

Table S1. Characteristics of the 30 *E. coli* MOB and RelN_{RNA} plasmids of our collection and their host strains

Plasmid ID ¹	Transfer type ²	Size bp	Mobilization gene type	Rop ³	Resistance genes on plasmid	Colicin type	TA system	Plasmid accession no	Host strain ID	Origin	Year of isolation	Strain phylogroup ⁴	Strain cMLST IP ⁵	
MOBrep_{B1} plasmid family, RGT Qu														
RCS76_pIII♦	C/Incl1	4,054	mobA1	nc				LT985285	13948	France	2004	C	7	
RCS35_pl	E	4,087	mobA1	nc				LT985232	565	France	2002	B1	87	
RCS49_pII	C/Incl1	4,074	mobA1	nc				LT985255	580	France	2002	B2	9	
RCS32	E	7,050	mobA1	nc	<i>bla</i> _{CTX-M-15}			LT985240	659	France	2001	B2	43	
MOBrep_{B2} plasmid family														
RCS90_pII	C/IncB/O	11,964	<i>MobA2</i>	nc	<i>strA/B</i>			LT985301	ECOR 24	Sweden	70-80s	A	176	
MOB_{RNA} plasmid type1 family, RGT P5-1														
RCS83_pIII	P	5,912	<i>mbe</i> ABC DE type 1	+				LT985292	ECOR 10	USA	70-80s	A	2	
RCS93_pIII	P	5,631	<i>mbe</i> ABCDE type 1	+				LT985311	CIP106223	United Kingdom	1932	D	IC	
RCS37_pl	C/Incl1	10,551	<i>mbe</i> ABCDE type 1	+	<i>bla</i> _{TEM-1}			LT985230	730	France	2002	F	IC	
RCS76_pII♦	C/Incl1	6,649	<i>mbe</i> ABCDE type 1	+		E1		LT985284	13948	France	2004	C	7	
RCS33_pII	C/Incl1	6,647	<i>mbe</i> ABCDE type 1	+		E1		LT985237	641	France	2002	B1	739	
RCS82_pII	P	23,526	<i>mbe</i> ABCDE type 1	+		E1	CcdAB	LT985303	ECOR 39	Sweden	70-80s	F	254	
MOB_{RNA} plasmid type 2 family														
RCS55_pII	C/Incl/M	6,859	<i>mbe</i> ABCDE type 2	+		S4		LT985386	694	France	2001	A	2	
RCS74_pII♦	C Incl1	7,133	<i>mbe</i> ABCDE type 2	+		S4		LT985282	13942	France	2004	NA	NA	
MOB_{RNA} plasmid type 3 family, RGT P5-2														
RCS48_pIII	C/Incl1	4,772	<i>mob</i> ABC	-				LT985246	720	France	2003	B2	9	
RCS49_pIII	C/Incl1	15,843	<i>mob</i> ABC	-	<i>bla</i> _{SHV-12}	<i>bla</i> _{TEM-1}		LT985254	580	France	2002	B2	9	
RCS91	E	9,89	<i>mob</i> ABC	-		<i>tetA(A)</i>		LT985299	ECOR 6	USA	70-80s	A	IC	
MOB_{RNA} plasmid type 4 family, RGT C11														
RCS12TR533_pl	E	14,248	<i>mob</i> BC	+	<i>bla</i> _{TEM-3}		cloacin	ParE/B	LT985216	533	France	1999	B2	33
RCS49_pIV	C/Incl1	20,798	<i>mob</i> BC	+	<i>bla</i> _{SHV-12}	<i>bla</i> _{TEM-1}	cloacin	ParE/B,LsoA/B	LT985257	580	France	2002	B2	9
MOB_{RNA} plasmid type 5 family, RGT P5-3														
RCS48_pII	C/Incl1	19,831	<i>mob</i>	+	<i>bla</i> _{SHV-12}	<i>bla</i> _{TEM-1}	<i>Δmer1</i>	LsoA/B	LT985247	720	France	2003	B2	9
RCS35_pII	E	14,365	<i>mob</i>	+	<i>bla</i> _{SHV-12}	<i>bla</i> _{TEM-1}		LsoA/B	LT985233	565	France	2002	B1	87
RCS93_pIV	P	4,913	<i>mob</i>	+			E1	-	LT985308	CIP106223	United Kingdom	1932	D	IC
RCS64_pl	C/Incl1	3,002	<i>mob</i>	+				parE/B	LT985294	650	France	2002	D	740
RelN_{RNA} plasmids type 1 family														
RCS87♦	E	6,047		-		<i>sul2</i>		MazE	LT985298	ECOR 18	USA	70-80s	A	132
RCS86_pl	E	6,069		-		<i>sul2</i>		MazE	LT985307	ECOR 4	USA	70-80s	A	188
RCS98♦	E	6,200		-		<i>strA/B</i>	<i>sul2</i>	MazE	LT985316	ECOR 17	Indonesia	70-80s	A	169
RCS92_pl♦	E	6,222		-		<i>strA/B</i>	<i>sul2</i>	MazE	LT985314	ECOR 25	USA	70-80s	A	177
RCS63	E	22,308		-	<i>bla</i> _{CTX-M-14}	<i>strA/B</i>	<i>sul2</i>	MazE	LT985269	631	France	2002	A	2
RelN_{RNA} plasmid type 2 family														
RCS92_pIII♦	E	3,174		+					LT985312	ECOR 25	USA	70-80s	A	177
RCS83_pII	P	2,999		+				HigAB	LT985291	ECOR 10	USA	70-80s	A	2
RelN_{RNA} plasmid type 3 family														
RCS83_pl	P	4,074		+				MazE	LT985290	ECOR 10	USA	70-80s	A	2

¹RGT, Relaxase Gene Type (Compain et al, 2014); ♦, plasmids isolated from animal: strains 13948 and 13942, *Bos taurus*; ECOR 17, *Sus scrofa domestica*; ECOR 18, *Macaca nigra*; ECOR 25, *Canis lupus familiaris*
²E, electroporation; C/, conjugation followed by conjugative plasmid Inc types; P, plasmidome

³Rop, repressor of primer; nc, not concerned; +, presence;- , absence

⁴NA, non-available

⁵IC, incomplete sequence type

Table S2. Description of backbone contents of the 10 plasmid families based on the 30 plasmids of our collection

Gene contents of the plasmid backbones according to the family type					
Family type	Replication gene	Mobilisation gene system	Presence of a <i>rop</i> gene	No of genes coding for proteins of unknown function	Other genes
MOBrep _{B1} plasmid family, RGT Qu	rep _{B1}	<i>mobA1</i>	NC	1	-
MOBrep _{B2} plasmid family	rep _{B2}	<i>mobA2</i>	NC	1	-
MOB _{RNA} plasmid type1 family, RGT P5-1	NC	<i>mbeABCDE</i> type 1	+	0	-
MOB _{RNA} plasmid type 2 family	NC	<i>mbeABCDE</i> type 2	+	0	-
MOB _{RNA} plasmid type 3 family, RGT P5-2	NC	<i>mobABC</i>	-	1	-
MOB _{RNA} plasmid type 4 family, RGT C11	NC	<i>mobBC</i>	+	0	-
MOB _{RNA} plasmid type 5 family, RGT P5-3	NC	<i>mob</i>	+	0	-
Rel _{RNA} plasmids type 1 family	NC	none	-	4	<i>mazE</i>
Rel _{RNA} plasmid type 2 family	NC	none	+	2	-
Rel _{RNA} plasmid type 3 family	NC	none	+	2	-

