

Table S1. Oligonucleotides used in this study

Primer	Sequence 5' → 3'
	<i>Homologous bases for joining PCR are bold</i> <i>Restriction sites are underlined</i> <i>Shine-Dalgarno sequences are italic</i>
Deletion and sequencing of <i>cspB</i>	
PF41	ATGATCGGAATTCTGGGGCTG
PF42	CCTATCACCTCAAATGGTTCGCTG GCATAAATTGATATGAAAACTGCAGGTG
PF43	CCGAGCGCCTACGAGGAATTTGTATCGT GAAATTCCTCCTAAAGCGATCATAAC
PF44	ACAGCTTTTAATTCAGGTGTCTCG
PF45	ACAAAATCATTAGAGGACCGTTTCTTAG
PF46	ATGAGTCCGCCGCTCTTAG
cat- fwd (kan)	CAGCGAACCATTTGAGGTGATAGG CGGCAATAGTTACCCTTATTATCAAG
cat-rev (kan)	CCGAGCGCCTACGAGGAATTTGTATCG CCAGCGTGGACCGGCGAGGCTAGTTACCC
Tc fwd2	CAGCGAACCATTTGAGGTGATAGG GCTTATCAACGTAGTAAGCGTGG
Tc rev	CCGAGCGCCTACGAGGAATTTGTATCG GAACTCTCTCCCAAAGTTGATCCC
Deletion and sequencing of <i>cspC</i>	
PF47	GAAGGGCAGGTACGGAAGATAG
PF48	CCTATCACCTCAAATGGTTCGCTG TTGTTGCCTCCTAGTGTGTAACC
PF49	CCGAGCGCCTACGAGGAATTTGTATCGT CTTCAATCGTTTATACAAACAGGCTC
PF50	TACGACCAGTTACCGATATACTTGC
PF51	TGAACAGGAGATTTAATGCTTTCTGATG
PF52	ACGGAGCAGGTATAATTGAAGCC
spec-fwd (kan)	CAGCGAACCATTTGAGGTGATAGG GACTGGCTCGCTAATAACGTAACGTGACTGGCAAG AG
spec-rev (kan)	CGATACAAATTCCTCGTAGGCGCTCGG CGTAGCGAGGGCAAGGGTTTATTGTTTTCTAAA ATCTG

Deletion and sequencing of <i>cspD</i>	
MB17	CGCCGAACTGGAAGAGTCATTCC
MB18	CCTATCACCTCAAATGGTTCGCTGGTTGAACCATTTACTTTACCGTTTTGCAT
MB19	CCGAGCGCCTACGAGGAATTTGTATCGGTAATCGTGGACCTCAAGCTTCTAATGTTG
MB20	GAAGCACTCCTTGAATCGCTGAAGC
MB21	GGCGAACTTGTCGATGAACATCAG
MB22	GGCAGCTGGCCTTGTTATGATC
kan fwd	AAAGAATTCGATAAACCCAGCGAACCATTGTA
kan rev	TTTGAATTCATCGATACAAATTCCTCGTAGGC
Deletion and sequencing of <i>veg</i>	
PF116	TCAAGAGTCAATATTCATGCGCTTG
PF119	CTGGTGGCAGTGAAAAAGGATG
PF120	CCGAGCGCCTACGAGGAATTTGTATCGTTGCATCCACCTCACTACATTATTG
PF121	CCTATCACCTCAAATGGTTCGCTGTTGTTTACTGCTTTTTGTTTTGCCC
PF122	GAAACGTCAGAGCCAATTTCCG
PF123	GTTTCGAATTATAGGAATAGAGCAAACAAG
PF124	AGCAGTTGAAACACCGATTGTC
mls-fwd	CAGCGAACCATTGAGGTGATAGGGATCCTTTAACTCTGGCAACCCTC
mls-rev	CGATACAAATTCCTCGTAGGCGCTCGGGCCGACTGCGCAAAAGACATAATCG
Construction of P_{cspB} - <i>lacZ</i> fusions	
PF151	TTTGAATTCTCATACGCTCTCTTAGTTGATAAACGT
PF152	TTTGGATCCAACATGAAATTTCTCCTAAAGCGATC
Construction of P_{cspC} - <i>lacZ</i> fusion	
PF97	TTTGAATTCAGGGGGCTTTGCGATTGAG
PF98	TTTGGATCCTCTAAAGATTTGAATCCGTCACTTTGG

Construction of P_{cspD}-<i>lacZ</i> fusion	
PF246	AGGGTATGTTTCTCTTTGATGTCTTTTG
PF247	CGGCAATAGTTACCCTTATTATCAAGATAAG
PF248	CTTATCTTGATAATAAGGGTAACTATTGCCG TCAGCCATCAATAAAAAGCGGTTAC
PF249	GTCACGACGTTGTAAAACGACGGGATCCCC GTTGAACCATTTTACTTTACCGTTTTGC
PF250	GGGGATCCCGTCGTTTTACAA
PF251	AACAAAATTCTCCAGTCTTCACATCG
Construction of P_{veg}-<i>lacZ</i> fusions	
PF127	AAAGAATTCAGAGAAAGGGCTTGGAGGTATTG
PF118	TTTGGATCCCCTAAATTCCCATCAAGCGATCTTTT
Construction of CspC[A58P] variant	
PF178	[5' Phosphorylated]ACGTTAGCAGCTTGAGGTCCACGAG
Qualitative PCR for <i>manR-manP</i>, <i>liaH-liaG</i>, <i>pyrR-pyrP</i>, <i>pyrP-pyrB</i> readthrough transcripts	
PF190	GTTTAAACAAGCCATTTTGAATCGTGA
PF191	CAATCGCATGAACAGTACCGC
PF192	GAGGTTCGTA CTGCCAGATCAC
PF193	GCTGAAGTGGCTGGCAAAC
PF196	GAACGCATTGAACAGATTGAGGG
PF197	CAGCCATCCTGTTCCAAGCT
PF198	CTGAGCAAGGTTGTCTGGACA
PF199	AGACGTCCACACCGATTGATTC
Quantative PCR for <i>manR-manP</i>, <i>liaH-liaG</i>, <i>pyrR-pyrP</i>, <i>pyrP-pyrB</i> readthrough transcripts	
PF201	AGCTGACGAAAGAAACCAATGT
PF202	CGAAATCAGCTCATTAAAATCGC
PF203	ACCGGCAGTGATCAACAGTT
PF204	GCGGCAAATGAATAAGCGGA

PF205	GGTCTTTGTATGCCTCTTTGCG
PF206	CCCAAGAGAAAGGTGTCGGG
PF207	CAGAGAGGCTTGGAAGGGTT
PF208	GCTAAGTTCATCATCGTCGT