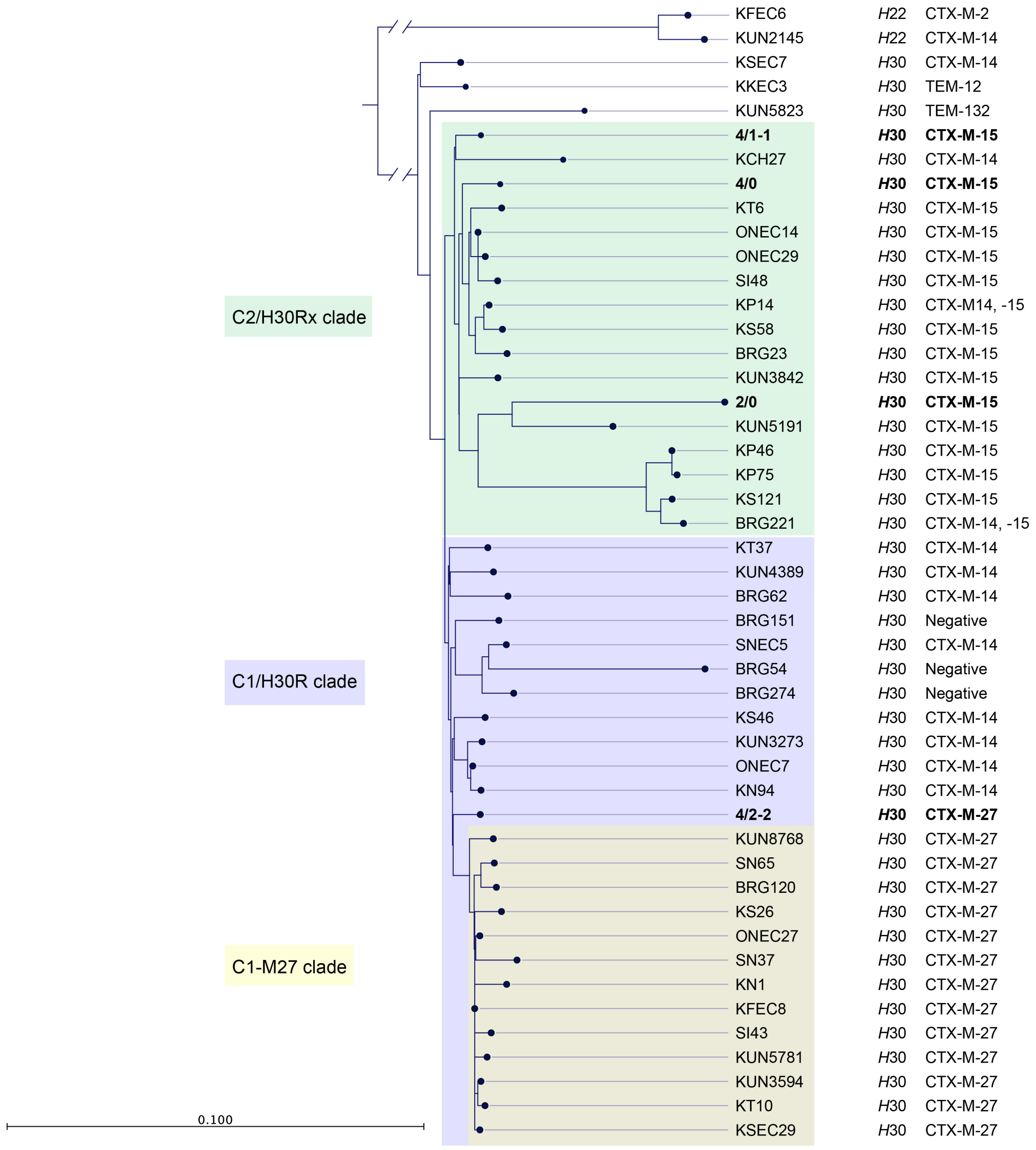

Figure S1. SNP-tree based of ST131 isolates on the dataset of Matsumura *et al.* (1). All sequences were aligned to EC958 and the sub-clades are marked as in (1). KFEC6 and KUN2145 were used as outgroups and have broken branch lengths.

