

EURL workshop May 2023

1. EURL AST EQAS 2022 (E. coli, Salmonella, Campylobacter, S. aureus) summary slides
2. Genomic Proficiency Test 2022 summary slides

- E. coli, Salmonella, Campylobacter, Staphylococcus
- E. coli, Salmonella
- E. coli

Participating countries in the 30th EURL-AR PT (n=33) that performed antimicrobial susceptibility testing of E. coli, Salmonella, Campylobacter and Staphylococcus (S. aureus). The map was created on MapChart.



Created with mapchart.net

Table 1. Panels of antimicrobials used in this EURL-AR proficiency test 2022.

<i>E. coli</i> & <i>Salmonella</i>		<i>Campylobacter</i>	<i>S. aureus</i>
Panel 1 (EUVSEC3)	Panel 2 (EUVSEC2)	Panel 1 (EUCAMP3)	Panel 1 (EUST2)
Amikacin (AMI) Ampicillin (AMP) Azithromycin (AZI) Cefotaxime (FOT or CTX) Ceftazidime (TAZ or CAZ) Chloramphenicol (CHL) Ciprofloxacin (CIP) Colistin (COL) Gentamicin (GEN) Meropenem (MERO) Nalidixic acid (NAL) Sulfonamides (SMX) Tetracycline (TET) Tigecycline (TGC) Trimethoprim (TMP)	Cefepime (FEP) Cefotaxime (FOT or CTX) Cefotaxime+clavulanic acid (F/C) Cefoxitin (FOX) Ceftazidime (TAZ or CAZ) Ceftazidime+clavulanic acid Ertapenem (ETP) Imipenem (IMI) Meropenem (MERO) Temocillin (TRM)	Chloramphenicol Ciprofloxacin (CIP) Ertapenem (ETP) Erythromycin (ERY) Gentamicin (GEN) Tetracycline (TET)	Cefoxitin (FOX) Chloramphenicol (CHL) Ciprofloxacin (CIP) Clindamycin (CLI) Erythromycin (ERY) Fusidic acid (FUS) Gentamicin (GEN) Kanamycin (KAN) Linezolid (LZD) Mupirocin (MUP) Penicillin (PEN) Quinupristin-dalfopristin

Table 1. Strain-antimicrobial combinations that were omitted from the evaluation.

Trial	Strain/antimicrobial combination omitted from the evaluation (Scores blanked)	%Deviation level
<i>E. coli</i>	EC-17.1/Cefoxitin	30.3
<i>E. coli</i>	EC-17.7/Chloramphenicol	53.1
<i>E. coli</i>	EC-17.7/Imipenem	48.5
<i>Salmonella</i>	S-17.1/Amikacin	31.3
<i>Salmonella</i>	S-17.2/Tigecycline	31.3
<i>Salmonella</i>	S-17.3/Imipenem	67.7
<i>Campylobacter</i>	C-17.8/Chloramphenicol	86.7
<i>S. aureus</i>	ST-17.1/Ciprofloxacin	34.6
<i>S. aureus</i>	ST-17.6/Quinopristin-dalfopristin	68.0

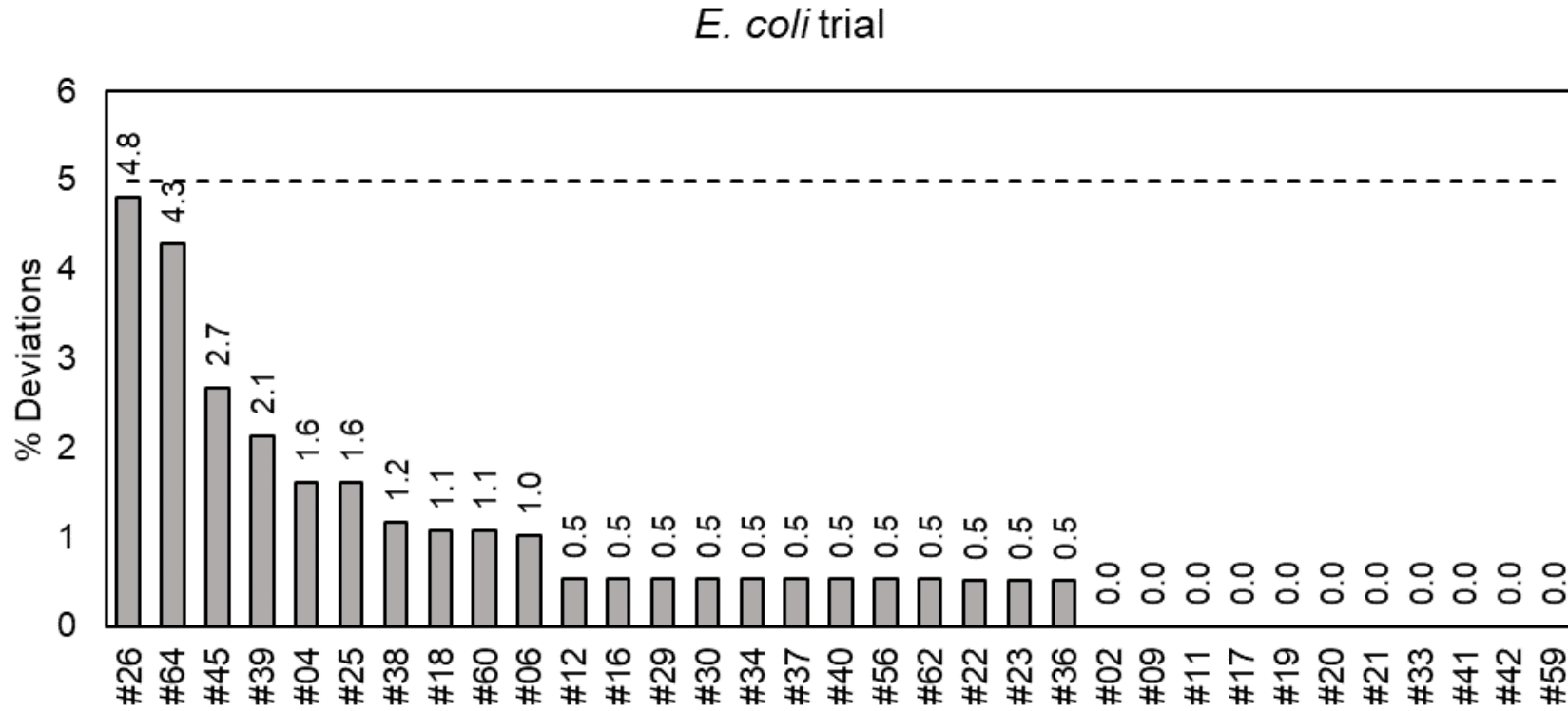


Figure 1. Percent deviation level for each laboratory, AST results, *E. coli* trial.

E. coli trial, ESBL categorisation

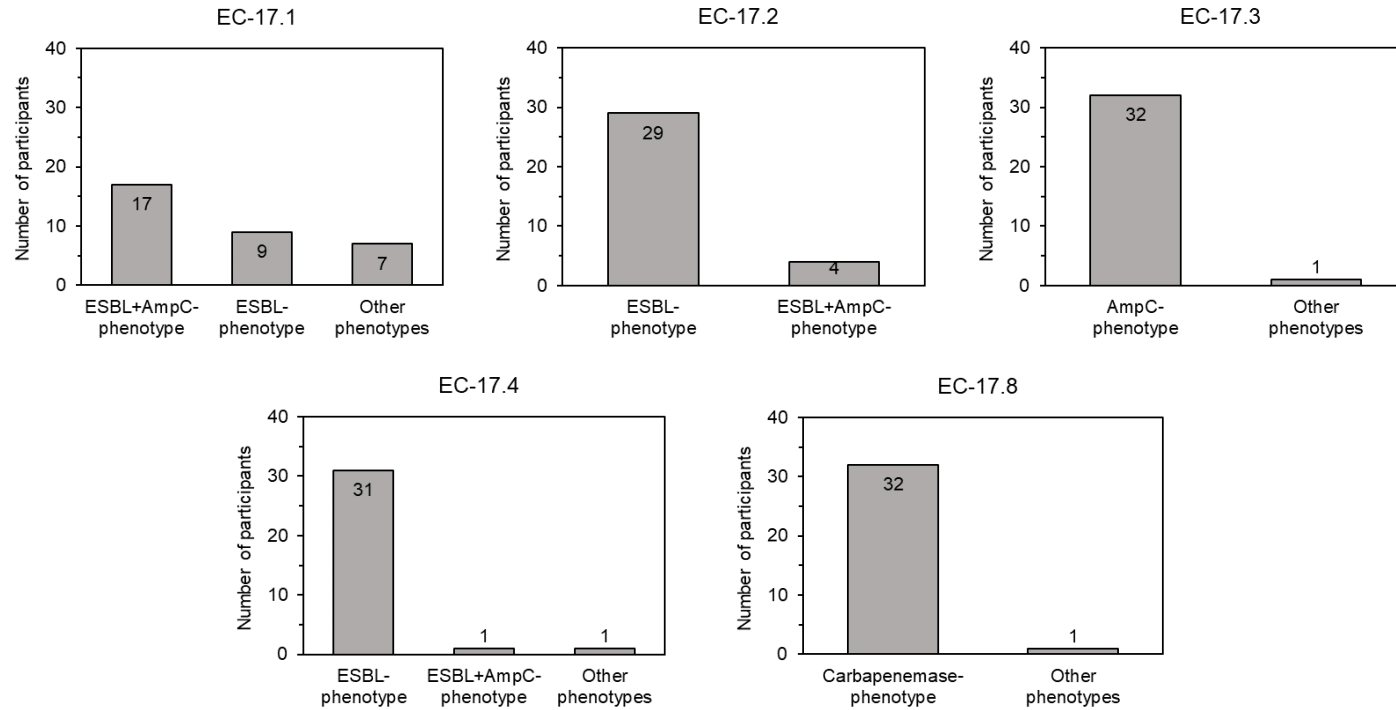


Figure 1. Obtained ESBL phenotypes for strains EC-17.1, EC-17.2, EC-17.3 EC-17.4 and EC-17.8.

