

Figure S1. BLAST comparisons of *S. sonnei* bla_{CTX-M-15} carrying IncI1 plasmid against five best overall-match plasmids. Rings were constructed using BRIG (BLAST Ring Image Generator) v0.95 software using p6607-69 (GenBank: CP045527.2) as reference sequence. Similarities with the reference plasmid are represented by the colored rings. From the center to outside: p6607-69, GC content, GC skew, pHNRD174, pKHSB1, pEC545_1, pSKLX3330, p2474-3. Genome accession numbers are indicated in the legend. Red and blue arrows above the rings correspond to gene features of interest. For each plasmid, we report species of isolation, Inc group plasmid, country, year, host, sample of isolation, disease, plasmid name, and plasmid size. For plasmid names ending with asterisk (*), the β-lactamase gene is bla_{CTX-M-55}. Not available = na.

E. coli, IncFII,
Canada, 2000,
Human, na, na
pC15-1a*
(92'353 bp)

K. pneumoniae, IncFII,
na, na,
na, na, na,
Plasmid unnamed4 *
(85'410 bp)

K. pneumoniae, IncFII,
Norway, 2015,
Human, blood, na,
Plasmid unnamed3 *
(89'709 bp)

E. coli, IncFII,
Sweden, 2008,
Human, blood, na,
pSUH-2 *
(79'945 bp)

E. coli, IncFII/IncN,
USA, na,
na, na, na
p94-1 *
(119'184 bp)

GC Content

GC Skew

GC Skew(-)

GC Skew(+)

