Gene	Name	Sequence (5'-3')	Experiment
отрС	ompC-F	GCGAAGGCATGACCAACAAC	qRT-PCR
ompC	ompC-R	AGGTCTGGGTGTACTGAGCA	qRT-PCR
ompF	ompF-F	ACCAACCGCAAGAAGCTCA	qRT-PCR
ompF	ompF-R	TTGGTGTAAGCGATGGACGG	qRT-PCR
recA	recA-F	GAAGACCGTTCCATGGATGT	qRT-PCR
recA	recA-R	GCGTGTTCAGCATCGATAAA	qRT-PCR
ftsl	Mut1ftsI	C*C*G*G*TCAGGGTTAATTTGCTGTA	TM-MAGE
		GCGTGCCACGTCTTTGATTTCGTGGCC	
		GTTAATTCGATAGTTAATTCGATAAGG	
		AATGGTATTGAGTA [§]	
ftsl	Mut2ftsI	C*C*A*T*GATGGCACCAAAGACCGG	TM-MAGE
		CGCGGAAACGGCGCCGCCGTAGTATT	
		TACCCGCCTGCGGATCGTTGAGAACA	
		ACAACCAGCGCGAAGC [§]	
ftsl	Mut1ftsIwt_F	ACCCCGGTCAGGGTTAATTC	Mutant screening PCR
ftsl	Mut1ftsIM_F	ACCCCGGTCAGGGTTAATTT	Mutant screening PCR
ftsl	Mut1ftsl_R	ACCATCACCGACGTGTTTGA	Mutant screening PCR
ftsl	Mut2ftsIwt_F	CTTCGCGCTGGTTGTTGTTA	Mutant screening PCR
ftsl	Mut2ftsIM_F	CTTCGCGCTGGTTGTTGTTC	Mutant screening PCR
ftsl	Mut2ftsI_R	CCTGTCCCCTCGCCTTGATT	Mutant screening PCR
ftsl	Mut1ftslwt2_F	CGTGGCCGTTAATTCGATAA	Mutant screening PCR
ftsl	Mut1ftsIM2_F	CGTGGCCGTTAATTCGATAG	Mutant screening PCR
ftsl	Mut1ftsI2_R	CGAAAGAGGCGATGCGTAAC	Mutant screening PCR
ompC	ompC_Xba_F	<i>CAGAATCTAGA</i> GTTTTGACATTCAGTG	Cloning in pACY184
		CTGTCA	
ompC	ompC_Hind_R	AACATAAGCTTTCATGCGAACGGTCGC	Cloning in pACY184
		AAGA	
отрС	ompC_F2	CAGACATTCAGAAATGAATGACGGT	Sequence verification
отрС	ompC_R2	AGTGCCACGCGGGTAAAGCT	Sequence verification
ompC	ompC_St38_F	TAGTGCTCATGGCGAAGGTA	Sequence verification
отрС	ompC_St38_R	GTACCGATCAGGCCAGTGT	Sequence verification
pACY184	pACY184_F	AAGAGATTACGCGCAGACCA	Sequence verification
pACY184	pACY184_R	ATAGTGACTGGCGATGCTGT	Sequence verification

 Table S3. Oligonucleotides used in this work

[§] * indicates a phosphorothioate bonds

ftsl mutation	Mutant name	Position	Mutation	Gene affected	*Effect
		1,64,569	A=>G	ydfA	NS
Control [§]	Magact 1	1,842,545	C=>T	gdhA	NS
Control	Wagect_1	2,236,418	G=>A	preA	NS
		2,426,060	426,060 A=>G hisJ		S
		92,411	Ins 12nt	<u>ftsI</u>	YRIN
VRIN	Mage 1a	777,276	(G) _{6→7}	tolA	FS
	Widge_id	979,184	C=>T	mukB	S
		4,261,075	G=>T	yjbM	NS
		92,457	G=>A	<u>fts1</u>	E349K
E349K	Mage_2b	380,022	(G) _{10→9}	frmR	IG
		1,475,884	A=>G	ydbD	S
1532L	Mage_3c	93,006	A=>C	<u>fts1</u>	1532L
	Maga 4b	92,411	Ins 12nt	<u>ftsI</u>	YRIN
TRIN+E349K	Wage_4b	92,457	G=>A	<u>ftsl</u>	E349K
		92,457	G=>A	<u>ftsl</u>	E349K
E349K +	Maga Fa	93,006	A=>C	<u>ftsl</u>	1532L
1532L	wage_5a	21,878	T=>C	ribF	NS
		2,958,079	A=>G	ptrA	NS
		92,411	Ins 12nt	<u>ftsl</u>	YRIN
YRIN+E349K	Maga 6b	92,457	G=>A	<u>ftsl</u>	E349K
+ I532L	INIGRE_OD	93,006	A=>C	<u>ftsl</u>	1532L
		994,214	C=>A	ssuC	NS

Table S4: Mutations detected in MG1655 strains derivatives mutated in *ftsl*.