E. coli trial, drug/bug deviation level

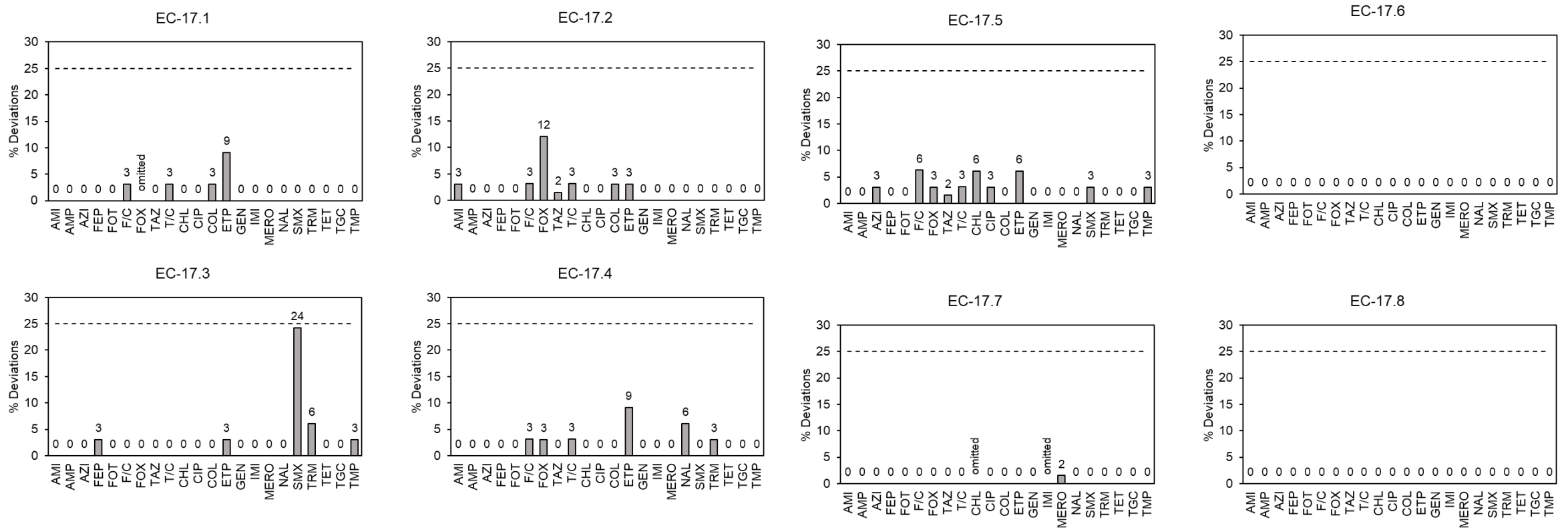


Figure 1. Percent deviation level for each strain-antimicrobial combination, E. coli trial.

Salmonella trial

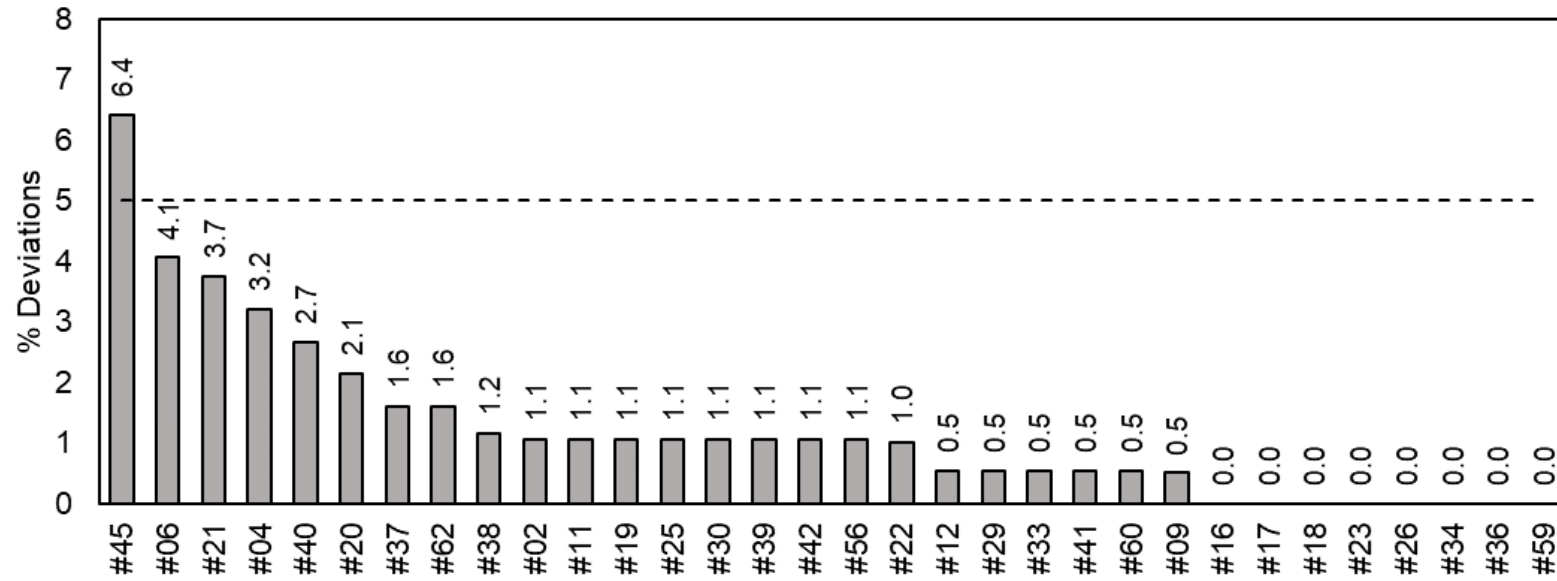


Figure 1. Percent deviation level for each laboratory, AST data, Salmonella trial.

Salmonella trial, drug/bug deviation level

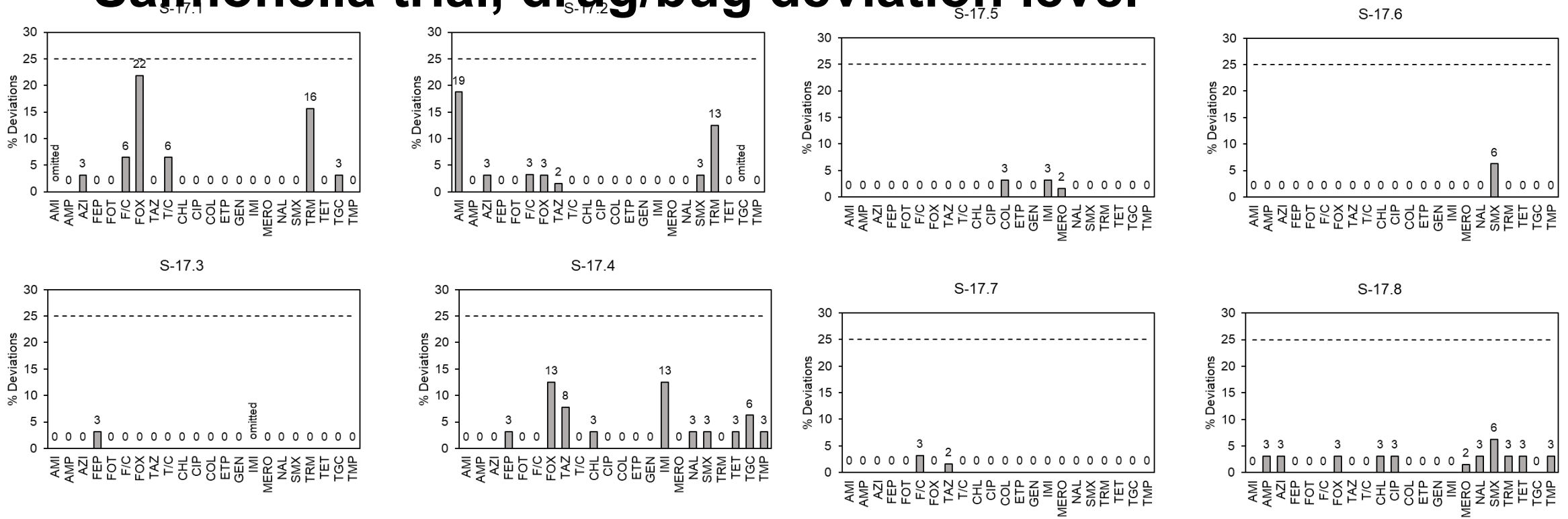


Figure 1. Percent deviation level for each strain-antimicrobial combination, Salmonella trial.

