Table S1 MICs of 39 fosfomycin-resistance *E. coli* isolates

Strain	MIC (mg/liter)							
	FOF[a]	FFC	GEN	AMK	CIP	TET	CTX	CST
SY301B	>512	128	128	2	16	64	>256	0.5
SY301F	>512	128	128	>256	8	128	256	0.5
SY303P	>512	256	64	>256	8	128	64	0.25
SY301L	>512	256	>256	>256	32	128	64	0.5
SY303M	>512	128	256	>256	16	128	128	0.5
SY305M	>512	128	128	>256	16	256	128	0.5
SY286M	>512	>512	128	>256	0.125	128	128	0.5
SY287M	>512	256	128	>256	0.25	128	256	0.5
SY284B	>512	256	64	>256	0.125	128	128	0.5
CH293B	>512	512	256	>256	128	64	>256	0.5
CH292B	>512	256	256	>256	128	128	>256	0.5
CH291M	>512	128	>256	>256	16	256	>256	0.5
CH281F	>512	128	128	256	32	128	>256	1
CH282M	>512	128	64	256	64	128	128	0.5
CH285F	>512	>512	128	>256	64	>256	128	0.5
DH286F	>512	256	64	>256	16	>256	128	0.5
DH286M	>512	256	64	>256	32	128	256	1
JL12G	>512	256	>256	>256	32	64	256	1
JL15P	>512	128	>256	>256	0.5	128	256	0.5
JL17P	>512	4	128	>256	0.125	128	32	0.5
JT14G	>512	128	256	256	0.125	32	128	0.5
JT14P	>512	256	256	128	0.25	32	128	1
HL12L	>512	256	256	4	0.125	16	128	0.5
HL36B	>512	128	128	4	0.125	128	256	0.5
HL40C	>512	128	128	2	0.125	128	>256	0.5
HB37B	>512	>512	256	256	64	256	64	0.5
HB35D	>512	512	256	256	0.25	256	128	0.5
HB38B	>512	4	64	128	8	16	128	0.5
HB38L	>512	256	128	>256	32	64	128	0.5
HB18F	>512	256	128	>256	64	64	64	1
HB13B	>512	128	>256	>256	64	256	>256	0.5
HB13M	>512	256	>256	>256	32	32	128	0.5
HB312G	>512	256	256	>256	16	64	128	1
SH312M	>512	512	64	256	16	64	>256	0.5
SH312N	>512	512	64	256	8	128	>256	0.5
SH21F	>512	128	32	2	8	256	>256	0.5
SH21G	>512	128	128	2	32	256	256	0.5
SH21M	>512	128	128	8	16	256	256	0.5
SH33L	>512	128	64	1	32	32	128	0.25

[a] FOF, fosfomycin; FFC, florfenicol; GEN, gentamicin; AMK, amikacin; CIP, ciprofloxacin; TET, tetracycline; CTX, cefotaxime; CST, colistin;

Table S2 Characteristics of the *fosA3*-positive *E. coli* isolates.

Isolate[a]	Source	Farm	Isolation date	PFGE pattern	MLST	Phylogroup	Resistance profile[b]
SY301B	pig feces	Fa1	06/2015	1	ST761	B2	FFC, CTX, TET, GEN, CIP
SY301F	pig liver	Fa2	06/2015	2	ST3315	B2	FFC, CTX, TET, GEN, AMK, CIP
SY303P	pig liver	Fa3	06/2015	3	ST5714	B2	FFC, CTX, TET, GEN, AMK, CIP
SY301L	pig kidney	Fa4	06/2015	4	ST5442	B2	FFC, CTX, TET, GEN, AMK, CIP
SY303M	pig liver	Fa5	06/2015	5	ST3944	B2	FFC, CTX, TET, GEN, AMK, CIP
SY305M	pig feces	Fa5	06/2015	5	ST3944	B2	FFC, CTX, TET, GEN, AMK, CIP
SY286M	cow milk	Fa6	06/2015	6	ST93	B2	FFC, CTX, TET, GEN, AMK
SY287M	cow milk	Fa6	06/2015	6	ST98	B2	FFC, CTX, TET, GEN, AMK
SY284B	cow milk	Fa7	06/2015	7	ST4683	B1	FFC, CTX, TET, GEN, AMK
CH293B	chicken faeces	Fa8	08/2015	8	ST10	B2	FFC, CTX, TET, GEN, AMK, CIP
CH292B	chicken faeces	Fa8	08/2015	8	ST10	B2	FFC, CTX, TET, GEN, AMK, CIP
CH291M	chicken faeces	Fa9	08/2015	9	ST410	B2	FFC, CTX, TET, GEN, AMK, CIP
CH281F	chicken faeces	Fa10	08/2015	10	ST5889	A	FFC, CTX, TET, GEN, AMK, CIP
CH282M	chicken faeces	Fa11	08/2015	11	ST1437	A	FFC, CTX, TET, GEN, AMK, CIP
CH285F	chicken faeces	Fa12	08/2015	12	ST448	B2	FFC, CTX, TET, GEN, AMK, CIP
DH286F	chicken faeces	Fa13	08/2015	13	ST2518	B2	FFC, CTX, TET, GEN, AMK, CIP
DH286M	chicken faeces	Fa14	08/2015	14	ST617	B2	FFC, CTX, TET, GEN, AMK, CIP
JL12G	cow milk	Fa15	08/2015	15	ST559	B2	FFC, CTX, TET, GEN, AMK, CIP
JL15P	cow milk	Fa16	08/2015	16	ST209	B2	FFC, CTX, TET, GEN, AMK
JL17P	cow milk	Fa16	08/2015	17	ST359	A	CTX, TET, GEN, AMK
JT14G	cow milk	Fa17	08/2015	18	ST5689	B1	FFC, CTX, TET, GEN, AMK
JT14P	cow milk	Fa18	08/2015	19	ST5714	B1	FFC, CTX, TET, GEN, AMK
HL12L	cow milk	Fa19	11/2015	20	ST195	D	FFC, CTX, TET, GEN
HL36B	cow milk	Fa20	11/2015	21a	ST4680	B1	FFC, CTX, TET, GEN
HL40C	farmer sputum	Fa20	11/2015	21b	ST4680	B1	FFC, CTX, TET, GEN
HB37B	chicken faeces	Fa21	02/2016	22	ST1725	B1	FFC, CTX, TET, GEN, AMK, CIP
HB35D	chicken faeces	Fa21	02/2016	23	ST48	B2	FFC, CTX, TET, GEN, AMK
HB38B	cow milk	Fa22	02/2016	24	ST2055	B1	CTX, TET, GEN, AMK, CIP
HB38L	cow milk	Fa23	02/2016	25	ST5693	B1	FFC, CTX, TET, GEN, AMK, CIP
HB18F	cow milk	Fa24	02/2016	26	ST1081	B1	FFC, CTX, TET, GEN, AMK, CIP
HB13B	chicken faeces	Fa25	02/2016	27	ST167	B2	FFC, CTX, TET, GEN, AMK, CIP
HB13M	cow milk	Fa26	02/2016	28	ST4463	B2	FFC, CTX, TET, GEN, AMK, CIP
HB312G	cow milk	Fa27	02/2016	29	ST685	B2	FFC, CTX, TET, GEN, AMK, CIP
SH312M	pig faeces	Fa28	04/2016	30	ST1488	B2	FFC, CTX, TET, GEN, AMK, CIP
SH312N	pig faeces	Fa29	04/2016	30	ST1313	B2	FFC, CTX, TET, GEN, AMK, CIP
SH21F	pig faeces	Fa30	04/2016	31	ST209	B2	FFC, CTX, TET, GEN, CIP
SH21G	pig faeces	Fa31	04/2016	32	ST354	D	FFC, CTX, TET, GEN, CIP
SH21M	pig faeces	Fa32	04/2016	33	ST648	D	FFC, CTX, TET, GEN, CIP
SH33L	cow milk	Fa33	04/2016	29	ST3743	B1	FFC, CTX, TET, GEN, CIP

