

1 **Table S1.** Primers for PCR, sequencing and RT-qPCR used in this study.

Name	Sequence 5'-3'	Amplicon size (bp)	Reference
DNA gyrase			
gyrAs-QRDR	TCCGTAATTGGCAAGACAAACG	543	This study
gyrAa-QRDR	CGGCCATCAGTTCATGGGCA		
gyrA741-1426s	GGCAATGCGTTATACGGAAA	685	This study
gyrA741-1426a	GGTTCATGATCTTCGGCTGA		
gyrA1376-1942s	TCGGTATCAACATGGTGGCA	566	This study
gyrA1376-1942a	TACGACGTTTGTACCGAAC		
gyrA1890-2490s	GATCCGTGAAGAGCTGGAGC	600	This study
gyrA1890-2490a	ACCTTCAGCGGAGAACAGCA		
gyrA2441-3089s	TTGACCTGACCAGCGGCGAA	648	This study
gyrA2441-3089a	AAGCCCAGACTTTGCAGCCTG		
gyrB-1-F	TAAAAGCGACGCAATCACAG	968	This study
gyrB-1-R	TGCGGAATGTTGTTGGTAAA		
gyrB-2-F	GGCAAAGAAGACCACTTCCA	1233	This study

gyrB-2-R	AGAAAGGTCAGCTTCCGTCA		
gyrB-3-F	TGGCGAAGCGTTAGAGAAAC	877	This study
gyrB-3-R	GGGATGATAATTGCGGATTG		
parCs	TCAGCGCCGCATTGTGTATG	253	This study
parCa	CAACCGGGATTCGGTGTAAC		

Regulators

marR-F	CTGTTCATGTTGCCTGCCAG	825	(1)
marR-R	CAGTCCAAAATGCTATGAATGG		
robA-F	CATCTGGACGCCCTGCATT	1172	(2)
robA-R	AGCCAATGGCCCCAGCATTA		
acrR-F	AAACCCATTGCTGCGTTTAT	821	(1)
acrR-R	AAACCGCAAGAATATCACGA		
soxSR-F	GCGCTATTGCCAGGGATGGT	1071	This study
soxSR-R	TGTGTTGACGTCGGGGGAAA		
soxS-F	TTTCTGATGGGACATAAATCTGCC	sequencing	(1)
plon-F	CCTGCGTTCCATCGTAGAAG	531	This study

plon-R	CCGTTGAAGCTTCTTTCTGC		
lon-end-F	GACCATTGAAACCGCATGTG	752	(3)
lon-end-R	GATCAATTGAGATTTATTCCTC		
lon3	CTATGAATCCTGAGCGTTCTG	729	(3)
lonR4	CACCGAGTTCTTTCTGAATAGC		
lon2	AAAATGATGTCTCCGATGTCG	1107	(3)
lonR3	CGCACGAACCACCGTTAA		
hns-F	CGGTGTTATCCACGAAACG	670	This study
hns-R	ATTGGCGGCACAAAATAAAG		
gadEp-F	G TTCAGCTTCGCCAGTTTGT	886	This study
gadEp-R	CTGCCAAAAGCCCTGTAAAA		

Efflux pumps

acrA-1F	CACCGGCAGTTTGAGGATCG	814	(2)
acrA-1R	GCGCGGATCAATCTGGCTTA		
acrA-2F	GTCGTTGCTGGACTGGGTCA	663	(2)
acrA-2R	ATGAACAAAAACAGAGGGTTTACG		

acrB-1F	TCAATGATGATCGACAGTATGGCT	616	(2)
acrB-1R	GGAACAACCTGGCGAGCAAAC		
acrB-2F	AGCGGAACGACCAGCATAAC	869	(2)
acrB-2R	GCGGGACGTGGTCAGAATAC		
acrB-3F	CCAGCCTGGTCAATCAGCTC	816	(2)
acrB-3R	GCGTGTTATGGCGGAAGAAG		
acrB-4F	CGAATACCGCCGACAGTACC	801	(2)
acrB-4R	GGATGAACCCGAATGAGCTG		
acrB-5F	CAGGATTTTGCCGAACCTCTCA	822	(2)
acrB-5R	ATAACCAGCAAGCCGCAAGC		
acrE-F	ATAGCCGAAGTTCGCCCACA	952	(2)
acrE-R	CTGCGGGGGTATCGGTAGTG		
acrF-1F	CAGTCAGGCGATTGGCGATA	935	(2)
acrF-1R	ACCACCGAGCCGTCACTGTT		
acrF-2F	CAGCGTTACCAGGGCAACAA	931	(2)
acrF-2R	ATTTTGCCGACGCTGTTGGT		

