

A**hfq CDS****Chromosomal hfq** ATAAGCATAT**AAGGAA**AAGAGAGAGATGGCTAAGGGGCAATCTTTAC**hfq2** ATAAGCATAT**AAGGAACACGCGGA**ATGGCTAAGGGGCAATCTTTAC**B****hfq2 sequence**

CAATTGAGAC GTATCGTGCG CAATTTTTTC AGAATCGAAA GGTTCAAAGT 50
 ACAAATAAGC ATATAAGGAA CACGCGGAAT GGCTAAGGGG CAATCTTTAC 100
 AAGATCCGTT CCTGAACGCA CTGCGTCGGG AACGTGTTCC AGTTTCTATT 150
 TATTTGGTGA ATGGTATTAA GCTGCAAGGG CAAATCGAGT CTTTTGATCA 200
 GTTCGTGATC CTGTTGAAAA ACACGGTCAG CCAGATGGTT TACAAGCACG 250
 CGATTTCTAC TGTGTCCCG TCTCGCCCGG TTTCTCATCA CAGTAACAAC 300
 GCCGTGGCG GTACCAGCAG TAACTACCAT CATGGTAGCA GCGCGCAGAA 350
 TACTCCGCG CAACAGGACA GCGAAGAAAC CGAATAAGGT TTCGGGCTGT 400
 TTTTTTACAC GGCTCGAGCC AGGCATCAA TAAAACGAAA GGCTCAGTCG 450
 AAAGACTGGG CCTTTCGTTT TATCTGTTGT TTGTCGGTGA ACGCTCTCTA 500
 CTAGATCAC ACTGGCTCAC CTTCGGGTGG GCCTTCTGTC GTTTATA 547

Fig. S1. Genetic structure of *hfq2* variant. (A) Sequence modification introduced into the RBS of the *hfq* gene while preserving the native *hfq* Shine-Dalgarno (SD) sequence and coding sequence (CDS). Blue nucleotides represent the native SD sequence (AAGGAA), green nucleotides indicate introduced nucleotide changes in the RBS, and red nucleotides correspond to the N-terminal region of the *hfq* CDS. (B) Complete nucleotide sequence of the *hfq2* variant construct spanning from the native promoter to transcription terminators. The promoter sequence is shown in orange, the UTR region in green, and the translation start codon (ATG) in red, the *hfq* CDS in underlined, and the transcription terminators (T1/TE) in blue.