Table S1. Primers used in construction of strains and plasmids.

Primers	Sequences (5′ to 3′)
DE-*rstB*-F	CGCGCGATAGAGCTAATGTATTGAGATCCGGTGGG CGTTGTGTAGGCTGGAGCTGCTTCG
DE-*rstB*-F	ATAGCACAGTTCCCGCCGCTCAACCAGCGTGCAA AATGCGCATATGAATATCCTCCTTAG
DE-*mgtA*(5′UTR)-F	ATTTTCCTTTTCCGGTAAGCCTGCCTCTGCTGTCTTA CCGGTGTAGGCTGGAGCTGCTTC
DE-*mgtA*(5′UTR)-R	GGCGGGTAATGATTTTTAGCATAGGTAATCCCTCCG CGCCATATGAATATCCTCCTTAGT
DE-*sitABCD*-F	TATTCGATGATTAATTAACCACATTGTTGCGAGGGA TACTTGTAGGCTGGAGCTGCTTCG
DE-*sitABCD*-R	ATTATGACCGTATGTTTCCTGAATAGCAGGCAAAA AAGTGATGAATATCCTCCTTAGTTC
DE-*mntH*-F	AGCATGAAACATAGCAAAGGCTATGTTTTTGAGGC AAAAGTGTAGGCTGGAGCTGCTTCG
DE-*mntH*-R	CCGATGACGCCCACGCATCGGGCCTGCTATCTTTCT GTCTATGAATATCCTCCTTAGTTC
DE-*ackApta*-F	CTGACGTTTTTTTAGCCACGTATCATAAATAGGTAC TTCCTGTAGGCTGGAGCTGCTTCG
DE-*ackApta*-R	ACAAGGCGTTCACGCCGCCATCCGGCATTAGCTTT TACTGCATATGAATATCCTCCTTAG
rstA-FLAG-F	CTATCTTTTTGCCCCTCATGCCTGGGACGAAACGA CGGGAGACTACAAGGACGACGATGACAAGTGATG TAGGCTGGAGCTGCTTCG
rstA-FLAG-R	ACTATGACTTGATAAAGGCAGGTAAAATCTGTCGG CTAACCATATGAATATCCTCCTTAG
CD-*rstA*-FLAG-F	GCGGATCCAATATGAACCGCATTGTATTTGTTGAAG
CD-*rstA*-FLAG-R	GCCTGCAGAACTCACTTGTCATCGTCGTCCTTGTAG TCTCC
SM-*rstA*(D52A)-F	CCCGATCTGGTTTTACTGGCTATTATGCTTCCAGGT AAA
SM-*rstA*(D52A)-R	TTTACCTGGAAGCATAATAGCCAGTAAAACCAGAT CGGG
CD-*phoP*-F	GCGGATCCAAGGGAGAAGAGATGATGCGCGTAC

CD-*phoP*-R	GCCTGCAGCATTAGCGCAATTCAAAAAGATATC

Table S2. Gene-specific primers used in quantitative real-time RT-PCR analysis.

Primers	Target genes	Sequences (5′ to 3′)
Q-feoB-F	*feoB*	GTTCGTCATCTACCTGATGTTC
Q-feoB-R	*feoB*	GCAGCCTGTAGCCAATCC
Q-rstA-F	*rstA*	GCATGACGATATGTCGCGATT
Q-rstA-R	*rstA*	ATCTCCAGCGCCAGAATATGA
Q-mgtA(a)-F	*mgtA* (5′UTR)	TAATTGCCACAAAACTTATG
Q-mgtA(a)-R	*mgtA* (5′UTR)	TCGCGGGAGAGGGGTGGGTT
Q-mgtA(b)-F	*mgtA* (coding region)	GGCAATGGAGCAGGAGACTCT
Q-mgtA(b)-R	*mgtA* (coding region)	CACCTCGGCAGCGTTTAATC
Q-mgtB-F	*mgtB*	TCGAAGCGGAAGCTTTTCAT
Q-mgtB-R	*mgtB*	TCATTGCGCCCATACACTTTC
Q-rrsH-F	*rrsH*	CCAGCAGCCGCGGTAAT
Q-rrsH-R	*rrsH*	TTTACGCCCAGTAATTCCGATT

Figure S1. Transcription of the *feoB* gene is activated in the *ackA-pta* deletion strain grown at acidic pH. RNA isolated from the wild-type (14028s) and *ackA-pta* deletion (EN252) strains grown in 2 mM Mg^{2+} N-minimal medium buffered at pH 7.7 (H) or 5.7 (L). The *feoB* mRNA levels were determined using qRT-PCR. Shown are the mean values and standard deviations of three independent experiments.