[a] The first two capital letters in each strain name represent different cities. SY, Shenyang; CH, Changchun; DL, Dehui; JL, Jilin; JT, Jiutai; HL, Hailaer; HB, Harbin; SH, Suihua; Shenyang belongs to Liaoning province; Changchun, Dehui, Jilin and Jiutai belong to Jilin Province; Hailaer belongs to Inner Mongolia autonomous region; Harbin and Suihua belong to Heilongjiang province. Isolates from healthy animals are underlined.

[b] AMK, amikacin; CTX, cefotaxime; CIP, ciprofloxacin; FFC, florfenicol; GEN, gentamicin; TET, tetracycline; the MIC value of florfenicol (≥32mg/L) was interpreted according to European Committee on Antimicrobial Susceptibility Testing (EUCAST). Transferable resistance phenotypes are underlined.

Table S3 Primers were used to investigate the four epidemic plasmids and the genetic environment of the *fosA3* gene in other plasmids

Plasmid		Primer[a]	Nucleotide sequence (5' to 3')	Product size (bp)	Annealing temperature (°C)
pECF12	PCR 1	repA_fw	GTGCAGGATGGTGTGACTGA	4179	52
		tnpA _rv	AGAAAGTCGCCATGCCGTTG		
	PCR 2	tnpA_fw	CTGCCAGCGTGAAGGAATAA	2518	51
		fosA3_rv	GACTATACCCACTACGCCTT		
	PCR 3	fosA3_fw	TCCAGCTTATGGCCGTCAGG	3790	49
		tetA _rv	TGATCACCGGCCCTGTAGCC		
	PCR 4	tetA_fw	CAAGCAGGATGTAGCCTGTG	3450	53
		strA_rv	GTGTCCCGCAATGCCGTCAA		
	PCR 5	strA_fw	GCCCAGTTCTCTTCGGCGTT	4947	54
		ΔTn3_rv	CATCGACCGGCGCTACTACG		
	PCR 6	ΔTn3_fw	TCCGCCATCTTGGTCAGGCC	4014	53
		IS26_rv	GGCACTGTTGCAAATAGTCG		
	PCR 7	IS26_fw	TTCTTCACGTTGTTGAGGAT	3889	50
		stbA_rv	CGAACAGTATTCATTTGATC		
	PCR 8	stbA_fw	ATCTATAATTAATAAAGAAT	4371	50
		ycgC_rv	TCCAGCATCACCGCCGGAAC		
	PCR 9	ycgC_fw	ACGATGAGCTGGAAACCGTC	4660	55
		psiB_rv	CAGTGACGCCGCCAGTGCCA		
	PCR 10	psiB_fw	TGGCAGCGAGTTCGGCGGCT	4707	55
		ydcA_rv	TCTCCTGCTGGCGTGGCCCG		
	PCR 11	ydcA_fw	CCATGTGTGATGCGGTGGAG	4211	52