AY458016

100% identity

70% identity

50% identity

CP032226

100% identity

70% identity

50% identity

CP034056

100% identity

70% identity

50% identity

CP041339

100% identity

70% identity

50% identity

CP041579

100% identity

70% identity

50% identity

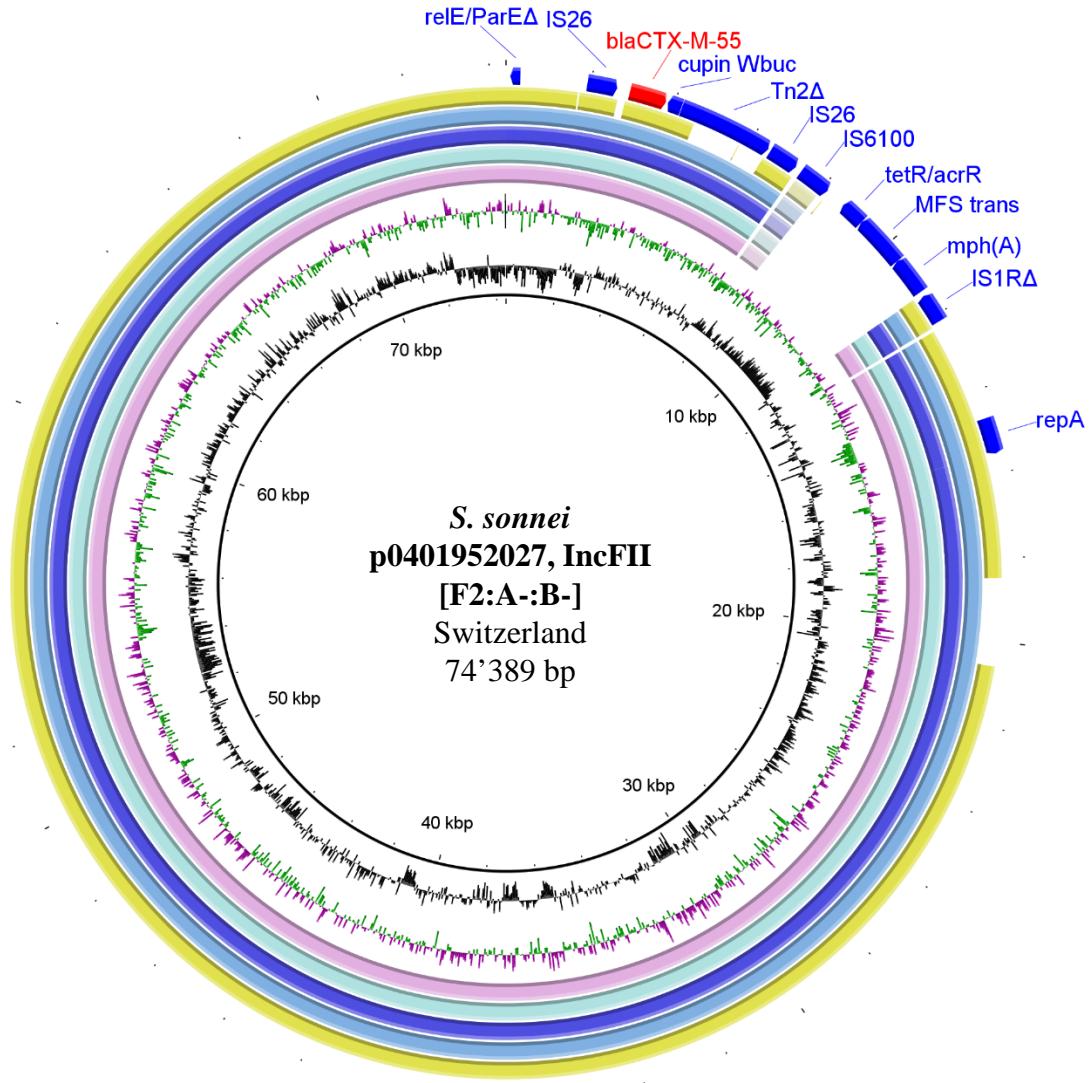


Figure S2. BLAST comparisons of *S. sonnei* *bla*_{CTX-M-55} carrying IncFII plasmid against five best overall-match plasmids. Rings were constructed using BRIG (BLAST Ring Image Generator) v0.95 software using p0401952027 (GenBank: CP049166) as reference sequence. Similarities with the reference plasmid are represented by the colored rings. From the center to outside: p0401952027, GC content, GC skew, pC15-1a, unnamed4, unnamed3, pSUH-2, p94-1. Genome accession numbers are indicated in the legend. Delta symbol (Δ) next to feature label corresponds to partial/incomplete gene CDS. Red and blue arrows above the rings correspond to gene features of interest. For each plasmid, we report species of isolation, Inc group plasmid, country, year, host, sample of isolation, disease, plasmid name, and plasmid size. For plasmid names ending with asterisk (*), the β -lactamase gene is *bla*_{CTX-M-15}. Not available = na.

E. coli, IncFII,
UAE, 2012,
Human, na, na
pEC743_3
(65'196 bp)

Citrobacter sp. CRE-46, IncFII,
na, na,
na, na, na,
Plasmid unnamed6
(76'953 bp)

S. flexneri, IncFII,
na, na,
na, na, na,
p2013C-3749-1
(71'053 bp)

E. coli, IncFIL/IncN,
na, na,
na, na, na,
pMG333
(134'435 bp)

E. coli, IncFII,
na, na,
na, na, na
pMG335
(73'874 bp)

GC Content

GC Skew

GC Skew(-)

GC Skew(+)