References

1. Matsumura Y, Pitout JDD, Gomi R, Matsuda T, Noguchi T, Yamamoto M, Peirano G, DeVinney R, Bradford PA, Motyl MR, Tanaka M, Nagao M, Takakura S, Ichiyama S. 2016. Global *Escherichia coli* Sequence Type 131 Clade with *bla*CTX-M-27 Gene. Emerg Infect Dis 22:1900–1907.

Table S1. Primers targeting plasmids without resistance genes of patient 2 and 7.

Primer target	Sequence (5' -> 3')
pat2.1_4.1kb	F ACGGAGTTACATCATGAGCA
	R AAATCATGGTGTTACAAGAC
pat2.1_2.3kb	F CGGTATTACAATTGCACA
	R GAGGATTTGATTGGTGCGGA
pat2.1_2.1kb	F AGTGAAAATGCGGATGTG
	R TGTGTGGAAAAGGTTGGG
pat2.1_1.5kb	F GATACCTGTGTAAACCTT
	R CTATCGCTACGTGACTGG
pat7.2_43kb	F TTATCCACACTAAACTGTTC
	R GTGCTATTAAGCGCTTTAGC
pat7.2_34kb	F TCAATAAGATGGGGTAAAATCC
	R TTATGATCCAGCGTTTAAA
pat7.2_4.1kb	F TCACAGCTTCAGCCACAC
	R TCACAGCTTCAGCCACAC
pat7.2_1.5kb	F AGGCAAAGAAAAACACCGA
	R GGGAGCAAAAACACGCAA

Table S2. Results from the NGS sequence analysis.

