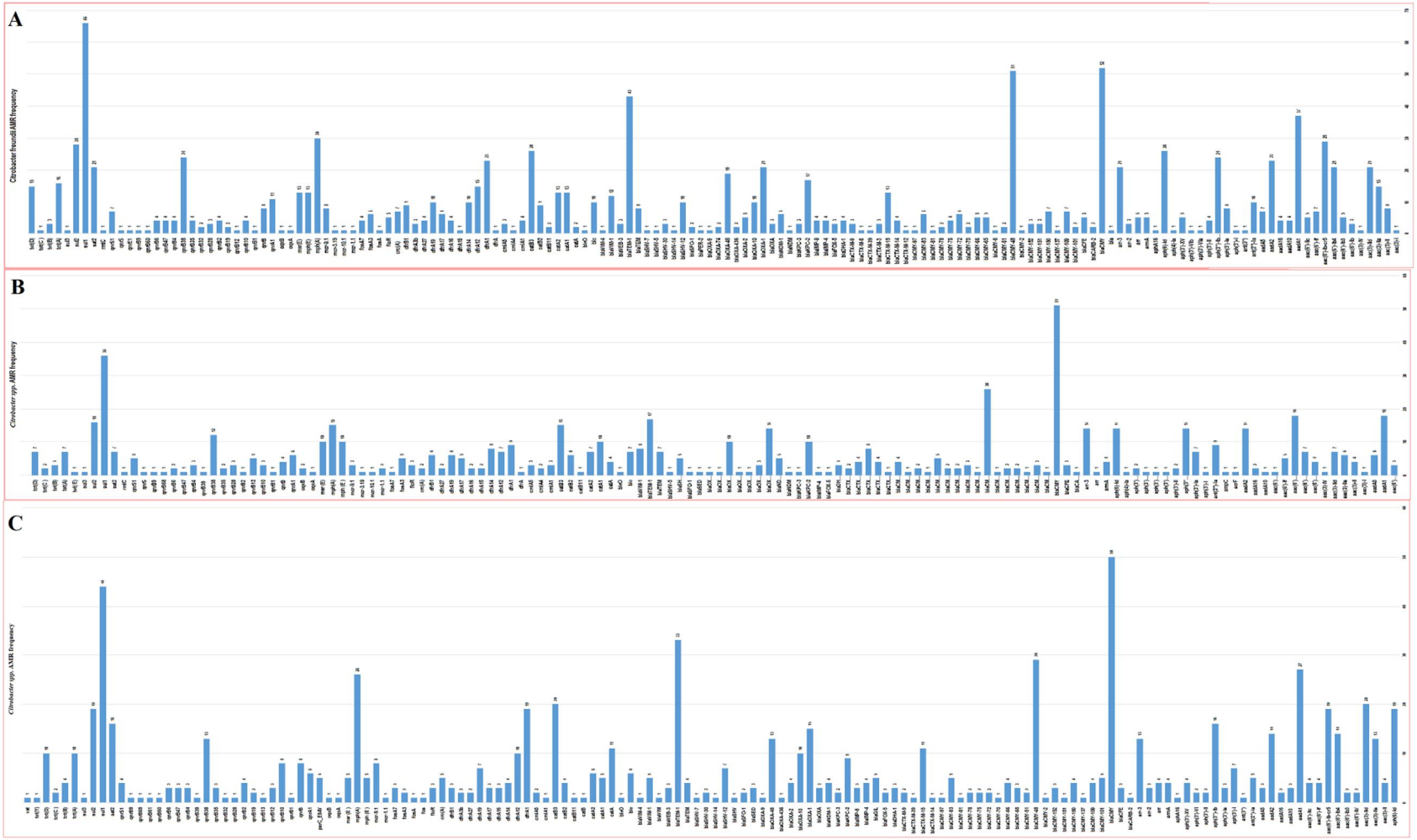




FQ = Fluoroquinolones resistance genes; COL = Colistin resistance genes; TET = Tetracycline resistance genes; F = Fosfomycn resistance gene; SXT = Sulphamethoxazole-trimethoprim resistance genes; B = Bleomycin resistance genes; RIF = Rifampicin resistance gene; S = Streptothricin resistance gene; L = Lincosamide resistance gene; V = Vancomycin resistance gene.