Salmonella trial, ESBL categorisation

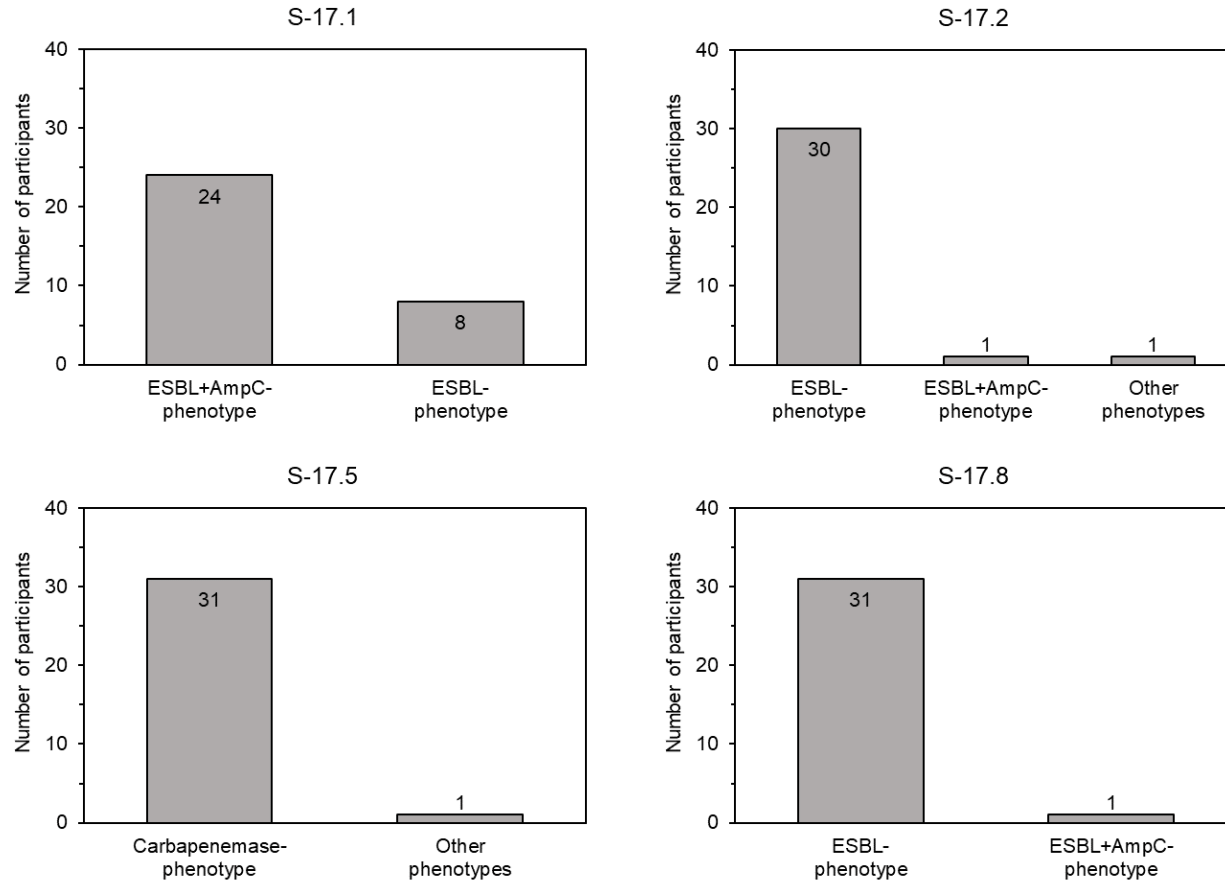


Figure 1. Obtained ESBL phenotypes for strains S-17.1, S-17.2, S-17.5 and S-17.8.

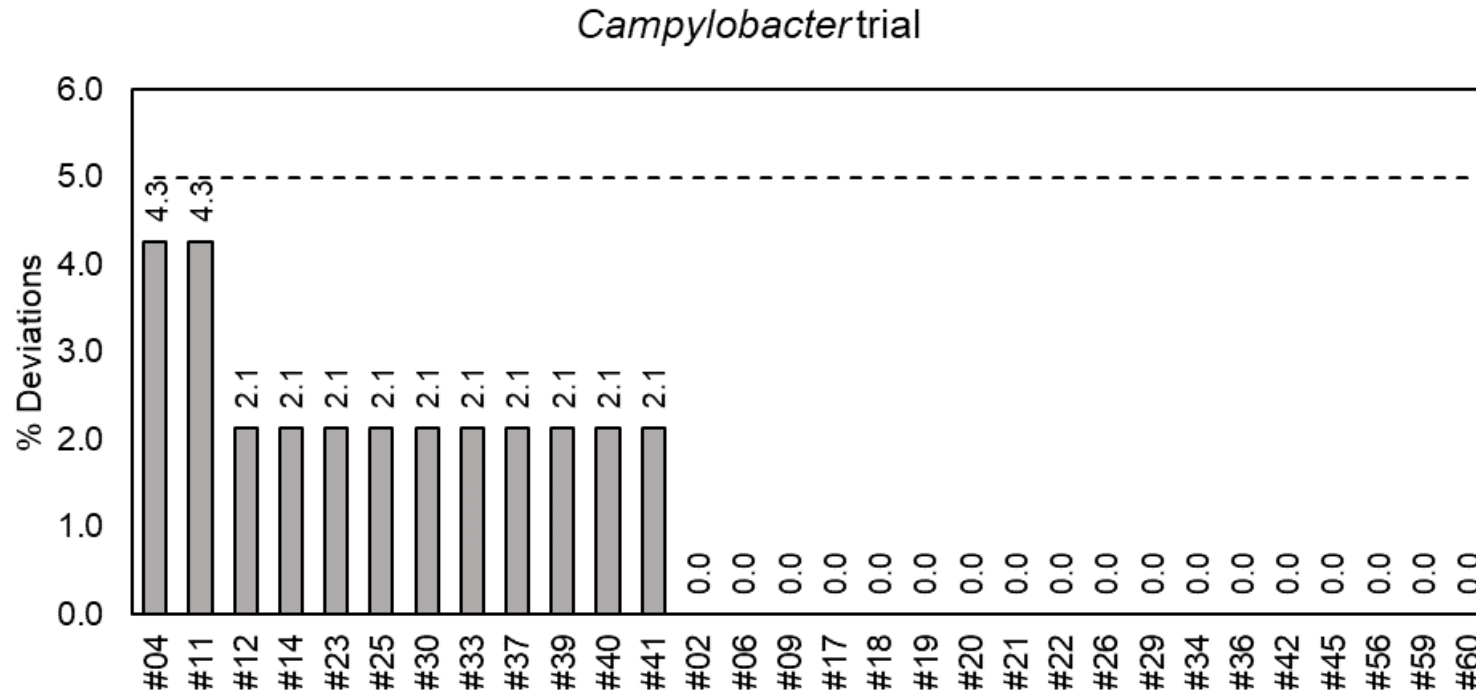


Figure 1. Percent deviation level for each laboratory, AST data, Campylobacter trial.

Campylobacter trial, drug/bug deviation level

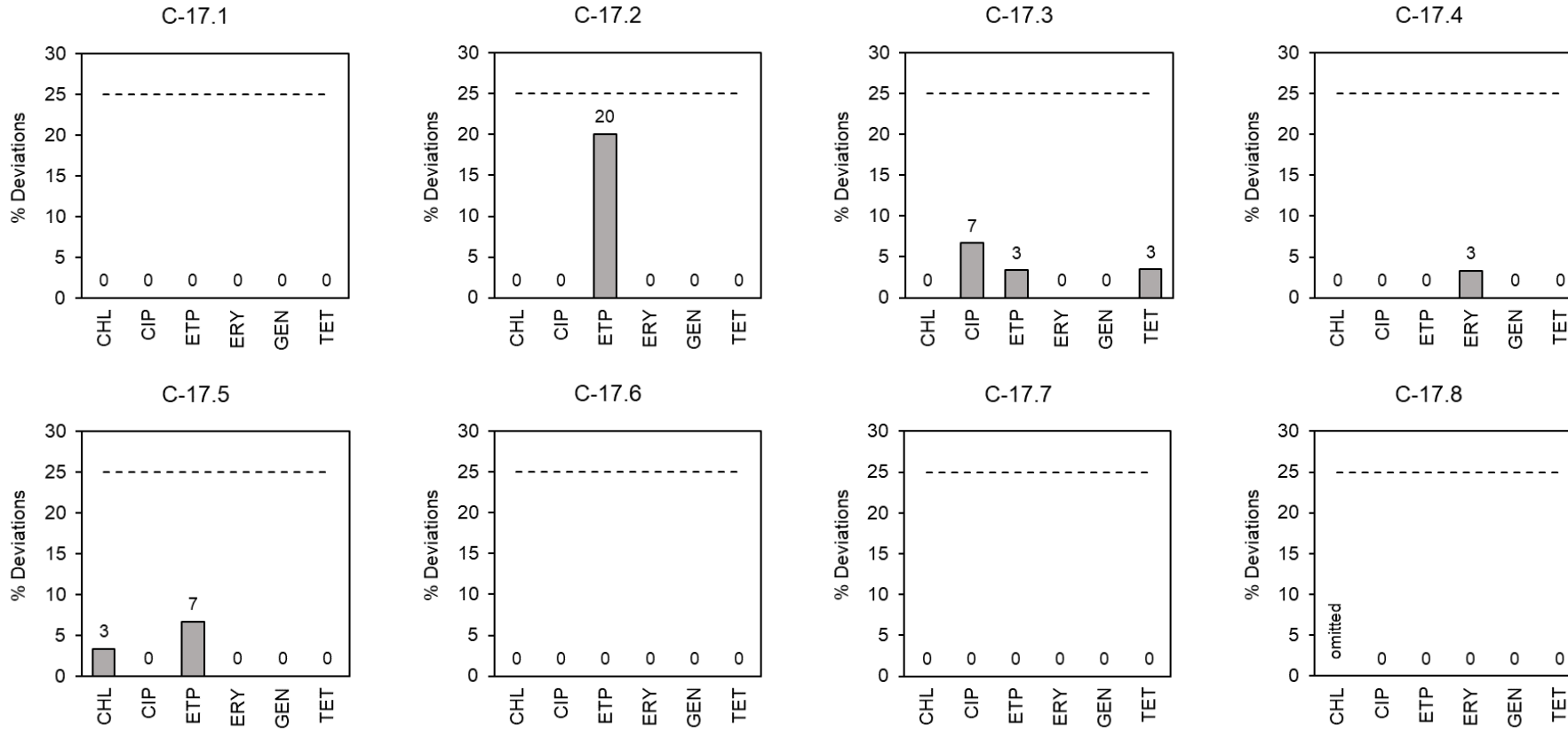


Figure 1. Percent deviation level for each strain-antimicrobial combination, Campylobacter trial.

