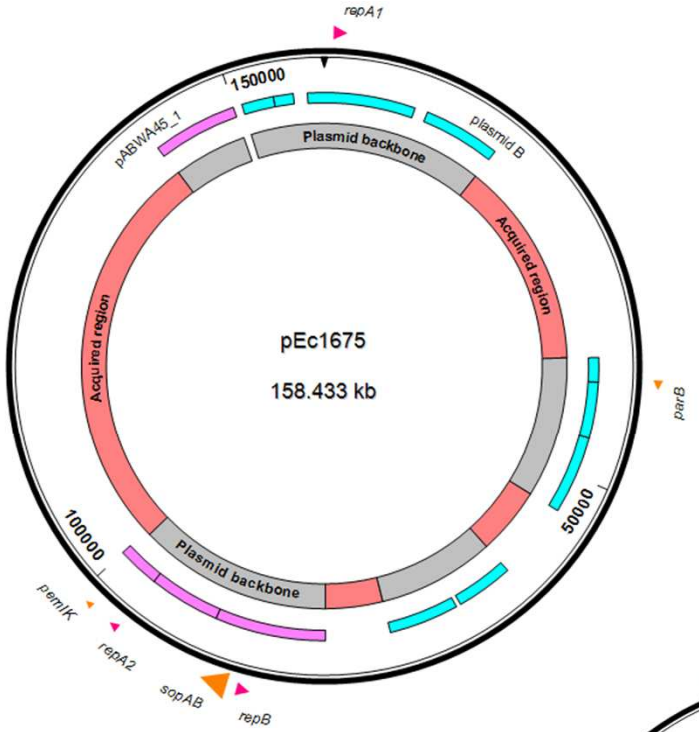
Table S1. Antimicrobial susceptibility of IMP-4-producing wildtype and recombinant strains.

Isolate	MIC (μg/ml) of:[a]															
	PIP	TZP	CTZ	CAZ	FEP	ATM	MER	ETP	GEN	AMK	CHL	TET	SXT	CIP	CST	TGC
E. aerogenes Ea1631	64	8	>8	16	8	≤0.12	0.5	1	16	1	>32	>32	>4	1	0.5	0.25
E. coli MT102 (pEa1631)	32	2	>8	8	4	≤0.12	≤0.12	0.25	32	≤0.25	2	1	≤0.03	≤0.06	≤0.12	0.12
E. coli Ec42	2	2	8	16	2	≤0.12	≤0.12	0.12	0.5	1	4	1	0.06	0.12	0.25	0.25
E. coli MT102 (pEc42)	≤1	≤1	8	8	2	≤0.12	≤0.12	0.03	≤0.25	≤0.25	2	0.5	≤0.03	≤0.06	0.25	0.12
E. coli Ec1675	32	2	>8	8	4	16	0.25	0.25	0.5	1	>32	1	>4	0.5	0.25	0.12
E. coli DH5α (pEc1675)	64	2	8	8	4	16	≤0.12	0.12	8	1	2	1	>4	≤0.06	0.25	0.25
P. penneri Pp47	16	≤1	8	>16	16	0.25	0.25	0.06	>32	2	>32	>32	>4	8	>16	2
E. coli MT102 (pPp47)	2	4	>8	8	16	≤0.12	0.25	0.25	16	≤0.25	2	32	≤0.03	≤0.06	≤0.12	0.25
P. mirabilis Pm60	16	≤1	8	16	16	0.25	0.5	0.12	>32	1	>32	>32	>4	4	>16	2
E. coli MT102 (pPm60)	4	4	>8	8	16	≤0.12	0.5	1	>32	≤0.25	2	>32	>4	≤0.06	≤0.12	0.25
E. coli Ec1677	16	2	>8	>16	>16	0.25	2	1	8	1	8	32	>4	4	>16	1
E. coli MT102 (pEc1677)	2	4	8	8	16	≤0.12	≤0.12	0.12	0.5	≤0.25	2	1	≤0.03	≤0.06	0.25	0.25