		traJ_rv	TTGCATGACCAACACCCAGC		
	PCR 12	traJ_fw	AGAGAGTTATATACGTCTGC	3489	50
		TraB_rv	AATGTACGGCAGTGATGGTC		
	PCR 13	TraB_fw	CGTCGCGAGCTGGATGTCCT	2610	55
		traV_rv	CGCTATCCATAATGCAGCCG		
	PCR 14	traV_fw	TCACTGCCGCGCCTGGCTGA	4814	55
		traU_rv	CAGGCTGAAGCCCAGGTTCA		
	PCR 15	traU_fw	GCAGTATCAAAGTCAGTCAG	4309	50
		traN_rv	TTTATCCCGGTATGCCCAGC		
	PCR 16	traN_fw	CTGCCAGGATCACCGGAGAC	3933	53
		trbF_rv	CTCCCGGCGCATACGGCGTT		
	PCR 17	trbF_fw	ACGGAATATTGAGTATAGTT	3914	50
		traG_rv	GGCTGCGGGTCATATTCGTC		
	PCR 18	traG_fw	CGCATAATATCAGTAATGAG	3711	50
		traD_rv	GAGACAACAAAGAAGGTAAT		
	PCR 19	traD_fw	ATATCATGCTTTACTGCCTG	4093	52
		traI_rv	CACCATTCCCGGGCGGTACA		
	PCR 20	traI_fw	GTGCGCTGATGGCCATGAAG	4404	55
		traX_rv	TCACAGCGCCAGAACGCCCA		
pECB11	PCR 21	repA_fw	GTGACTGATCTTCAACAA	3950	49
		tnp_rv	CTTTGCCACGGACATATC		
	PCR 22	tir_fw	TTTGCCGATAAGTCCATA	3828	53
		ISCR2_rv	AAGCGGGTTAGGTTGA		
	PCR 23	ISCR2_fw	CTATCTGGCCTCGGATGC	4707	51
		tetA_rv	GCGCTGTCGGATCGTT		
	PCR 24	tetA_fw	AGGCAAGCAGGATGTAGC	3438	50

	strA_rv	GTCAATCCCGACTTCT		
PCR 25	strA_fw	TTCTCTTCGGCGTTAGCA	4997	53
	ΔTn21_rv	GCGCCGACCGAGTTCAT		
PCR 26	ΔTn21_fw	GCGCTGCTGCTCGAAACT	4381	50
	res/mod_rv	TAACAGCGCGAAAGA		
PCR 27	res/mod_fw	TTGCGGCGTATGTTCTC	3523	48
	res/mod_rv	CCATAAAGGCGAGGTAAA		
PCR 28	res/mod_fw	TACCGCTATCCTTGTATT	4587	49
	exc1_rv	ATGGCACTGGTATCAATC		
PCR 29	exc1_fw	TGCCGGTAGCTTGGACTC	3529	49
	fosA3_rv	ATAGCGGAGCCTATCTCT		
PCR 30	fosA3_fw	TCACTGCGGTTATCTTTC	3353	50
	bla$_{\text{CTX-M-55}}$_rv	GAAACGTTCCGTCTCGAC		
PCR 31	bla$_{\text{CTX-M-55}}$_fw	GCCGACGCTAATACATCG	2037	50
	IS26_rv	GGCACTGTTGCAAATAGTCG		
PCR 32	IS26_fw	CAGATACGCCCAGCGGCCAT	4980	55
	met_rv	GTTGAGCCGCTGCCTGCAAA		
PCR 33	met_fw	GGCTGCAACCAGCCTGTAAT	3220	55
	ycjA_rv	TGCCTGCCAGCGCCATCACT		
PCR 34	ycjA_fw	AGACGTGCCGGACAGTGAAT	5010	53
	ssb_rv	CGGTGACGTAACGGGTAATA		
PCR 35	ssb_fw	CATGGCAGTTCGTGGCATTA	3939	55
	psiA_rv	TCCAGGTCATGCTCTGCCAC		
PCR 36	psiA_fw	TGGCTGTATGCCGTCGATGT	4621	49
	traM_rv	CTCTGATATCGTCAACCATA		
PCR 37	traM_fw	TCAGGAACTGCTTCAATGCT	4526	50

		traB_rv	CGCTCCATTCCCTGACCGAT		
	PCR 38	traB_fw	GGTGACGTACCAGTCTGTGC	4232	53
		traC_rv	CGCTGAACCACACCGGCCTC		
	PCR 39	traC_fw	CACAGTGAAGCCAACCTGAA	4820	53
		trbC_rv	GGATTCGCCCTGACCTGCTG		
	PCR 40	trbC_fw	CTGACAGCAGGACTGTTTAT	4043	50
		traF_rv	ATTAATGACCTGCGCCAGCT		
	PCR 41	traF_fw	AGGAGCCGGATATTATGCAG	4544	50
		traG_rv	ATGCCCACCAGAATGGTCTG		
	PCR 42	traG_fw	ACAGGCTGAATCTCGATACA	3905	49
		hp_rv	TAATTCCTTATGCCTGAGAG		
	PCR 43	hp_fw	TGTTGGTGAGAATAATCAAT	4027	50
		traI_rv	GTTCTGGCCAGCACGTCCGT		
	PCR 44	traI_fw	TCACAGGCTATCCGAGAGGC	3004	55
		traI_rv	CGCGCCGGTCCTCATTCAGG		
	PCR 45	traI_fw	GAACTGCGGGAGGCGGTATA	3250	50
		finO_rv	TTATTTCTCATCAAGCACGG		
pECXH3	PCR 46	IS903_fw	TCAGGCAATACGCACGCTTT	4178	53
		IS26_rv	CACGATTTACCGCTGGGTTC		
	PCR 47	IS26_fw	AGCAAGCGCGCGACCATAGG	3860	53
		orf2_rv	CCAGCGCCCTGTTTAACTAT		
	PCR 48	orf2_fw	GCCATGTACCAGCACATCCC	4583	54
		hp_rv	CCCAACGCTGCCCGAGATGC		
	PCR 49	hp_fw	GTAGGCGCCGCCCTATACCT	3173	50
		hp_rv	TCAGTCAGATCCATCCGACT		
pECM13	PCR 50	repZ_fw	GTGACCGGCGAGCAGAGCCT	4699	52