*NC, not concerned

**+, presence; -, absence

Table S3. Characteristics of the MOB_{repB1} plasmids

No	Plasmid ID	Accession no	Co-integration	Plasmid size bp	Colicin operon type	Toxin/antitoxin system	Restriction/methylation system	antibiotic resistance gene	other genes	Bacterial host ID	Geographic origin
1	pIGWZ12	DQ311641.1		4 072						<i>Escherichia coli</i> CZD1527	Poland
2	pSF-468-4	CP012629.1		4 072						<i>Escherichia coli</i> strain SF-468	USA
3	pEC732_4	CP015142.1		4 072						<i>Escherichia coli</i> strain Ecol_732	Thailand
4	RCS32	LT985240.1		7 050				<i>bla</i> _{CTX-M-15}		<i>Escherichia coli</i> strain 659	France
5	pEC867_3	CP018980.1		4 074						<i>Escherichia coli</i> strain Ecol_867	Canada
6	VNB151-sc-2315230 p2	LT795116.1		4 239						<i>Salmonella enterica</i> serovar Typhimurium VNB151-sc-2315230	United Kingdom
7	pE35BA_1	KT693145.1		4 130						<i>Escherichia coli</i> strain E35BA	Spain
8	RCS49_pIII	LT985255.1		4 074						<i>Escherichia coli</i> strain 580	France
9	pV294-c	LC056560.1		4 157						<i>Escherichia coli</i> plasmid pV294-c	India
10	pMRSN346647_4.1	CP018208.1		4 074						<i>Escherichia coli</i> strain MRSN346647	USA
11	pSTM6-4	CP019648.1		4 083						<i>Salmonella enterica</i> serovar Typhimurium strain TW-Stm6	Australia
12	pYU39_5.1	CP011432.1		5 093						<i>Salmonella enterica</i> Serovar Typhimurium strain YU39	Mexico
13	pSD4.0	JX566767.1		4 060						<i>Salmonella enterica</i> subsp. enterica serovar Derby	Germany
14	RCS76_pIII	LT985285.1		4 054						<i>Escherichia coli</i> strain 13948	France
15	pSMS35_4	CP000973.1		4 074						<i>Escherichia coli</i> SMS-3-5	USA
16	pEC224_7	CP018941.1		4 062						<i>Escherichia coli</i> strain Ecol_224	Viet Nam
17	pSE11-6	AP009246.1		4 082						<i>Escherichia coli</i> SE11	Japan
18	pEC08-4	JX238443.1		4 082						<i>Escherichia coli</i> strain EC08	Sweden
19	p2PCN033	CP006634.1		4 086						<i>Escherichia coli</i> PCN033	China
20	pE2022_4	KT693143.1		4 082						<i>Escherichia coli</i> strain E2022	Spain
21	pEC29-1	JX238447.1		4 082						<i>Escherichia coli</i> strain EC29	Sweden
22	pFV9873_1	KT693144.1		4 081						<i>Escherichia coli</i> strain FV9873	Spain
23	FH182_scaffold-9	LM996766.1		4 161						<i>Escherichia coli</i> FH182	Norway
24	pVR50F	CP011140.1		4 075						<i>Escherichia coli</i> VR50	Australia
25	pEC542_4	CP018966.1		4 087						<i>Escherichia coli</i> strain Ecol_542	Viet Nam
26	pMNCRE44_2	CP010878.1		4 088						<i>Escherichia coli</i> strain MNCRE44	USA
27	pEC958B	HG941720.1		4 080						<i>Escherichia coli</i> ST131 strain EC958	Australia
28	pEC299-2	JX238458.1		4 088						<i>Escherichia coli</i> strain EC299	Sweden
29	RCS35_pI	LT985232.1		4 087						<i>Escherichia coli</i> 565	France
30	pEC648_4	CP008718.1		4 073						<i>Escherichia coli</i> strain ST648	China
31	pC06114_7	CP016041.1		4 071						<i>Escherichia coli</i> isolate Co6114	Germany
32	pEC881_5	CP019024.1		4 063						<i>Escherichia coli</i> strain Ecol_881	Colombia
33	pEC147-4	JX238455.1		4 071						<i>Escherichia coli</i> strain EC147	Sweden
34	pEC224_6	CP018942.1		4 063						<i>Escherichia coli</i> strain Ecol_224	Viet Nam
35	pEC545_4	CP018972.1		4 073						<i>Escherichia coli</i> strain Ecol_545	Viet Nam
36	pECAZ153_4	CP018996.1		4 073						<i>Escherichia coli</i> strain Ecol_AZ153	China
37	pMRY16-002	AP017616.1		4 073						<i>Escherichia coli</i> 20Ec-P-124	Japan
38	pV004-b	LC056155.1		4 110						<i>Escherichia coli</i> strain V004	India
39	pEC08-3	JX238442.1		4 071						<i>Escherichia coli</i> strain EC08	Sweden
40	pV044-c	LC056172.1		3 976						<i>Escherichia coli</i> V044	India

Table S4. Characteristics of the MOB_{repB2} plasmids

No	Plasmid ID	Accession no	Co-integration	Plasmid size bp	Colicin operon type	Toxin/antitoxin system	Restriction/methylation system	antibiotic resistance gene	other genes	Bacterial host ID	Geographic origin
1	pEC147-3	JX238454.1		3 904						<i>Escherichia coli</i> strain EC147 plasmid pEC147-3	Sweden
2	p931-3904	CP016386.1		3 904						<i>Salmonella enteric</i> a subsp. enterica serovar Typhimurium	USA
3	pSF-088-3	CP012638.1		3 904						<i>Escherichia coli</i> strain SF-088	USA
4	pN13-01290_3-3	CP012935.1		3 905						<i>Salmonella enterica</i> subsp. enterica serovar Heidelberg	Canada
5	pSAN1-1677	CP019896.1		3 904						<i>Salmonella enteric</i> a subsp. enterica serovar Anatum SAN222	USA
6	pBS512_5	CP001060.1		5 114						<i>Shigella boydii</i> CDC 3083-94	USA
7	p75-02_5	CP019693.1		5 114						<i>Shigella sonnei</i> strain 75/02	Hungary
8	pCFSAN030807_6	CP023651.1		5 114						<i>Shigella sonnei</i> strain CFSAN030807 plasmid	USA
9	pSTY2-1899	CP019895.1		3 910						<i>Salmonella enterica</i> subsp. enterica serovar Typhimurium	USA
10	pCROD3	FN543505.1		3 910						<i>Citrobacter rodentium</i> ICC168	United Kingdom
11	pCVM19633_4,	CP001126.1		4 585						<i>Salmonella enterica</i> subsp. enterica serovar Schwarzengrund	USA
12	RCS90_pII	LT985301.1		11 964				<i>strA/B</i>		<i>Escherichia coli</i> strain ECOR 24	Sweden

Table S5. Characteristics of the MOB_{RNA} type 1 plasmids

No	Plasmid ID	Accession no	Co-integration	Plasmid size bp	Colicin operon type	Toxin/antitoxin system	Restriction/methylation system	antibiotic resistance gene	other genes	Bacterial host ID	Geographic origin
1	RCS33_pII	LT985237		6 647	Colicin E1					<i>Escherichia coli</i> strain 641	France
2	RCS76_pII	LT985284		6 649	Colicin E1					<i>Escherichia coli</i> strain13948	France
3	pH1519-7	KJ484632.1		7 036	Colicin E1					<i>Escherichia coli</i>	Switzerland
4	pEC276_KPC	CP018949.1		16 559	Colicin E1			<i>bla</i> _{KPC-2}		<i>Escherichia coli</i> strain Ecol_276	USA
5	pCE-R2-11-0435_6	CP016519.1		6 647	Colicin E1					<i>Salmonella enterica</i> serovar Heidelberg strain CE-R2-11-0435	Canada
6	FHI99 scaffold-9	LM997248.1		9 449	Colicin E1					<i>Escherichia coli</i> genome assembly FHI99,	Norway
7	pEC224_5	CP018943.1		6 647	Colicin E1					<i>Escherichia coli</i> strain Ecol_224	Viet Nam
8	pSF-468-3	CP012628.1		6 647	Colicin E1					<i>Escherichia coli</i> strain SF-468	USA
9	pSH14-028_6	CP016513.1		6 647	Colicin E1					<i>Salmonella enterica</i> serovar Heidelberg strain SH14-028	Canada
10	H8 plasmid C	CP010175.1		6 647	Colicin E1					<i>Escherichia coli</i> strain H8	China
11	ColE1	J01566.1		6 646	Colicin E1					<i>Escherichia coli</i>	-
12	pEC881_4	CP019025.1		6 647	Colicin E1					<i>Escherichia coli</i> strain Ecol_881	Colombia
13	pEC158	HQ425708.1		5 706			Eco8I type II			<i>Escherichia coli</i> strain G8	Poland
14	pSL491_5	CP001148.1		5 880					transporter	<i>Salmonella enterica</i> serovar Virchow str. SL491	USA
15	pSLy5	CP015917.1		8 972	Colicin E1					<i>Escherichia coli</i> strain 210205630	USA
16	plasmid pC	AY079201.1		5 269			Eco29KI type II			<i>Salmonella enteritidis</i> serovar Enteritidis	Czech republic
17	EC11 p4	CP027259.1		6 812	colicin N					<i>Escherichia coli</i> strain EC11	China
18	pACN001-C	KC853436.1		5 784						<i>Escherichia coli</i> ACN001	China
19	TGH10 Plasmid	CP012744.1	chromosome		- Colicin E1					<i>Klebsiella pneumoniae</i> strain TGH10	Belgium
20	RCS37_pl	LT985230		10 551				<i>bla</i> _{TEM-1}		<i>Escherichia coli</i> strain 730	France
21	FHI58 scaffold-5	LM995959.1		9 649	Colicin E1		EcoRI type II			<i>Escherichia coli</i> FHI58	Norway
22	FHI63 scaffold-18	LM996433.1		9 690	Colicin E1		EcoRI type II			<i>Escherichia coli</i> FHI63	Norway
23	pSE11-4	AP009244.1		6 929						<i>Escherichia coli</i> SE11	Japan
24	pSPI12	GU949535.1		4 080						<i>Salmonella enterica</i> serovar Pullorum strain S06004	China
25	pSFD10	AY048853.1		4 091						<i>Salmonella choleraesuis</i> strain 79500	China
26	pSMS35_8	CP000972.1		8 909	Colicin E1					<i>Escherichia coli</i> SMS-3-5	USA
27	pEC159	JN692546.1		6 292			EcoRV type II			<i>Escherichia coli</i>	Poland
28	pLG13	AF251289.1		6 293			EcoRV type II			<i>Escherichia coli</i>	Russia
29	pWQ799	L39794.1		6 915					glycosyltransferase	<i>Salmonella enterica</i> serovar Borreze	Canada
30	pETEC_5	CP000801.1		5 033						<i>Escherichia coli</i> E24377A	USA
31	p75	FN822749.1		7 497						<i>Escherichia coli</i> ETEC 1392/75	United Kingdom
32	pEC34B	HQ622576.1		6 952			EcoO34I type II			<i>Escherichia coli</i> strain NCTC 9034	Poland
33	pDT1	HF565445.2		5 262	Colicin Js					<i>Shigella sonnei</i> EG211	Vietnam
34	p12579_5	CP003114.1		5 954			Eco12579 type II			<i>Escherichia coli</i> O55:H7 str. RM12579	USA
35	pFAM21845_3	CP017223.1		5 828			Ssoll type II			<i>Escherichia coli</i> strain FAM21845	Switzerland
36	pHSD	Y16897.2		5 571			Ecl18KI type II			<i>Enterobacter cloacae</i> HSD	Russia
37	pSTd4	HQ730898.1		5 569			StyD4I type II			<i>Salmonella enterica</i> serovar Typhi	Poland
38	pO26_3	AP010956.1		5 686			CfrBI type II			<i>Escherichia coli</i> O26:H11 str. 11368	Japan
39	pSD5.6	JX566769.1		5 784			CfrBI type II			<i>Salmonella enterica</i> serovar Derby	Germany
40	pEC16II	KU932034.1		7 939					Cupin ABC transporter	<i>Escherichia coli</i>	Finland
41	pHUSEC41-3	HE603112.1		7 930					Cupin ABC transporter	<i>Escherichia coli</i> HUSEC41	Germany