[a]PIP, piperacillin; TZP, piperacillin-tazobactam (inhibitor fixed at 4 μg/ml); CTX, cefotaxime; CAZ, ceftazidime; FEP, cefepime; ATM, aztreonam; MEM, meropenem; ETP, ertapenem; GEN, gentamicin; AMK, amikacin; CHL, chloramphenicol; TET, tetracycline; SXT, trimethoprim-sulfamethoxazole; CIP, ciprofloxacin; CST, colistin; TGC, tigecycline.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Plasmid backbone
Acquired region
pEc1675
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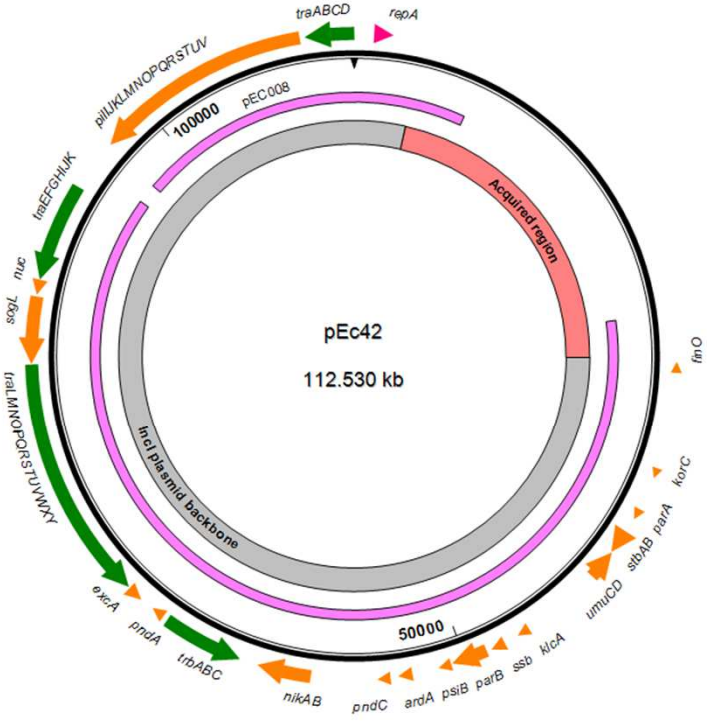
parB
50000
100000
Acquired region
Plasmid backbone
pemIK
repA2
sopAB
repB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sogL
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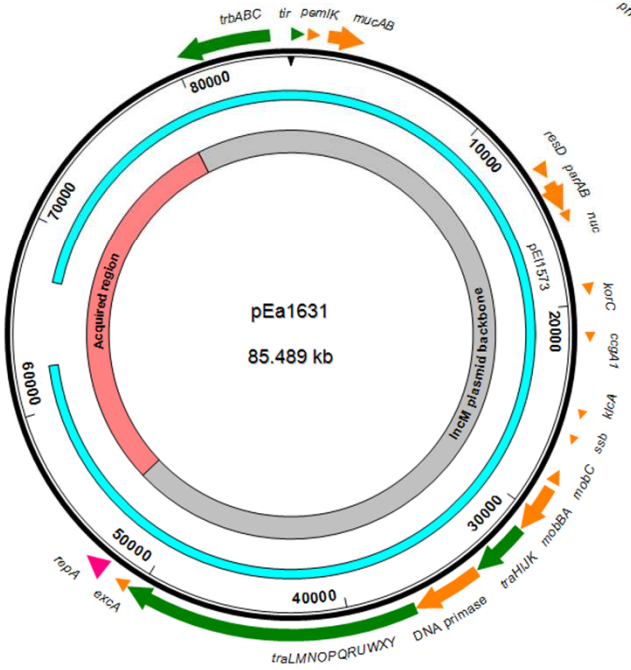
Acquired region
IncI plasmid backbone
pEc42
112.530 kb
finO
korC
stbAB
parA
umuCD
50000
excA
pndA
trbABC
nikAB
pndC
ardA
psiB
parB
ssb
klcA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tir
pemIK
mucAB
80000
10000
resD
parAB
nuc
70000
pEI1573
Acquired region
IncM plasmid backbone
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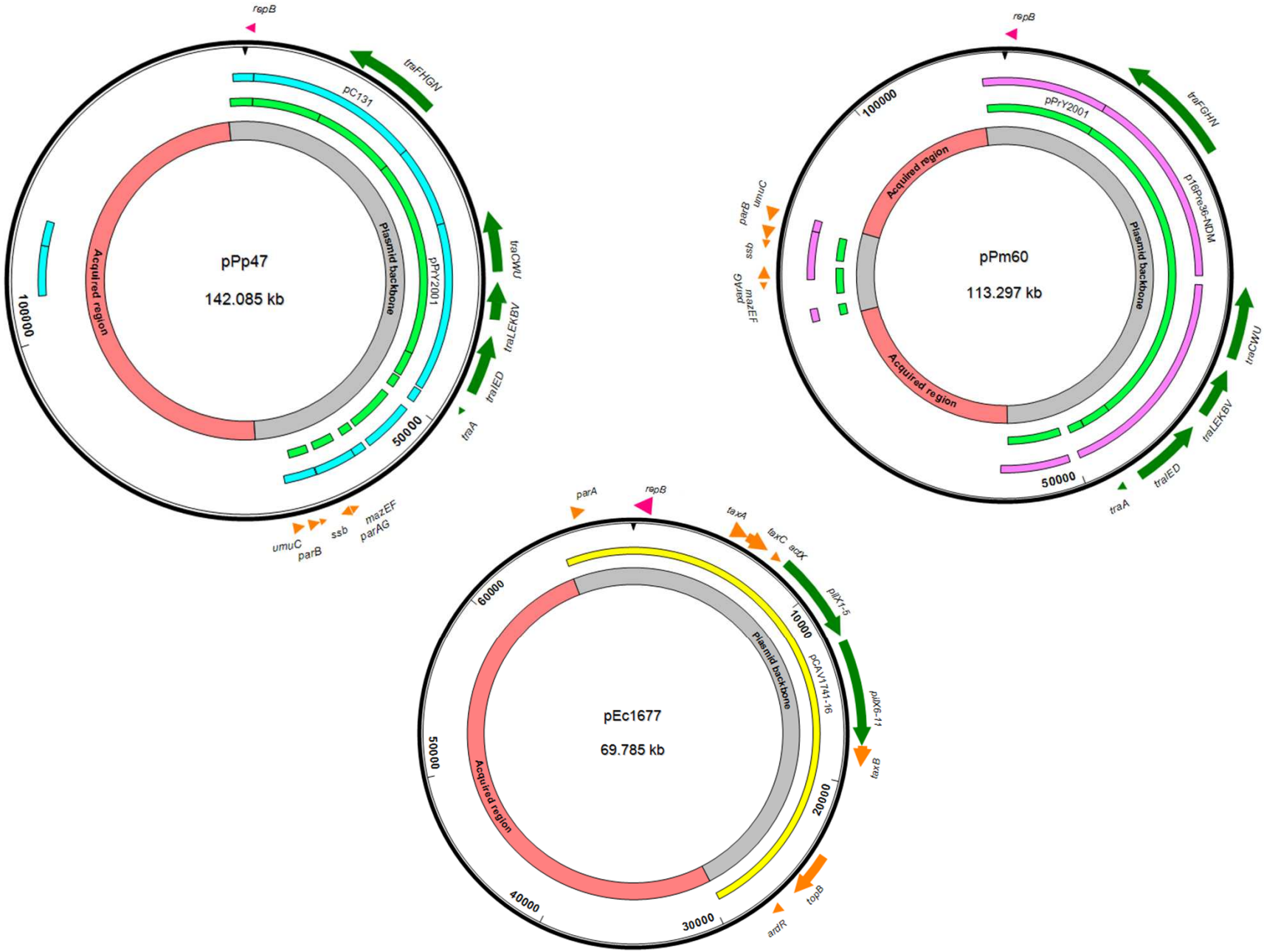
85.489 kb
korC
20000
ccgA1
klcA
ssb
60000
mobC
mobBA
traHIJK
30000
50000
repA
excA
40000
DNA primase
traLMNOPQRUWXY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pC131
pPrY2001
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traLEKBV
traIED
traA
umuC
parB
ssb
mazEF
parAG
pPm60
113.297 kb
repB
traFGHN
pPrY2001
pTGPre96-NDM
Plasmid backbone
Acquired region
Acquired region
100000
50000
parB
umuC
ssb
parAG
mazEF
traCWU
traLEKBV
traIED
traA
pEc1677
69.785 kb
parA
repB
taxA
taxC
acdX
pilX1-5
pilX6-11
taxB
pCAV1741-16
Plasmid backbone
Acquired region
60000
10000
20000
30000
40000
50000
ardR
topB

Figure S1. Overview of the plasmids pEa1631, pEc42, pEc1675, pPp47, pPm60 and pEc1677. The innermost circles show the main regions of the plasmids. Similarities with other plasmids are shown in the next circle; each color represents a unique plasmid. In the outer circle, indicative genes and the direction of transcription are shown by arrows. Replicons of the plasmid are indicated as pink arrows. Genes responsible for plasmid transfer and maintenance are shown in green and orange, respectively.