	IS26_rv	TCATGGATTTAAATCCCAGC		
PCR 51	IS26_fw	CACTGTCGATTTTTATCTCT	4358	49
	IS26_rv	CCTACGTGAAGGTCAATGGC		
PCR 52	IS26_fw	ATCCGTTTCAGTTTGCCATG	5621	55
	ISCfr1_rv	CGTTCGCAGCGAGAGACGAG		
PCR 53	ISCfr1_fw	CTGGTCGTCGGCTACTGCTA	5585	52
	ISCR1_rv	TAGACGAAGTCTTCCCCAAG		
PCR 54	ISCR1_fw	TGAGCGAGCGTATTCAGCTC	4705	53
	IntI1_rv	TGATCCGCATGCCCGTTCCA		
PCR 55	IntI1_fw	ATGTCCACTGGGTTCGTGCC	4797	49
	smc_rv	AGTTAAGCCTGAACAATACA		
PCR 56	smc_fw	AGGCCAGATCCATCACTCGT	3718	49
	tir_rv	CTCAAGCTTCTCGATTATGG		
PCR 57	tir_fw	CAGTACCGGAAGCAGTTATT	4250	50
	res_rv	TTATGGAATTCTTTTGAGCA		
PCR 58	res_fw	CACATGCTGTATGCCGGTAT	4195	50
	umuC_rv	GCAGTTGAGCCCTACTCAAT		
PCR 59	umuC_fw	GCCAGCTGCAGTGCTGTGTT	4541	55
	ychA_rv	TTCGTCTTCGGTCAGCCACT		
PCR 60	ychA_fw	TATCCGGGCTGGATCAGCAT	4241	55
	parB_rv	TGTTCGGCAGGGTGCATATC		
PCR 61	parB_fw	TGAGCGTGCCGCTGGCCTCA	2958	55
	psiA_rv	CGCCAGAGTGGTTCCTCCTG		
PCR 62	psiA_fw	TGTGGCTGGCTGCCGTGGAT	4552	55
	tnp_rv	GCCTGCTTAATCTGCTCCGG		
PCR 63	tnp_fw	ACTCCCGCAGGTCATGGTGG	4282	50

	nikB_rv	TGGTACTGGCGTGTAGTCAC		
PCR 64	nikB_fw	TATGACAGTGTACGCCATAC	4500	49
	trbC_rv	TGATATCGATATCCGTGACA		
PCR 65	trbC_fw	GTGGCTGTTGTCTGTCCTTC	3320	52
	trbA_rv	CTGTACTGGCAGATGGTGAT		
PCR 66	trbA_fw	AGCCATTGCTGTGCTTCGTT	4218	49
	traY_rv	GCAGGATTCTCTTTATCTAT		
PCR 67	traY_fw	TCCTCCTAGGAAATTAATTA	4883	49
	traU_rv	AGGGATAACTTCAACGTTCC		
PCR 68	traU_fw	CGAACTGAACCTAACTTATT	3612	50
	traT_rv	ACACAATCAGTGACACACGA		
PCR 69	traT_fw	GTACTGGTGATTTCAGCTTT	4250	49
	traN_rv	TCTCTGACAGTTAATCTGTC		
PCR 70	traN_fw	CCACTGGTTACGTTCAGGAT	3655	52
	SogL/SogS_rv	GATGACAAACAAAGCACCGG		
PCR 71	SogL/SogS_fw	AGGTATCGGTGGAGTCGTCG	4747	55
	traI_rv	CCATCATTCGCCCTGAACGC		
PCR 72	traI_fw	TTGGCTTCAAGCGTCAGGTC	3925	50
	traE_rv	TACATCATGCTGTCGCATGA		
PCR 73	traE_fw	TCAATATTACCCCGCAATAT	4645	50
	pilV_rv	TTACAGGCATATGTGGTTCG		
PCR 74	pilV_fw	ACGTTATTCAGGTTATTTGA	4180	49
	pilQ_rv	CATTACATACAAACTCAGCT		
PCR 75	pilQ_fw	CCTGCCGGTGAGGCCTTTAC	4766	50
	pilN_rv	CACCACCGGATTCAATATGA		
PCR 76	pilN_fw	ATAATGGATTTGCTGGCGTA	2920	52

	pilL_rv	AGAGTCAGCGTGCCAGAGAC		
PCR 77	pilL_fw	GGCTGCATTCTCTTGTCTGA	3368	50
	traC_rv	ATGACCACGACAGAACATCC		

[a]PCR1 to PCR20 were designed per the complete sequence of pECF12 and PCR2 to PCR6 were used to investigate the type I structure of *fosA3* environment; PCR21 to PCR45 were designed per the complete sequence of pECB11 and PCR22 to PCR31 were used to investigate the type II structure of fosA3 environment; PCR46 to PCR49 were designed per the sequence of pECXH3, and which were used to investigate the type III structure of *fosA3* environment; PCR50 to PCR77 were designed per the complete sequence of pECM13 and PCR50 to PCR55 were used to investigate the type IV structure of *fosA3* environment.