Isolate	Chromosome /plasmid	Size (bp)	MLST	Replicon [a]	Best match in GenBank (identity/query coverage)	Resistance genes [b]	Virulence genes [c, d]
2/0	p2/0.1	135,053		FIA, FIB, FII	pEcIMT16316 (CP023816.1) (99%/80%)	*dfrA17*, *aadA5*, *sul1*, *bla*$_{\text{TEM-1b}}$, *mphA*, *tetA(B) (partial)*	
	Chromosome		ST131			*bla*$_{\text{CTX-M-15}}$ *(ISEcp1/ctx-m-15* (3214 bp) inserted in *mppA*), Resistance mutations conferring resistance to; Quinolones [*gyrA* (S83L, D87N, A828S) and *parC* (S80I, E84V, A192V, A471G, D475E, Q481H)]	*gad*, *sat*, *iha*, *nfaE*, *ireA*, *iss*
2/1	p2/1.1	153,195		FIA, FIB, FII	pEcIMT16316 (CP023816.1) (99%/80%)	*bla*$_{\text{CTX-M-15}}$, *dfrA17*, *aadA5*, *sul1*, *bla*$_{\text{TEM-1b}}$, *mphA*, *tetA(B) (partial)*	
	Chromosome		ST131			*bla*$_{\text{CTX-M-15}}$ *(ISEcp1/ctx-m-15* (3214 bp) inserted in *mppA*), Resistance mutations conferring resistance to; Quinolones [*gyrA* (S83L, D87N, A828S) and *parC* (S80I, E84V, A192V, A471G, D475E, Q481H)]	*gad*, *sat*, *iha*, *nfaE*, *ireA*, *iss*
2/2	p2/2.1	153,195		FIA, FIB, FII	pEcIMT16316 (CP023816.1) (99%/80%)	*bla*$_{\text{CTX-M-15}}$, *dfrA17*, *aadA5*, *sul1*, *bla*$_{\text{TEM-1b}}$, *mphA*, *tetA(B) (partial)*	
	Chromosome		ST131			*bla*$_{\text{CTX-M-15}}$ *(ISEcp1/ctx-m-15* (3214 bp) inserted in *mppA*), Resistance mutations conferring resistance to; Quinolones [*gyrA* (S83L, D87N, A828S) and *parC* (S80I, E84V, A192V, A471G, D475E, Q481H)]	*gad*, *sat*, *iha*, *nfaE*, *ireA*, *iss*
2/3	p2/3.1	153,195		FI A, FIB, FII	pEcIMT16316 (CP023816.1) (99%/80%)	*bla*$_{\text{CTX-M-15}}$, *dfrA17*, *aadA5*, *sul1*, *bla*$_{\text{TEM-1b}}$, *mphA*, *tetA(B) (partial)*	
	Chromosome		ST131			*bla*$_{\text{CTX-M-15}}$ *(ISEcp1/ctx-m-15* (3214 bp) inserted in *mppA*), Resistance mutations conferring resistance to; Quinolones [*gyrA* (S83L, D87N, A828S) and *parC* (S80I, E84V, A192V, A471G, D475E, Q481H)]	*gad*, *sat*, *iha*, *nfaE*, *ireA*, *iss*
2/4	p2/4.1	130,502		FIA, FIB, FII	pEcIMT16316 (CP023816.1) (99%/80%)	*dfrA17, aadA5, sul1, bla*$_{\text{TEM-1b}}$, *mphA*	
	Chromosome		ST131			*bla*$_{\text{CTX-M-15}}$ *(ISEcp1/ctx-m-15* (3214 bp) inserted in *mppA*), Resistance mutations conferring resistance to; Quinolones [*gyrA* (S83L, D87N, A828S) and *parC* (S80I, E84V, A192V, A471G, D475E, Q481H)]	*gad*, *sat*, *iha*, *nfaE*, *ireA*, *iss*
4/0	p4/0.1	138,672		FIA, FII	*E. coli* NCTC 13441 plasmid (LT632321.1) (100%/96%)	*bla*$_{\text{CTX-M-15}}$, *dfrA17, aadA5, sul1, mphA, tetA(A), catB3 (partial), bla*$_{\text{OXA-1}}$, *aac(6')-Ib-cr, aac(3')IIa*	
	p4/0.2	110,452		ND	pECOH89 (HG530657) (98%/91%)		
	(p4/0.3) cryptic plasmid						*cci*
	Chromosome		ST131			Resistance mutations conferring resistance to; Quinolones [*gyrA* (S83L, D87N, A828S) and *parC* (S80I, E84V, A192V, A471G, D475E, Q481H)]	*gad*, *sat*, *iha*, *nfaE*, *ireA*, *iss, nf1*
4/1-1	p4/1-1.1	181,324		FIA, FIB, FII	pYDC107_184 (CP025708.1) (99%/86%)	*aph(3')1a, bla*$_{\text{CTX-M-15}}$, *sul1, bla*$_{\text{TEM-1b}}$, *mphA, tetA(A), catB3 (partial), bla*$_{\text{OXA-1}}$, *aac(6')-Ib-cr, aadA2, dfrA12*	
	p4/1-1.2	33,067		IncX4	pBS512_33 (CP001059) (99%/100%)		
	Chromosome		ST131			Resistance mutations conferring resistance to; Quinolones [*gyrA* (S83L, D87N, A828S) and *parC* (S80I, E84V, A192V, A471G, D475E, Q481H)]	*gad*, *sat*, *iha*, *iss*
4/1-2	p4/1-2.1	112,141		ND	pKPX-2 (AP012056) (99%/86%)		
	p4/1-2.2	96,190		*IncFIB(pQil)*	pNDM-1fa (CP014757) (99%/56%)	*bla*$_{\text{CTX-M-15}}$, *dfrA1, sul1, bla*$_{\text{TEM-1b}}$, *tetA(A), catA1, catB3 (partial), bla*$_{\text{OXA-1}}$, *qnrS1, aac(6')-Ib-cr, aac(3')IIa, strAB*	