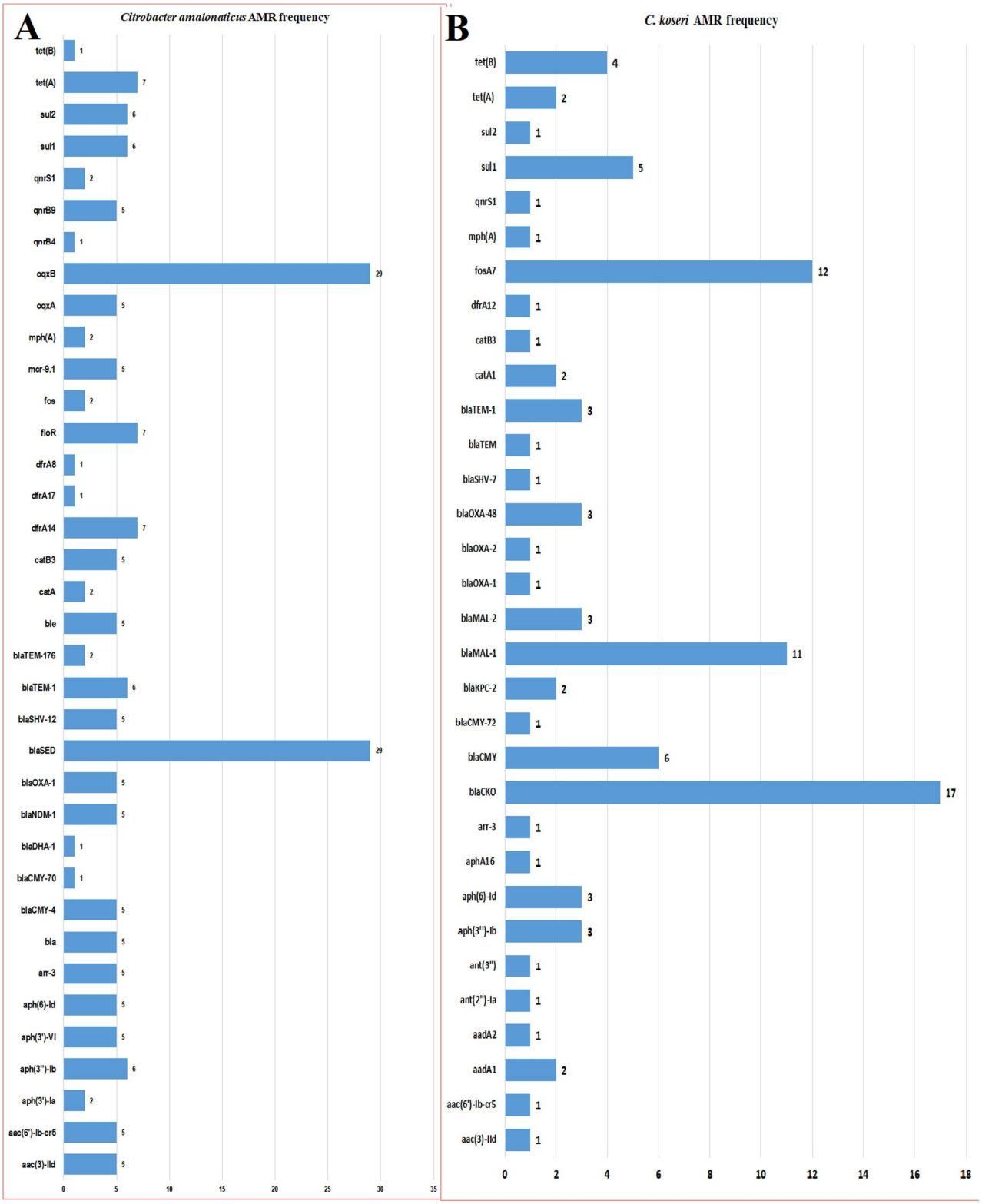
S4

Fig. S5 (A-C). Count of antibiotic resistance genes (ARGs) in *Citrobacter freundii* (A), and *Citrobacter species* (B and C). The sum of each unique ARG and its variants are computed and shown as a bar chart to depict the most abundant ARGs.