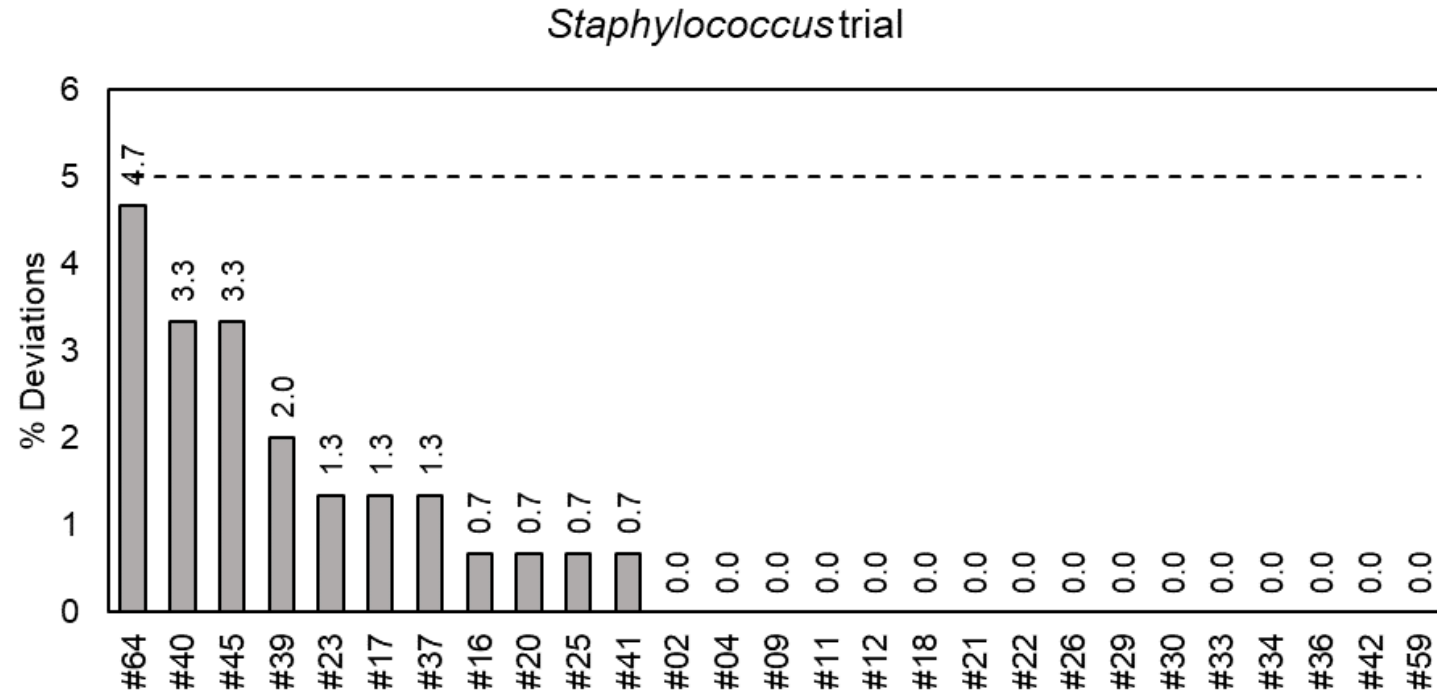


Figure 1. Percent deviation level for each laboratory, AST data, S. aureus trial.

S. aureus trial, drug/bug deviation level

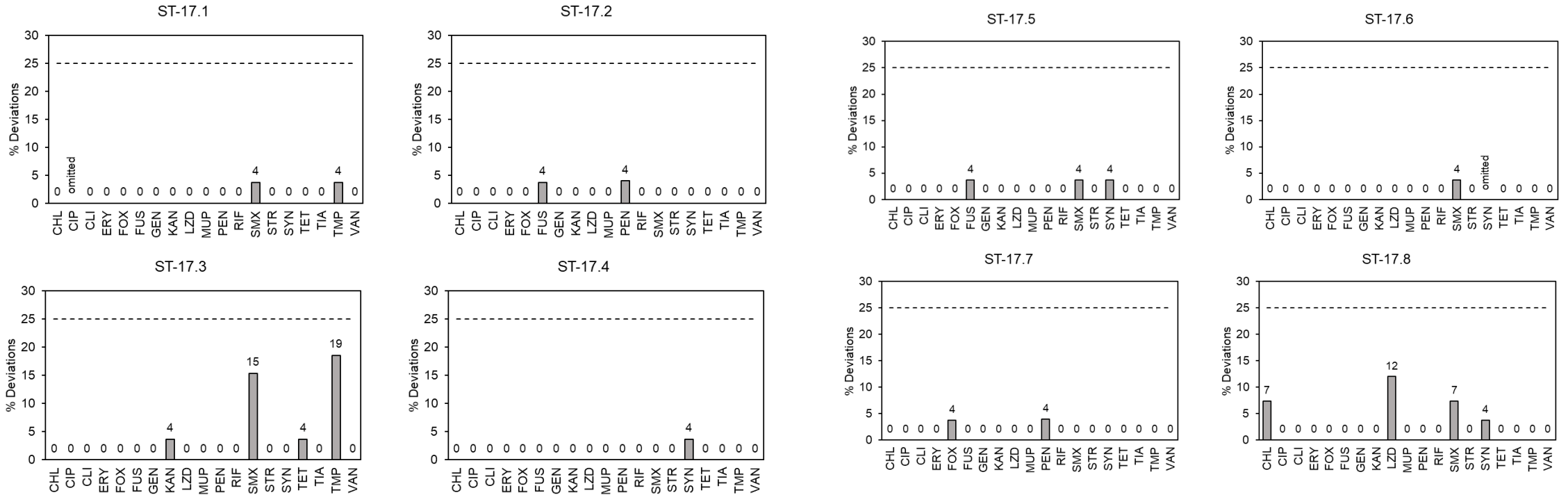
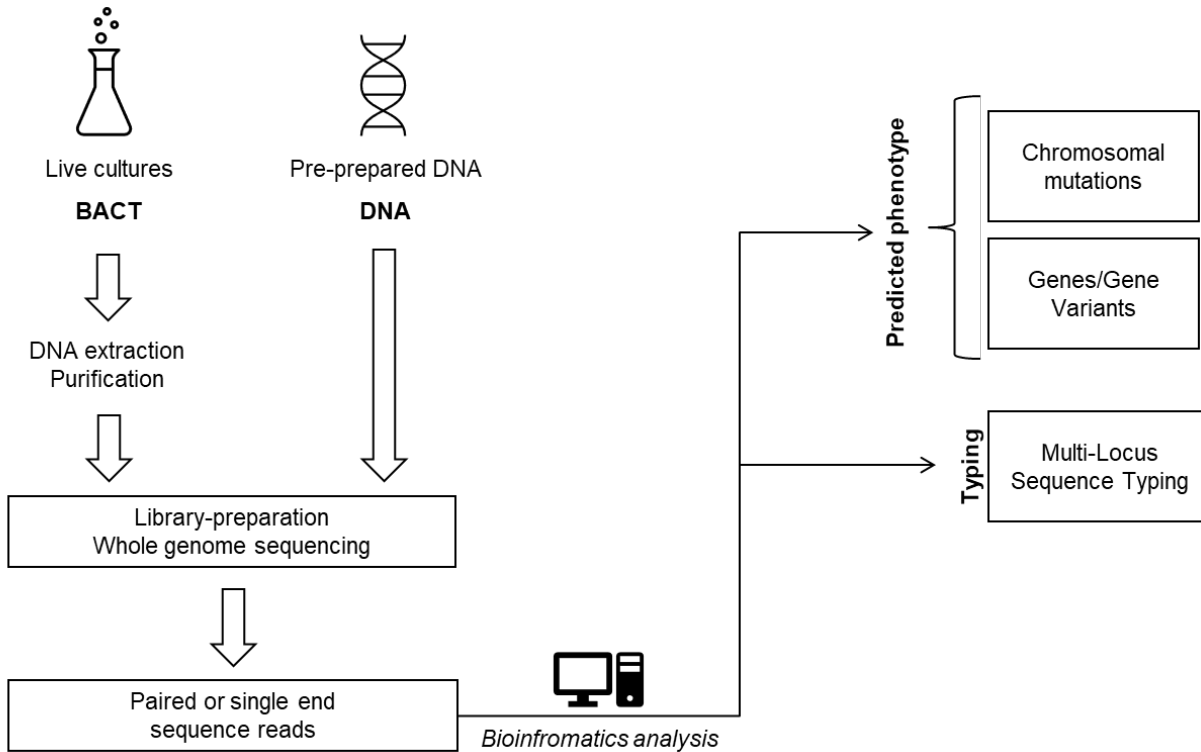


Figure 1. Percent deviation level for each strain-antimicrobial combination, S. aureus trial.



Schematic overview of the downstream processing of live culture samples (BACT) and pre-prepared DNA samples (DNA).

Species	Strain code	Type of sample
<i>S. aureus</i>	GENOMIC22-001	BACT/DNA
	GENOMIC22-002	BACT/DNA
<i>E. coli</i>	GENOMIC22-003	BACT/DNA
	GENOMIC22-004	BACT/DNA
<i>E. faecalis/E. faecium</i>	GENOMIC22-005	BACT/DNA
	GENOMIC22-006	BACT/DNA

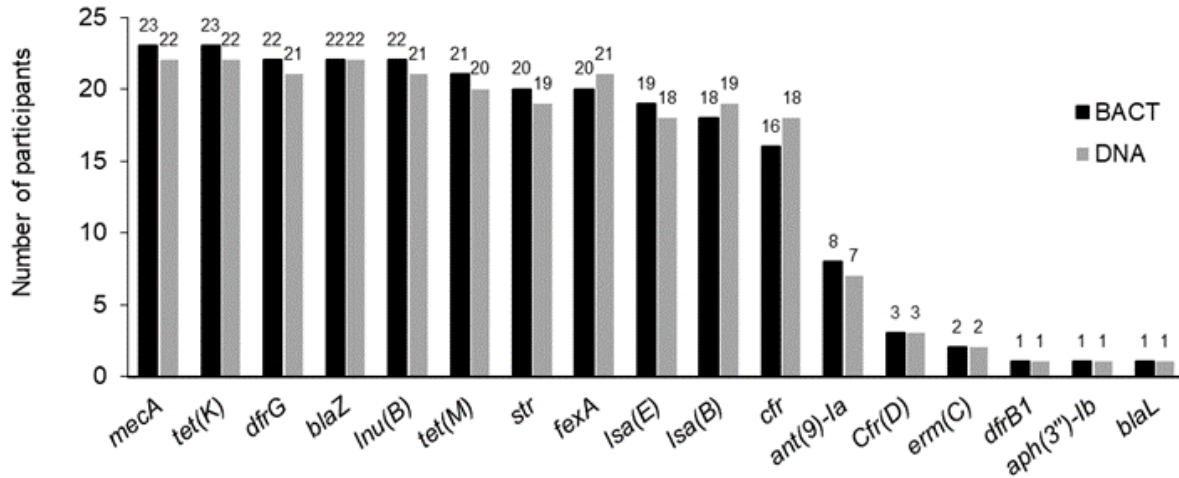
Strains included in DTU Genomic PT 2022. Two types of sample were analysed for each strain: DNA isolated from live cultures (BACT) and pre-prepared DNA (DNA).

