

## Supplementary Materials For:

# An efficient stress-free strategy to displace stable bacterial plasmids

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**Supplementary Table S1. Plasmids used and constructed in this work**

Plasmid name	Size (kb)	Selectable marker	Key properties	Reference and source
pAKE604	7.219	Ap <sup>R</sup> Km <sup>R</sup>	pMB1 replicon; mcs; <i>sacB</i> ;	(1)
pGEM-T Easy	3.015	Ap <sup>R</sup>	T-tailed vector for cloning PCR products	Promega
F	99.159	None	RepFIA RepFIB RepFIC/FIIA Tra <sup>+</sup>	NC_002483
F'proAB lacZΔM15	>100	<i>proAB</i>	RepFIA RepFIB RepFIC/FIIA Tra <sup>+</sup>	(2)
pO157	94.601/ 92.077	None	RepFIB RepFIC/FIIA Tra <sup>-</sup>	(3,4)
p1658/97	125.491	Ap <sup>R</sup> AG <sup>R</sup> Su <sup>R</sup>	<i>bla</i> <sub>SHV-5</sub> Tra <sup>+</sup>	(5)
pKDSC50	49.503	None	RepFIB RepFIIA Tra <sup>-</sup>	(6)
RK2	60.099	Ap <sup>R</sup> Km <sup>R</sup> Tc <sup>R</sup>	IncP-1α	(7)
pRK24	65 (approx)	Ap <sup>R</sup> Tc <sup>R</sup> TrpE <sup>+</sup>	IncP-1α	(8)
R751	53.339	Tp <sup>R</sup>	IncP-1β	(9,10)
pCURE1	10.211	Ap <sup>R</sup> Km <sup>R</sup>	pMB1 replicon; oriT <sub>RK2</sub> ; <i>sacB</i> ; anti-pO157	This work
pCURE2	12.002	Ap <sup>R</sup> Km <sup>R</sup>	pMB1 replicon; oriT <sub>RK2</sub> ; <i>sacB</i> ; anti-IncF	This work
pCURE11	9.419	Ap <sup>R</sup> Km <sup>R</sup>	pMB1 replicon; oriT <sub>RK2</sub> ; <i>sacB</i> ; anti-IncP	This work

AG<sup>R</sup>, resistance to the entire spectrum of clinically used aminoglycosides due to the presence of *aadA1*, *aacA4* and *aacC1*; Ap<sup>R</sup>, ampicillin resistance; Km<sup>R</sup>, kanamycin resistance; Tc<sup>R</sup>, tetracycline resistance; Tp<sup>R</sup>, trimethoprim resistance; mcs, multiple cloning site.

Supplementary Table S2. Primers used in this work

Sequence (all sequences are written 5'-3')	Coordinates	Plasmid template (Accession no.)	Genetic region
ACATTAAACGAGAGTAATCCCC	2351-2372	pO157 (AF074613)	<i>repFIIA copAB</i>
GTCGACTGAAGATCAGTCACACCATCC	3033-3053	pO157 (AF074613)	<i>repFIIA copAB</i>
GCTGACAAGCTGGTTCAGCAGAAC	48,289-48,307	pO157 (AF074613)	<i>repFIB</i>
TCTAGAGGAGGCTCGATCCAGTAAAC	49,890-49,871	pO157 (AF074613)	<i>repFIB</i>
TCTAGACCATACGAAACGGGAATGC	51,692-51,710	pO157 (AF074613)	<i>letA (ccdA)</i>
AAGCTTACATCCACAACAGACGATAAC	52,149-52,170	pO157 (AF074613)	<i>letA (ccdA)</i>
AAGCTTAGGAAAAGTGAATGGTTCAG	73,752-73,732	pO157 (AF074613)	<i>flmB (sok)</i>
GAATCCAACACACACCAGACAAGAG	73,988-73,969	pO157 (AF074613)	<i>flmB (sok)</i>
GGATCCGCCAGACGACTCATA	49,141-49,157	F (AP001918)	<i>repFIA (incC)</i>
CTCGAGCGGATAGCCAATTCAGA	49,459-49,476	F (AP001918)	<i>repFIA (incC)</i>
CTCGAGGGAACGGACTGGAACA	24,300-24,317	pKDSC50 (NC_002638)	<i>repFIIA copAB</i>
GGATCCCGTGTGCGTAATGAGTGAA	25,046-25,062	pKDSC50 (NC_002638)	<i>repFIIA copAB</i>
GCTAGCACACGCTGGGTTTACTG	40,448-40,466	p1658/97; (AF550679)	<i>pemI</i>
GGATCCAGCGAGACAAGCCAGATT	40,840-40,857	p1658/97; (AF550679)	<i>pemI</i>
CTGGTACCTCTCGCACAGCGATTTTC	124,521-124,504	p1658/97; (AF550679)	<i>srnC (sok)</i>
TTGCTAGCCGCTTGAGGCTTTCTGC	124,254-124,270	p1658/97; (AF550679)	<i>srnC (sok)</i>
GGATCCAGCCCCTCAAATGTCAA	12,366-12,385	RK2 (L27758)	<i>oriV</i>
CTCGAGGCGTGGACTCAAGGCTCT	12,973-12,992	RK2 (L27758)	<i>oriV</i>
GTCGACTGGTGGTCTTGCTTGAG	58,236-58,253	RK2 (L27758)	<i>korA-incC</i>
AGATCTAAGGACGAGTTTTAGCGG	59,449-59,466	RK2 (L27758)	<i>korA-incC</i>
GAATTCAGCGCATTTCCCGAC	35,029-35,044	RK2 (L27758)	<i>parD</i>
GGATCCAGCCGTGAGGATGTAGG	35,395-35,377	RK2 (L27758)	<i>parD</i>

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