	Chromosome		ST147			*oqxAB, bla*$_{\text{SHV-11}}$ Resistance mutations conferring resistance to; Quinolones [*gyrA* (S83L) and *parC* (S80I)]]	
4/2-1	p4/2-1.1	152,425		FIA, FIB, FII	pCA28 (CP009232) (99%/88%)	*bla*$_{\text{CTX-M-15}}$, *dfrA17, aadA5, sul1*, *bla*$_{\text{OXA-1}}$, *aac(6')-Ib-cr, aac(3')IIa, catB3 (partial)*	
	p4/2-1.2	33,067		IncX4	pBS512-33 (CP001059) (99%/100%)		
	Chromosome		ST167			*tetA(B)* Resistance mutations conferring resistance to; Quinolones [*gyrA* (S83L, D87N) and *parC* (S80I), *nfsA* (In frame deletion of amino acids 77-79)]	*gad, iss, capU*
4/2-2	p4/2-2.1	125,877		FIA, FIB, FII	pCA28 (CP009232) (99%/95%)	*bla*$_{\text{CTX-M-27}}$, *dfrA17, aadA5, sul1, sul2, mphA, tetA(A), strAB*	*senB*
	Chromosome		ST131			Resistance mutations conferring resistance to; Quinolones [*gyrA* (S83L, D87N, A828S) and *parC* (S80I, E84V, A192V, A471G, D475E, Q481H)]	*gad*, *sat*, *iha*, *iss*
4/2-3	p4/2-3.1	73,669		*IncFIB(pQil)*	pNDM-1fa (CP014757) (99%/53%)	*bla*$_{\text{CTX-M-15}}$, *dfrA1, sul1, bla*$_{\text{TEM-1b}}$, *tetA(A), catB3 (partial), bla*$_{\text{OXA-1}}$, *qnrS1, aac(6')-Ib-cr, aac(3)IIa, strAB*	
	Chromosome		ST147			*oqxAB, bla*$_{\text{SHV-11}}$ Resistance mutations conferring resistance to; Quinolones [*gyrA* (S83L) and *parC* (S80I)]	
4/3-1	p4/3-1.1	152,425		FIA, FIB, FII	pCA28 (CP009232) (99%/88%)	*bla*$_{\text{CTX-M-15}}$, *dfrA17, aadA5, sul1*, *bla*$_{\text{OXA-1}}$, *aac(6')-Ib-cr, aac(3')IIa, catB3 (partial)*	
	p4/3-1.2	67,839		FII	pVR50A (CP011135) (99%/92%)	*bla*$_{\text{TEM-1b}}$	
	p4/3-1.3	33,067		IncX4	pBS512-33 (CP001059) (99%/100%)		
	Chromosome		ST167			*tetA(B)* Resistance mutations conferring resistance to; Quinolones [*gyrA* (S83L, D87N) and *parC* (S80I), *nfsA* (In frame deletion of amino acids 77-79)]	*gad, iss, capU*
4/3-2	p4/3-2.1	181,324		FIA, FIB, FII	pYDC107_184 (CP025708.1) (99%/86%)	*bla*$_{\text{CTX-M-15}}$, *sul1*, *bla*$_{\text{TEM-1b}}$, *mphA, tetA(A), catB3 (partial), bla*$_{\text{OXA-1}}$, *aac(6')-Ib-cr, aph(3')1a, aadA2, dfrA12*	
	p4/3-2.2	33,067		IncX4	pBS512-33 (CP001059) (99%/100%)		
	Chromosome		ST131			Resistance mutations conferring resistance to; Quinolones [*gyrA* (S83L, D87N, A828S) and *parC* (S80I, E84V, A192V, A471G, D475E, Q481H)]	*gad*, *sat*, *iha*, *iss*
4/4	p4/4.1	125,877		FIA, FIB, FII	pCA28 (CP009232) (99%/95%)	*bla*$_{\text{CTX-M-27}}$, *dfrA17, aadA5, sul1, sul2, mphA, tetA(A), strAB*	*senB*
	p4/4.2	67,839		FII	pVR50A (CP011135) (99%/92%)	*bla*$_{\text{TEM-1b}}$	
	p4/4.3	33,067		IncX4	pBS512-33 (CP001059) (99%/100%)		
	Chromosome		ST131			Resistance mutations conferring resistance to; Quinolones [*gyrA* (S83L, D87N, A828S) and *parC* (S80I, E84V, A192V, A471G, D475E, Q481H)]	*gad*, *sat*, *iha*, *iss*
7/0	p7/0.1	113,718		FII, FIB	pMVAST0167 (CP014493) (99%/90%)	*dfrA17, sul1, mphA, aadA5*	*senB*
	Chromosome		ST405			*bla*$_{\text{CTX-M-14}}$ Resistance mutations conferring resistance to; Quinolones [*gyrA* (S83L, D87N) and *parC* (S80I)]	*gad*, *eilA*, *air*
7/1	p7/1.1	118,997		FII, FIB	pMVAST0167 (CP014493) (99%/90%)	*dfrA17, sul1, mphA, aadA5, erm(B)*	*senB*
	p7/1.2	42,913		ND	pO157_Sal (CP001927) (77%/65%)		
	Chromosome		ST405			*bla*$_{\text{CTX-M-14}}$ Resistance mutations conferring resistance to;	*gad*, *eilA*, *air*