42 pV097-a	LC056262.1	4 081			<i>Escherichia coli</i> strain V097	India
43 p5217	EU580135.1	5 217			<i>Escherichia coli</i> strain E2348/69	Canada
44 pSB13	HQ404303.1	5 424		Sbo13I type II	<i>Shigella boydii</i>	Poland
45 pSF301-3	JF813188.1	4 043			<i>Shigella flexneri</i> strain 2a 301	China
46 pSFxv_4	CP001387.1	4 042			<i>Shigella flexneri</i> 2002017	China
47 ColJs	AF282884.1	5 210 Colicin Js			<i>Shigella sonnei</i> Colicin Js type 7 producer	Czech Republic
48 RCS82_pII	LT985303	23 526 Colicin E1	<i>CCDAVB</i> (<i>Replicon FIR</i>)		<i>Escherichia coli</i> ECOR 39	Sweden
49 FHI90 scaffold-9	LM997292.1	6 983 Colicin E1			<i>Escherichia coli</i> FHI90	Norway
50 pColE1-MRE600	CP014198.2	7 057 Colicin E1			<i>Escherichia coli</i> strain MRE600	United Kingdom
51 plasmid B M6	CP010188.1	6 039			<i>Escherichia coli</i> strain M6	China
52 pCFSAN017963_02,	CP017722.1	7 665		CfrBI type II	<i>Salmonella enterica</i> serovar Minnesota strain CFSAN017963	USA
53 RCS83_pIII	LT985292	5 912			<i>Escherichia coli</i> ECOR 10	USA
54 p14408_3	LT599828.1	11 988 Colicin R			<i>Escherichia coli</i> NRZ14408	Germany
55 C8 plasmid C	CP010128.1	7 982 Colicin E1			<i>Escherichia coli</i> strain C8	China
56 pMRSN346355_5.3	CP018126.1	5 310		<i>aph(3')-I</i>	<i>Escherichia coli</i> strain MRSN346355	USA
57 pECAZ146_6	CP018985.1	5 631		EamA family transporter	<i>Escherichia coli</i> strain Ecol_AZ146	Italy
58 pJJ1886_3,	CP006787.1	5 631			<i>Escherichia coli</i> JJ1886	USA
59 pVR50D	CP011138.1	5 631		Permease transporter (DMT)	<i>Escherichia coli</i> VR50	Australia
60 RCS93_pIII	LT985310	5 631			<i>Escherichia coli</i> CIP106224	United Kingdom

Table S6. Characteristics of the MOB_{RNA} type 2 plasmids

No	Plasmid ID	Accession no	Co-integration	Plasmid size bp	Colicin operon type	Toxin/antitoxin system	Restriction/methylation system	antibiotic resistance gene	other genes	Bacterial host ID	Geographic origin
1	pECAZ146_4	CP018987.1		6 994	Colicin K					<i>Escherichia coli</i> strain Ecol_AZ146	Italy
2	FHI99, scaffold scaffold-7	LM997246.1		6 965	Colicin K					<i>Escherichia coli</i> genome assembly FHI99, scaffold scaffold-7	Norway
3	FHI100, scaffold scaffold-5	LK985402.1		6 965	Colicin K					<i>Escherichia coli</i> genome assembly FHI100, scaffold scaffold-5	Norway
4	RCS74_pII	LT985282.1		7 133	Colicin S4					<i>Escherichia coli</i> strain 13942-1	France
5	FHI89, scaffold scaffold-10_	LM997028.1		7 008	Colicin K					<i>Escherichia coli</i> genome assembly FHI89, scaffold scaffold-10	Norway
6	Pvr50c	CP011137.1		6 989	Colicin K					<i>Escherichia coli</i> VR50	Australia
7	pColK-K235	AY929248.1		8 318	Colicin K					<i>Escherichia coli</i>	Slovenia
8	FHI65, scaffold scaffold-9_	LM996510.1		8 785					transporter	<i>Escherichia coli</i> genome assembly FHI65, scaffold scaffold-9	Norway
9	RCS55_pII	LT985386.1		6 859	Colicin S4					<i>Escherichia coli</i> strain 694	France
10	pSYM12	KM107848.1		7 111	Colicin S4					<i>Escherichia coli</i> strain G1/2	Germany
11	FHI87, scaffold scaffold-7	LM996983.1		6 668	Colicin D					<i>Escherichia coli</i> genome assembly FHI87, scaffold scaffold-7	Norway
12	FHI20, scaffold scaffold-5_	LM995793.1		6 664	Colicin D					<i>Escherichia coli</i> genome assembly FHI20, scaffold scaffold-5	Norway
13	pColD-157	Y10412.1		6 675	Colicin D					<i>Escherichia coli</i> plasmid pColD-157 DNA	Germany
14	pO177C1	CP024615.1		6 675	Colicin D					<i>Escherichia coli</i> strain SMN152SH1	USA
15	pO177C3	CP024053.1		6 675	Colicin D					<i>Escherichia coli</i> strain SMN197SH3	Canada
16	D10 plasmid B	CP010159.1		6 822	Colicin 10					<i>Escherichia coli</i> strain D10	China
17	FHI42, scaffold scaffold-8	LK999928.1		5 959	Colicin 10					<i>Escherichia coli</i> genome assembly FHI42, scaffold scaffold-8	Norway
18	pACN001-E	KC853438.1		6 822	Colicin 10					<i>Escherichia coli</i> ACN001	China
19	pO111_5	AP010965.1		6 673	Colicin D					<i>Escherichia coli</i> O111:H- str. 11128	Japan
20	pO104:H7_S1	KM085451.1		6 819	Colicin 10					<i>Escherichia coli</i> O104:H7 strain RM9387	USA
21	pO104:H7_S2	KM085452.1		6 673	Colicin D					<i>Escherichia coli</i> O104:H7 strain RM9387	USA
23	FHI30, scaffold scaffold-7	LM995877.1		6 144	Colicin K					<i>Escherichia coli</i> genome assembly FHI30, scaffold scaffold-7	Norway
23	FHI23, scaffold scaffold-9	LM995623.1		4 222						<i>Escherichia coli</i> genome assembly FHI23, scaffold scaffold-9	Norway
24	FHI6, scaffold scaffold-9_	LM996333.1		7 424	Colicin D					<i>Escherichia coli</i> genome assembly FHI6, scaffold scaffold-9	Norway
25	FHI97, scaffold scaffold-14	LM997189.1		7 409	Colicin D					<i>Escherichia coli</i> genome assembly FHI97, scaffold scaffold-14	Norway

