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.