Table S2 Primers used for various purposes in this study

target	sequence (5'→ 3')
M-strain specific:	
mmar_3798 forward	TGGAAGATATCGGGAACTGC
mmar_3798 reverse	TTAGCGGCGAAAGACTTGAT
kdpC forward	TGCCGCAGTACTTCCAGAG
kdpC reverse	ACGCCTTGAAAGACATCCAG
E11-strain specific	
mmarE11_00270 forward	TGCACGAATTGCTCTTCAAC
mmarE11_00270 reverse	ACGACATGCTGACGTACTCG
mmarE11_28790 forward	CAAGCTCACAACCGTGAAAA
mmarE11_28790 reverse	CGAATATCGCCAAACCTGAT
pRAW-specific primers	
virB4 homologue forward	GGCATAGGATTTGCCGTATC
virB4 homologue reverse	AGCTTGAAGCCAACATCGAC
relaxase forward	CTACCGCGACTACAACACCA
relaxase reverse	GGGGTGAACGTGAGGTCATA
eccC$_{P1}$ forward	TGCGRCTGGTGGTGGTGACT
eccC$_{P1}$ reverse	GGCGAACTCGTCAATGACCA
eccA$_{P1}$ forward	CACCCAAGCGATGTGYCTTC
eccA$_{P1}$ reverse	GCCATCAGCTTGGTCAGTTC
primers for complementation	
eccBC6 AflII forward	TTTTT*CTTAAG*GCAACGGCGCAGAACCGATT
eccBC6 HindIII reverse	TTTTT*AAGCTT*CGTAGCCGCTCTGAAGGACA
eccC6 AflII forward	TTTTT*CTTAAG*GCAGACCGAACGCGTCTATC
virb4-like HindIII forward	TTT*AAGCTT*ATGAGCCAGACCGTGGTGAG
virb4-like PacI reverse	TTTT*TTAATTAA*GCATCACGACCGGCCAATTC

The introduced restriction sites in the primers used for complementation are shown in italics. pRAW-specific primers contain two ambiguity bases to increase detection (based on pMyong sequence homology).