CP015072

100% identity

70% identity

50% identity

CP029734

100% identity

70% identity

50% identity

CP034932

100% identity

70% identity

50% identity

MK878892.2

100% identity

70% identity

50% identity

MK878893.2

100% identity

70% identity

50% identity

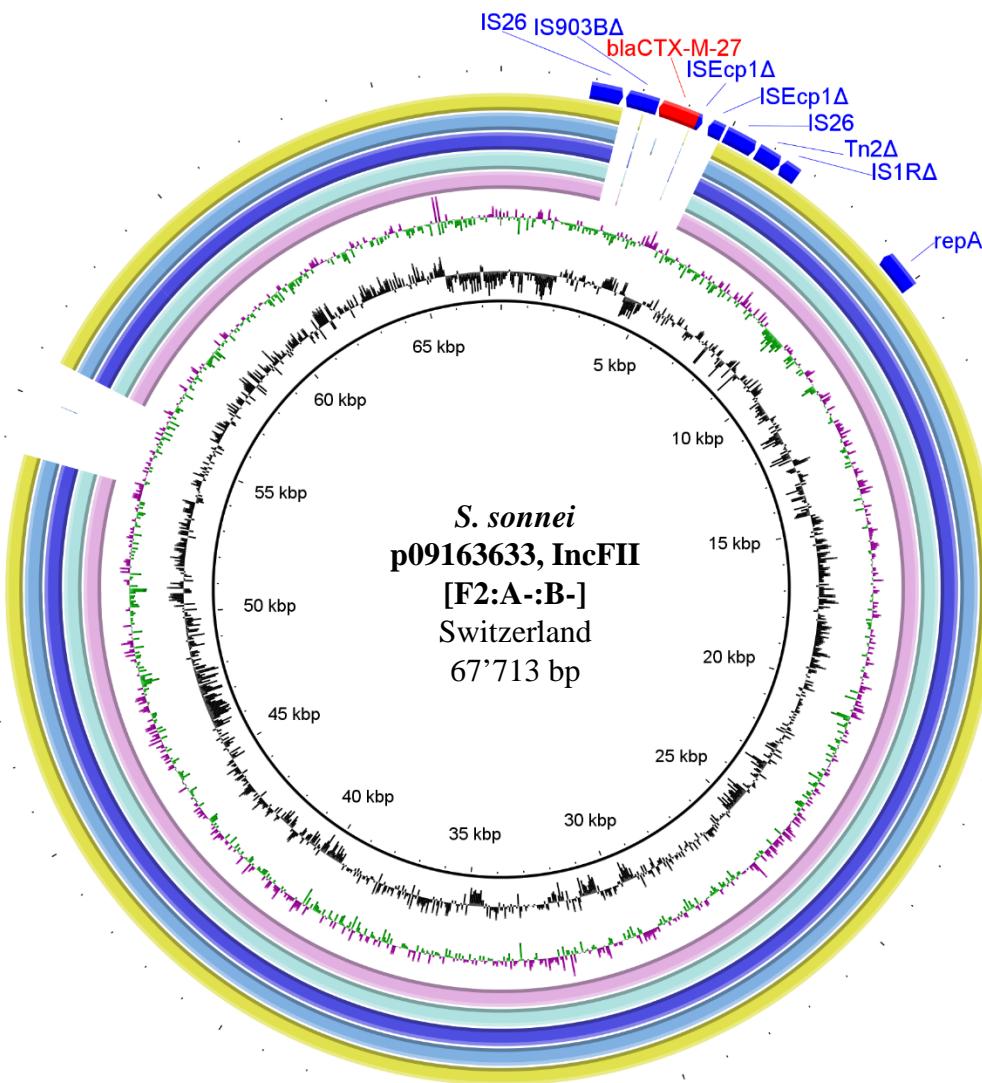


Figure S3. BLAST comparisons of *S. sonnei* *bla*_{CTX-M-27} carrying IncFII plasmid against five best overall-match plasmids. Rings were constructed using BRIG (BLAST Ring Image Generator) v0.95 software using p09163633 (GenBank: CP049168) as reference sequence. Similarities with the reference plasmid are represented by the colored rings. From the center to outside: p09163633, GC content, GC skew, pEC743_3, unnamed6, p2013C-3749-1, pMG333, pMG335. Genome accession numbers are indicated in the legend. Red and blue arrows above the rings correspond to gene features of interest. Delta symbol (Δ) next to feature label corresponds to partial/incomplete gene CDS. For each plasmid, we report species of isolation, Inc group plasmid, country, year, host, sample of isolation, disease, plasmid name, and plasmid size. Not available = na.

S. flexneri, IncFII (pSE11),
Australia, 2017,
Human, na, na
pAUSMDU00010535_02
(83'548 bp)

S. flexneri, IncFII (pSE11),
na, na,
na, na, na,
pKSR100
(73'047 bp)

S. flexneri, IncFII (pSE11),
Australia, 2016,
Human, feces, na,
Plasmid 3
(76'615 bp)

S. flexneri, IncFII (pSE11),
Canada, na,
Human, feces, na,
pSf2
(79'827 bp)

S. flexneri, IncFII (pSE11),
Canada, na,
Human, feces, na
pSf3
(72'398 bp)

GC Content

GC Skew

GC Skew(-)

GC Skew(+)