Figure S2. The Fur protein represses transcription of the *feoB* gene at acidic pH in the presence of iron. RNA isolated from the wild-type (14028s), *rstA* deletion (JH101), and *fur* deletion (JH352) strains grown in 2 mM Mg^{2+} N-minimal medium at pH 5.7 in the presence (20 μM) or absence of $FeSO_4$. The *feoB* mRNA levels were determined using qRT-PCR. Shown are the mean values and standard deviations of three independent experiments.

Figure S3. Expression of the *mgtB* gene is promoted only when *Salmonella* starves for Mg^{2+}. The wild-type (14028s) and *phoPQ* deletion (DS267) strains were grown to OD_{600}=0.4 in N-minimal medium at pH 7.7 with 2 mM Mg^{2+} and transferred to the medium at pH 7.7 or 5.7 in the presence (10 mM) or absence of Mg^{2+}. After 30 min, RNA was isolated from the strains, and the levels of *mgtB* mRNA determined by qRT-PCR. Shown are the mean values and standard deviations of three independent experiments.

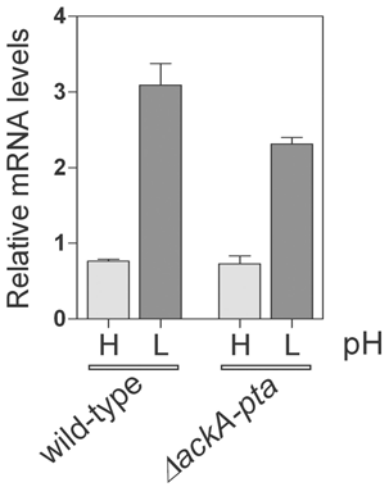

Figure S1

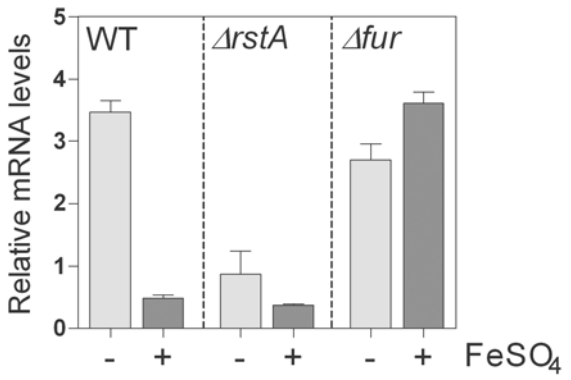

Figure S2

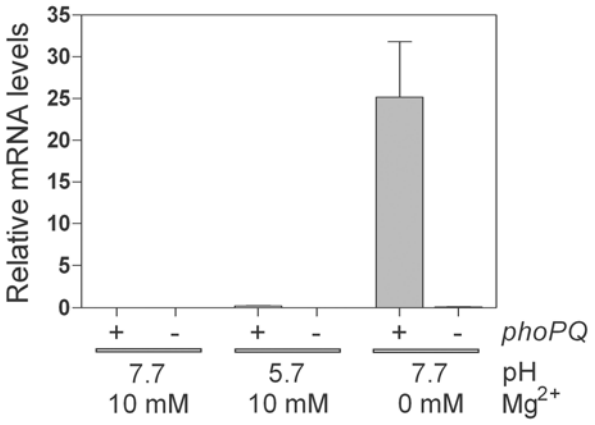
Relative mRNA levels
35
30
25
20
15
10
5
0
+ - + - + -
phoPQ
7.7
10 mM
5.7
10 mM
7.7
0 mM
pH
Mg2+

Figure S3