Supplemental Materials

TABLE S1. Primers used in this study

Primer[a]	Sequence (5'-3')	Reference
RPA primers		
cytoC553_G27_RPA_F	GGTTATTGTGGCTTTAGG	this study
cytoC553_RPA_R	GGGATGTATTTGGCTAAAG	this study
hydA_RPA_F	GGTTGCACATGGCAGAATG	this study
hydA_G27_RPA_R	GCCTTCTACCATTAAAATG	this study
pfr-RPA-F	GCGGCTGAAGAATACGAG	(26)
pfr-RPA-R	CTGATCAGCCAAATACAA	(26)
serB_G27_RPA_F	GCTATGAATGGCGAAACAG	this study
serB_RPA_R	CCCTGTAATGATTGGTCGC	this study
qRT-PCR primers		
cyto c553_RT-F	CGCAAACGCTTTAATGGCAACCGA	this study
cyto c553_RT-R	CAGGATTCTTGTTGGCACCGCTTT	this study
hydA_RT-F	ATTGAAATGGGCGGGCATGATGAG	this study
hydA_RT-R	TGCCATGTGCAACCAAATCACAGG	this study
pfr_RT-F	TGAGCATGAGTTCTTGGTGC	(Gilbreath, et al.)[b]
pfr_RT-R	TTAAACCACATGCTCCACCGCTTG	(Gilbreath, et al.)[b]
serB_RT-F	GGCGTTTGATCTCATTAGCGCCTT	this study
serB_RT-R	AGCGTGTTACTGAAAGCCGCATCT	this study
G27_16S RT-F	ATGGATGCTAGTTGTTGGAGGGCT	(15)
G27_16S RT-R	TTAAACCACATGCTCCACCGCTTG	(15)
EMSA primers		
Cyto c553 EMSA-F	ACCCATGCTTATTTTCATAGGAATTG	this study
Cyto c553 EMSA-R	AGCCACAATAACCTTTTTCATCG	this study
hydA_EMSA-F1	CAGAGCTCCCGAACGCTTTGGC	this study
hydA_EMSA-R	TCATCGTAGAACATCGCCACTCC	this study
pfr EMSA-F	CCCCTTTTTACCTAATTCTC	(27)
pfr EMSA-R	CCTTATTCACTTGTTCGTTTAG	(27)
pfr EMSA MUT3-F	CCCCTTTTTACCTAATTCGT	this study
rpoB EMSA-F	CCAAAGAGGGTAAAGAGAGCG	(10)
rpoB EMSA-R	CCTCTCCATCGCTTCTCTAAC	(10)
serB_EMSA-F1	GCCTATGAACATGAGCAACACATC	this study
serB_EMSA-R1	GGAGTCAAAATCAAAAACGGCTAG	this study

serB_EMSA-F2	CAAAGGAGATACTATGTTATCAAAAGACATC	this study
serB_EMSA-R2	GCATGCTCGTATTCTTCAGCC	this study
Junctional PCR primers		
hydAB_Jxn-F	TGGCCGATAAAGTCGGCACG	this study
hydAB_Jxn-R	CTTTGAGCGATGAATCCTGC	this study
hydBC_Jxn-F	AATCGCTGATTTAACCCAGCC	this study
hydBC_Jxn-R	ACCCCTTTATAAAAGCTGGAATTAGG	this study
hydCD_Jxn-F	TCCCTGTGCATGTTTATATGG	this study
hydCD_Jxn-R	CATCTATAATATCCACGCTAGG	this study
hydDE_Jxn-F	AACGCTTTAGAAACAGCCC	this study
hydDE_Jxn-R	TGATCTCAGCGCTCGCTTGG	this study
pfr_serB_jxn-R	TCTGTCTCGCCATTCATAGC	this study
pfr_serB_jxn-F	TCTTGCAATGGTATGTGTCTG	this study
serB_fucT_jxn-F	GCATCAATGAGCCTAATTTAGCCC	this study
serB_fucT_jxn-R	CTGGCTGATCCAAGGGGATTGC	this study
Primer Extension and TSS primers		
Cyto_c553 PE	GCCATTAAAGCGTTTGCGAACGCC	this study
Cyto_c553_TSS_map-F	AATCCAGGCATAACGCTTGAG	this study
Cyto_c553_TSS_map-R	CCTTTTTCATCGTTTGTCTCCTCTAC	this study
hydA_PE	GCGTTCTTCAATCTTTTGATAGGTC	this study
hydA_TSS_map-F	CCCCCAGAGCTCCCGAACGC	this study
hydA_TSS_map-R	CATCGTAGAACATCGCCACTCC	this study
serB_PE	CAGCATTGACTAGCGTGGAGTC	this study
*pfr*SOE primers		
PFR_ApoMT_SOE_F	CTTTTTCATTA**gtgtgt**ATGCTATAATTATG	this study
PFR_ApoMT_SOE_R	CATAATTATAGCAT**acacac**TAATGAAAAAG	this study
PFR_PE	CCTTATTCACTTGTTCGTTTA	this study
PFR_ApoMT2_SOE_F	GGTGTTCTTTC**gtgtgt**TTTGCAAG	this study
PFR_ApoMT2_SOE_R	CTTGCAAA**acacac**GAAAGAACACC	this study
Footprinting primers		
hydA_FAM_F	FAM-CAGAGCTCCCGAACGCTTTGGC	this study
pfr_PE_FAM	FAM-CCTTATTCACTTGTTCGTTTA	this study
PFR_large_ftptng_F	GGTTAAATTGCCCTTTCG	this study
FA primers		