CP045943

100% identity

70% identity

50% identity

LN624486

100% identity

70% identity

50% identity

LR213457

100% identity

70% identity

50% identity

MG767299

100% identity

70% identity

50% identity

MG767302

100% identity

70% identity

50% identity

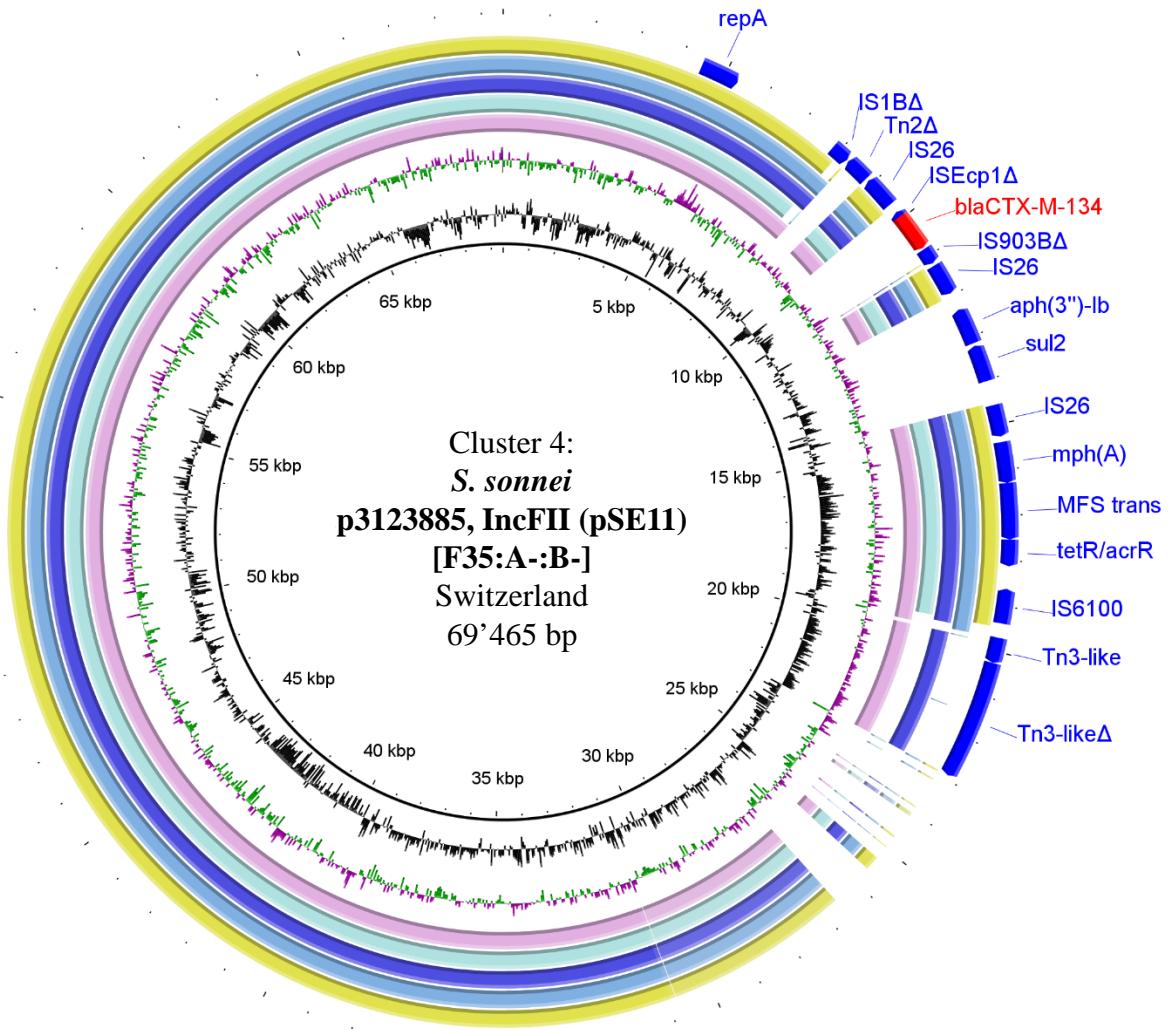


Figure S4. BLAST comparisons of *S. sonnei* bla_{CTX-M-134} carrying IncFII (pSE11) plasmid against five best overall-match plasmids. Rings were constructed using BRIG (BLAST Ring Image Generator) v0.95 software using p3123885 (GenBank: CP049164) as reference sequence. Similarities with the reference plasmid are represented by the colored rings. From the center to outside: p3123885, GC content, GC skew, pAUSMDU00010535_02; pKSR100, Plasmid 3, pSf2, pSf3. Genome accession numbers are indicated in the legend. Red and blue arrows above the rings correspond to gene features of interest. Delta symbol (Δ) next to feature label corresponds to partial/incomplete gene CDS. For each plasmid, we report species of isolation, Inc group plasmid, country, year, host, sample of isolation, disease, plasmid name, and plasmid size. Not available = na.

Table S1. Antimicrobial susceptibility tests for the *S. sonnei* isolates collected during 2016-2019 in Switzerland and analyzed in the present study

<i>S. sonnei</i> strain	<i>bla</i> _{ESBL}	MIC, mg/L ^a																					
		CAZ	CTX	FEP	ATM	PTZ	TIM	IMP	MEM	ERT	DOR	LEV	CIP	SXT	AK	GEN	TOB	DOX	MIN	TIG	COL	POL	AZT ^c
L4094	<i>bla</i> _{CTX-M-3}	≤1	16	≤2	4	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	≤1	≤0.25	1/19	≤4	≤1	≤1	≤2	≤2	≤0.25	≤0.25	≤0.25	np
1205-3131	<i>bla</i> _{CTX-M-3}	≤1	8	≤2	≤2	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	≤1	≤0.25	2/38	≤4	≤1	≤1	≤2	≤2	≤0.25	≤0.25	≤0.25	12
7111-69	<i>bla</i> _{CTX-M-3}	2	16	4	4	≤8/4	32/2	≤1	≤1	≤0.25	≤0.125	≤1	≤0.25	2/38	≤4	≤1	≤1	≤2	≤2	≤0.25	≤0.25	≤0.25	np
509-1022	<i>bla</i> _{CTX-M-3}	2	16	4	8	≤8/4	32/2	≤1	≤1	≤0.25	≤0.125	≤1	≤0.25	>4/76	≤4	≤1	≤1	16	≤2	≤0.25	≤0.25	≤0.25	np