Table S7. Characteristics of the MOB_{RNA} type 3 plasmids

No	Plasmid ID	Accession no	Co-integration	Plasmid size bp	Colicin operon type	Toxin/antitoxin system	Restriction/methylation system	antibiotic resistance gene	other genes	Bacterial host ID*	Geographic origin	Plant disease
1	pSZECL_b	KU302804.1		3 223						<i>Enterobacter cloacae</i> strain SZECL1	China	
2	pV046-a	LC056197.1		3 629						<i>Escherichia coli</i> strain V046	India	
3	pSTY4-2010K-1587	CP016867.1		3 223						<i>Salmonella enterica</i> serovar Typhimurium str. CDC 2010K-1587 strain USDA-ARS-USMARC-1908	USA	
4	pKpN01-COL	CP012991.1		3 223						<i>Klebsiella pneumoniae</i> strain KpN01	Canada	
5	pKP13b	CP003994.1		3 223						<i>Klebsiella pneumoniae</i> Kp13	Brazil	
6	pCAV1741-3223	CP011652.1		3 223						<i>Citrobacter freundii</i> strain CAV1741	USA	
7	pCAV1492-3223	CP011637.1		3 223						<i>Serratia marcescens</i> strain CAV1492	USA	
8	pCAV1311-3223	CP011569.1		3 223						<i>Enterobacter cloacae</i> strain CAV1311	USA	
9	pCAV1176-3223	CP011658.1		3 223						<i>Enterobacter hormaechei</i> strain CAV1176	USA	
10	pCAV1042-3223	CP018666.1		3 223						<i>Klebsiella pneumoniae</i> strain CAV1042	USA	
11	p_incR_DHQP1002001	CP016812.1	IncR	65 887						<i>Klebsiella pneumoniae</i> strain DHQP1002001	USA	
12	KSB1_4E plasmid unnamed 4	CP024503.1		3 223						<i>Klebsiella pneumoniae</i> strain KSB1_4E	Australia	
13	INF322 plasmid unnamed 5	CP024487.1		3 223						<i>Klebsiella pneumoniae</i> strain INF322	Australia	
14	pV266-a	LC056487.1		2 965						<i>Escherichia coli</i> strain V266	China	
15	pRK10	EU697813.1		4 241						<i>Serratia marcescens</i> strain ACE2	India	
16	pEC867_KPC	CP018981.1		14 029				<i>bla</i> _{KPC-3}		<i>Escherichia coli</i> strain EcoI_867	Canada	
17	pSAN2-06-0624	CP019997.1		4 018						<i>Salmonella enterica</i> serovar Anatum str. USDA-ARS-USMARC-1765	USA	
18	p34977-5.006kb	CP010375.2		5 007						<i>Enterobacter hormaechei</i> subsp. steigerwaltii strain 34977	USA	
19	pSZECL_g	KU302809.1		5 522						<i>Enterobacter cloacae</i> strain SZECL1	China	
20	AR_0365 plasmid unnamed4	CP027141.1		4 604						<i>Enterobacter cloacae</i> complex 'Hoffmann cluster III' strain AR_0365	USA	
21	pASM4	CP019843.1		4 667						<i>Enterobacter cloacae</i> strain R11	China	
22	pEC278	AY589571.1		4 669						<i>Escherichia coli</i> strain 278B	UK	
23	pSD4.6	JX566768.1		4 664						<i>Salmonella enterica</i> subsp. enterica serovar Derby	Germany	
24	p09-036813-1A_4	CP016528.1		4 096						<i>Salmonella enterica</i> serovar Heidelberg strain 09-036813-1A	Canada	
25	pCAV1321-4310	CP011606.1		4 310						<i>Citrobacter freundii</i> strain CAV1321	USA	
26	pLK39	GQ353340.1		4 029						Endophytic <i>Salmonella</i> sp LOB-07	Brazil	Solanum lycocarpum
27	pDSJ01	CP017582.1		4 277						<i>Pantoea stewartii</i> subsp. stewartii DC283	USA	Corn pathogen
28	pSW100	L37403.1		4 272						<i>Pantoea stewartii</i> (Erwinia)SW2	USA	Corn pathogen
29	pSA01AB09084001_4	CP016532.1		4 245						<i>Salmonella enterica</i> serovar Heidelberg strain SA01AB09084001	Canada	
30	RCS91_p	LT985299.1		9 890				<i>tet</i> (A)		<i>Escherichia coli</i> strain ECOR 6	USA	
31	pK	AY079200.1		4 245						<i>Salmonella enterica</i> serovar Enteritidis	Czech Republic	
32	pSYM7	KM107843.1		4 452						<i>Escherichia coli</i> strain G5	Germany	
33	pHL1 Eco1524I	EU863203.1		5 850			Eco1524 Type II			<i>Escherichia coli</i> strain 1524a	Tunisia	
34	pBERT	AF025795.1		4 656						<i>Salmonella enterica</i> serovar Berta	USA	
35	pCN061p2	CP006638.1		5 754						<i>Escherichia coli</i> PCN061	China	
36	pCY-MdT	KF998105.1		5 933				<i>aaC</i> (6')-Ib		<i>Enterobacter cloacae</i> strain CY01	China	
37	pMdT1	JX457478.1		5 931				<i>aac</i> (6')-Ib		<i>Salmonella enterica</i> serovar Typhimurium	Spain	
38	pSEEH1578_03	CP004857.1		4 773						<i>Salmonella enterica</i> serovar Heidelberg str. 41578	USA	

39	pSH1148_4.8	JX494965.1	4 775		<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Heidelberg	USA	
40	RCS48_pIII	LT985246.1	4 772		<i>Escherichia coli</i> strain 720	France	
41	RCS49_pIII	LT985254.1	15 843	<i>bla</i> _{SHV-12} <i>bla</i> _{TEM-1}	<i>Escherichia coli</i> strain 580	France	
42	pDSJ02	CP017583.1	4 368		<i>Pantoea stewartii</i> subsp. <i>stewartii</i> DC283	USA	Corn pathogen
43	pSW200	L42525.1	4 368		<i>Pantoea stewartii</i> (Erwinia)SW2	USA	Corn pathogen
44	CFSAN001921 plasmid unmamed	CP006051.1	4 675		<i>Salmonella enterica</i> serovar Typhimurium var. 5- str. CFSAN001921	USA	
45	pSTY3-2010K-1587	CP016866.1	4 675		<i>Salmonella enterica</i> serovar Typhimurium str. CDC 2010K-1587 strain USDA-ARS-USMARC-1908	USA	
46	pEC3	D45188.1	3 000		<i>Pectobacterium carotovorum</i> (Erwinia carotovora)	Japan	Solanum tuberosum
47	pSCC1	CP021895.1	5 524		<i>Pectobacterium carotovorum</i> strain SCC1 (Erwinia carotovora)	Finland	Solanum tuberosum
48	pUCD5000	AF022806.1	5 229		<i>Tatumella morbirosei</i> (Pantoea citrea)	USA	pineapple pink disease
49	pTPqnrS-1a	AM746977.1	10 066	<i>qnrS1</i>	<i>Salmonella enterica</i> serovar Typhimurium	United Kingdom	
50	p10k	CP025337.1	10 047	<i>qnrS1</i>	<i>Salmonella enterica</i> serovar Typhimurium strain BL10	Taiwan	
51	pHLR25	HE652087.1	10 047	<i>qnrS1</i>	<i>Salmonella enterica</i> serovar Typhimurium HLR25	Spain	
52	pQnrS1-cp17s	JN393220.1	10 047	<i>qnrS1</i>	<i>Salmonella enterica</i> serovar Typhimurium strain 484	Viet Nan	
53	pSQR1	KJ187750.1	10 047	<i>qnrS1</i>	<i>Salmonella enterica</i> serovar Typhimurium strain AC06.010	Taiwan	
54	pST728/06-2	EU715253.1	10 107	<i>qnrS1</i>	<i>Salmonella enterica</i> serovar Typhimurium	Taiwan	

