

S2 Table | Primers used in this study.

Name	Sequence (forward/reverse)	Length/Description
$\Delta ravA$	A: GAATTCCAAGATGCTCTACCCCGAC B: AAGCTTAGCTTCCGGATCGTGTTG C: AAGCTTGAGAAAGAACTTGGCAGT D: GTCGACAAGTGCAGATGCCCGAAG	AB 403 bp; CD 301 bp; For pKS- <i>ravA</i> construction
$\Delta ravR$	A: GGATCCCTGACCAATGCGTTGCGG B: AAGCTTCGGGATCACAGGGCTCCA C: AAGCTT CATGATGAGTTGCGGAAC D: GTCGACGGCATCATCAACAAGCAC	AB 300 bp; CD 303 bp; For pKS- <i>ravR</i> construction
$\Delta ravS$	A: GGATCCCATTGCCCGCTCCATGAG B: AAGCTTGTGTTCTTCCACGATCTG C: AAGCTTCTGATCGTGATGCGTGAG D: GTCGACCGATATGGAAGATCATCA	AB 299 bp; CD 277 bp; For pKS- <i>ravS</i> construction
<i>ravR</i> ^{ΔEAL}	A: GGATCCGCACGGTAGCGACGAAAT B: GGTACCATGCGCATTGGTGGCCGA C: GGTACCGCCGGCATGGCGCTCCGC D: TCGACGTGTCGGGGTAGAGCATC	AB 315 bp; CD 275 bp; For pKS- <i>ravR</i> ^{ΔEAL} construction
<i>ravR</i> ^{D496A}	A: GGATCCCTGACCAATGCGTTGCGG B: GTCGACGGCATCATCAACAAGCAC C: AGGTGATCCTCTCCGCCAGCGCATGA D: GCGGAGAGGATCACCTGCACATCGTTG	AB 2274 bp; For pKS- <i>ravR</i> ^{D496A} construction
<i>ravS</i> ^{H500A}	A: GGATCC CATTGCCCGCTCCATGAG B: GTCGAC CGATATGGAAGATCATCA C: CATCTCGCGGACCTGGCCGACGACATC D: GCCAGGTCGCGGAGATGGCGCGGCGTTTC	AB 2262 bp; For pKS- <i>ravS</i> ^{H500A} construction
C- <i>ravA</i>	A: GTCGACCGAAGTGCAGATGCCCGA B: GGTACCCTACCGCGGCTGCCGCAC	AB 1509 bp; For pHM2 - <i>ravA</i> construction
C- <i>ravR</i>	A: GAATTCTCGCTGCTTTCCAGCACTTC B: TGAGGTCGTCGCGGACCATGTGGAGCCCTGTGATC C: ATGGTCCGCGGACGACCTCA D: GGTACCCTATTCCCGGCCGTTCCG	AB 334 bp; CD 1722 For pHM2 - <i>ravR</i> construction
C- <i>ravS</i>	A: GAATTCTCGCTGCTTTCCAGCACTTC B: GGTACCCTCAACGTCCACCATCTTC	AB 2410 bp; For pHM2 - <i>ravS</i> construction
OX- <i>ravS</i>	A: AAGCTTATGCACCAACACGTTGCC B: GAGCTCTCAACGTCCACCATCTTCAG	AB:2094 bp; For pBBR- <i>ravS</i> or pBBR- <i>ravS</i> ^{H500A} construction
RT- <i>fliC</i>	A: GCTTCACCACGCAGATCCG B: TGGTGGCGTTGGCTGACTGC	AB 144 bp; For qRT-PCR analysis of <i>fliC</i>
RT- <i>fliD</i>	A: CGAGAACGCCAACAACG B: GATCGCTTTACGGTCGTCG	AB 142 bp; For qRT-PCR analysis of <i>fliD</i>

