Table S2. Primers used in this study [a]

Primer name	Sequence (5'→3')[b]	Restriction site	Application
*katA*_pME6032_FW	cggaattcATGGAAGAGAAGACCCGCC	EcoRI	Generation of pME*katA*
*katA*_pME6032_RV	ggggtaccTCAGTCCAGCTTCAGGCC	KpnI	Generation of pME*katA*
*sodB*_pME6032_FW	cggaattcATGGCTTTCGAATTGCCGC	EcoRI	Generation of pME*sodB*
*sodB*_pME6032_RV	ccgctcgagGTTCTGATCAGACTCAGGC	XhoI	Generation of pME*sodB*
*bfrB*_pME6032_FW	cggaattCATGAAAGGCGACAAGAAAG	EcoRI	Generation of pME*bfrB*
*bfrB*_pME6032_RV	ccgctcgAGGCCGCCGGCGCTTC	XhoI	Generation of pME*bfrB*
TnpRL13-2	CAGCAACACCTTCTTCACGA		Sequencing of transposon insertion mutants
TnpRL17-1	AACAAGCCAGGGATGTAACG		Sequencing of transposon insertion mutants

[a] Unless otherwise stated, PCRs were performed using the genomic DNA of *P. aeruginosa* PAO1 as the template.
[b] The restriction site used for cloning is underlined in the primer sequence.