* Plant pathogens are highlighted in green

Table S8. Characteristics of the MOB_{RNA} type 4 plasmids

No	Plasmid ID	Accession no	Co-integration	Plasmid size bp	Colicin operon type	Toxin/antitoxin system	Restriction/methylation system	antibiotic resistance gene	other genes	Bacterial host ID	Geographic origin
1	pKPN-819	CP008799.1	IncX3	58 050	Cloacin	ParE1		<i>aac6'-lb-Tn3</i> , <i>bla</i> _{TEM-1}		<i>Klebsiella pneumoniae</i> KPNIH24	USA
2	plasmid 15S	FJ223606.1		23 753	Cloacin	ParE ₁		<i>aac6'-lb-Tn3</i> , <i>bla</i> _{KPC-2}		<i>Klebsiella pneumoniae</i> strain S15	USA
3	pECAZ161_KPC	CP019010.1	Inc unknown	55 746	Cloacin	ParE1		<i>bla</i> _{TEM-1} , <i>bla</i> _{KPC-3}		<i>Escherichia coli</i> strain EcoL_AZ161	USA
4	pIGMS32	DQ298019.1		9 294	Cloacin	ParE ₁				<i>Klebsiella pneumoniae</i>	poland
5	pAAC154-a9e	CP009877.1		15 100	Cloacin	ParE1		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i> strain KPNIH31	USA
6	AR_0125 plasmid tig00000007	CP021860.1		24 749	Cloacin	ParE ₁		<i>aac6'-lb-Tn3</i> , <i>bla</i> _{KPC-3}		<i>Klebsiella pneumoniae</i> strain AR_0125	USA
7	HUG07 plasmid p4	CP019776.1		14 027	Cloacin	ParE1		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i> strain KPN_KPC_HUG_07	Switzerland
8	pAAC154-a50	CP007728.1		15 096	Cloacin	ParE ₁		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i> KPNIH10	USA
9	pCAV1453-14	CP018353.1		13 841	Cloacin	ParE1		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i> strain CAV1453	USA
10	ColEST258	JN247853.1		13636	Δ Cloacin	ParE ₁		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i>	Italia
11	pAp	CP024651.1		14 241	Cloacin	ParE1		<i>bla</i> _{TEM-1}		<i>Escherichia coli</i> strain BH100 substr. MG2014	Brazil
12	pCAV1417	CP018348.1		9 940	Cloacin	ParE ₁				<i>Klebsiella pneumoniae</i> strain CAV1417	USA
13	pBIC-1c	CP022576.1		13 841	Cloacin	ParE1		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i> strain BIC-1	France
14	pCKO3	CP000823.1		9 294	Cloacin	ParE ₁				<i>Citrobacter koseri</i> ATCC BAA-895	USA
15	AR_0047 plasmid tig00000004	CP021543.1		15 271	Cloacin	ParE1		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i> strain AR_0047	USA
16	AR0098 plasmid tig00000004	CP020112.1		13 841	Cloacin	ParE ₁		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i> strain AR_0098	USA
17	p38544-85.403kb	CP010362.1	IncR	85 403	Cloacin	ParE1		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i> strain 38544	USA
18	pKP64477e	MF150119.1		9 294	Cloacin	ParE ₁				<i>Klebsiella pneumoniae</i> strain A64477	Brazil
19	pMNCRE53_1	CP018433.1		15 273	Cloacin	ParE1		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i> strain MNCRE53	USA
20	pNY9_6	CP015391.1		11 090	Δ Cloacin	ParE ₁				<i>Klebsiella pneumoniae</i> strain NY9	USA
21	pDMC1097	CP011979.1		20 222	Cloacin	ParE1		<i>Δbla</i> _{TEM-1}		<i>Klebsiella pneumoniae</i> DMC1097	USA
22	pUHKPC33-13.841kb	CP011993.1		13 841	Cloacin	ParE ₁		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i> UHKPC33	USA
23	AR_0024 plasmid unitig_1	CP026710.1		9 294	Cloacin	ParE1				<i>Citrobacter koseri</i> strain AR_0024	USA
24	p500_1420-13.838kb	CP011984.1		13 838	Cloacin	ParE1		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i> 500_1420	USA
25	pMNCRE78_1	CP018431.1		18 890	Cloacin	ParE ₁		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i> strain MNCRE78	USA
26	pKPN-c8b	CP009778.1		15 271	Cloacin	ParE1		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i> strain KPNIH32	USA
27	pCR14_4	CP015396.1	IncFII	110 092	Cloacin	ParE ₁		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i> strain CR14	USA
28	KP30835 plasmid unnamed3	CP027698.1		9 291	Cloacin	ParE1				<i>Klebsiella pneumoniae</i> strain KP30835	USA
29	pAAC154	JF828150.1		15 101	Cloacin	ParE ₁		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i> strain U3156199	Israel
30	pCN1_2	CP015384.1		15 100	Cloacin	ParE1		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i> strain CN1	USA
31	pBK13043-3	CP020840.1		11984	Δ Cloacin	ParE ₁		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i> strain BK13043	USA
32	AR_0053 plasmid unitig_4	CP021779.1		15 028	Cloacin	ParE1		<i>aac6'-lb-Tn3</i>		<i>Enterobacter cloacae</i> strain AR_0053	USA
33	AR_0009 plasmid tig000000054	CP024884.1		9 294	Cloacin	ParE ₁				<i>Klebsiella aerogenes</i> strain AR_0009	USA
34	pAUSMDU8119-1	CP025009.1	IncFIIK	176 049	Cloacin	ParE1		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i> strain AUSMDU00008119	Australia
35	pKPN-294	CP008832.1		13 841	Cloacin	ParE ₁		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i> KPR0928	USA
36	pNJST258C2	CP006919.1		25 284	Cloacin	ParE1		<i>aac6'-lb-Tn3</i> , <i>bla</i> _{KPC-3}		<i>Klebsiella pneumoniae</i> 30684/NJST258_2	USA
37	AR0115 plasmid tig00000005	CP020075.1		22 062	Cloacin	ParE1		<i>bla</i> _{TEM-1} , <i>bla</i> _{KPC-3}		<i>Klebsiella pneumoniae</i> strain AR_0115	USA
38	ColE-LS6	JX442973.1		14 709	Cloacin	ParE ₁		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i>	Italia
39	AR0117 plasmid unitig_5	CP020066.1	IncN	72 663	Cloacin	ParE1		<i>aac6'-lb-Tn3</i> , <i>bla</i> _{KPC-3}		<i>Klebsiella pneumoniae</i> strain AR_0117	USA
40	pCAV1217-9294	CP018672.1		9 294	Cloacin	ParE ₁				<i>Klebsiella pneumoniae</i> strain CAV1217	USA
41	p34618-13.841kb	CP010394.1		13 841	Cloacin	ParE1		<i>aac6'-lb-Tn3</i>		<i>Klebsiella pneumoniae</i> strain 34618	USA

42 pEA1509_B	FO203353.1	9 294	Cloacin	ParE ₁		<i>Klebsiella aerogenes</i> EA1509E	France
43 pKp_Goe_917-4	CP018445.1	9 294	Cloacin	ParE ₁		<i>Klebsiella pneumoniae</i> strain Kp_Goe_822917	Germany
44 pNJST258N4	CP006928.1	14 249	Cloacin	ParE ₁	<i>bla</i> _{TEM-1}	<i>Klebsiella pneumoniae</i> 30660/NJST258_1	USA
45 pUHKPC07-13.841kb	CP011988.1	13 841	Cloacin	ParE ₁	<i>aac6'-lb</i> -Tn3	<i>Klebsiella pneumoniae</i> UHKPC07	USA
46 RCS12TR533	LT985216.1	14 248	Cloacin	ParE ₁	<i>bla</i> _{TEM-3}	<i>Escherichia coli</i> strain 533	France
47 Ea18A UFPE plasmid	MG786902.1	9 453	Cloacin	ParE ₁		<i>Enterobacter cloacae</i> strain Ea18A UFPE	Brazil
48 FDAARGOS_287 plasmid 2	CP022075.2	9 293	Cloacin	ParE ₁		<i>Citrobacter koseri</i> strain FDAARGOS_287	USA
49 FDAARGOS_393 plasmid	CP023528.1	9 195	Cloacin	ParE ₁		<i>Citrobacter koseri</i> strain FDAARGOS_393	USA
50 p18-43_04	CP023557.1	9 293	Cloacin	ParE ₁		<i>Klebsiella pneumoniae</i> ST2017:950142398	South Africa
51 RCS49_pIV	LT985257.1	20 798	Cloacin	ParE ₁	<i>bla</i> _{TEM-1} , <i>bla</i> _{SHV-12}	<i>Escherichia coli</i> strain 580	France
52 JM45 plasmid p2	CP006658.1	12 207	Cloacin	ParE ₁	<i>retA</i>	<i>Klebsiella pneumoniae</i> JM45	china
53 pMRSN480738_10.0	CP024463.1	10 046	Cloacin	ParE ₁		<i>Klebsiella pneumoniae</i> strain QS17-0161	Thailand
54 AR_0079 plasmid unnamed3	CP028998.1	10 077	Cloacin	ParE ₂	<i>tolA</i> , <i>copG</i>	<i>Klebsiella pneumoniae</i> strain AR_0079	USA
55 KP36 plasmid 3	CP017388.1	10 077	Cloacin	ParE ₂	<i>tolA</i> , <i>copG</i>	<i>Klebsiella pneumoniae</i> strain KP36	Taiwan
56 FDAARGOS_444 plasmid 3	CP023944.1	10 061	Cloacin	ParE ₂	<i>tolA</i> , <i>copG</i>	<i>Klebsiella pneumoniae</i> strain FDAARGOS_444	Canada
57 p69-3	CP025459.1	10 060	Cloacin	ParE ₂	<i>tolA</i> , <i>copG</i>	<i>Klebsiella pneumoniae</i> strain KP69	China
58 p10K_L111	CP030130.1	10 060	Cloacin	ParE ₂	<i>tolA</i> , <i>copG</i>	<i>Klebsiella pneumoniae</i> strain 160111	Taiwan
59 p1_020079	CP029379.1	11 970	Cloacin	ParE ₂	<i>tolA</i> , <i>copG</i> , <i>retA</i>	<i>Klebsiella pneumoniae</i> strain SCKP020079	China
60 p1_095649	CP026582.2	10 060	Cloacin	ParE ₂	<i>tolA</i> , <i>copG</i>	<i>Klebsiella pneumoniae</i> strain WCHKP649	China
61 p2_020036	CP028580.1	12 746	Cloacin	ParE ₂	<i>tolA</i> , <i>copG</i> , <i>retA</i>	<i>Klebsiella pneumoniae</i> strain WCHKP36	China
62 p5-L388	CP029224.1	11 970	Cloacin	ParE ₂	<i>tolA</i> , <i>copG</i> , <i>retA</i>	<i>Klebsiella pneumoniae</i> strain L388	China
63 pGSU10-3-4	AP018675.1	10 061	Cloacin	ParE ₂	<i>tolA</i> , <i>copG</i>	<i>Klebsiella pneumoniae</i> GSU10-3	japon

*aac6'-lb, Tn3: Tn1331 derivative

**CopG: ribbon-helix-helix protein, CopG family; retA: (group II intron reverse transcriptase/maturase); TolA: cell envelope integrity protein