Table S4. Annotation of ORFs in plasmid pECF12

Gene name	location (start-end)	size (aa[a])	aa identity (%)	Alignment region of the match	homolog description
repA1	1-870	290	100	1-290/290	plasmid replication protein RepA [*Escherichia coli* 7A8]
tir	1809-2462	217	100	1-217/217	transfer inhibition protein [*Escherichia coli*]
pemI	2555-2812	85	100	1-85/85	stable plasmid inheritance [*Escherichia coli*]
pemk	2736-3146	136	100	1-136/136	stable inheritance protein PemK [*Escherichia coli* UMNK88]
Δ*tnpA*	4409-3846	177	100	1-177:14-190/177[b]	Tn3 transposase, tnpA [*Escherichia coli*]
fosA3	6617-6201	138	100	1-138/138	Fosfomycin resistance protein FosA3 [*Escherichia coli*]
IS*26*	6991-7707	238	100	1-238/238	Tnp1 superfamily, IS*26* transposase [*Escherichia coli*]
res	8339-9076	245	100	1-245/245	Ser-recombinase, resolvase [*Escherichia coli* 75]
tetA	10937-9663	424	100	1-424/424	tetracycline efflux protein TetA [*Escherichia coli* UMNK88]
tetR	10941-11618	225	100	1-225/225	tetracycline resistance repressor protein TetR [*Escherichia coli*]
strB	13034-12198	278	100	1-278/278	streptomycin phosphotransferase, StrB [*Escherichia coli* W26]
strA	13525-13034	163	100	1-163/163	streptomycin phosphotransferase, StrA [*Escherichia coli*]
Δ*sul2*	14713-13898	271	100	1-271:13-283/271	dihydropteroate synthase type-2 [*Escherichia coli* UMEA 3215-1]
IS*5075*	16405-15401	334	100	1-334/334	IS*5075* transposase [*Escherichia coli* SMS-3-5]
ΔTn*3*	18190-16484	568	100	1-568/568	Tn3 family transposase [*Escherichia coli* SMS-3-5]
IS*26*	19018-18302	238	100	1-238/238	transposase of IS26 [*Escherichia coli*]
bla$_{\text{CTX-M-55}}$	20392-19517	291	100	1-291/291	Beta-lactamase CTX-M-55 [*Escherichia coli*]
IS*26*	21530-20814	238	100	1-238/238	Tnp1 superfamily IS26, transposase of IS26 [*Escherichia coli*]
stbA	25179-24217	320	100	1-320/320	stable plasmid inheritance protein A, stbA[*Escherichia coli*]
ycgA	25696-26379	227	100	1-227/227	DNA methylase family protein,YcgA [*Escherichia coli*]
ycgB	26615-27049	144	100	1-144/144	transcription-repair coupling factor,YcgB [*Escherichia coli*]
yciA	27734-28321	195	100	1-195/195	YciA [*Escherichia coli*]
ycgC	28766-29188	140	100	1-140/140	ycgC [*Escherichia coli* DEC8C]
ssb	30177-30743	188	100	1-188/188	single-strand binding protein, Ssb [*Escherichia coli*]
parB	31095-32516	473	100	1-473/473	parB, ParB-like partition protein [*Escherichia coli*]
psiB	33187-33621	144	100	1-144/144	plasmid SOS inhibition protein B [*Escherichia coli*]
psiA	33618-34337	239	100	1-239/239	plasmid SOS inhibition protein PsiA [*Escherichia coli* F18+]

ydbA	36172-37533	453	100	1-453/453	YdbA [*Escherichia coli*]
ydcA	37580-38143	187	100	1-187/187	YdcA, DNA-methyltransferase-like protein [*Escherichia coli*]
yubP	38887-39708	273	100	1-273/273	YubP [*Escherichia coli*]
ygfA	40005-40652	215	100	1-215/215	lytic transglycosylase YgfA [*Escherichia coli*]
traM	40929-41312	127	100	1-127/127	type IV conjugative transfer protein TraM [*Escherichia coli*]
traJ	41443-42189	248	98	1-248/248	conjugal transfer protein TraJ [*Escherichia coli* LAU-EC10]
traA	42544-42909	121	99	1-121/121	conjugal transfer protein TraA [*Escherichia coli* O26:H11]
traE	43257-43823	188	100	1-188/188	type IV conjugative transfer system protein TraE [*Escherichia coli*]
traK	43810-44538	242	100	1-242/242	type IV conjugative transfer secretin TraK [*Escherichia coli*]
traB	44538-45965	475	100	1-475/475	type IV conjugative transfer system protein TraB [*Escherichia coli*]
traP	45955-46545	196	100	1-196/196	type IV conjugative transfer system protein TraP [*Escherichia coli*]
traV	46989-47504	171	100	1-171/171	type IV conjugative transfer system TraV [*Escherichia coli*]
traW	51027-51659	210	100	1-210/210	type IV conjugative transfer system TraW [*Escherichia coli*]
traU	51656-52648	330	100	1-330/330	conjugal transfer pilus assembly protein TraU [*Escherichia coli*]
trbC	53594-54232	212	100	1-212/212	type IV conjugative transfer system TrbC [*Escherichia coli*]
traN	55045-56895	616	100	1-616/616	conjugative transfer protein TraN [*Escherichia coli*]
traF	57142-57915	257	100	1-257/257	conjugative transfer pilus assembly protein TraF [*Escherichia coli*]
trbB	58299-58844	181	100	1-181/181	Putative conjugative transfer protein TrbB [*Escherichia coli*]
trbF	59102-59494	130	100	1-130/130	probable conjugal transfer protein TrbF [*Escherichia coli*]
traH	59481-60854	457	100	1-457/457	type IV conjugative transfer system pilus TraH [*Escherichia coli*]
traG	60851-63667	938	100	1-938/938	type IV conjugative transfer system TraG [*Escherichia coli*]
traT	64243-64977	244	100	1-244/244	type IV conjugative transfer system TraT [*Escherichia coli*]
traD	65968-68175	735	100	1-735/735	conjugal transfer protein TraD [*Escherichia coli*]
traI	68175-73445	1756	99	1-1756/1756	type IV conjugative transfer relaxase protein [*Escherichia coli*]
traX	73465-74211	248	100	248/248	type IV conjugative transfer pilin acetylase [*Escherichia coli*]

[a] aa, amino acids.

[b] Query alignment region:match alignment region/total aa of the match.

