

A *B. subtilis hfq* MAKGQSLQDPFLNALRRERVPVSIYLVNGIKLQGQIESFDQFVILKLN-TVSQMVKHAI 59
E. coli hfq M-KPINIQDQFLNQIRKENTYVTVFLNNGFQLRGQVKGFDFNFTVLESEGKQQLIYKHAI 59
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B. subtilis hfq STFAPQK-----NVQLELE---
E. coli hfq STVVPSPVSHHSNAGGGTSSNYHHGSSAQNTSAQQDSEETE
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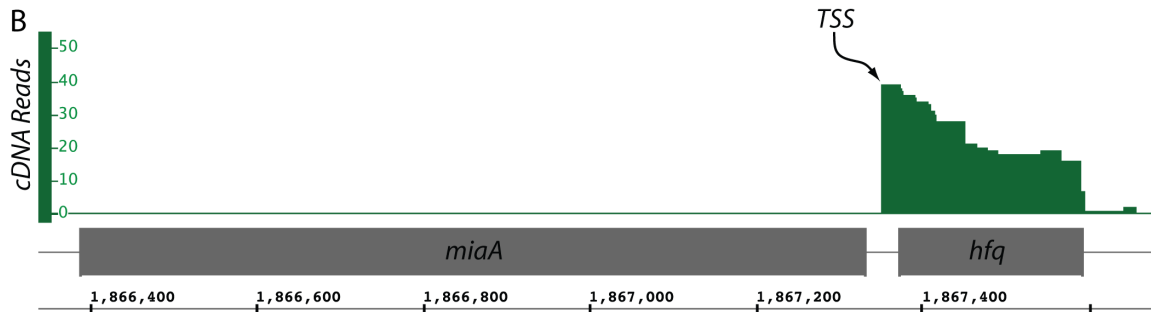


Figure S1. Organization of *hfq*. (A) The Hfq sequences from *B. subtilis* and *E. coli* are shown as an alignment to highlight the C-terminal truncation in *B. subtilis* (and many other Gram-positive bacteria). (B) Approximately 600 *B. subtilis* transcription start sites were determined in a previous study (Irnov *et al.*, 2010). We examined these data and found that they supported a single transcription start site upstream of *hfq*, suggesting that it is a monocistronic transcript.