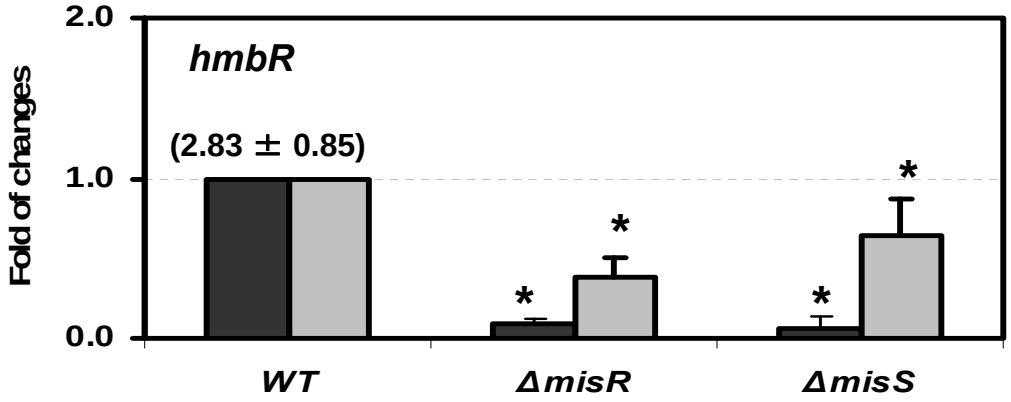

Fig. S1. The expression of *hmbR* is affected by the *misR* and *misS* mutations. Total RNAs were isolated from the wild type strain IR3287, the *misR* mutant (SZT1009) and the *misS* mutant (SZT1010) grown in the presence (gray bars) or absence (black bars) of 50 μM desferal for 3 hours and the *hmbR* expression assayed by qRT-PCR. The relative changes in transcriptional level between the mutants and the wild type strain were calculated by the $2^{-\Delta\Delta Ct}$ method (21). The transcriptional level of the wild type strain under the iron-rich condition was used as the calibrator. Subsequently, the transcription level of the wild type strain under each condition was set as 1 and then used to normalize those of the mutants. The iron-induction ratio of the wild type strain was shown in parenthesis as mean value ± standard deviation. Each qRT-PCR was examined in triplicate and was repeated with two independent preparations of RNA. Significant differences in transcription were noted by asterisks as determined by Student's t test with a 2-tailed distribution ($P < 0.01$).

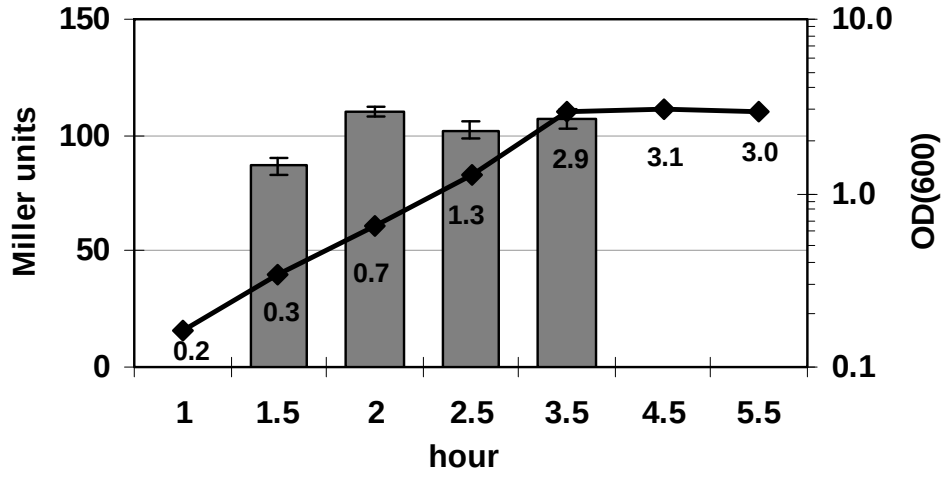

Fig. S2. The expression of *hmbR* is not growth phase dependent. The *hmbR::lacZ* reporter strain R103 integrated at the native locus was grown in GC broth and samples collected at four time points. Data presented are the mean values and standard deviations of one representative experiment. The values of OD_{600} are labeled along the line graph, while the corresponding activities shown in gray bars. No significant difference in transcription was noted from the mid-log phase to the early stationary phase.