Table S9. Characteristics of the MOB_{RNA} type 5 plasmids

No	Plasmid ID	Accession no	Co-integration	Plasmid size bp	Colicin operon type	Toxin/antitoxin system	Restriction/methylation system	antibiotic resistance gene	other genes	Bacterial host ID	Geographic origin
1	p9705	AB040037.1		3 172						<i>Escherichia coli</i> O157:H7	Japon
2	pCRP3	AF311902.1		3 172						<i>Citrobacter rodentium</i> strain DBS100 pl	USA
3	pSS046_spB	CP000642.1		5 153	Colicin E1					<i>Shigella sonnei</i> Ss046	China
4	pHUSEC41-4	HE603113.1		5 153	Colicin E1					<i>Escherichia coli</i> HUSEC41 O104:H4	Germany
5	pCoIE1-H22	AY913943.1		5 159	Colicin E1					<i>Escherichia coli</i> strain H22	Brazil
6	pCFSAN030807_5	CP023650.1		5 153	Colicin E1					<i>Shigella sonnei</i> strain CFSAN030807	USA
7	FHI29 scaffold-5	LM995843.1		6 815	Colicin B	ParE3				<i>Escherichia coli</i> genome assembly FHI29	Norway
8	53G plasmid B	HE616530.1		5 153	Colicin E1					<i>Shigella sonnei</i> 53G	?
9	RCS93_pIV	LT985308.1		4 913	Colicin E1					<i>Escherichia coli</i> strain CIP106223	United Kingdom
10	FHI74 scaffold-12	LM996601.1	IncFIB -ΔFII	55 304						<i>Escherichia coli</i> genome assembly FHI74	Norway
11	plasmid p3	CP023374.1		3 173						<i>Escherichia coli</i> strain 1283	United Kingdom
12	pO104:H7_S3	KM085453.1		3 173						<i>Escherichia coli</i> O104:H7 strain RM9387	USA
13	pEC34A	HQ622575.1		3 770						<i>Escherichia coli</i> strain NCTC 9034	Poland
14	RCS64_Pi	LT985294.1		3 002		ParE3				<i>Escherichia coli</i> strain 650	France
15	FHI4 scaffold-7	LM995913.1		4 147					rrt*	<i>Escherichia coli</i> genome assembly FHI4	Norway
16	plasmid I	AF218051.1		4 053					rrt*, csp**	<i>Salmonella enterica</i> serovar enteritidis strain 2159	Czech Republic
17	AR435 plasmid unnamed8	CP029121.1		3 174						<i>Escherichia coli</i> strain AR435	USA
18	pB1020	JQ319772.1		3 174						<i>Klebsiella pneumoniae</i> strain BB1089	Spain
19	pCARB35_05	CP031658.1		3 174						<i>Escherichia coli</i> strain UK_Dog_Liverpool	United Kingdom
20	pV044-c	LC056177.1		2 607						<i>Escherichia coli</i> strain V044	India
21	Nissle 1917	CP007799.1	chromosome							<i>Escherichia coli</i> Nissle 1917	Germany
22	pYU39_2.7	CP011435.1		2 677						<i>Salmonella enterica</i> serovar Typhimurium strain YU39	Mexico
23	pSAN2-1677	CP019897.1		3 126						<i>Salmonella enterica</i> serovar Anatum str. USDA-ARS-USMARC-1677 isolate SAN222	USA
24	p2.3	KU166868.1		3 609					cholin binding	<i>Salmonella enterica</i> serovar Enteritidis strain S1080	Russia
25	CFSAN001921 plasmid	CP006052.1		3 609					cholin binding	<i>Salmonella enterica</i> serovar Typhimurium var. 5- str. CFSAN001921	USA
26	p75-02_7	CP019695.1		2 690						<i>Shigella sonnei</i> strain 75/02	Hungary
27	pCFSAN030807_8	CP023653.1		2 690						<i>Shigella sonnei</i> strain CFSAN030807	USA
28	FDAARGOS_448 plasmid unnamed4	CP023958.1		3 264						<i>Escherichia coli</i> strain FDAARGOS_448	USA
29	pSL491_3	CP001149.1		3 176						<i>Salmonella enterica</i> serovar Virchow str. SL491	USA
30	p3K	CP007488.1		3 208					<i>aph(3)-I</i>	<i>Salmonella enterica</i> subsp. enterica strain SA972816	China
31	pU302S	AY333433.1		3 208					<i>aph(3)-I</i>	<i>Salmonella enterica</i> serovar typhimurium	USA
32	pec22	HQ848325.1		11 957			Eco22T1 type II			<i>Escherichia coli</i> strain TB22	Poland
33	p4821	Y14016.1		3 307		LsoA/B				<i>Escherichia coli</i> O157:H7	Germany
34	pOSAK1	AB011548.2		3 306		LsoA/B				<i>Escherichia coli</i> O157:H7 str. Sakai	Japon
35	pN13-01290_3-1	CP012933.1		3 319		LsoA/B				<i>Salmonella enterica</i> serovar Heidelberg strain N13-01290	Canada
36	NTP16	L05392.1		8 255		LsoA/B			<i>aph(3)-I bla</i> _{TEM-1} variant	<i>Salmonella enterica</i> serovar Typhimurium	United Kingdom
37	p1PCN033	CP006633.1		3 319		LsoA/B				<i>Escherichia coli</i> PCN033	China
38	pCERC7	KX356458.1		9 712		LsoA/B			<i>bla</i> _{TEM-1}	<i>Escherichia coli</i> strain 11.1-R1 ST131	Australia
39	pST12	HG428760.1		8 275		LsoA/B			<i>bla</i> _{TEM-144} ESBL	<i>Salmonella enterica</i> serovar Derby str. T12	Uruguay
40	pAnkS	DQ916413.1		8 271		LsoA/B			<i>bla</i> _{TEM-1}	<i>Salmonella enterica</i> serovar typhimurium	Turkey
41	RCS35_pII	LT985233.1		14 365		LsoA/B			<i>bla</i> _{SHV-12} , <i>bla</i> _{TEM-1}	<i>Escherichia coli</i> strain 565	France
42	pEco70745_3	CP023261.1		3 735					cholin binding	<i>Escherichia coli</i> strain CCUG 70745	Sweden
43	pV147-c	LC056399.1		1 922						<i>Escherichia coli</i> strain V147	India

44	pV263-c	LC056464.1	2 271			<i>Escherichia coli</i> strain V263	India
45	FDAARGOS_433 plasmid unnamed8	CP023904.1	4 011	AbiEii		<i>Escherichia coli</i> strain FDAARGOS_433	USA
46	RCS48_pII	LT985247.1	19 831	LsoA/B	<i>bla</i> _{SHV-12} , <i>bla</i> _{TEM-1}	<i>Escherichia coli</i> strain 720	France
47	FHI85 scaffold-7	LM996934.1	3 741			<i>Escherichia coli</i> genome assembly FHI85	Norway
48	pEC404/03-4	AP014807.1	8 599		<i>bla</i> _{TEM-1}	<i>Escherichia coli</i> O119:H6	Brazil