Table S5. Annotation of ORFs in plasmid pECB11

Gene designation	**location (start-end)**	**size (aa[a])**	**aa identity (%)**	**Alignment region of the match**	**homologue description**
repA1	1-858	285	100	1-285/285	plasmid replication initiator RepA [*Escherichia coli*]
repA4	1221-1607	128	100	1-128/128	replication initiation protein RepA4 [*Escherichia coli*]
tir	1797-2450	217	100	1-217/217	CAAX amino terminal protease Tir protein [*Escherichia coli*]
tnp	4367-3834	177	100	1-177/177	Tn3 transposase [*Escherichia coli*]
IS*26*	4445-5161	238	100	1-238/238	transposase tnpAIS26 [*Escherichia coli*]
IS*CR2*	5374-6297	307	100	1-307/307	putative transposase of ISCR2 [*Escherichia coli* EC1865]
virD2	6328-7212	294	100	1-294/294	type IV secretory pathway protein VirD2 [*Escherichia coli*]
floR	7429-8643	404	100	1-404/404	florfenicol-chloramphenicol exporter FloR [*Escherichia coli*]
lysR	8671-8976	101	100	1-101/101	putative transcriptional regulator protein LysR [*Escherichia coli*]
tetA	10517-9243	424	100	1-424/424	tetracycline repressor protein TetA class A [*Escherichia coli*]
tetR	10521-11198	225	100	1-225/225	tetracycline repressor protein TetR [*Escherichia coli*]
strB	12614-11778	278	100	1-278/278	aminoglycoside resistance protein StrB [*Escherichia coli*]
strA	13105-12614	163	100	1-163/163	streptomycin phosphotransferase, StrA [*Escherichia coli*]
Δ*sul2*	14293-13478	271	100	1-271:13-283/271[b]	dihydropteroate synthase type-2 [*Escherichia coli* UMEA]
IS*5075*	15985-14981	334	100	1-334/334	Transposase, similar to IS5075 [*Escherichia coli*]
Δ*tnp*	17770-16064	568	100	1-568:421-988/568	transposase for transposon Tn21 [*Escherichia coli* BIDMC 19A]
mobA	18113-18850	245	100	1-245/245	relaxation protein MobA [*Escherichia coli*]
rel	18863-19447	194	100	1-194/194	relaxation protein [*Escherichia coli*]
res/mod	22126-19490	878	100	1-878/878	type III restriction and modification system [*Escherichia coli*]
res/mod	24179-22131	682	100	1-682/682	type III restriction/modification enzyme [*Escherichia coli*]
exc1	27775-27326	149	100	1-149/149	Putative entry exclusion protein 1 (Exc1) [*Escherichia coli*]
IS*26*	28074-28790	238	100	1-238/238	transposase tnpAIS26 [*Escherichia coli*]
orf2	29290-30078	262	100	1-262/262	CadC-like protein, transcriptional regulator [*Escherichia coli*]
fosA3	31017-30601	138	100	1-138/138	fosfomycin resistance protein FosA3 (plasmid) [*Escherichia coli*]
IS*26*	31391-32107	238	100	1-238/238	transposase tnpAIS26 [*Escherichia coli*]
bla$_{\text{TEM-1}}$	32235-32900	221	100	1-221/221	beta-lactamase protein TEM-1b [*Escherichia coli* UMNF18]

orf477	33159-33635	158	100	1-158/158	ORF477 [*Escherichia coli*]
bla$_{\text{CTX-M-55}}$	34557-33682	291	100	1-291/291	extended-spectrum beta-lactamase CTX-M-55 [*Escherichia coli*]
IS*26*	34979-35695	238	100	1-238/238	transposase tnpAIS26 [*Escherichia coli*]
stbB	38382-38029	117	100	1-117/117	stable plasmid inheritance protein B [*Escherichia coli*]
stbA	39344-38382	320	100	1-320/320	stable plasmid inheritance protein A (plasmid) [*Escherichia coli*]
met	39861-40544	227	100	1-227/227	DNA methylase family protein [*Escherichia coli*]
ycgB	40780-41214	144	100	1-144/144	transcription-repair coupling factor, YcgB [*Escherichia coli*]
ychA	41214-42041	275	100	1-275/275	YchA (plasmid) [*Escherichia coli*]
yciA	41914-42486	190	100	1-190/190	YciA [*Escherichia coli*]
klcA	42459-42884	141	100	1-141/141	anti-restriction protein klcA [*Escherichia coli*]
ycjA	42931-43353	140	100	1-140/140	YcjA (plasmid) [*Escherichia coli*]
ydbA	44861-46222	453	100	1-453/453	YdbA (plasmid) [*Escherichia coli*]
ydcA	46269-46832	187	100	1-187/187	YdcA [*Escherichia coli*]
ssb	47648-48214	188	100	1-188/188	single-strand binding protein, Ssb [*Escherichia coli*]
Δ*yefA*	50128-50589	153	100	1-153:39-191/153	YefA (plasmid) [*Escherichia coli*]
psiB	50658-51092	144	100	1-144/144	plasmid SOS inhibition protein B [*Escherichia coli*]
psiA	51089-51808	239	100	1-239/239	plasmid SOS inhibition protein A [*Escherichia coli*]
yubP	53568-54389	273	100	1-172/273	yubP protein [*Escherichia coli* FVEC1302]
ygfA	55333-54686	215	100	1-215/215	lytic transglycosylase YgfA [*Escherichia coli*]
traM	55610-55993	127	100	1-127/127	conjugal transfer protein TraM [*Escherichia coli*]
traJ	56124-56870	248	100	1-248/248	conjugal transfer protein TraJ [*Escherichia coli*]
traA	57225-57590	121	100	1-121/121	conjugal transfer protein TraA [*Escherichia coli*]
traL	57605-57916	103	100	1-103/103	conjugal transfer pilus assembly protein TraL [*Escherichia coli*]
traE	57938-58504	188	100	1-188/188	conjugal transfer protein TraE [*Escherichia coli*]
traK	58491-59219	242	100	1-242/242	conjugal transfer protein TraK [*Escherichia coli*]
traB	59219-60646	475	100	1-475/475	conjugal transfer protein TraB [*Escherichia coli*]
traP	60636-61226	196	100	1-196/196	conjugal transfer protein TraP [*Escherichia coli*]
Δ*traV*	61778-62185	135	100	1-135:37-171/135	conjugal transfer protein TraV [*Escherichia coli*]
traC	62803-65328	841	100	1-841/841	conjugal transfer protein TraC [*Escherichia coli*]