pfr-FA_LABEL	5FluorT/TCATTATCATTTATGCTAT	(Gilbreath, et al.)[b]
pfr-FA_UNLABELED	TTCATTATCATTTATGCTAT	this study
pfr-FA_COMPLEMENT	ATAGCATAAATGATAATGAA	(Gilbreath, et al.)[b]
pfr-FA_SCRAM-1	TTCATTA**gtgtgt**ATGCTAT	(Gilbreath, et al.)[b]
pfr-FA-SCRAM-2	ATAGCAT**acacac**TAATGAA	(Gilbreath, et al.)[b]

[a]Mutations in *apo*-Fur box are in bold, lowercase. FAM and FluorT labeling is as indicated.

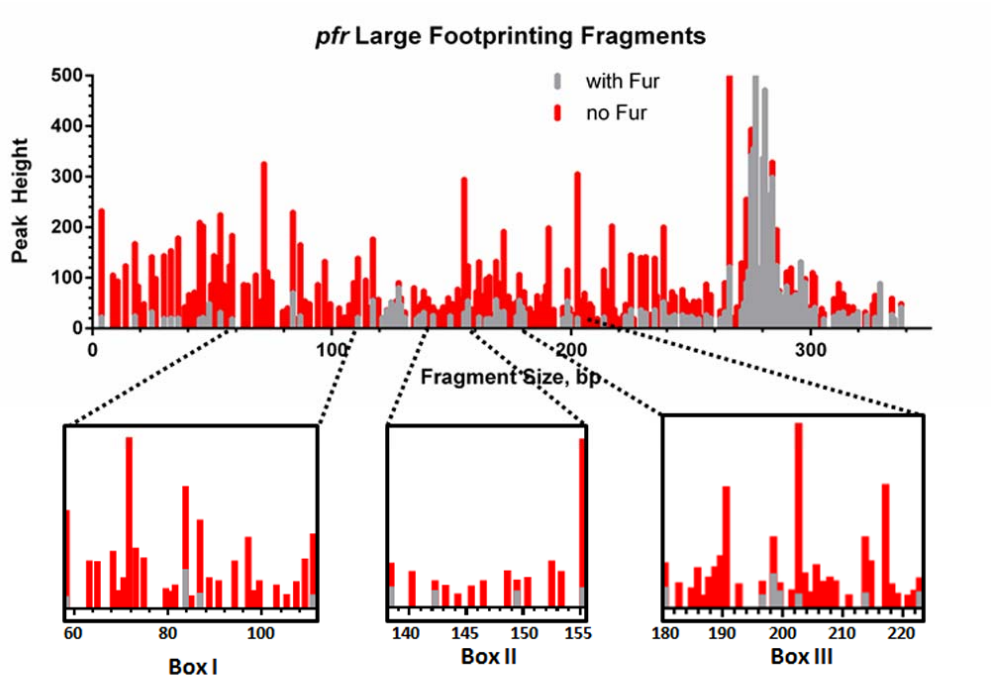
[b]**Gilbreath JJ, Pich OQ, Benoit SL, Besold AN, Cha JH, Maier RJ, Michel SL, Maynard EL, Merrell DS.** 2013. Random and site-specific mutagenesis of the *Helicobacter pylori* ferric uptake regulator provides insight into Fur structure-function relationships. Mol Microbiol **89:**304-323.

FIG. S1

DNase I footprinting of the *pfr* Large promoter fragment. A 3' end fluorescently labeled fragment of the *pfr* large promoter fragment was subjected to DNase I digestion in the absence and presence of *apo*-Fur (Panel A). Protected regions are those with reduced peak height and/or entirely missing peaks in the presence of *apo*-Fur (gray lines) as compared to digestion fragments in the absence of Fur (red lines). Protected regions are magnified in the boxed regions. The sequence of the *pfr* large promoter fragment utilized in the footprinting experiments is shown in Panel B. The conserved *apo*-Fur box sequences are in red, and the protected regions as identified through DNase I footprinting are given in blue (note that the second protected region does encompass the second AAATGA sequence, which is in red). The -10 and -35 promoter elements are shown in bold italics; the ATG start codon is in bold underlined text. The previously reported protected regions for the *pfr* promoter (5) are underlined.

Figure S1

A



B

GGTTAAATTGCCCTTTCGTTTTAAAGATAAACATTGTAGCATTTTTAGATTTAAGAATGCTTTTTATATATTATATAAAAA
TATCCCCTTTTAACCCCCTAGTTGATACCAACCCCTTTTTACCTAATTCTCATTAAATAGATTTTTATGATAAAATCTAAG
CTTTATCAAGCCATTAGCCGGTGTTCTTTCTCATTTTTTGCAAGTTTTTAAAAATTTTCATACTCTTG***TTTACT***TTTTCAT
TATCATTTATGC***TATAAT***TATGGGACAACTTAAACCAACACAAAGGAGATACTATGTTATCAAAAGACATCATTAAGTTGC
TAAACGAACAAGTGAATAAGG