RT- <i>flgA</i>	A: GGAATCGGGAATCGTCTGAC B: ATCGGGAGTGGGGAATCG	AB 123 bp: For qRT-PCR analysis of <i>flgA</i>
RT- <i>flgB</i>	A: CGAAGGCAATCTACCGACCG B: GCCTCGCCGGTCTCAGCTTG	AB 135 bp: For qRT-PCR analysis of <i>flgB</i>
RT- <i>flhA</i>	A: CGATGAACGCCCCGCCG B: GAACAGCGCATCCAGCACC	AB 122 bp: For qRT-PCR analysis of <i>flhA</i>
RT- <i>flhB</i>	A: CGAACGCACCGAACTACCC B: CTCAGCGCGGTCTTCATCC	AB 175 bp: For qRT-PCR analysis of <i>flhB</i>
RT- <i>motA</i>	A: CATCGTCGTCATCGTCAGTG B: ATCTTGCCCTGGCGTGCTC	AB 138 bp: For qRT-PCR analysis of <i>motA</i>
RT- <i>motB</i>	A: GTTCGCACAGCACGGGTTC B: CGTGCGGCCGTCATCTC	AB 153 bp: For qRT-PCR analysis of <i>motB</i>
RT- <i>tmRN</i> A	A: GCAGCTTTCCTCGTTAATCC B: CATGCTTATCCCTCCGTTAG	For qRT-PCR analysis of <i>tmRNA</i>
RavA	A: CATATGACTGCCAAGTTCTTCTC B: CTCGAGCCGCGGCTGCCGCACCG	AB 1227 bp; For pET-RavA construction
RavR	A: CATATGTGGAGCCCTGTGATC B: CTCGAGTTCCCGGCCGTTCCGCAA	AB 1722 bp; For pET-RavR construction
RavS ^{ΔTM}	A: CATATGAACCGCATGCTCGACCTG B: CTCGAGACGTCCACCATCTTCAGG	AB 1956 bp; For pET-RavS ^{ΔTM} construction
RavA ^{H164} A	A: GCTGCCGGCGTCGCGGCTGAGATCAAT B: GCCGCGACGCCGGCAGCGAGCTGGC	For pET-RavA ^{H164A} construction
RavR ^{D496} A	A: AGGTGATCCTCTCCGCCAGCGCATGA B: GCGGAGAGGATCACCTGCACATCGTTG	For pET-RavR ^{D496A} or pKS-ravR ^{D496A} construction
RavS ^{H500} A	A: CATCTCGCGCGACCTGGCC GACGACATC B: GCCAGGTGCGCGGAGATGGCGCGGCGTTC	For pKS-ravS ^{H500A} construction
R-EAL	A: CATATGAGCGAAAGCATCATTGCG B: CTCGAGGGACTCGGCCGACATCGG	AB 741 bp; For pET-EAL construction
S-PAS-A	A: CATATGGCACTTTTACAAGCCAAGTTCC B: CTCGAGACGTTCGGTACGTCCTG	AB 732 bp; For pET-PAS-A construction
S-PAS-B	A: CATATGGAGCAGTTCCGCGAGCTG B: CTCGAGGGGCTCGCTCAGGTCCG	AB 336 bp; For protein pET-PAS-B construction
RavS ^{ΔN}	A: CATATGGAGCAGTTCCGCGAGCTG B: CTCGAGACGTCCACCATCTTCAGG	AB 1041 bp; For protein pET-RavS ^{ΔN} construction
S-DHp-C A	A: CATATGGAGCGCATGCGCGATGCA B: CTCGAGACGTCCACCATCTTCAGG	AB 702 bp; For pET-DHP-CA construction
S-DHP	A: CATATGGAGCGCATGCGCGATGCA B: CTCGAGGAGCTGCGGCGGCCGACG	AB 279 bp; For pET-DHP construction
S-CA	A: GAATTCGAGAACCTGTACTTCCAAGGGGATGCATT GGGGCTGGAAGC B: CTCGAGACGTCCACCATCTTCAGG	AB 423 bp; For pMAL-CA construction

RavS ^{S636} _A	A: CTTTCGCCTGGAAGTCGCCGACGATGGC B: GCGACTTCCAGGCGAAAGCCGTTGCCG	For pET-DHP-CA ^{S636A} construction
RavS ^{D637} _A	A: CGCCTGGAAGTCAGCGCCGATGGCGACG B: GCGCTGACTTCCAGGCGAAAGCCGT	For pET-DHP-CA ^{D637A} construction
RavS ^{D638} _A	A: CTGGAAGTCAGCGACGCTGGCGACGGG B: GCGTCGCTGACTTCCAGGCGAAAGCCG	For pET-DHP-CA ^{D638A} construction
RavS ^{G639} _A	A: GAAGTCAGCGACGATGCCGACGGGTTC B: GCATCGTCGCTGACTTCCAGGCGA	For pET-DHP-CA ^{G639A} construction
RavS ^{D640} _A	A: GTCAGCGACGATGGCGCCGGGTTTCGAA B: TCGCCATCGCCGCTGACTTCCAGGCG	For pET-DHP-CA ^{D640A} construction
RavS ^{L652} _A	A: CCGCGTGGTTTGGGGGCGATCGTGATG B: GCCCCCAAACCACGCGGACCTTCCGG	For pET-DHP-CA ^{L652A} construction
RavS ^{L653A}	A: CGTGGTTTGGGGCTGGCCGTGATGCGTG B: GCCAGCCCAAACCACGCGGACCTTCC	For pET-DHP-CA ^{L653A} construction
RavS ^{R656} _A	A: GGGCTGATCGTGATGGCTGAGCGTGCGC B: GCCATCACGATCAGCCCAAACCACG	For pET-DHP-CA ^{R656A} and pKS- <i>ravS</i> ^{R656A} construction
RavS ^{E657} _A	A: CTGATCGTGATGCGTGCGGTGCGCA B: GCACGCATCACGATCAGCCCAAACC	For pET-DHP-CA ^{E657A} construction
RavS ^{L666} _A	A: ACCGTCGGCGGTGCGGCCGCGATAGAA B: GCCGCACCGCCGACGGTTTGCGCACGC	For pET-DHP-CA ^{L666A} construction