*rrtI: retron reverse transcriptase

**cps: cold shock gene

Table S10. Characteristics of the RelN_{RNA} type1 plasmids

No	Plasmid ID	Accession no	Co-integration	Plasmid size bp	Colicin operon type	Toxin/antitoxin system	Restriction/methylation system	antibiotic resistance gene	other genes	Bacterial host ID	Geographic origin
1	FDAARGOS_434 unnamed	CP023872.1		6 172		MazE		<i>suL2</i> , <i>APH(3'')-Ib</i> , <i>APH(6)</i>		<i>Escherichia coli</i> strain FDAARGOS_434	Canada
2	pCFSAN030807_2	CP023647.1		8 401		MazE		<i>suL2</i> , <i>tet(A)</i> , <i>APH(3'')-Ib</i> , <i>APH(6)-Id</i>		<i>Shigella sonnei</i> strain CFSAN030807	usa
3	FDAARGOS_90 unnamed4	CP014100.1		8 421		MazE		<i>strA/B</i> , <i>suL2</i> , <i>tet(A)</i>		<i>Shigella sonnei</i> strain FDAARGOS_90	USA
4	FHI72 scaffold-18	LM996860.1		8 420		MazE		<i>strA/B</i> , <i>suL2</i> , <i>tet(A)</i>		<i>Escherichia coli</i> genome assembly FHI72	Norway
5	p62	FN822747.1		6 222		MazE		<i>strA/B</i> , <i>suL2</i>		<i>Escherichia coli</i> ETEC 1392/75	Honk Kong
6	p9123 plasmid family	AY360321.1		6 222		MazE		<i>strA/B</i> , <i>suL2</i>		<i>Escherichia coli</i>	United Kingdom
7	p6148/pE2348-2	EU580136.1 FM180570.1		6 147		MazE		<i>strA/B</i> , <i>suL2</i>		<i>Escherichia coli</i> strain E2348/69 0127:H6	United Kingdom
8	pQ1-1	HM371192.1		6 200		MazE		<i>strA/B</i> , <i>suL2</i>		<i>Escherichia coli</i> strain Q1	China
9	pCERC2	KX291024.1		6 200		MazE		<i>strA/B</i> , <i>suL2</i>		<i>Escherichia coli</i> strain 10.1-R1	Australia
10	pEC299-4	JX238460.1		6 199		MazE		<i>strA/B</i> , <i>suL2</i>		<i>Escherichia coli</i> strain EC299	Sweden
11	C2 plasmid A	CP010118.1		8 410		MazE		<i>strA/B</i> , <i>suL2</i> , <i>tet(A)</i>		<i>Escherichia coli</i> strain C2	China
12	FDAARGOS_90 unnamed5	CP014101.1		8 420		MazE		<i>strA/B</i> , <i>suL2</i> , <i>tet(A)</i>		<i>Shigella sonnei</i> strain FDAARGOS_90	USA
13	pCN061p3	CP006639.1		6 222		MazE		<i>strA/B</i> , <i>suL2</i>		<i>Escherichia coli</i> PCN061	China
14	pMG828-5	DQ995355.1		8 985		MazE		<i>suL2</i> , <i>bla</i> _{AMPc}		<i>Escherichia coli</i>	Taiwan
15	RCS98	LT985316.1		6 200		MazE		<i>strA/B</i> , <i>suL2</i>		<i>Escherichia coli</i> strain ECOR 17	Indonesia
16	pABC-3	KT988306.1		6 779		MazE		<i>strA/B</i> , <i>suL2</i> , <i>dfrA14</i>		<i>Shigella sonnei</i> strain c8225	Chili
17	pSS046_spA	CP000641.1		8 420		MazE		<i>strA/B</i> , <i>suL2</i> , <i>tet(A)</i>		<i>Shigella sonnei</i> strain Ss046	China
18	RCS86_pl	LT985307.1		6 069		MazE		<i>suL2</i>		<i>Escherichia coli</i> strain ECOR 4	USA
19	pSFxv 3	CP001386.1		6 200		MazE		<i>strA/B</i> , <i>suL2</i>		<i>Shigella flexneri</i> 2002017	China
20	WCHEC005237 p1_005237	CP026572.1		6 200		MazE		<i>suL2</i> , <i>APH(3'')-Ib</i> , <i>APH(6)-Id</i>		<i>Escherichia coli</i> strain WCHEC005237	China
21	pKKTET7	AF497970.1		8 400		MazE		<i>strA/B</i> , <i>suL2</i> , <i>tet(A)</i>		<i>Shigella sonnei</i>	South Korea
22	pVI678	EF090911.1		6 222		MazE		<i>strA/B</i> , <i>suL2</i>		<i>Escherichia coli</i>	Norway
23	pETEC_6	CP000798.1		6 199		MazE		<i>strA/B</i> , <i>suL2</i>		<i>Escherichia coli</i> E24377A	USA
24	p12579_4	CP003113.1		6 211		MazE		<i>strA/B</i> , <i>suL2</i>		<i>Escherichia coli</i> O55:H7 str. RM12579	USA
25	p8401	CP012198.1		8 401		MazE		<i>strA/B</i> , <i>suL2</i> , <i>tet(A)</i>		<i>Escherichia coli</i> strain ECwhn14	China
26	pFORC11.3	CP010832.1		8 405		MazE		<i>strA/B</i> , <i>suL2</i> , <i>tet(A)</i>		<i>Shigella sonnei</i> strain FORC_011	South Korea
27	RCS63	LT985269.1		22 308		MazE		<i>strA/B</i> , <i>suL2</i> , <i>bla</i> _{CTX-M-14}		<i>Escherichia coli</i> strain 631	France
28	pSS4	AF534183.1		8 401		MazE		<i>strA/B</i> , <i>suL2</i> , <i>tet(A)</i>		<i>Shigella sonnei</i>	South Korea
29	RCS92_pl	LT985314.1		6 222		MazE		<i>strA/B</i> , <i>suL2</i>		<i>Escherichia coli</i> strain ECOR 25	USA
30	1283 p7	CP023375.1		6 800		MazE		<i>suL2</i> , <i>DfrA14</i> , <i>APH(6)-Id</i>		<i>Escherichia coli</i> strain 1283	United Kingdom
31	pCERC1	JN012467.1		6 790		MazE		<i>strA/B</i> , <i>suL2</i> , <i>dfrA14</i>		<i>Escherichia coli</i> strain S1.2.T2R	Australia
32	pT108	JN412137.1		9 007		MazE		<i>suL2</i> , <i>bla</i> _{AMPc}		<i>Escherichia coli</i> strain 108	Thailand
33	RCS87	LT985298.1		6 047		MazE		<i>suL2</i>		<i>Escherichia coli</i> strain ECOR 18	USA
34	SA20084699 unnamed2	CP022499.1	IncQ	38 945		MazE		<i>suL2</i> , <i>DfrA14</i> , <i>APH(3'')</i> , <i>APH(6)-Id</i>		<i>Salmonella enterica</i> serovar Manhattan strain SA20084699	Canada
35	pRF1	AB076707.2		6 066		MazE		<i>suL2</i>		<i>Salmonella enterica</i> serovar Choleraesuis	Japon

Table S11. Characteristics of the Rel_{RNA} type 2 plasmids

No	Plasmid ID	Accession no	Co-integration	Plasmid size bp	Colicin operon type	Toxin/antitoxin system	Restriction/methylation system	antibiotic resistance gene	other genes	Bacterial host ID	Geographic origin
1	pCol-let	AF197335.1		5 847	Colicin Y					<i>Escherichia coli</i>	USA
2	pCuv8 clone	MG648905.1		4 000		HigA/B				<i>Escherichia coli</i>	France
3	RCS83_pII	LT985291.1		2 999		HigA/B				<i>Escherichia coli</i> strain ECOR 10	USA
4	M10 plasmid E	CP010205.1		3 258		HigA/B				<i>Escherichia coli</i> strain M10	China
5	pEC886	HQ659758.1		9 261			ecoVIII type II	<i>bla</i> _{TEM-1}		<i>Escherichia coli</i> strain 886	Poland
6	pEC156	AF158026.1		4 312			ecoVIII type II			<i>Escherichia coli</i>	?
7	pEC71-2	JX238450.1		4 315			ecoVIII type II			<i>Escherichia coli</i> strain EC71	Sweden
8	pEC881_6	CP019023.1		3 256		HigA/B				<i>Escherichia coli</i> strain EcoI_881	Colombia
9	pColG	DQ286390.1		4 715		AbiEii/Gii				<i>Escherichia coli</i> strain CA46	Slovenia
10	FDAARGOS_313 plasmid unnamed3	CP022068.1		19 849		HigA/B		<i>bla</i> _{TEM-1}		<i>Salmonella enterica</i> strain FDAARGOS_313	USA
11	pD90-4	CP022454.1		17 636		AbiEii/Gii				<i>Salmonella enterica</i> serovar Indiana strain D90	China
12	pC06114_8	CP016042.1		3 205						<i>Escherichia coli</i> isolate Co6114	Germany
13	pNMEC-O75B	CP030113.1		6 465		ToxN/AbiQ				<i>Escherichia coli</i> strain MCJCHV-1	USA
14	AR_452 plasmid unnamed3	CP030330.1		6 395		ToxN/AbiQ				<i>Escherichia coli</i> strain AR_452	USA
15	pO26_4	AP010957.1		4 073						<i>Escherichia coli</i> O26:H11 str. 11368	Japan
16	pO26-S3	FJ004637.1		4 073						<i>Escherichia coli</i> strain H30 serovar O26:H11	USA
17	MS6671_plasmid_D	LN824137.1		4 715		AbiEii/Gii				<i>Klebsiella pneumoniae</i> genome assembly MS6671.v1	Australia
18	p48896_5	CP024434.1		4 715		AbiEii/Gii				<i>Klebsiella pneumoniae</i> strain DA48896	Pakistan
19	pSE12-02541	KY807920.1		17 156				<i>bla</i> _{TEM-1} , <i>mrc-5</i>		<i>Salmonella enterica</i> serovar Paratyphi B isolate 12-02541	Germany
20	pEC1066	MG587003.1		12 201				<i>mrc-5-2</i> variant		<i>Escherichia coli</i>	Germany
21	pEC2380	MG587004.1		11 708				<i>mrc-5-2</i> variant		<i>Escherichia coli</i>	Germany
22	pSE13-SA01718	KY807921.1		12 201				<i>mrc-5</i>		<i>Salmonella enterica</i> serovar Paratyphi B 13-SA01718	Germany
23	p4.4	MG948564.1		6 760			type III			<i>Salmonella enterica</i> serovar Enteritidis strain S17861	Russia
24	RCS92_pIII	LT985312.1		3 174					<i>fehE</i>	<i>Escherichia coli</i> strain ECOR 25	USA
25	pO26-S2	FJ386570.1		3 174					<i>fehE</i>	<i>Escherichia coli</i> strain H30	Canada
26	pSYM2	KM107838.1		4 197			EcorII-C type II			<i>Escherichia coli</i> strain G3/10	Germany
27	pKPN2	AF300473.1		4 196			MKpn2kl type II			<i>Klebsiella pneumoniae</i>	Russia
28	pSe_kan	HQ230976.1		7 132				<i>aphA1</i>		<i>Salmonella enterica</i> serovar Typhimurium	USA
29	pSBardo-Kan	HQ230977.1		8 198				<i>aphA1</i>		<i>Salmonella enterica</i> serovar Bardo	USA
30	pSFxv_5	CP001388.1		3 180					<i>fehE</i>	<i>Shigella flexneri</i> 2002017	China
31	pSF301-2	JF813187.1		3 178					<i>fehE</i>	<i>Shigella flexneri</i> strain 2a 301	China
32	p2457TS2	AY028316.1		3 179					<i>fehE</i>	<i>Shigella flexneri</i> 2a	China
33	2mDa plasmid	M25995.1		3 048					<i>fehE</i>	<i>Shigella flexneri</i> 2mDa	USA