						Quinolones [*gyrA* (S83L, D87N, R237H, D678E) and *parC* (S80I)]	
7/2	p7/2.1	113,737		FII, FIB	pMVAST0167 (CP014493) (99%/90%)	*dfrA17, sul1, mphA, aadA5*	*senB*
	p7/2.2	42,913		ND	pO157_Sal (CP001927) (77%/65%)		
	p7/2.3	34,371		ND	pN-Cit (JQ996149) (99%/97%)		
	Chromosome		ST405			*bla*$_{\text{CTX-M-14}}$ Resistance mutations conferring resistance to; Quinolones [*gyrA* (S83L, D87N, R237H, D678E) and *parC* (S80I)]	*gad, eilA*, *air*
7/3	p7/3.1	113,737		FII, FIB	pMVAST0167 (CP014493) (99%/90%)	*dfrA17, sul1, mphA, aadA5*	*senB*
	p7/3.2	42,913			pO157_Sal (CP001927) (77%/65%)		
	Chromosome		ST405			*bla*$_{\text{CTX-M-14}}$ Resistance mutations conferring resistance to; Quinolones [*gyrA* (S83L, D87N, R237H, D678E) and *parC* (S80I)]	*gad, eilA*, *air*
7/4	p7/4.1	113,737		FII, FIB	pMVAST0167 (CP014493) (99%/90%)	*dfrA17, sul1, mphA, aadA5*	*senB*
	Chromosome		ST405			*bla*$_{\text{CTX-M-14}}$ Resistance mutations conferring resistance to; Quinolones [*gyrA* (S83L, D87N, R237H, D678E) and *parC* (S80I)]	*gad, eilA*, *air*

a) PlasmidFinder, b) ResFinder, c) VirulenceFinder, ND = not detected.

d) Virulence genes: *gad* (glutamate decarboxylase), *sat* (secreted autotransporter toxin), *iha* (adherence protein), *nfaE* (diffuse adherence fibrillar adhesin), *ireA* (siderophore receptor), *iss* (increased serum survival), cci (Cloacin), *cnf1* (Cytotoxic necrotizing factor), *capU* (Hexosyltransferase homolog), *senB* (Enterotoxin), *eilA* (Salmonella HilA homolog), *air* (Enteroaggregative immunoglobulin repeat protein)

Table S3 Chromosomal differences in the isolates from patients 2 and 7.

Isolate	Reference position chromosome	Type	Nucleotide change	Amino acid change	Predicted protein/function
2/0	Reference				
2/1	3434924	SNV	C56T	Gly19Gln	glycosyl transferase family 1
	4668147	Insertion	409_410insA		*psiE*
2/2	888155	SNV	C541T	G181R	IS66 family transposase
	2020099	SNV	T175C	L59syn	hypothetical protein
	3434571	SNV	G409A	R137C	glycosyl transferase family 1
	4668147	Insertion	409_410insA		*psiE*
2/3	888155	SNV	C541T	G181R	IS66 family transposase
	1326915	SNV	G56T	A19D	alpha/beta hydrolase
	2020099	SNV	T175C	L59syn	hypothetical protein
	3434571	SNV	G409A	R137C	glycosyl transferase family 1
	3434829	SNV	T151A	K51*	glycosyl transferase family 1
	3434896	SNV	C84A	W28C	glycosyl transferase family 1
	4668147	Insertion	409_410insA		*psiE*
2/4	130442	Deletion	A		Upstream of *hcp* or *aroP*
	268798	SNV	A288C	G96syn	*fliN*
	398005..398017	Deletion	13 nt	H65fs	*lacZ*
	654994	SNV	C904T	V302I	anion permease
	855484..913513	Deletion	58029 nt		IS21 element, hypothetical proteins, toxin/antitoxin, antirestriction protein, transcriptional regulator, GTPase, *repB* family protein, IS66 element, ATPase, *ymgB/arlR* family protein, *evgA/S*, type 1 fimbriae protein
	1428692	SNV	C -> T		Downstream of hypothetical protein
	1630779	SNV	G -> A		11bp upstream of a partial *oppA*
	1708252	SNV	C -> T		92bp upstream of glutathione S-transferase
	1866244	SNV	T29C	L10P	*mdtK* (*norM*)
	2319432	Insertion	146_147insT	N49fs	glycosyltransferase family 2
	2319446	Deletion	133delT	T45fs	glycosyltransferase family 2
	2974171	SNV	G277A	D93N	*ompA* family protein, *yfiB*
	3110475	Deletion	451delA	N152fs	*barA*
	3412884	SNV	C324G	D108E	antitoxin
	3437226	SNV	G137A	T46M	ABC transporter ATP-binding protein
	3875935	SNV	C1685T	P562L	RNA-binding transcriptional accessory protein
	3880465	SNV	C -> T		Downstream of transposase and methyl ester esterase
	4111641	Insertion	1667_1670insGGAT	T558fs	adhesin
	4668147	Insertion	409_410insA		*psiE*
	4718098..4737449	Deletion	19351 nt		integrase, transcriptional regulator, DNA-binding protein, DNA methyltransferase, DNA helicase, *dprA*,
	4829724	Deletion	G		108bp upstream of an autotransporter outer membrane beta-barrel domain-containing protein
	5016654	SNV	A257C	L86*	*fecR*