19-0822-3296	<i>bla</i> _{CTX-M-3}	2	32	8	8	≤8/4	32/2	≤1	≤1	≤0.25	≤0.125	≤1	≤0.25	>4/76	8	≤1	2	>16	4	0.5	≤0.25	≤0.25	np
LC-1477-18 ^b	<i>bla</i> _{CTX-M-3}	2	16	4	4	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	≤1	≤0.25	>4/76	≤4	≤1	≤1	16	≤2	≤0.25	≤0.25	≤0.25	12
6607-69	<i>bla</i> _{CTX-M-15}	>16	>32	8	>16	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	≤1	≤0.25	>4/76	≤4	≤1	≤1	16	4	0.5	≤0.25	≤0.25	np
19-0821-3486	<i>bla</i> _{CTX-M-15}	≤1	16	≤2	4	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	≤1	≤0.25	>4/76	≤4	≤1	≤1	>16	4	≤0.25	≤0.25	≤0.25	np
0401930105	<i>bla</i> _{CTX-M-15}	≤1	8	≤2	4	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	≤1	≤0.25	>4/76	≤4	≤1	≤1	16	≤2	≤0.25	≤0.25	≤0.25	np
6904-27	<i>bla</i> _{CTX-M-15}	2	8	≤2	4	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	≤1	≤0.25	>4/76	≤4	≤1	≤1	16	≤2	≤0.25	≤0.25	≤0.25	np
19-1125-3493	<i>bla</i> _{CTX-M-15}	2	8	≤2	≤2	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	≤1	≤0.25	>4/76	≤4	≤1	≤1	16	4	≤0.25	≤0.25	≤0.25	np
19-0820-1561 ^d	<i>bla</i> _{CTX-M-15}	2	16	≤2	8	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	>8	>2	>4/76	≤4	≤1	≤1	≤2	≤2	0.5	≤0.25	≤0.25	>128
0401952027 ^d	<i>bla</i> _{CTX-M-55}	8	>32	4	>16	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	≤1	≤0.25	>4/76	≤4	≤1	≤1	16	4	≤0.25	≤0.25	≤0.25	>128
09163633	<i>bla</i> _{CTX-M-27}	4	>32	≤2	8	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	≤1	≤0.25	>4/76	≤4	≤1	≤1	16	≤2	≤0.25	≤0.25	≤0.25	np
3123885 ^d	<i>bla</i> _{CTX-M-134}	≤1	16	≤2	≤2	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	4	>2	>4/76	≤4	≤1	≤1	16	4	0.5	≤0.25	≤0.25	>128
7103-58 ^d	-	≤1	≤1	≤2	≤2	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	8	>2	>4/76	≤4	≤1	≤1	16	4	0.5	≤0.25	≤0.25	>128
7103-28 ^d	-	≤1	≤1	≤2	≤2	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	4	>2	>4/76	≤4	≤1	≤1	16	≤2	≤0.25	≤0.25	≤0.25	>128
6407-57 ^d	-	≤1	≤1	≤2	≤2	≤8/4	≥32/2	≤1	≤1	≤0.25	≤0.125	8	>2	>4/76	≤4	≤1	≤1	16	4	0.5	≤0.25	≤0.25	>128