Table S12. Characteristics of the Rel_{RNA} type 3 plasmids

No	Plasmid ID	Accession no	Co-integration	Plasmid size bp	Colicin operon type	Toxin/antitoxin system	Restriction/methylation system	antibiotic resistance gene	other genes	Bacterial host ID	Geographic origin
1	pCAV1752-4374	CP018358.1		4 374						<i>Klebsiella oxytoca</i> strain CAV1752	USA
2	pEC542_KPC	CP018968.1	IncP-6	44 320						<i>Escherichia coli</i> strain Ecol_542	Viet Nam
3	FDAARGOS_429 plasmid unnamed1	CP023876.1		10 343		AbiEii (a)				<i>Raoultella planticola</i> strain FDAARGOS_429	Canada
4	FDAARGOS_430 plasmid unnamed2	CP023880.1		10 345		AbiEii (a)				<i>Raoultella planticola</i> strain FDAARGOS_430	Canada
5	INF322 plasmid unnamed3	CP024485.1		4 228						<i>Klebsiella pneumoniae</i> strain INF322	Australia
6	pKPN2312-5	CP011315.1		4 831		AbiEii (b)				<i>Klebsiella pneumoniae</i> strain 234-12	Germany
7	KSB1_7F-sc-2280268 plasmid unnamed2	CP031816.1		4 110						<i>Klebsiella pneumoniae</i> strain KSB1_7F-sc-2280268	Australia
8	pCAV1042-2781	CP018665.1		2 781						<i>Klebsiella pneumoniae</i> strain CAV1042	USA
9	pMRSN480738_2.8	CP024464.1		2 780						<i>Klebsiella pneumoniae</i> strain QS17-0161	Thailand
10	pKlebB-k17/80	AF156893.2		5 258	<i>klebicin B</i>					<i>Klebsiella pneumoniae</i>	USA
11	INF125-sc-2279943 plasmid unnamed2	CP031797.1		4 269						<i>Klebsiella pneumoniae</i> strain INF125-sc-2279943	Australia
12	p4_020019	CP028552.1		4 686						<i>Klebsiella variicola</i> strain WCHKP19	China
13	pX39-5	CP023982.1		3 374		MazE				<i>Klebsiella variicola</i> strain X39	China
14	KSB1_5D plasmid unnamed6	CP024197.1		3 825		MazE				<i>Klebsiella pneumoniae</i> isolate KSB1_5D	Australia
15	H1 plasmid B	CP010162.1		4 075		MazE			<i>fepE</i>	<i>Escherichia coli</i> strain H1 plasmid B	China
16	RCS83_pl	LT985290.1		4 074		MazE			<i>fepE</i>	<i>Escherichia coli</i> strain ECOR 10	USA
17	pKPN1482-5	CP020845.1		9 510					alcohol dehydrogenase	<i>Klebsiella pneumoniae</i> strain KPN1482	USA
18	p1_095845	CP031882.1		5 733						<i>Klebsiella pneumoniae</i> strain WCHKP095845	China
19	pKP13c	CP003995.1		5 065		AbiEii (a)				<i>Klebsiella pneumoniae</i> Kp13	Brazil
20	FDAARGOS_442 plasmid unnamed4	CP023930.1		4 166		AbiEii (a)				<i>Klebsiella pneumoniae</i> strain FDAARGOS_442	Canada
21	p48896_6	CP024435.1		4 167		AbiEii (a)				<i>Klebsiella pneumoniae</i> strain DA48896	Pakistan
22	pKpn114	EU932690.1		4 211		AbiEii (a)				<i>Klebsiella pneumoniae</i> strain 0773	China
23	pKpn70742_3	CP023252.1		4 426		AbiEii (a)				<i>Klebsiella pneumoniae</i> strain CCUG 70742	Sweden
24	pKp_Goe_641-5	CP018739.1		3 541						<i>Klebsiella pneumoniae</i> strain Kp_Goe_121641	Germany
25	pKpvST101_7	CP031375.1		8 469						<i>Klebsiella pneumoniae</i> strain KpvST101_OXA-48	United Kingdom
26	pKO_JKo3_4	AP014955.1		3 897						<i>Klebsiella oxytoca</i>	Japon
27	pKPN535a	MH595533.1	InQ	14 873						<i>Klebsiella pneumoniae</i> strain KPN535	Brazil
28	FDAARGOS_436 plasmid unnamed3	CP023908.1		4 000						<i>Klebsiella pneumoniae</i> strain FDAARGOS_436	Canada
29	p1_020046	CP028779.1		3 999						<i>Klebsiella pneumoniae</i> strain SCKP020046	China
30	pCAV1344-3741	CP011619.1		3 741						<i>Klebsiella pneumoniae</i> strain CAV1344	USA
31	pDA33140-9	CP029585.1		8 809		AbiEii (a)				<i>Klebsiella pneumoniae</i> strain DA33140	Sweden
32	AR_0158 plasmid tig00003569alt	CP021700.1		8 364						<i>Klebsiella pneumoniae</i> strain AR_0158	USA
33	FDAARGOS_440 plasmid unnamed	CP023920.1		4 619						<i>Klebsiella pneumoniae</i> strain FDAARGOS_440	Canada
34	KSB1_5D plasmid unnamed4	CP024195.1		4 660						<i>Klebsiella pneumoniae</i> isolate KSB1_5D	Australia
35	pMRSN479404_4.7	CP024044.1		4 660						<i>Klebsiella pneumoniae</i> strain QS17-0029	Thailand
36	FDAARGOS_445 plasmid unnamed2	CP024579.1		4 163						<i>Klebsiella pneumoniae</i> strain FDAARGOS_445	Canada
37	pCR14_5	CP015397.1		9 456					<i>aac6'-lb-Tn3</i>	<i>Klebsiella pneumoniae</i> strain CR14	USA
38	pKPN7	CP000652.1		3 478						<i>Klebsiella pneumoniae</i> MGH 78578	USA

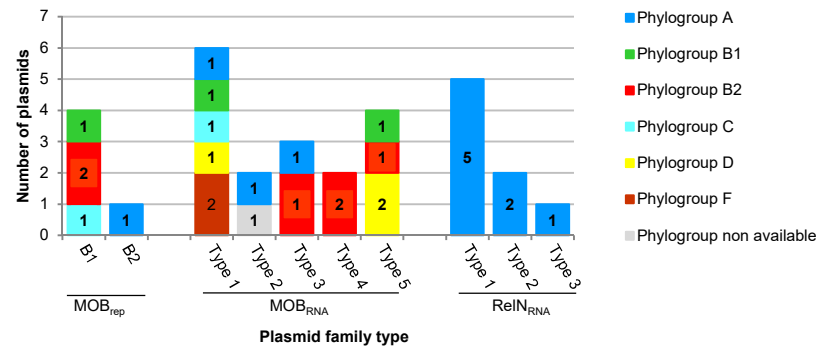


Fig. S1. Phylogenetic distribution of the parental *E. coli* strains of the 30 plasmids of our collection according to the family type of the plasmids. Phylogroups are shown according to the given colour code. The number of sequence types using the Pasteur Institut scheme in each phylogroup is indicated

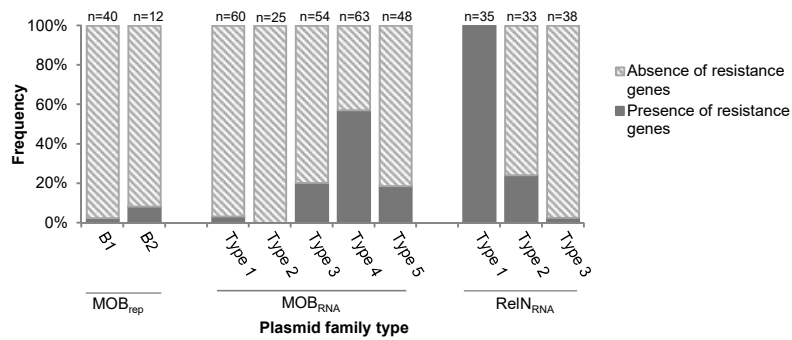


Fig. S2. Frequencies of the plasmids carrying at least one antibiotic resistance gene according to their family type. Numbers of plasmids in each of the families are indicated above the columns of the graph

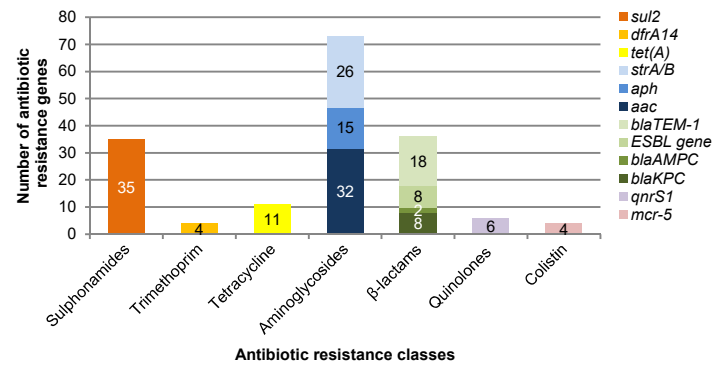


Fig. S3. Number of antibiotic resistance genes carried by the plasmids according to the antibiotic class they belong