[§]Control strain was obtained by submitting the MGF strain to TM-MAGE steps but without incorporating mutations in *ftsI.* [§]NS, non-synonymous, S, synonymous; FS Frameshift, IG intergenic. Mutations resulting of site directed mutagenesis are indicated in red

	Replicon	Size (bp)	Number of CDS	Antibiotic resistance genes
Chromosome		4,747,851	4,452	bla _{CMY-2}
p <i>Ec</i> MAD1	IncFIB, IncFIA, IncQ1	98,473	15	dfrA17, mph(A), aadA5, sul1, tet(B), aac(3)-IId, aac(6')Ib-cr, bla _{OXA-1} , bla _{CTX-M-15} , bla _{TEM-1B} , sul2, strA, strB
p <i>Ec</i> MAD2	IncX3, ∆ColKP3	51,479	65	qnrS1, bla _{OXA-181}
p <i>Ec</i> MAD3	Col (BS512)	2,088	2	-

Table S5: Genomic features of the E. coli ST410 isolate Ec-MAD

Table S6 Antibiotics susceptibility testing of the ST410 isolate Ec-MAD

Resistant	Amoxicillin, Ticarcillin, Piperacillin, Cefepime, Cefalotin, Amoxicillin- Clavulanate, Ceftazidime, Piperacillin-Tazobactam, Cefoxitin, Cefuroxime, Ticarcillin, Clavulanate, Aztroonam, Maxalactam, Cefotaxime, Strontomucin							
	Clarythromycin, Tetracycline, Erythromycin, Rifampicin, Ciprofloxacin,							
	Nalidixic Acid, Trimethoprim, Tobramycin							
Intermediate	Mecillinam, Ertapenem, Kanamycin and Gentamicin							
Suscentible	Imipenem, Meropenem, Doripenem, Amikacin, Azithromycin,							
Susceptible	Chloramphenicol, Tigecycline and Colistin							

Table S7. Distribution and effect of point mutations in the OXA-181 *E. coli* ST410 subclade

 MRCA

Region	SNPs	Synonymous	Non- Synonymous	Start/Stop	Functional SNP [*]	IG⁵
Non- recombinant	84	23	46	2	25	11
Recombinant ^{&}	1622 (197)	1303 (169)	205 (16)	2	9 (1)	112 (11)

*As determined by the SIFT algorithm[5],[§]Intergenic regions, [&]In bracket the number of SNPs in the 16.5 kb region of the *dcw* gene cluster common to the five recombinant regions in *Ec* ST410 isolates.