acrF-3F	CGCTGCTTAAACCCGTCTCTG	962	(2)
acrF-3R	CAGTCGCGGAGAGCCATACA		
acrF-4F	CGCTGGGTGGGACTTACGTT	851	(2)
acrF-4R	TTATCCTTTAAAGCAACGGCGGA		
acrD-L1-F	TCATTGCCCGTTGAACAATA	969	This study
acrD-L1-R	AACCAGAGCGATAGCTTCCA		
acrD-L2-F	GTGTTCCCTGTTCCCTGCGTTT	986	This study
acrD-L2-R	AGCAAGGAAATGGCGTACAG		
acrS-F	TTACATGACACTTAATTCATTCGTTTGA	1321	(2)
acrS-R	TGCACATCGCTGCCTTCAGT		
mdtF-F	CACAAACCTAACGCCCTGTT	662	This study
mdtF-R	AACATCGGCGTATCTTCCAG		
mdtEp-F	GAGCGACATCGTCACCCTGG	447	(4)
mdtEp-R	GTCATCGCAGGCGGTGAGCA		
mdtF1-F	CATTCGTCCGGGTATCAAAG	753	This study
mdtF1-R	AGTTGACCACCGGAAATCTG		

mdtF2-F	CAGATTTCCGGTGGTCAACT	921	This study
mdtF2-R	TTCAAACAGCGTGTTGAAGC		
mdtF3-F	GTACCGCGTCAGGTTTTGAT	522	This study
mdtF3-R	CGACCAGGTCTGCCATAAAT		
mdtF4-F	CATCCCGTCAATGGAGATTT	711	This study
mdtF4-R	GCAGGAAAGAGTAAGGCTGAA		
ydhE-F1	CTTCTTTTTGCTGCCCATTC	696	This study
ydhE-R1	GAAACCATGGCAAGGAACAT		
ydhE-F2	ATG TTCCTTGCCATGGTTTC	919	This study
ydhE-R2	TCAACGTGTATATCCCCGGT		
ydhEp-F	TTCTCGTCAATCGACACCAG	360	This study
ydhEp-R	GACAAAACCCATCGCAGTTT		

LPS synthesis

rfaE-F	ATGAAAGTAACGCTGCC	1455	(5)
rfaE-R	GATCTGTGAACCGCTTTCC		
rfaH-F	CCACGGATGCTAATGTCAAA	677	This study

rfaH-R	CCCATTATACGGCGTTCATC		
lpcA-1F	GTACTTCTCGCTTTTGGCGG	801	(6)
lpcA-1R	AATTTTCAGGTCGGATGCGG		
gmhB-F	TCAGGTTTATGCGAAGAGCA	706	This study
gmhB-R	GAAGACAAGCGGAAAAATGC		
rfaD-F	CAGACATTCGTGTCTGAGATTG	1068	This study
rfaD-R	GGAGCGTGCGATAGAGACTT		
rfaF-F	ATACATGGCCTGGCTGAATC	1147	This study
rfaF-R	GGGCAACGTATGGAGAACAT		
rfaC-1F	CACCGCCGCTATCCCATAAA	1367	(6)
rfaC-2R	AGAAAGGGGAAGAATAAGGT		
rfaL-F	TGGTATGTAGGGCTCCAAGAG	1501	This study
rfaL-R	AATTTGGTCCCCGAATCATC		
rfaQ-F	GCGCATAAAGTCACGTTGAA	1139	This study
rfaQ-R	TCGCTAGTGGAAAAGCCATT		
rfaG-F	AGCATCTTTACCACGCCAAA	1219	This study

rfaG-R	GGAAAAGCTGTTGCCAGAAG		
rfaP-F	TTCATAATCTGCAACCCAATTT	995	This study
rfaP-R	GAGAATGCTCGCCATTATGC		
rfaS-F	AGAAACAGCTTCGCCGATAA	1110	This study
rfaS-R	TGAACATGGCAAGCGTTAAG		
rfaB-F	TTCCATAAGCGATGTCCAGA	1263	This study
rfaB-R	TGATGTCAACGATTGTTTCTGA		
rfaI-F	ATGGCAGGAAATGAGTCCAC	1164	This study
rfaI-R	CTGCGTCGATCGATGAATTT		
rfaJ-F	TTTCATCGGTAAAAACAACCAA	1243	This study
rfaJ-R	GCTGAAACCGAACAATAGCA		
rfaY-F	AGGGCCCGAAAGAAAAATAA	917	This study
rfaY-R	GAGTCTGTTATCTTTGCCGAAA		
rfaZ-F	TTCCTAAGCGCATTTTTATACCA	995	This study
rfaZ-R	GCGTTTGAAAGGGAAACCAG		
rfaU-F	CACGCAGCATTCCAATTATC	1298	This study

rfaU-R GACATCAGTGCAGAAGAATCAAA

Others

yoaA-F	CGCCCTCATCCTGACATAAT	1994	This study
yoaA-R	ATAAAAAGGCGCGCATCATA		
yoaAseq-F	TTACAAAAGTGCGCTGATCG	sequencing	This study
yoaAseq-R	AGCGTTGCTGAGGTGAAGAT		
surA-F	TTACCACGTAATCCGCAGTG	1397	This study
surA-R	ACA ACTAAGTCCGGGCCAAT		
topB1-F	CGAGTTTGGCATTGAACTGA	945	This study
topB1-R	CGGATTCTGATTCCCGTTTA		
topB2-F	GTCAACCGGCTATTGTCACC	1107	This study
topB2-R	TTTTCGCACTACGTTTACGC		
rbsA-F	CAACAAACCGCAGAAAGTCA	1643	This study
rbsA-R	GAAATAACGGCGACCAGAGA		
rbsA-F2	AATGGTTGAAATCGCCAAAG	sequencing	This study
rbsA-R2	AACGGGTAACGACTTCATGC		

