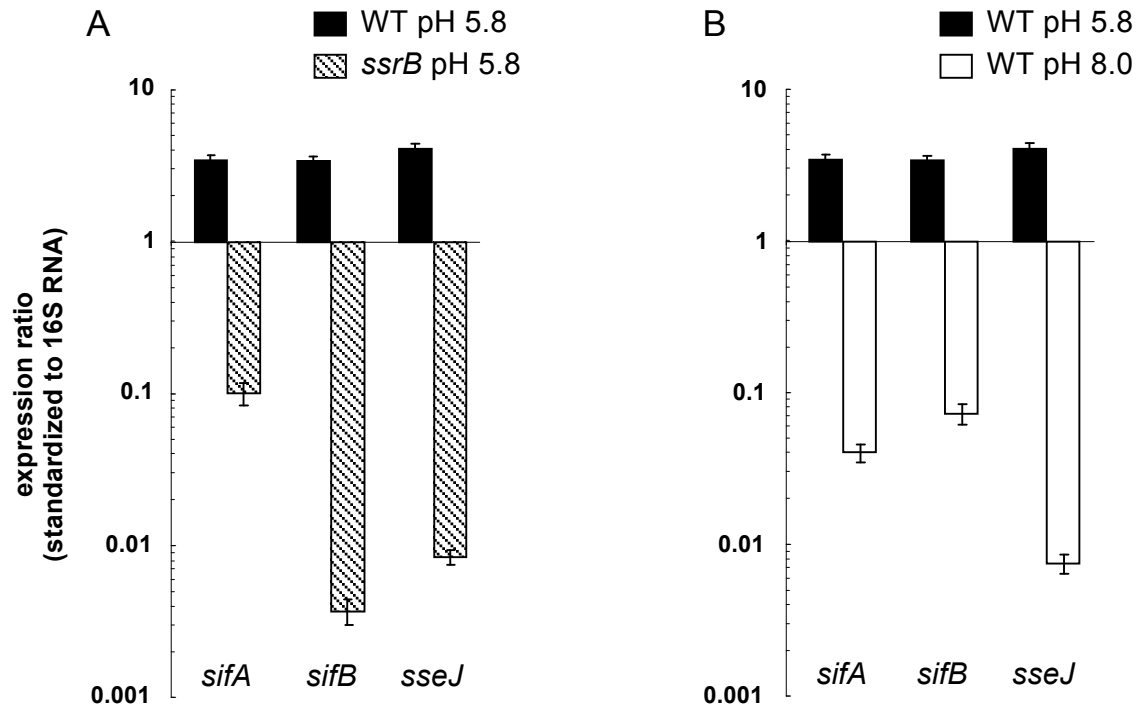


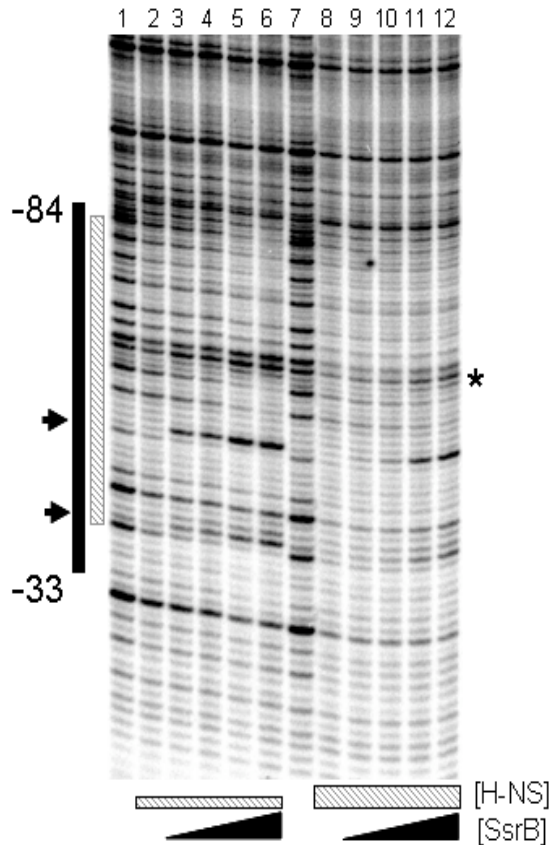
## Supplemental Material

### Supplemental Table 1. Oligonucleotides.

DW245 tatagtcgtaattaatcattactc  
DW247 caggcatgaagtttattcaag  
DW249 cattccctatagtaatcggcac  
DW250 ctcccgatagtaattggcat  
DW460 taagacgttcaggcgttctctgt  
DW461 aacagccgctttgtgttctgagc  
DW462 tgttgatactcagtctgccacct  
DW463 tttctgcatggcgataagcgtct  
DW655 acgaattcaacatgcaccaccaccaccacagcgaagcacttaaattctg  
DW656 agctgcagttattccttgatcaggaaatctcc  
DW671 caagctttatctcaactgcgggcgc  
DW672 ggaattcccttcggcataaaaaacgcatg  
DW685 aagcttcattactggaataggtggtattcg  
DW686 gaattcctttctctaaaaataatagtgcg  
DW696 cctgtccaacactcaatggcatag  
DW702 aggcgcttcccatcccaaac  
DW712 gaagctttctccttacyyyattaaacacgc  
DW713 cgaattcataagttgtctgttttctgag  
DW716 caagcttctatactggagtaaaatgactac  
DW717 atgaaagcatcgctcacaatgcc  
DW718 tgcacggcagctctcgtaatagca



**Supplemental Figure 1. Transcription of *sifA*, *sifB* and *sseJ* is strongly *ssrB*- and pH-dependent.** (A) qRT-PCR of *sifA*, *sifB* and *sseJ* transcript levels. Reactions were performed with the indicated gene specific primers and RNA harvested from wild type or *ssrB* null strains grown to mid-log phase in N9 minimal medium at acid pH. (B) qRT-PCR of *sifA*, *sifB* and *sseJ* transcript levels at low and high pH. Transcript levels were normalized to 16S RNA as described in Experimental Procedures. Error bars represent +/- 1 standard deviation.



### Supplemental Figure 2. SsrB antagonizes H-NS binding to *sifA* DNA

DNase I co-footprinting assays were employed to examine SsrB binding to *sifA* DNA in the presence of H-NS. Reactions were performed as described in Experimental Procedures. *sifA* template was pre-bound with 200 or 400 nM H-NS (indicated by the hatched rectangles) for 10 minutes at RT. Increasing concentrations of SsrB (indicated by the black triangles) from 100-800 nM in 2-fold increments were added for an additional 10 minutes. The presence of H-NS alone does not reveal discrete footprints, but a region of higher affinity within the SsrB binding site is apparent (delineated by the hatched rectangle; compare the DNase I sensitivity between lanes 1 and 2 and between lanes 7 and 8 both within and outside of the delineated region). At 200 nM H-NS (lanes 2-6), increasing concentrations of SsrB (lanes 3-6) result in the formation of SsrB-specific hypersensitive sites and an SsrB footprint (indicated by the black triangle) although the footprint is less apparent than when in the absence of H-NS (compare to Figure 1, panel B). When 400 nM H-NS is pre-bound to *sifA* template, the SsrB footprint is not readily apparent (i.e. it is not distinct from the H-NS region of protection) but the hypersensitive sites begin to reappear with increasing SsrB concentrations, as do sites not protected from cleavage in the presence of SsrB alone (indicated by the asterisk, compare to Figure 1, panel B).