6110-62	-	≤1	≤1	≤2	≤2	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	≤1	≤0.25	>4/76	≤4	≤1	≤1	≤2	≤2	≤0.25	≤0.25	≤0.25	np
6105-15	-	≤1	≤1	≤2	≤2	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	≤1	≤0.25	>4/76	≤4	≤1	≤1	16	4	0.5	≤0.25	≤0.25	np
6101-40	-	≤1	≤1	≤2	≤2	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	≤1	≤0.25	>4/76	≤4	≤1	≤1	16	4	0.5	≤0.25	≤0.25	np
6412-75	-	≤1	≤1	≤2	≤2	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	4	>2	2/38	≤4	≤1	≤1	≤2	≤2	≤0.25	≤0.25	≤0.25	np
6502-32	-	≤1	≤1	≤2	≤2	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	≤1	≤0.25	>4/76	≤4	≤1	≤1	16	4	0.5	≤0.25	≤0.25	np
7111-23	-	≤1	≤1	≤2	≤2	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	≤1	≤0.25	>4/76	≤4	≤1	≤1	≤2	≤2	≤0.25	≤0.25	≤0.25	np
7109-28	-	≤1	≤1	≤2	≤2	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	≤1	≤0.25	>4/76	≤4	≤1	≤1	8	≤2	0.5	≤0.25	≤0.25	np
7001-38	-	≤1	≤1	≤2	≤2	≤8/4	≤16/2	≤1	≤1	≤0.25	≤0.125	≤1	≤0.25	>4/76	≤4	≤1	≤1	≤2	≤2	≤0.25	≤0.25	≤0.25	np

Note. Antibiotics (susceptibility MIC cutoff in mg/L, according to EUCAST 2019): CAZ, ceftazidime (≤1); CTX, cefotaxime (≤1); FEP, ceferipime (≤1); ATM, aztreonam (≤1); TIM, ticarcillin-clavulante (≤8); PTZ, piperacillin-tazobactam (≤8); IMP, imipenem (≤2); MEM, meropenem (≤2); ERT, ertapenem (≤0.5); DOR, doripenem (not available); LEV, levofloxacin (≤0.25); CIP, ciprofloxacin (≤0.25); SXT, trimethoprim-sulfamethoxazole (≤2/38); AK, amikacin (≤8); GEN, gentamicin (≤2); TOB, tobramycin (≤2); DOX, doxycycline (not available); MIN, minocycline (not available); TIG, tigecycline (≤0.5 for *E. coli* and *Citrobacter koseri*); COL, colistin (≤2); POL, polymyxin B (not available); AZT, azithromycin (≤16); np, not performed

^a All MICs obtained using GNX2F Sensititre panels

^b This strain was detected in Italy

^c MICs were obtained implementing the Etest

^d These strains possessed genes conferring resistance to macrolides [i.e., *erm(B)* and/or *mph(A)*], therefore MIC for AZT was tested