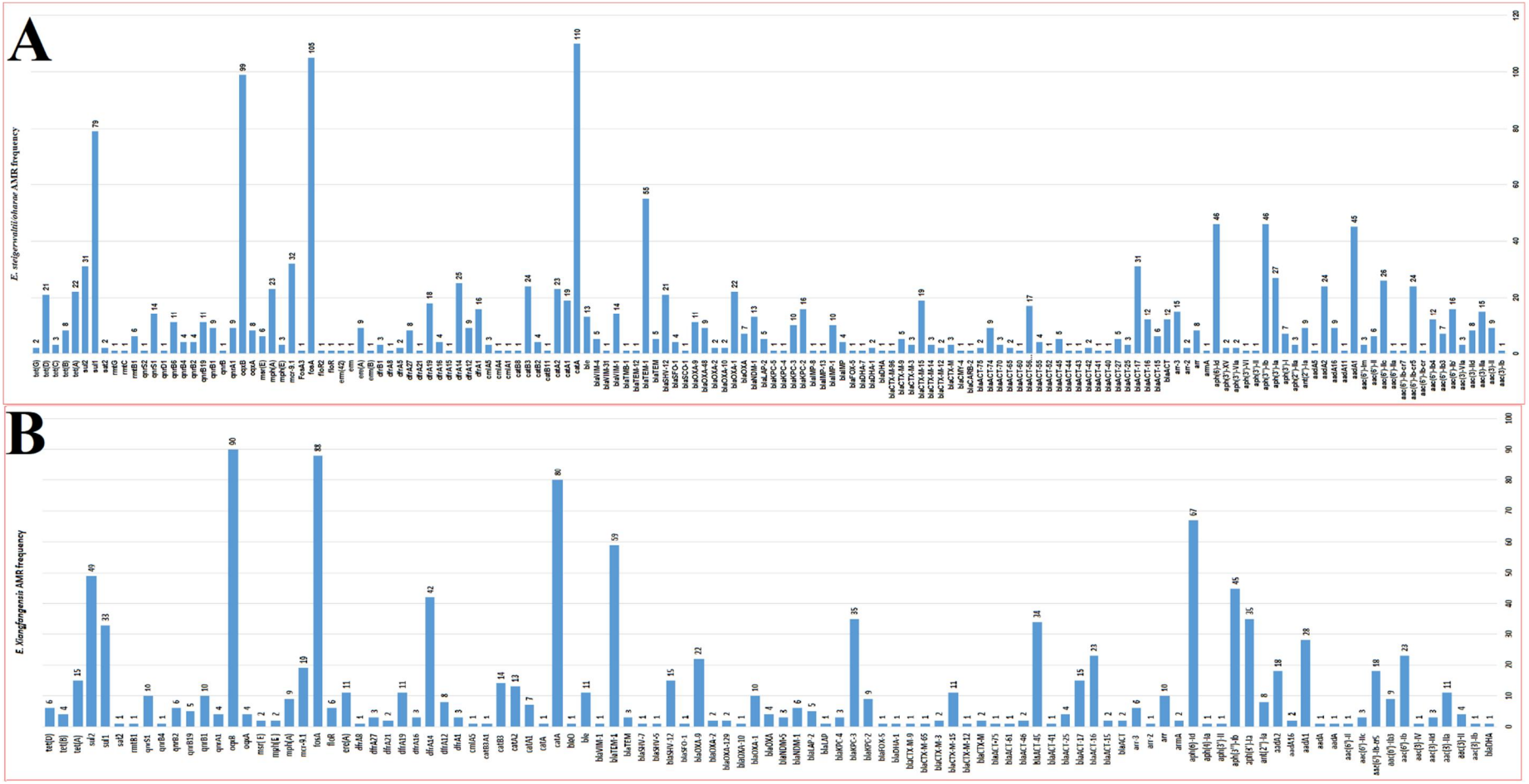
S5A-C

Fig. S6 (A-B). Count of antibiotic resistance genes (ARGs) in *Citrobacter amalonaticus* (A), and *Citrobacter koseri* (B). The sum of each unique ARG and its variants are computed and shown as a bar chart to depict the most abundant ARGs.