Overview of antimicrobials included in DTU Genomic PT 2022, for *S. aureus*, *E. coli* and *E. faecalis/E. faecium*

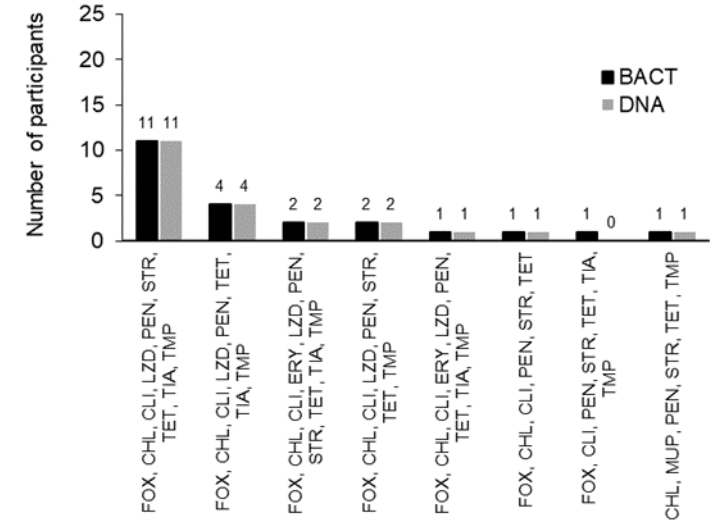
Antimicrobial	Abbreviation	Class	<i>S. aureus</i>	<i>E. coli</i>	<i>E. faecalis/E. faecium</i>
Amikacin	AMI	Aminoglycoside	-	X	-
Ampicillin	AMP	Beta-lactam	-	X	X
Azithromycin	AZI	Macrolide	-	X	-
Cefepime	FEP	Beta-lactam	-	X	-
Cefotaxime	FOT	Beta-lactam	-	X	-
Cefoxitin	FOX	Beta-lactam	X	X	-
Ceftazidime	TAZ	Beta-lactam	-	X	-
Chloramphenicol	CHL	Amphenicol	X	X	X
Ciprofloxacin	CIP	Quinolone	X	X	X
Clindamycin	CLI	Lincosamide	X	-	-
Colistin	COL	Polymyxin	-	X	-
Ertapenem	ETP	Beta-lactam	-	X	-
Erythromycin	ERY	Macrolide	X	-	X
Fusidate	FUS	Steroid antibacterial	X	-	-
Gentamicin	GEN	Aminoglycoside	X	X	X
Imipenem	IMI	Beta-lactam	-	X	-
Kanamycin	KAN	Aminoglycoside	X	-	-
Linezolid	LZD	Oxazolidinone	X	-	X
Meropenem	MERO	Beta-lactam	-	X	-
Mupirocin	MUP	Pseudomonic acid	X	-	-
Nalidixic acid	NAL	Quinolone	-	X	-
Penicillin	PEN	Beta-lactam	X	-	-
Rifampin	RIF	Rifamycin	X	-	-
Streptomycin	STR	Aminoglycoside	X	-	-
Sulfamethoxazole	SMX	Folate pathway antagonist	X	X	-
Teicoplanin	TEI	Glycopeptide	-	-	X
Temocillin	TRM	Beta-lactam	-	X	-
Tetracycline	TET	Tetracycline	X	X	X
Tiamulin	TIA	Pleuromutilin	X	-	-
Tigecycline	TGC	Tetracycline	-	X	X
Trimethoprim	TMP	Folate pathway antagonist	X	X	-
Vancomycin	VAN	Glycopeptide	X	-	X

GENOMIC22-001

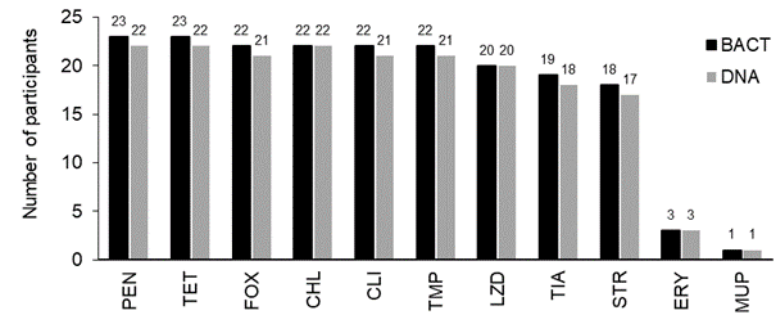
AMR genes - *S. aureus*, GENOMIC22-001



Predicted AMR phenotypic profile
S. aureus, GENOMIC22-001

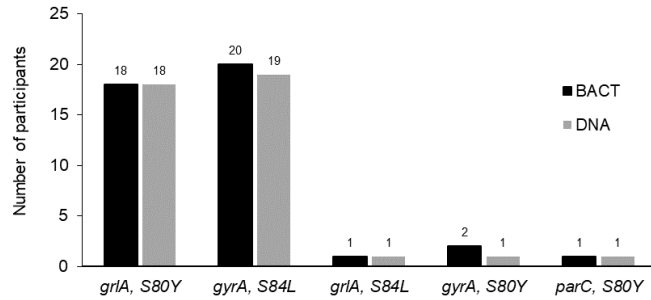


Predicted AMR phenotype (individual antimicrobials)
S. aureus, GENOMIC22-001

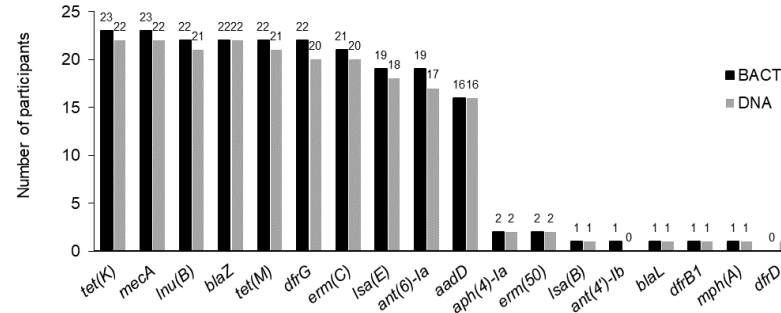


GENOMIC22-02

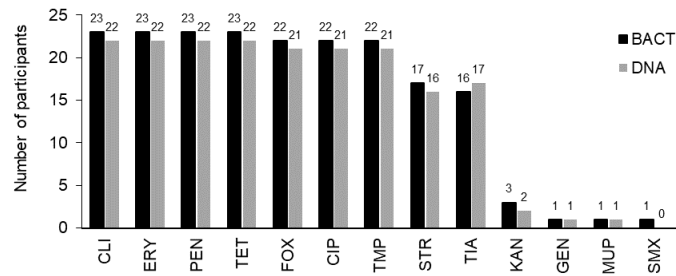
AMR Chr. mutations - *S. aureus*, GENOMIC22-002



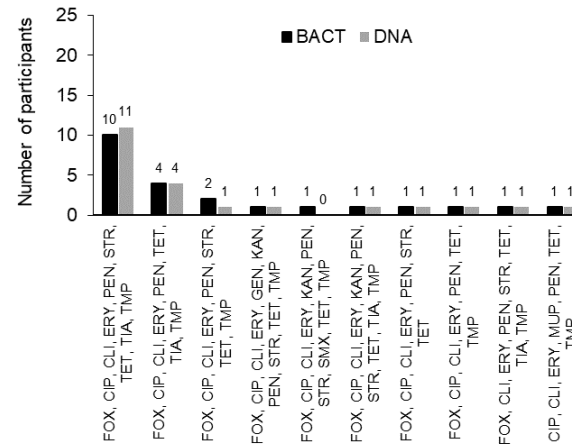
AMR genes - *S. aureus*, GENOMIC22-002



Predicted AMR phenotype (individual antimicrobials) *S. aureus*, GENOMIC22-002

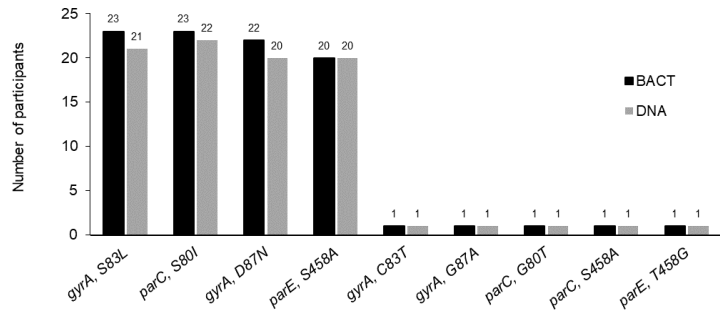


Predicted AMR phenotypic profile *S. aureus*, GENOMIC22-002

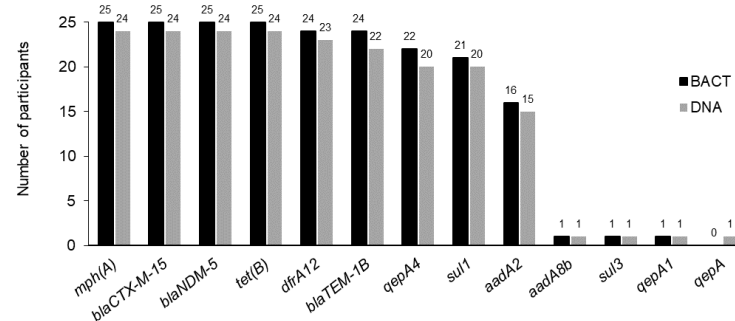


GENOMIC22-03

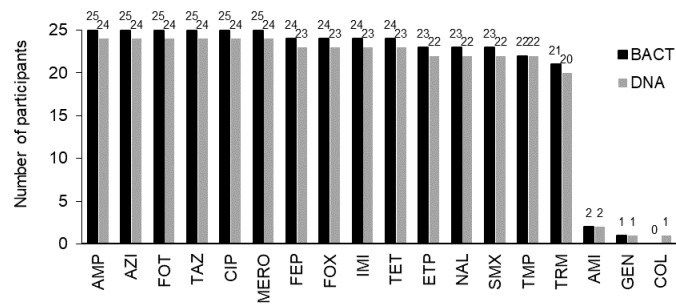
AMR Chr. mutations - *E. coli*, GENOMIC22-003