trbI	65325-65711	128	100	1-128/128	conjugal transfer protein TrbI (plasmid) [*Escherichia coli*]
traW	65708-66340	210	100	1-210/210	conjugal transfer pilus assembly protein TraW [*Escherichia coli*]
traU	66337-67329	330	100	1-330/330	F pilin assembly, TraU [*Escherichia coli*]
ygeA	67356-67664	102	100	1-102/102	ygeA protein [*Escherichia coli* DEC8D]
trbC	68275-68913	212	100	1-212/212	conjugal transfer protein TrbC (plasmid) [*Escherichia coli*]
HNH	69307-69729	140	100	1-140/140	HNH endonuclease family protein [*Escherichia coli* DEC1B]
traN	69726-71576	616	100	1-616/616	conjugal transfer protein TraN [*Escherichia coli*]
traF	71823-72596	257	100	1-257/257	conjugative transfer pilus assembly protein TraF [*Escherichia coli*]
trbB	72980-73525	181	100	1-181/181	conjugal transfer protein TrbB [*Escherichia coli*]
trbF	73783-74175	130	100	1-130/130	putative conjugal transfer protein TrbF [*Escherichia coli*]
traH	74162-75535	457	100	1-457/457	conjugal transfer pilus assembly protein TraH [*Escherichia coli*]
traG	75601-78348	915	100	1-915/915	conjugal transfer protein TraG, partial [*Escherichia coli*]
traS	78381-78902	173	100	1-173/173	conjugal transfer entry exclusion protein TraS [*Escherichia coli*]
traT	78924-79658	244	100	1-244/244	conjugative transfer protein TraT [*Escherichia coli*]
hp	79861-80598	245	100	1-245/245	transmembrane protein (plasmid) [*Escherichia coli*]
Δ*traD*	80649-82157	502	100	1-500/500	conjugal transfer protein TraD [*Escherichia coli*]
traI	82886-88156	1756	100	1-1756/1756	conjugal transfer protein TraI [*Escherichia coli*]
traX	88176-88922	248	100	1-248/248	conjugal transfer protein, TraX [*Escherichia coli*]
finO	88977-89537	186	100	1-186/186	conjugal transfer fertility inhibition protein FinO [*Escherichia coli*]

[a] aa, amino acids.

[b] Query alignment region:match alignment region/total aa of the match.

Table S6. Annotation of ORFs in plasmid pECXH3

Gene designation	**location (start-end)**	**size (aa[a])**	**aa identity (%)**	**Alignment region of the match**	**homologue description**
IS*903*	1309-386	307	99	1-307/307	IS*903* transposase (plasmid) [*Escherichia coli*]
bla$_{\text{CTX-M-65}}$	2264-1389	291	100	1-291/291	CTX-M-65 beta-lactamase [*Escherichia coli*]
fipA	3395-2769	208	100	1-208/208	fipA [Plasmid pKM101]
IS*26*	4709-3993	238	100	1-238/238	IS*26* transposase, (plasmid) [*Escherichia coli*]
IS*26*	6112-5396	238	100	1-238/238	IS*26* transposase, (plasmid) [*Escherichia coli*]
fosA3	6486-6902	138	100	1-138/138	fosfomycin resistance protein FosA3 [*Escherichia coli*]
hp	7114-7443	109	100	1-109/109	hypothetical protein A6V31_17905 [*Proteus mirabilis*]
orf1	7425-6907	172	100	1-172/172	Orf1 (plasmid) [*Escherichia coli*]
orf2	8213-7425	262	100	1-262/262	Orf2 (plasmid) [*Escherichia coli*]
IS*26*	9429-8713	238	100	1-238/238	IS26 transposase, (plasmid) [*Escherichia coli*]
tetR	10909-10250	219	99	1-219/219	tetracycline repressor protein TetR [*Escherichia coli* SE11]
tet(A)	11002-12192	396	100	1-396/396	Tetracycline efflux protein TetA [*Proteus mirabilis*]
hp	12096-12434	112	100	1-112/112	conserved hypothetical protein (plasmid) [*Escherichia coli*]
orf	13184-12717	155	100	1-155/155	orf [*Escherichia coli*]
merR	13782-13375	135	100	1-135/135	MerR family transcriptional regulator [*Proteus mirabilis*]
hp	13878-14774	298	100	1-298/298	sodium: proton antiporter [Gammaproteobacteria]
hp	14778-15290	170	100	1-170/170	lipoprotein signal peptidase [*Escherichia coli*]

[a] aa, amino acids.