icdA-F	GCGGTATTCGCTCTCTGAAC	844	This study
icdA-R	GTTACGGTTTTTCGCGTTGAT		
rpoB-F	AGGTCGTCACGGTAACAAGG	803	This study
rpoB-R	TACCCAGCGAACGAATCTCT		
gudD-F	GGTCAACAGCGTAGCGAAGT	736	This study
gudD-R	CAAACGGTTCTTTGGTCAGG		
ygeG-F	GTGATGAATGGGCAAATCAA	425	This study
ygeG-R	TTCAATATATGCCTGCGCTTT		
pYejA-F	ACAGGCGCGATGGCTAAG	408	This study
pYejA-R	CGGTTGAAATTATCGAAGGTG		
sdhC-F	CGTCAGGACGATAGCGGTAG	721	This study
sdhC-R	TTGTAATGATTTTGTGAACAGCCTA		
EIE38512-F	CTCACCAGCATTTCGTGTTC	254	This study
EIE38512-R	GAACGGCCTCAGTAGTCTCG		
RT-qPCR			
mdh-F	TGACCAAACGCATCCAGAAC	118	(7)

mdh-R	GCACGAACCAGAGACAGACC		
rpsL-F	GCAAAAACGTGGCGTATGTACTC	104	(8)
rpsL-R	TTCGAAACCGTTAGTCAGACGAA		
RTqnrA-F	ACGCCAGGATTTGAGTGACAGCC	118	(9)
RTqnrA-R	GGCGCCGCTTTCAATGAAACTGC		
RTblaFOX-F	AACATGGGGTATCAGGGAGATG	190	(10)
RTblaFOX-R	CAAAGCGCGTAACCGGATTGG		
RTsul1-F	CACCGGAAACATCGCTGCA	158	(11)
RTsul1-R	AAGTTCCGCCGCAAGGCT		
RTacrA-F	CTTAGCCCTAACAGGATGTG	189	(12)
RTacrA-R	TTGAAATTACGCTTCAGGAT		
RTmdfA-F	CATTGGCAGCGATCTCCTTT	103	(8)
RTmdfA-R	TTATAGTCACGACCGACTTCTTTCA		
RTydhE-F	CTGGCGGCAGCGGTAA	108	(8)
RTydhE-R	TGCCATACAGACACCCACCATA		
RTacrE-F	CCTCCTGCCCTCCTTTATTCTG	100	(2)

RTacrE-R	AACGGTAACCTGCGGTTAC		
RTtolC-F	GGTACGTTGAACGAGCAGGATC	116	(2)
RTtolC-R	CCATCAGCAATAGCATTCTGTTCC		
RTmdtE-F	AATGTCACCTCGCCGATTAC	199	(13)
RTmdtE-R	TGCCCTGAACCTGTTTGATT		
RTmdtF-F	CCGTACCGGTGGTTATTCTC	193	(13)
RTmdtF-R	ATCGATTTATGCGTCGCTTC		
RTmarA-F	CATAGCATTTTGGACTGGAT	170	(12)
RTmarA-R	TACTTTCCTTCAGCTTTTGC		
RTSoxS-F	CCATTGCGATATCAAAAATC	210	(12)
RTSoxS-R	ATCTTATCGCATGGATTGAC		
RTfis-F	CGGTAAACAGGCACTGAAGA	134	This study
RTfis-R	CTGGTTACCACGGGTGTATTG		
RTdsrA-F	CATCAGATTTCTGGTGTAACGAA	65	This study
RTdsrA-R	GGTCGGGATGAAACTTGCT		
RTevgA-F	TGCTATTTCCCCTTCTCTCAACC	84	(13)

RTevgA-R	TTCTTGTTTCGATAAGGAGTCGAGTT		
RTompF-F	ACGCTGACGTTGGTTCTTTC	190	This study
RTompF-R	AAGTTCAGGCCATCAACCAG		
RTompC-F	TACGGCCAGTGGGAATATCA	165	This study
RTompC-R	CAGTACGTCGGTCCAGGAAG		
pRS415 cloning			
pYejA-F	GGCCCGgaattcGATTAGCCGCCCGTTACC	176	This study
pYejA-R	CACCGCCggatccCTGCAACGGATTCCTTT		
pYejAmut-R	CACCGCCggatccCTGTAACGGATTCCTTT		
pSdhC-F	GGCCCGgaattcCGACAAACTATATGTAGG	264	This study
pSdhC-R	CACCGCCggatccGCTGTTCTTATTATCCCT		
pRS415-Rn	GGCCTCTTCGCTATTACGC	sequencing	This study

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