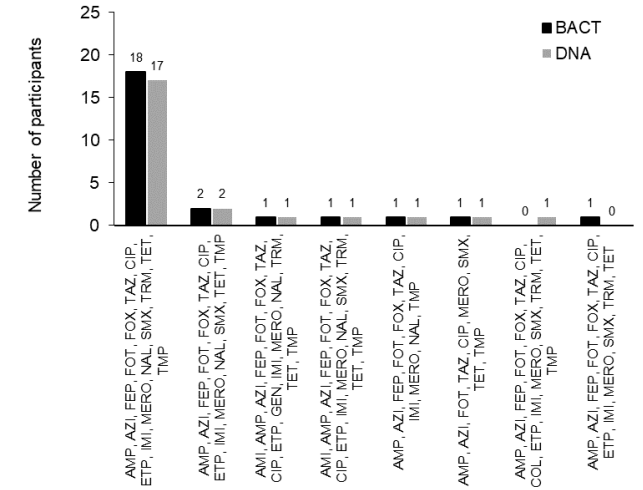
AMR genes - *E. coli*, GENOMIC22-003



Predicted AMR phenotype (individual antimicrobials) *E. coli*, GENOMIC22-003

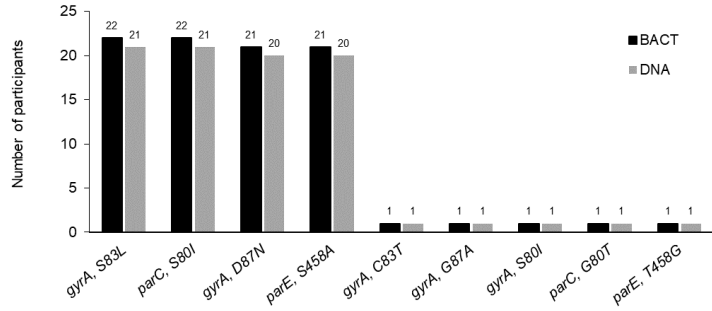


Predicted AMR phenotypic profile *E. coli*, GENOMIC22-003

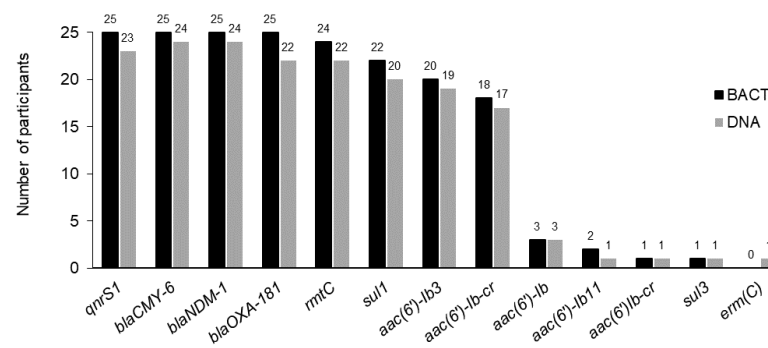


GENOMIC22-04

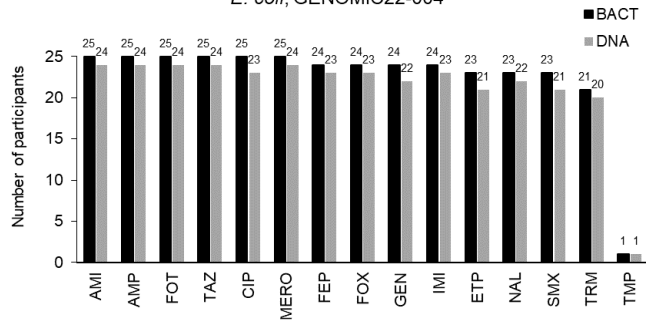
AMR Chr. mutations - *E. coli*, GENOMIC22-004



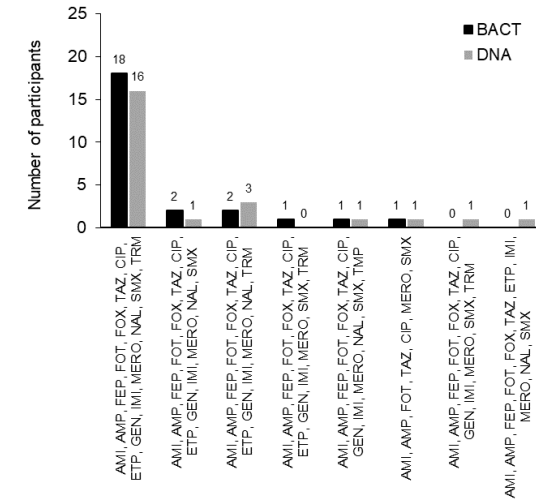
AMR genes - *E. coli*, GENOMIC22-004



Predicted AMR phenotype (individual antimicrobials) *E. coli*, GENOMIC22-004

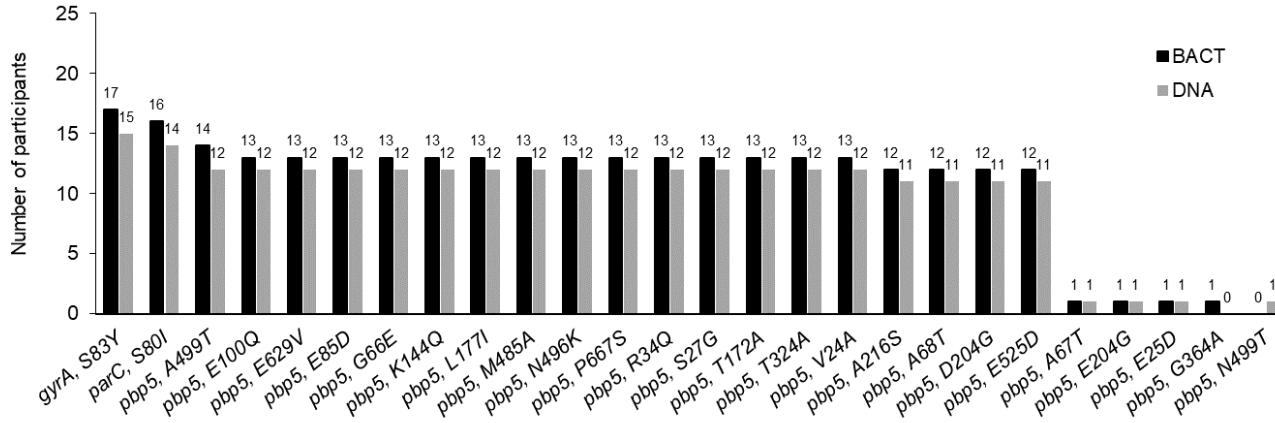


Predicted AMR phenotypic profile *E. coli*, GENOMIC22-004

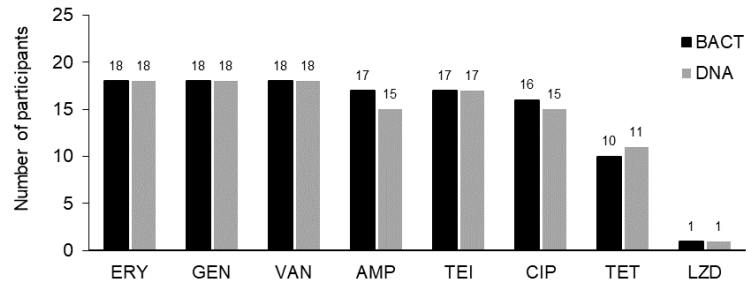


GENOMIC22-05

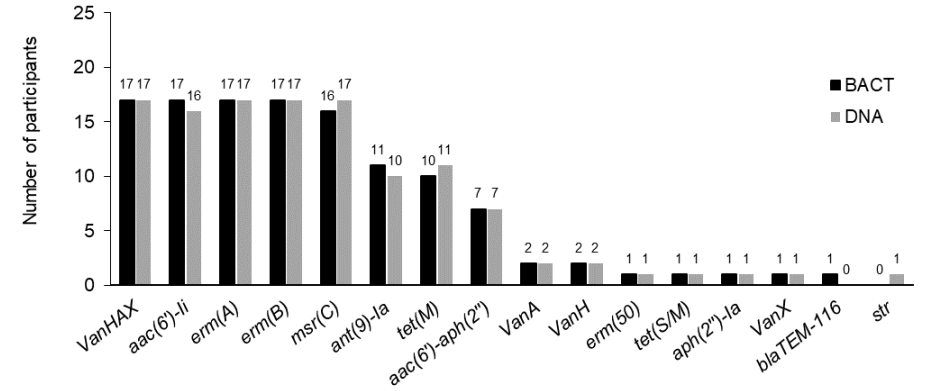
AMR Chr. mutations - *E. faecium*, GENOMIC22-005



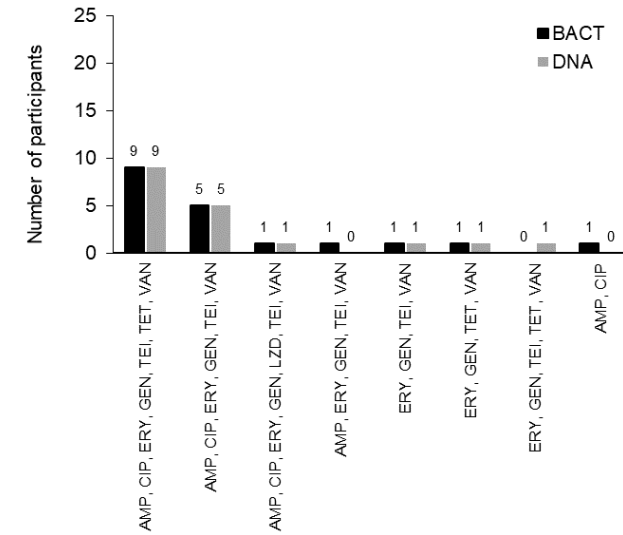
Predicted AMR phenotype (individual antimicrobials) *E. faecium*, GENOMIC22-005