Table S3 continued.

Isolate	Reference position chromosome	Type	Nucleotide change	Amino acid change	Predicted protein
7/0	Reference				
7/1	639458	SNV	C1020T		CuzA/CzcA family heavy metal efflux RND transporter
	925324	SNV	G310A	Gln104*	glutathione S-transferase
	2002107	SNV	G310A		3bp upstream of DUF481 domain-containing protein
	2317218	SNV	T991C	Phe331Leu	hypothetical protein
	2333618	SNV	C279G		IS200/IS605 family transposase
	2339750	Insertion	704_705insA	Leu235fs	O102 family O-antigen polymerase
	2407185	SNV	G267T		Phage major tail tube protein
	2407200	SNV	C252T		Phage major tail tube protein
	2407205	SNV	C247A	Ala83Ser	Phage major tail tube protein
	2407257	SNV	C195A		Phage major tail tube protein
	2407839	SNV	G816T		Phage tail protein
	2407851	SNV	A804G		Phage tail protein
	2407866	SNV	T789A		Phage tail protein
	2407899	SNV	A756G		Phage tail protein
	2407902	SNV	A753G		Phage tail protein
	2407932	SNV	G723T		Phage tail protein
	2407956	SNV	C699T		Phage tail protein
	2407965	SNV	A690G		Phage tail protein
	2408016	SNV	G639A		Phage tail protein
	2408124	SNV	A531G		Phage tail protein
	2408151	SNV	T504C		Phage tail protein
	2408159	SNV	C496T	Gly151Ser	Phage tail protein
	2408175	SNV	G480A		Phage tail protein
	2408202	SNV	A453C		Phage tail protein
	2408217	SNV	A438T		Phage tail protein
	2408247	SNV	G408A		Phage tail protein
	2408301	SNV	C354T		Phage tail protein
	2411114	SNV	G1236A		Phage tail protein
	2411117	SNV	G1233A		Phage tail protein
	2411156	SNV	G1194A		Phage tail protein
	2411159	SNV	G1191C		Phage tail protein
	2411162	SNV	T1188C		Phage tail protein
	2411164	SNV	C1186T	Ala396Thr	Phage tail protein
	2411178	SNV	T1172A	Tyr391Phe	Phage tail protein
	2411378	SNV	C972A		Phage tail protein
	2411381	SNV	A969C		Phage tail protein
	2411408	SNV	A942G		Phage tail protein
	2411417	SNV	A933G		Phage tail protein
	2411436	SNV	G914A	Thr305Met	Phage tail protein
	2411480	SNV	C870T		Phage tail protein
	2411492	SNV	A858G		Phage tail protein
	2411510	SNV	A840C		Phage tail protein
	2411552	SNV	G798A		Phage tail protein
	2411555	SNV	A795G		Phage tail protein
	2411567	SNV	T783C		Phage tail protein
	2411600	SNV	T750C		Phage tail protein
	2411629	SNV	T721C		Phage tail protein
	2411666	SNV	A684C		Phage tail protein
	2411669	SNV	C681T		Phage tail protein
	2411674	SNV	T676G	Lys226Glu	Phage tail protein
	2411676-77	SNV	GT673-674CG	Thr225Arg	Phage tail protein
	2411768	SNV	T582C		Phage tail protein
	2942538	SNV	A787G	Cys263Arg	*der*
	3370102	SNV	A315G		IS66 family insertion sequence
	3526713	SNV	G1709A	Gly570Asp	*rpoD*
	4302774	SNV	T628C	Cys210ASer	undecaprenyl-phospatate alpha-N-acetylglucosaminyl 1-phosphate transferase
	4475933	Deletion	G		Downstream of RHS element sequence and hypothetical
	4535303	SNV	T2289C		*rpoB*
	4714412	SNV	G799A	His267Tyr	*cadC*
	4757500	SNV	C237G		*eutJ, dnaK, uidC*
	5097335	SNV	C575T	Arg192His	DNA-binding response regulator

