

Table S4. Strains, plasmids, and oligonucleotides used in this study.

Strains		
Organism	Description	Source
<i>E. coli</i> TOP10	For general cloning	Invitrogen
<i>E. coli</i> XL1-Blue	For general cloning	QB3 Macrolab
<i>E. coli</i> S17-1	Conjugation donor strain	(1)
<i>E. coli</i> WM3064	Strain APA752; barcoded <i>mariner</i> transposon vector (Kan <sup>R</sup> ) in <i>E. coli</i> conjugation strain	(2)
<i>P. syringae</i> B728a	Wild type strain (Rif <sup>R</sup> )	(3)
<i>P. syringae</i> B728a	Whole genome barcoded <i>mariner</i> transposon library (Rif <sup>R</sup> Kan <sup>R</sup> )	This work
<i>P. syringae</i> B728a	Whole genome barcoded <i>mariner</i> transposon library (Rif <sup>R</sup> Kan <sup>R</sup> ), in $\Delta mexB$ genotype	This work
<i>P. syringae</i> B728a	$\Delta mexB$ (Rif <sup>R</sup> Kan <sup>R</sup> )	This work
<i>P. syringae</i> B728a	$\Delta mexB$ (Rif <sup>R</sup> ) – cured of pFLP2 $\Omega$	This work
<i>P. syringae</i> B728a	p519-MexAB (Rif <sup>R</sup> Kan <sup>R</sup> )	This work
<i>P. syringae</i> B728a	$\Delta mexB$ p519-MexAB (Rif <sup>R</sup> Kan <sup>R</sup> )	This work
<i>P. syringae</i> B728a	$\Delta mexB$ p519-MexAB-OprM (Rif <sup>R</sup> Kan <sup>R</sup> )	This work
<i>P. syringae</i> B728a	$\Delta mexF$ (Rif <sup>R</sup> Kan <sup>R</sup> )	This work
<i>P. syringae</i> B728a	$\Delta mexB \Delta mexF$ (Rif <sup>R</sup> Kan <sup>R</sup> )	This work
<i>P. syringae</i> B728a	$\Delta muxB$ (Kan <sup>R</sup> )	This work
<i>P. syringae</i> B728a	$\Delta mexB \Delta muxB$ (Kan <sup>R</sup> )	This work
<i>P. syringae</i> B728a	$\Delta mexK$ (Rif <sup>R</sup> Kan <sup>R</sup> )	This work
<i>P. syringae</i> B728a	$\Delta mexB \Delta mexK$ (Rif <sup>R</sup> Kan <sup>R</sup> )	This work

Plasmids			
Plasmid name	Description	Antibiotic	Reference
pKD13	Source of kanamycin resistance	Kan	(4)
pTsacB	Suicide plasmid to introduce DNA into <i>P. syringae</i>	Tet	(5)
pFLP2 $\Omega$	Contains Flp recombinase	Spec	(6)
p519ngfp	<i>lac</i> promoter and <i>pnpt2</i> in front of <i>gfp</i>	Kan	(7)
p519-MexAB	<i>mexAB</i> and upstream 1161 bp, replacing <i>gfp</i> in p519ngfp	Kan	This work
p519-MexAB-OprM	<i>mexAB-oprM</i> and upstream 1161 bp, replacing <i>gfp</i> in p519ngfp	Kan	This work
pT:2968-kan	To delete <i>mexF</i> , contains <i>Psyr</i> _2968 flanking regions bordering kan <sup>R</sup> cassette, inserted into SmaI site of pTsacB	Tet Kan	This work
pT:2483-kan	To delete <i>mexB</i> , contains <i>Psyr</i> _2483 flanking regions bordering kan <sup>R</sup> cassette, inserted into SmaI site of pTsacB	Tet Kan	This work
pT:0346-kan	To delete <i>mexK</i> , contains <i>Psyr</i> _0346	Tet Kan	This work

	flanking regions bordering kan <sup>R</sup> cassette, inserted into SmaI site of pT <i>sacB</i>		
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Primers used to construct MexAB (*Psyr\_4007-8*) and MexAB-OprM (*Psyr\_4007-9*) expression plasmids. Restriction cut sites are lowercase.

Name	Sequence
XbaI 4007 F	TAA <b>t</b> ctagaTTTTCTGCGGGGCAATACT
EcoRI 4008 R	ATga <b>a</b> ttcGAACGCGGTA <b>a</b> ACTGCAAGTG
EcoRI 4009 R	ATga <b>a</b> ttcCACTGATCGCAGGTGTGTTT

Bold sequence complements FRT-Kan sequence for splicing by overlap extension protocol. The primers used for TnSeq mapping and BarSeq amplification are described (2).

Name	Sequence
FRT-KanF	GTGTAGGCTGGAGCTGCTTC
FRT-KanR	ATTCCGGGGATCCGTCGACC
4008 up F	AGCACAGCCCTATACCCTGA
FRT 4008 up R	<b>GAAGCAGCTCCAGCCTACACTTACTCCCCTTTGCTGCCTG</b>
FRT 4008 down F	<b>GGTCGACGGATCCCCGGAATTG</b> CAGTTACCGCGTTCATTC
4008 down R	AGGAAGGTCAGGTTGCTGTC
2968 up F	GGGATGAATTCACCGGTCGT
FRT 2968 up R	<b>GAAGCAGCTCCAGCCTACACCGGACGAGTCCCTTAGCCGC</b>
FRT 2968 down F	<b>GGTCGACGGATCCCCGGAATG</b> AGTGCGTACAAAGTCTTCATCCCG
2968 down R	TTGTCGTAGTCGCTGAACGC
2483 up F	GCAGCTATCAAGTGGCGTTG
FRT 2483 up R	<b>GAAGCAGCTCCAGCCTACACGGTTTTTCCACCTTGCCGAG</b>
FRT 2483 down F	<b>GGTCGACGGATCCCCGGAATG</b> TGAGCTTTCGCTTGTTGCC
2483 down R	GAGCGGTCCATCGCGATATT
0346 up F	CAAAGTGCGCGAAGTAACCC
FRT 0346 up R	<b>GAAGCAGCTCCAGCCTACACTG</b> ACTGGCGACGGTGAATAC
FRT 0346 down F	<b>GGTCGACGGATCCCCGGAATG</b> GCTGCTGACGCGGTAATC
0346 down R	CTGCGAAGTGGTGCAGCAA

Primers used to confirm deletion strains.

Name	Sequence
4008 check F	CAGTGGCTGTAGCAAGAAGGA
4008 check R	TTTGTTGCGCACTGAACAGC
2968 check F	GTA <b>a</b> CTGGAGCAGCCAGTCAA
2968 check R	CCAGCAGGACCAGAAAGTCC
2483 check F	TTCCAGGAAGGGCAGATGGT
2483 check R	AGGTGCATGATCGCAAAGGT
0346 check F	ACGTTGCTCGATAACCCGAA
0346 check R	TCCGAACGTTTCGCAGAGAT

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