AMR genes - *E. faecium*, GENOMIC22-005

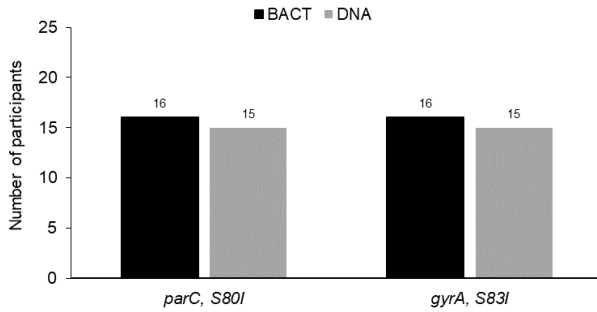


Predicted AMR phenotypic profile *E. faecium*, GENOMIC22-005

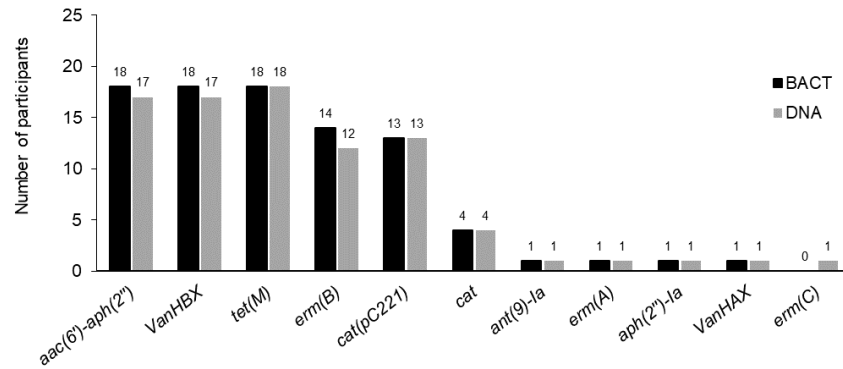


GENOMIC22-06

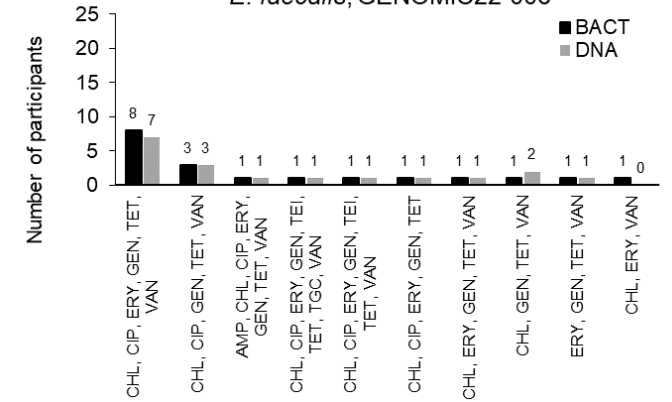
AMR Chr. mutations - *E. faecalis*, GENOMIC21-006



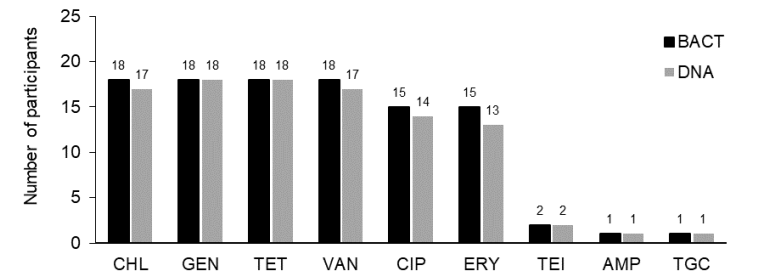
AMR genes - *E. faecalis*, GENOMIC21-006



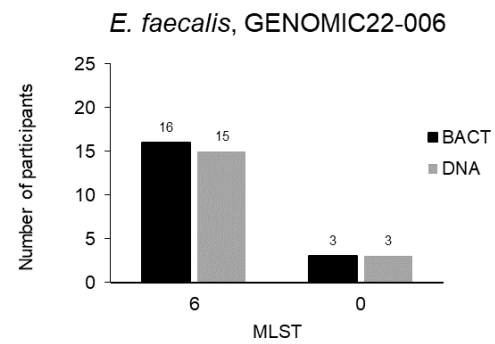
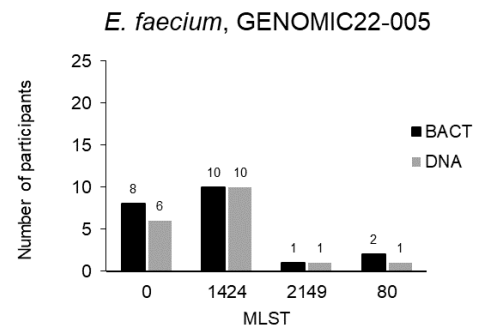
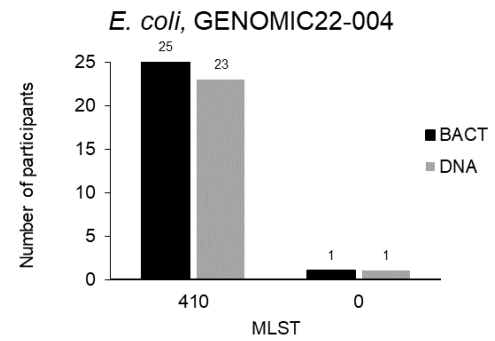
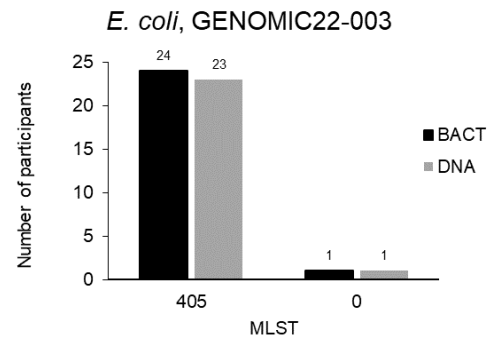
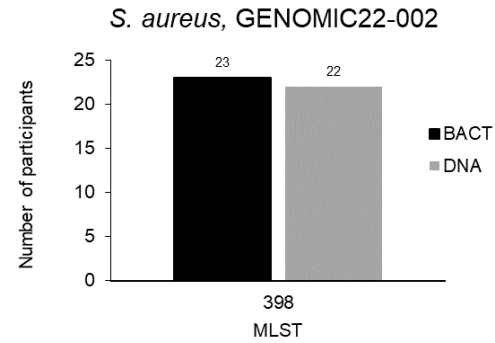
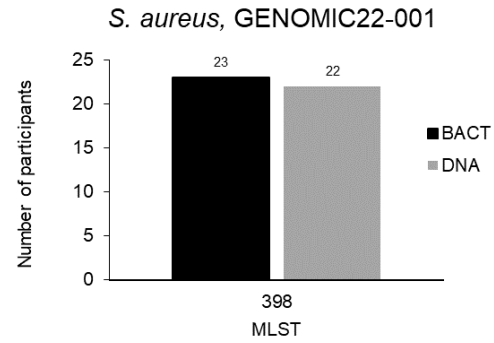
Predicted AMR phenotypic profile
E. faecalis, GENOMIC22-006



Predicted AMR phenotype (individual antimicrobials)
E. faecalis, GENOMIC22-006



MLST





contigs >200bp

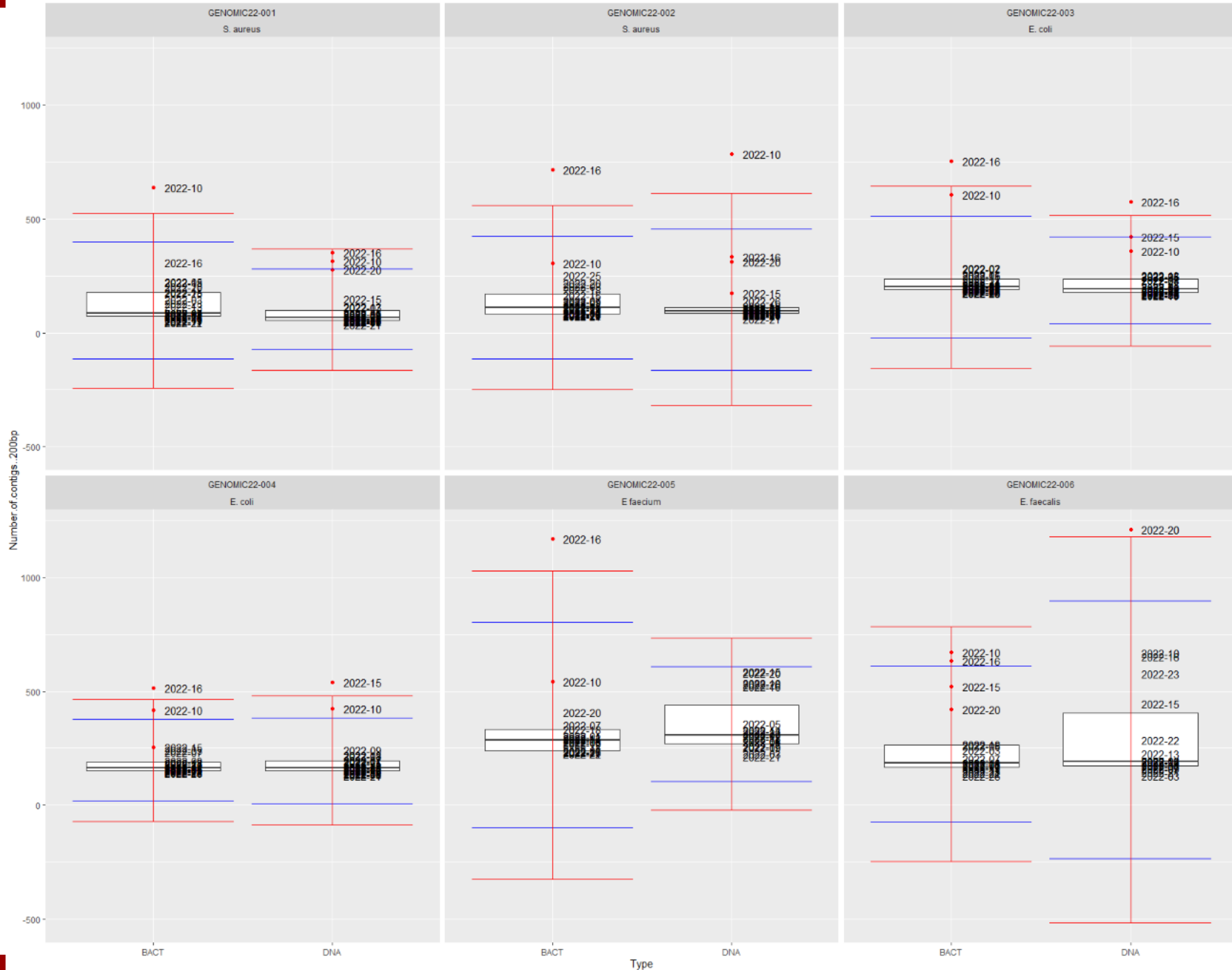
Number of contigs longer than 200 bp per isolate per source (live culture/purified DNA)