Locus Tag	Gene	ene Product N		SIFT Score*	Median Info ^{&}	Chromosomal region	Functional class		
EcMAD_00039	caiD	crotonobetainyl-CoA hydratase	S181N	0.01	2.75	Non-recombinant	Nitrogen metabolism		
EcMAD_00067	yabl	hypothetical protein	G254V	0	3.38	Recombinant	Conserved hypothetical		
EcMAD_00068	thiQ	thiamin ABC transporter - ATP binding subunit	T66M	0.03	2.76	Recombinant	Transporter		
EcMAD_00075	setA	sugar / lactose efflux transporter SetA	V27G	0.01	2.76	Recombinant	Transporter		
EcMAD_00088	ftsl	essential cell division protein FtsI; penicillin-binding protein 3	1536L	0.02	2.75	Recombinant	Cell envelope		
EcMAD_00134	yadE	putative polysaccharide deacetylase lipoprotein	P171S	0.01	2.77	Recombinant	Cell envelope		
EcMAD_00143	htrE	putative outer membrane usher protein	V662I	0.05	2.75	Recombinant	Cell envelope		
EcMAD_00152	hrpB	putative ATP-dependent helicase	C332S	0.01	2.76	Recombinant	DNA metabolism		
EcMAD_00152	hrpB	putative ATP-dependent helicase	P553L	0.01	2.76	Recombinant	DNA metabolism		
EcMAD_00155	fhuC	iron (III) hydroxamate ABC transporter - ATP binding subunit	T72A	0.03	2.77	Recombinant	Transporter		
EcMAD_00362	brnQ	branched chain amino acid transporter BrnQ	D385N	0	2.77	Non-recombinant	Transporter		
EcMAD_00854	nfsA	NADPH nitroreductase monomer	R203H	0	2.77	Non-recombinant	Stress response		
EcMAD_00986	rarA	acid phosphatase	A300V	0	2.77	Non-recombinant	DNA metabolism		
EcMAD_01114	ymdA	putative protein	I21S	0.03	2.83	Non-recombinant	Conserved hypothetical		
EcMAD_01472	tehA	TehA TDT transporter	P246L	0	2.77	Non-recombinant	Transporter		
EcMAD_01480	hicB	antitoxin of the HicA-HicB toxin-antitoxin system	T34A	0	2.75	Non-recombinant	Stress response		
EcMAD_01535	dosP	c-di-GMP phosphodiesterase, heme-regulated	G524D	0.02	2.76	Non-recombinant	Stress response		
EcMAD_01541	yddB	putative porin protein	G406C	0	2.78	Non-recombinant	Cell envelope		
EcMAD_01796	astE	succinylglutamate desuccinylase	A45V	0.03	2.78	Non-recombinant	Carbon metabolism		
EcMAD_01900	edd	phosphogluconate dehydratase	R312H	0.05	3.22	Non-recombinant	Carbon metabolism		
EcMAD_02162	yegV	putative kinase	I181T	0	2.77	Non-recombinant	Conserved hypothetical		
EcMAD_02201	yohC	putative inner membrane protein	L134Q	0	2.78	Non-recombinant	Conserved hypothetical		
EcMAD_02264	сстВ	protoheme IX ABC transporter - membrane subunit CcmB	G147S	0	2.77	Non-recombinant	Transporter		
EcMAD_02280	отрС	outer membrane porin C	R191L	0.03	3.14	Non-recombinant	Cell envelope		
EcMAD_02311	glpB	glycerol-3-phosphate dehydrogenase, membrane anchor subunit	V289M	0.02	2.76	Non-recombinant	Carbon metabolism		
EcMAD_02425	emrK	EmrKY-TolC multidrug efflux transport system - membrane protein	N248I	0	2.75	Non-recombinant	Transporter		
EcMAD_02511	таеВ	malate dehydrogenase	A172S	0.04	3.14	Non-recombinant	Carbon metabolism		
EcMAD_02714	nrdE	ribonucleoside-diphosphate reductase 2	F84L	0.01	3.3	Non-recombinant	DNA metabolism		
EcMAD_02760	hycl	hydrogenase 3 maturation protease	A63V	0.02	2.79	Non-recombinant	Carbon metabolism		
EcMAD_02802	casC	Cascade subunit C	P125S	0	2.75	Non-recombinant	DNA metabolism		
EcMAD_03071	gss	glutathionylspermidine amidase / glutathionylspermidine synthetase	P100S	0.01	2.81	Non-recombinant	Nitrogen metabolism		
EcMAD_03159	ebgR	EbgR DNA-binding transcriptional repressor	198T	0	2.77	Non-recombinant	C. metabolism Regulation		
EcMAD_03286	yrbG	inner membrane protein YrbG	G219V	0.01	2.76	Non-recombinant	Conserved hypothetical		
EcMAD_03840	emrD	multidrug efflux transporter EmrD	G323D	0	2.76	Non-recombinant	Transporter		

Table S8. Mutations predicted with a functional effect using the SIFT algorithm

* Ranges from 0 to 1, mutation is predicted to be functional for values equal or below 0.05. [&]Median for the whole alignment of the information content calculated for each position. This value ranges from 0, when all 20 amino acids are identified to 4.32 when only one amino acid is found.

	qnrB4	qnrS1	aac(3)-IId	aac(6')Ib-cr	aadA5	blaCMY-2	blaCMY-42	<i>bla</i> CTX-M-15	<i>bla</i> DHA-1	blaOXA-1	<i>bla</i> OXA-181	<i>bla</i> TEM-1B	dfrA17	mph(A)	strA	strB	Su/1	sul2	tet(A)	tet(B)
83B9	+	+	+	+	+	+		+	+	+	+	+	+	+	+	+	+	+		+
<i>Ec</i> MAD		+	+	+	+	+		+		+	+	+	+	+	+	+	+	+		+
94G8		+			+		+	+			+		+	+			+	+	+	
92B7		+		+	+			+		+	+		+	+			+		+	
93G1		+		+	+			+		+	+		+	+			+		+	
32139			+	+	+			+		+		+	+	+	+	+	+	+		+

 Table S10. Antibiotic resistance gene content of ST410 isolates analysed in Fig. 7^{*}

* β -lactamase genes are highlighted with colours; + indicates that the gene is present.