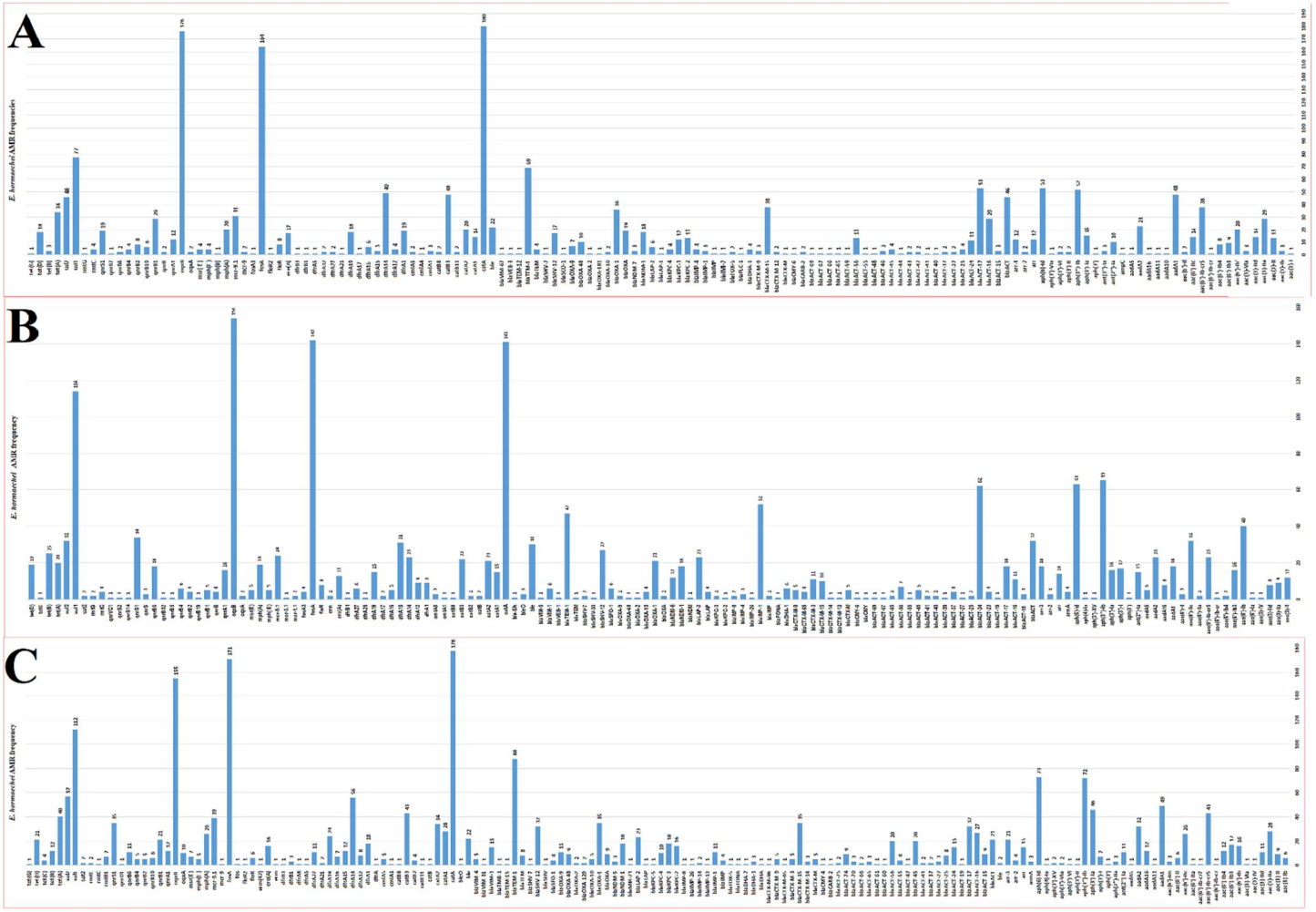
S6A-B

Fig. S7 (A-B). Count of antibiotic resistance genes (ARGs) in *Enterobacter steigerwaltii* and *oharae* (A), and *Enterobacter xiangfangensis* (B). The sum of each unique ARG and its variants are computed and shown as a bar chart to depict the most abundant ARGs.