Blue whisker present 2 standard deviations from the mean

Red whiskers present 3 standard deviations from the mean

Genomes larger than 110% or smaller than 90% of expected size have been excluded

Could >500bp be a better parameter?





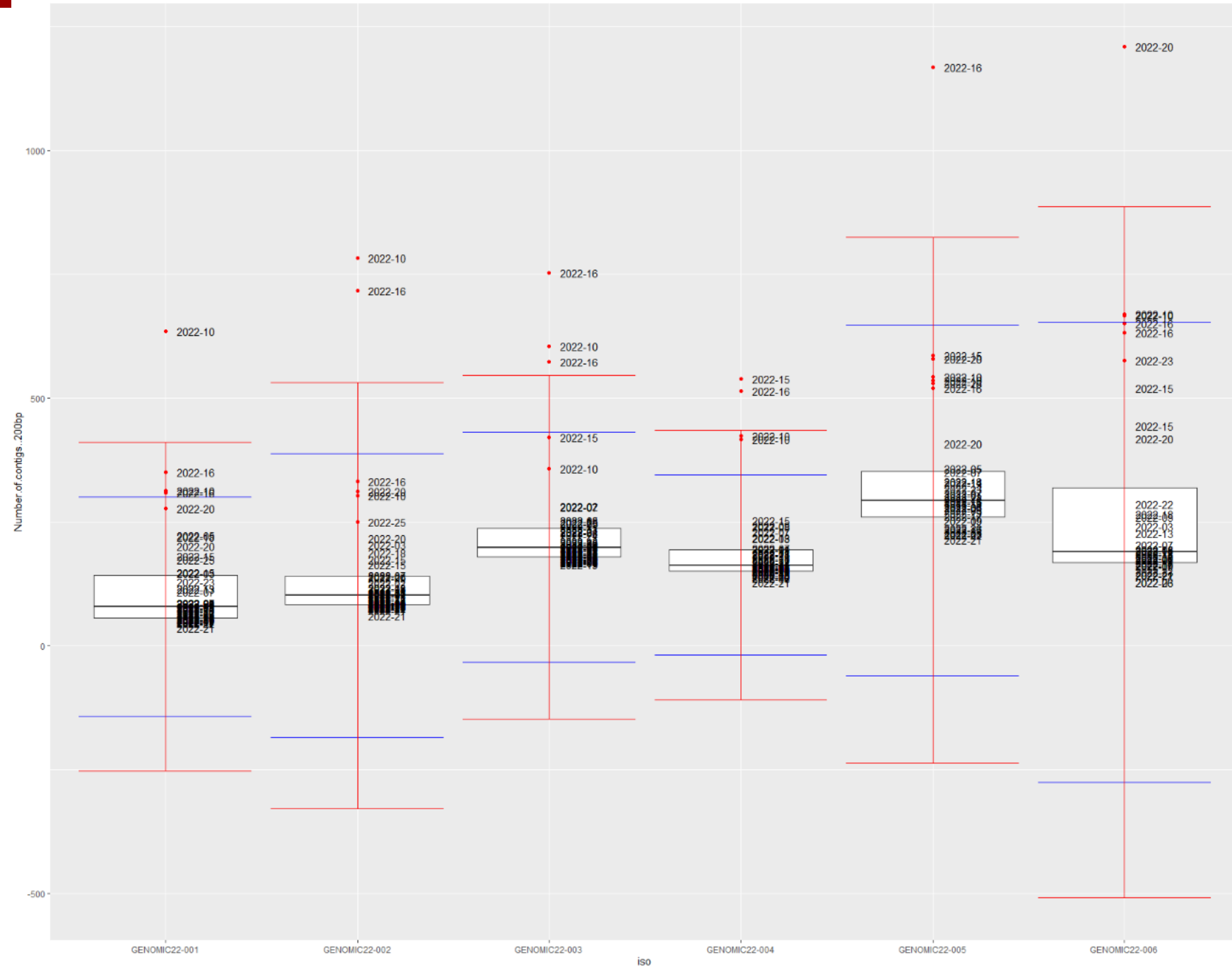
contigs >200bp

Number of contigs longer than 200 bp per isolate

Blue whisker present 2 standard deviations from the mean

Red whiskers present 3 standard deviations from the mean

Genomes larger than 110% or smaller than 90% of expected size have been excluded



N50

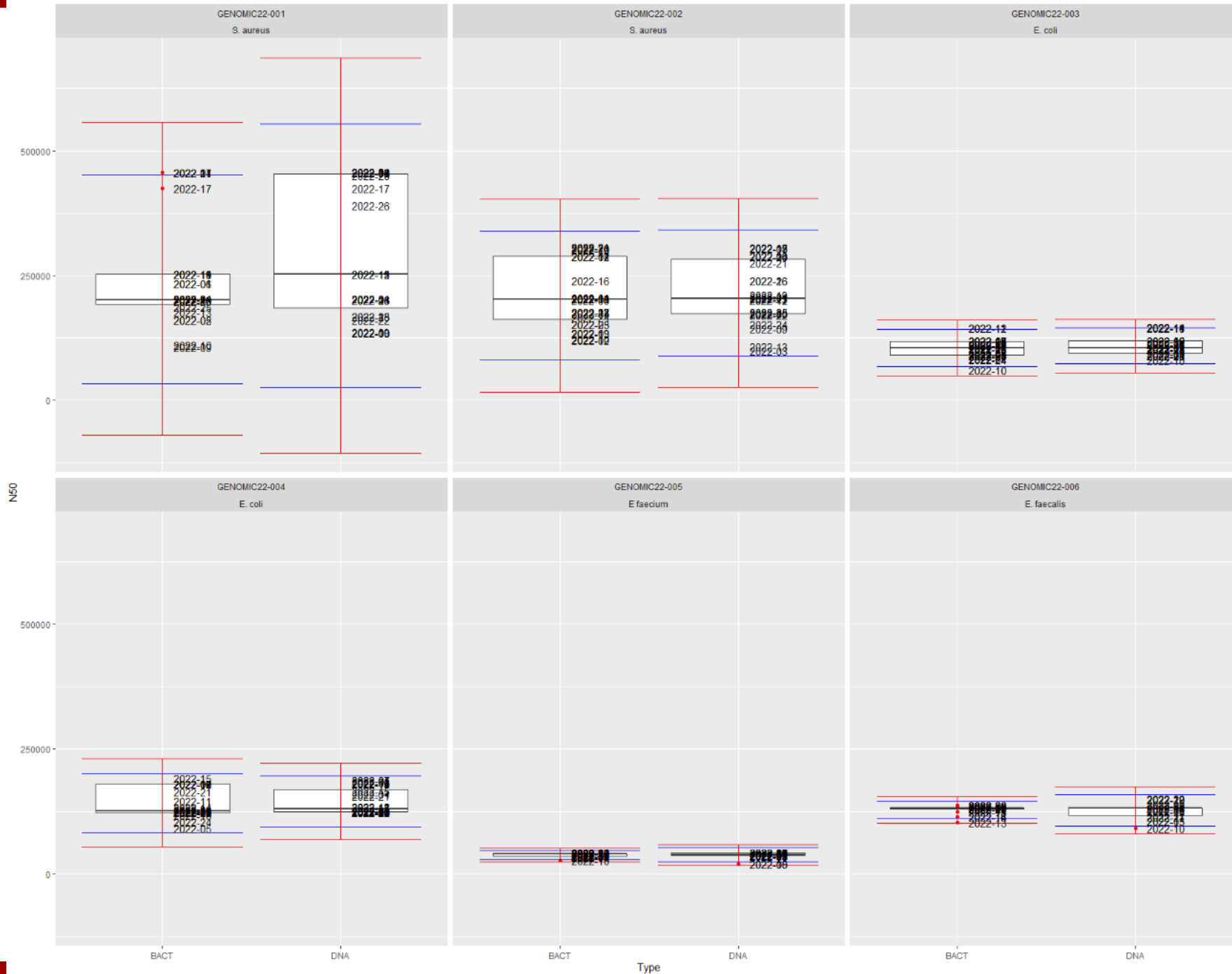
N50 per isolate per source

Blue whisker present 2 standard deviations from the mean

Red whiskers present 3 standard deviations from the mean

Genomes larger than 110% or smaller than 90% of expected size have been excluded

3 genomes below 3 SD in isolates GENOMIC22-005 and -006





Proportion of reads mapping to reference

Boxplot per isolate

Thresholds applied for scoring were minimal >80%, and preferably >90%

Generally lower mapping proportion in GENOMIC22-005 (*Enterococcus faecium*)