7/2	3526713	SNV	G1709A	Gly570Asp	*rpoD*
	4096597^4096598	Insertion	16 nt		UDP-galactose LPS alpha 1,2-galactosyltransferase
	4278336	SNV	C273 G		23s rRNA
	4714412	SNV	G799A	His267Tyr	*cadC*
7/3	3526713	SNV	G1709A	Gly570Asp	*rpoD*
	4714412	SNV	G799A	His267Tyr	*cadC*
7/4	1633270..1637761	Deletion	4491 nt		autotransporter barrel domain-containing lipoprotein (cut after 4580bp, 5421bp gene), transcriptional regulator, serine threonine kinase, SIR2 family protein, ISNCY family transposase (first 293bp left, gene 1033bp)

Table S4 Best plasmid matches for the ESBL-plasmids in ST131.

Plasmid	Match in GenBank	Sequence identity (%)	Query coverage (%)	ST type	Size plasmid (kbp)	Accession nr
p2/0.1	*E coli* IMT16316 pEcIMT16316	99	80	648	184	CP023816.1
	E. coli ZH193 plasmid pZH193	99	77	131	210	CP014498.1
p4/0.1	*E. coli* NCTC 13441 plasmid: p.	100	96	131	161	LT632321.1
p4/1-1.1	*E. coli* YDC107 plasmid pYDC107_184	99	86	964	184	CP025708.1
	E. coli CREC-532 CREC-532_1	99	86	167	216	CP024831.1
	E. coli CREC-629 CREC-629_1	99	86	167	176	CP024816.1
	E. coli NCTC 13441 plasmid: p.	100	66	131	161	LT632321.1
p4/4.1	*E. coli* CA28 plasmid pCA28	99	95	44	172	CP009232.1
	E. coli AR_0372 plasmid unnamed1	99	95	405	170	CP027130.1
	E. coli AR_0014 plasmid unitig_1_pilon	99	95	167	173	CP024860.1
	E. coli CA14 plasmid pCA14	99	88	131	155	CP009231.1

Table S5 Small cryptic plasmids.