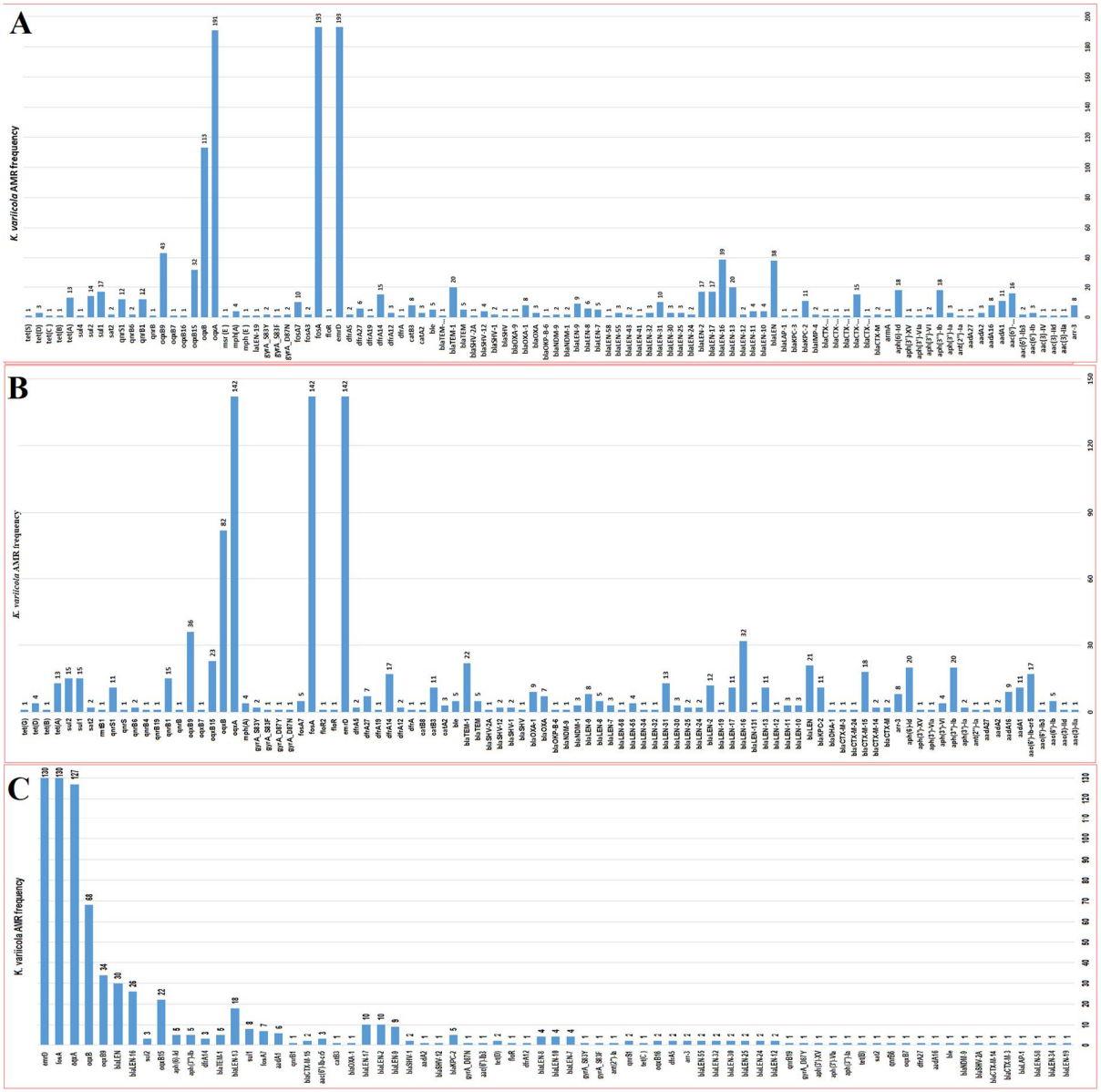
S7A-B

Fig. S8 (A-C). Count of antibiotic resistance genes (ARGs) in *Enterobacter hormaechei* (A, B and C). The sum of each unique ARG and its variants are computed and shown as a bar chart to depict the most abundant ARGs.