Table S7. Annotation of ORFs in plasmid pECM13

Gene designation	**location (start-end)**	**size (aa^{a})**	**aa identity (%)**	**Alignment region of the match**	**homologue description**
repZ	1-765	255	100	1-255/255	IncFII RepA protein [*Escherichia coli* 2.3916]
rep	900-307	197	99	1-197/197	replication initiation protein (plasmid) [*Escherichia coli*]
IS*26*	4111-4827	238	100	1-238/238	transposase of IS26, IS6 family [*Escherichia coli*]
bla$_{\text{CTX-M-14}}$	5130-6005	291	100	1-291/291	extended-spectrum beta-lactamaseCTX-M-14[*Escherichia coli*]
fosA3	6617-7033	139	100	1-139/139	Fosfomycin resistance protein FosA3 [*Escherichia coli*]
IS*26*	9029-8313	238	100	1-238/238	transposase of IS26, IS6 family [*Escherichia coli*]
aac(3)-IId	9250-10110	286	100	1-286/286	aminoglycoside 3-N-acetyltransferase [*Escherichia coli*]
tmrB	10123-10665	180	100	1-180/180	Tunicamycin resistance protein [*Escherichia coli*]
IS*Cfr1*	12892-14262	456	100	1-456/456	ISCfr1, TnpA [*Escherichia coli*]
bla$_{\text{TEM-1}}$	15083-15943	286	100	1-286/286	TEM-1 beta-lactamase [*Escherichia coli*]
rmtB	16113-16868	251	100	1-251/251	16S rRNA methylase RmtB [*Escherichia coli*]
IS*CR1*	19002-17461	513	100	1-513/513	ISCR1 transposase [*Escherichia coli*]
sul1	20333-19407	279	100	1-279/279	dihydropteroate synthase, sul1 [*Escherichia coli*]
qacEdelta1	20587-20240	115	100	1-115/115	quarternary ammonium compounds [*Escherichia coli*]
aadA2	21542-20751	263	100	1-263:10-272/263^{b}	aminoglycoside nucleotidyltransferase [*Klebsiella pneumoniae*]
intI1	22592-23605	337	100	1-337/337	IntI1 integrase [*Escherichia coli*]
IS*26*	24598-23882	238	100	1-238/238	transposase of IS26, IS6 family [*Escherichia coli*]
chem	24577-25965	462	99	16-462/447	chemotaxis protein [Enterobacter hormaechei subsp. oharae]
smc	28744-27188	518	100	1-518/518	recF/RecN/SMC N terminal domain protein [*Escherichia coli*]
tir	30185-31288	367	100	1-367/367	nucleotide-binding containing TIR-like [*Escherichia coli*]
res	33953-34732	259	100	1-259/259	resolvase [*Escherichia coli* KTE191]
yefA	34879-35556	225	100	1-225/225	ParB-like nuclease YefA [*Escherichia coli*]
stbA	36310-37344	344	100	1-344/344	plasmid partitioning and stability StbA [*Escherichia coli*]
umuC	39029-37755	424	100	1-424/424	UV protection protein UmuC [*Escherichia coli*]
yubD	41199-41882	227	100	1-227/227	putative DNA methylase YubD [*Escherichia coli* ACN001]
ychA	42552-43379	275	100	1-275/275	YchA [*Escherichia coli*]
parB	46437-48485	682	100	1-682	ParB-like partition protein [*Escherichia coli* KTE191]

psiA	48971-49690	239	100	1-239/239	plasmid SOS inhibition protein A, PsiA [*Escherichia coli*]
ardA	50512-51246	244	100	1-244/244	antirestriction protein ArdA [*Escherichia coli*]
tnp	52832-53794	320	100	1-320/320	transposase [*Escherichia coli*]
ydiA	54901-55749	282	100	1-282/282	YdiA protein [*Escherichia coli* ACN001]
nikB	56831-59449	872	100	1-872/872	relaxase NikB [*Escherichia coli*]
trbC	62754-60463	763	100	1-763/763	conjugal transfer protein TrbC [*Escherichia coli* EC4402]
trbB	63817-62747	356	100	1-356/356	TrbB protein [*Escherichia coli* ACN001]
trbA	65044-63836	402	100	1-402	conjugal protein TrbA [*Escherichia coli* ACN001]
traY	70091-67854	745	100	1-745/745	IncI1 conjugal transfer protein TraY [*Escherichia coli*]
traW	71934-70732	400	100	1-400/400	conjugal transfer protein, TraW [*Escherichia coli* KO11FL]
traU	75559-72515	1014	100	1-1014/1014	conjugal protein TraU [*Escherichia coli* W26]
traT	76449-75649	266	100	1-266/266	conjugal transfer protein TraT [*Escherichia coli*]
traP	78371-77667	234	100	1-234/234	conjugal transfer protein TraP [*Escherichia coli*]
traO	79660-78371	429	100	1-429/429	conjugal transfer protein TraO [Salmonella enterica subsp]
traN	80646-79663	327	100	1-327/327	conjugal transfer protein TraN (plasmid) [*Escherichia coli*]
traM	81349-80657	230	100	1-230/230	conjugal transfer protein TraM [*Escherichia coli*]
SogL/SogS	85478-81711	1255	100	1-1255/1255	SogL/SogS DNA primase [*Escherichia coli*]
traK	86479-85568	303	100	1-303/303	conjugal transfer protein TraK (plasmid) [*Escherichia coli*]
traJ	87569-86421	382	100	1-382/382	conjugative transfer protein (plasmid) [*Escherichia coli*]
traI	88384-87566	272	100	1-272/272	plasmid conjugative transfer protein TraI [*Escherichia coli*]
traF	91080-89878	400	100	1-400/400	conjugal transfer protein TraF [*Escherichia coli*]
traE	91989-91165	274	100	1-274/274	plasmid conjugative transfer protein TraE [*Escherichia coli*]
rci	93294-92140	384	99	1-384:12-395/384	Shufflon-specific DNA recombinase, Rci [*Escherichia coli*]
pilV	96348-95239	369	100	1-369/369	conjugal transfer protein pilV [*Escherichia coli*]
pilU	97019-96336	227	100	1-227/227	conjugal transfer prepilin peptidase PilU [*Escherichia coli*]
pilR	99276-98179	365	100	1-365/365	conjugal transfer protein PilR [*Escherichia coli*]
pilQ	99289-100842	517	100	1-517/517	conjugal transfer protein PilQ [*Escherichia coli*]
pilO	103923-102628	431	100	1-431/431	conjugative transfer protein PilO [*Escherichia coli* ETEC]
piN	105598-103916	560	100	1-560/560	IncI1 conjugal transfer protein PilN [*Escherichia coli*]

pilL	107116-106049	355	100	1-355/355	conjugal transfer protein PilL [*Escherichia coli*]
traC	110070-109387	227	100	1-227/227	conjugational TraC protein [*Escherichia coli* ETEC 1392/75]

[a] aa, amino acids.

[b] Query alignment region:match alignment region/total aa of the match.