Isolate	Plasmid	Plasmid size/replicon[a]	Best match in GenBank (identity/query coverage)
2/0	p2/0.2	4063 bp / ND	pEC147-4 (JX238455) (99%/100%)
	p2/0.3	2331 bp / ND	No match
	p2/0.4	2105 bp / Col(BS512)	pEC135-1 (JX238451) (99%/100%)
	p2/0.5	1552 bp / ND	pJJ1886 (CP006785) (100%/100%)
2/1	p2/1.2	4063 bp / ND	pEC147-4 (JX238455) (99%/100%)
	p2/1.3	2331 bp / ND	No match
	p2/1.4	2105 bp / Col(BS512)	pEC135-1 (JX238451) (99%/100%)
	p2/1.5	1552 bp / ND	pJJ1886 (CP006785) (100%/100%)
2/2	p2/2.2	4063 bp / ND	pEC147-4 (JX238455) (99%/100%)
	p2/2.3	2331 bp / ND	No match
	p2/2.4	2105 bp / Col(BS512)	pEC135-1 (JX238451) (99%/100%)
	p2/2.5	1552 bp / ND	pJJ1886 (CP006785) (100%/100%)
2/3	p2/3.2	4063 bp / ND	pEC147-4 (JX238455) (99%/100%)
	p2/3.3	2331 bp / ND	No match
	p2/3.4	2105 bp / Col(BS512)	pEC135-1 (JX238451) (99%/100%)
	p2/3.5	1552 bp / ND	pJJ1886 (CP006785) (100%/100%)
2/4	p2/4.2	4063 bp / ND	pEC147-4 (JX238455) (99%/100%)
	p2/4.3	2331 bp / ND	No match
	p2/4.4	2105 bp / Col(BS512)	pEC135-1 (JX238451) (99%/100%)
	p2/4.5	1552 bp / ND	pJJ1886 (CP006785) (100%/100%)
4/0	p4/0.3	10,612 bp / ColRNAI	p2 (CP006658) (99%/94%)
4/1-1	p4/1-1.3	7939 bp / ND	pHUSEC41-3 (99%/100%)
	p4/1-1.4	5167 bp / ND	pASL01a (JQ480155) (99%/100%)
4/1-2	p4/1-2.3	8809 bp / ND	pKpn113c (CP003995) (99%/67%)
	p4/1-2.4	2044 bp / ND	No match
4/2-1	p4/2-1.3	5163 bp / ND	pASL01a (JQ480155) (99%/100%)
			Differ from 4/1-1 at 50 positions
	p4/2-1.4	2640 bp / ND	pSJ-2 (CP011067) (100%/100%)
	p4/2-1.5	2089 bp / Col(BS512)	pEC147-2 (JX238453) (99%/100%)
4/2-2	p4/2-2.2	5167 bp / ND	pASL01a (JQ480155) (99%/100%)
	p4/2-2.3	4087 bp / ND	pMNCRE44_2 (CP010878) (100%/100%)
4/2-3	p4/2-3.2	8809 bp / ND	pKpn113c (CP003995) (99%/67%)
	p4/2-3.3	2044 bp / ND	No match
4/3-1	p4/3-1.4	7939 bp / ND	pHUSEC41-3 (99%/100%)
	p4/3-1.5	5163 bp / ND	pASL01a (JQ480155) (99%/100%)
			Differ from 4/1-1 at 50 positions
	p4/3-1.6	2640 bp / ND	pSJ-2 (CP011067) (100%/100%)
	p4/3-1.7	2089 bp / Col(BS512)	pEC147-2 (JX238453) (99%/100%)
4/3-2	p4/3-2.3	7939 bp / ND	pHUSEC41-3 (99%/100%)
	p4/3-2.4	5167 bp / ND	pASL01a (JQ480155) (99%/100%)
	p4/3-2.5	4087 bp / ND	pMNCRE44_2 (CP010878) (100%/100%)
4/4	p4/4.4	7939 bp / ND	pHUSEC41-3 (HE603112) (99%99%)
	p4/4.5	5167 bp / ND	pASL01a (JQ480155) (99%/100%)
	p4/4.6	4087 bp / ND	pMNCRE44_2 (CP010878) (100%/100%)
	p4/4.7	4072 bp / ND	pMNCRE44_2 (CP010878) (100%/98%)
7/0	p7/0.2	4072 bp / ND	pSF-486-4 (CP012629) 100%/100%)
	p7/0.3	1552 bp / ND	pJJ1886 (CP006785) (99%/100%)
7/1	p7/1.3	4072 bp / ND	pSF-486-4 (CP012629) 100%/100%)
	p7/1.4	1552 bp / ND	pJJ1886 (CP006785) (99%/100%)
7/2	p7/2.4	4072 bp / ND	pSF-486-4 (CP012629) 100%/100%)
	p7/2.5	1552 bp / ND	pJJ1886 (CP006785) (99%/100%)
7/3	p7/3.3	4072 bp / ND	pSF-486-4 (CP012629) 100%/100%)
	p7/3.4	1552 bp / ND	pJJ1886 (CP006785) (99%/100%)
7/4	p7/4.2	4072 bp / ND	pSF-486-4 (CP012629) 100%/100%)
	p7/4.3	1552 bp / ND	pJJ1886 (CP006785) (99%/100%)

a) PlasmidFinder, ND = not detected