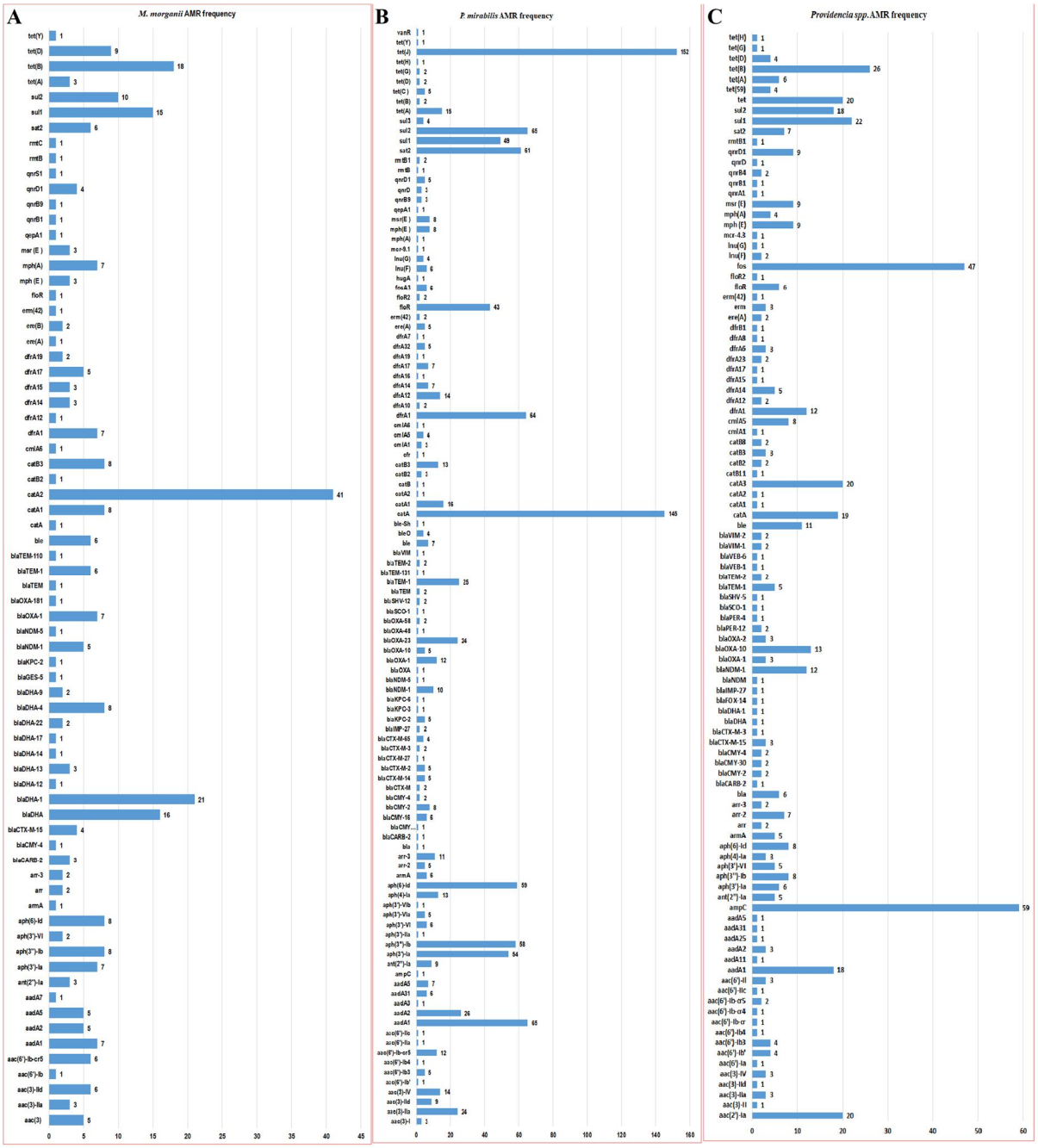
S8 A-C

Fig. S9 (A-C). Count of antibiotic resistance genes (ARGs) in *Klebsiella variicola* (A, B and C). The sum of each unique ARG and its variants are computed and shown as a bar chart to depict the most abundant ARGs.



S9 A-C

Fig. S10 (A-C). Count of antibiotic resistance genes (ARGs) in *Morganella morganii* (A), *Proteus mirabilis* (B) and *Providencia species* (C). The sum of each unique ARG and its variants are computed and shown as a bar chart to depict the most abundant ARGs.



S10 A-C