Contents:

Supplemental Materials and Methods

Replication run out flow cytometry

Samples of BB1185 (*sda*$^+$) and SH455 (Δ*sda*) were grown in LB and LB+100 μM $MnCl_2$ at 26ºC to mid exponential phase (OD_{600} of 0.3-0.5) or at 37ºC to 3 hours after the onset of stationary phase. The strains contained a *flgM*Δ80 mutation that upregulated autolysins, reducing cell chaining for single cell analysis in the flow cytometer (S. Biller, personal communication). At each timepoint, a 5 mL aliquot was removed and chloramphenicol was added to a final concentration of 200 μg/mL, then incubated at 30ºC for 6 hours to allow current rounds of DNA replication to finish while inhibiting initiation of new rounds of replication. After the 6 hour incubation, the samples were diluted to an OD_{600} of 0.1 with T-base medium and 11 mL of cold 100% ethanol (-20ºC) was added to 4 mL of diluted sample and promptly mixed to fix the cells. The fixed cells were allowed to incubate for at least 15 minutes before being pelleted by centrifugation at 8000 x *g* for 10 minutes at 4ºC. The cell pellets were washed twice with equal volumes of 200 mM of Tris-HCl at pH 7.5 and then resuspended in 2 mL of 200 mM of Tris-HCl at pH 7.5. Samples were incubated with 100 μg/mL of RNase A (Sigma) at 60ºC for 1 hour then stained with 5 μg/mL Propidium Iodide (Molecular Probes). The stained samples were incubated for 5 minutes at room temperature and 1 to 20 dilutions were made of each sample using 200 mM of Tris-HCl at pH 7.5 with 5 μg/mL Propidium Iodide. The amount of DNA per cell was measured on a BD FACSCalibur Flow Cytometer (BD Biosciences) for 10,000 cells, thus indicating the number of origins of replication at the time of chloramphenicol treatment for the population.

DNA microarrays and statistical analysis

DNA microarray slides consisting of >99% of the annotated protein coding sequences in *B. subtilis* were prepared by spotting onto CMT-GAPS slides (Corning) as described in Britton *et al.* (2002). JH642 (*sda*$^+$) and BB668 (Δ*sda*) samples were grown at 37ºC in LB or LB supplemented with 100 μM $MnCl_2$ to mid exponential phase (OD_{600} of 0.3-0.5), T_0 (the onset of stationary phase), and T_3 (3 hours after the onset of stationary phase) for RNA extraction for use in the DNA microarrays. Three biological replicates were collected for each sample at each timepoint. Samples were immediately mixed with an equal volume of cold methanol at -20ºC and kept on ice for 2 minutes before centrifugation for 5 minutes at 4ºC. Cell pellets were stored at -80ºC until RNA extraction. RNA was isolated using RNeasy mini kits (Qiagen), treating with DNase on the column as described in the manufacturer's protocol to remove genomic DNA. The quality of the RNA was assessed by running approximately 2 μg of RNA on a 1% agarose gel and visualizing the 23S and 16S bands. Reference RNA was generated by pooling RNA from all samples.

Labeled cDNA was generated from 10 μg of RNA from samples or the reference pool as described in Wall *et al.* (10), with sample cDNA labeled with Cy5 and reference cDNA labeled with Cy3. The labeled reference cDNA was pooled and aliquots prepared for each hybridization (aliquots were stored at -80ºC). Hybridizations were performed essentially as described previously (10). The array slides were scanned using an Agilent DNA Microarray Scanner (Agilent) and images were processed and analyzed using GenePix 3.0 software (Axon Instruments, Inc.).

For each of the 36 arrays, raw data from GenePix file were background corrected by fitting a normexp model (5) to remove non-target hybridization signal and normalized using loess method

to remove systematic intensity-dependent bias. To identify the genotype and manganese effect at each time point, we fitted a two-way factorial model for each gene:

$$y_{ijk} = \mu + \alpha_i + \beta_j + \gamma_{ij} + \varepsilon_{ijk},$$

where y_{ijk} is the gene expression under condition (α_i, β_j), μ is the base line expression level, α_i is the gene expression response to genotype i (1: wild type; 2: mutant), β_j is the gene expression response to manganese state i (1: +Mn(II); 2: -Mn(II)), γ_{ij} is the genotype-dependent gene expression response to manganese state, and ε_{ijk} is a Gaussian error. From the model, we estimated the main effects of manganese, genotype and interaction at each timepoints and computed their significance using moderated t-statistic. The estimated effects were then tested across time using F-statistic to check if they changed over time. All the model fittings and statistical tests were carried out in Bioconductor package LIMMA (3, 7). For all statistical tests involved, false discovery rate is estimated by converting p-values into q-values according to ref. (8). Relative differences in gene expression for several regulons and other groups of genes are shown in Tables S3-S7 (provided in the same file as the supplementary materials and methods, Figs. S1, and Tables S1-S2). Relative differences in gene expression for all regulons (for which we have annotations based on DBTBS and other references) are listed in Table S8, provided as a separate PDF file. The microarray data and statistical analysis are provided as an Excel file (Table S9), and the data will be deposited in the Stanford Microarray Database.

Plasmid and strain construction

The plasmids used in this study are listed in Table S1 and were constructed by amplification of genomic DNA by PCR then digestion and ligation of the insert and vector plasmid. The specific oligonucleotides used to amplify the insert as well as the vector plasmid identity and

enzymes used for each plasmid constructed are detailed in Table S1. Oligonucleotide sequences used in this study are listed in Table S2.

The following strains were generated through plasmid integration by double crossover at either *amyE* or thrC: AM48 (*amyE*), BB424 (*amyE*), KM81 (*amyE*), KM96 (*amyE*), SH350 (*thrC*), SH507 (*amyE*), SH517 (*amyE*), and SH536 (*amyE*). The strain containing *flgM*Δ80 and Δ*sda* (SH455) was constructed in several steps due to the fact that both mutations do not contain selectable markers. First, an *aroD*::*erm* deletion allele was created using long flanking homology PCR (9) with the oligonucleotides OSH78, OSH79, OSH99, OSH100, OSH101, and OSH102, and integrating the resulting DNA fragment into the chromosome of BB1185 (*flgM*Δ80). By transformation, *sda* is approximately 95% linked to *aroD* (2, 6). The Δ*sda* allele was moved into the *flgM*Δ80 background by transforming SH430 with genomic DNA from BB668 (Δ*sda*) and selecting for *aroD*$^+$ on agar plates as described in reference (6). The presence of the Δ*sda* allele was confirmed by PCR analysis of the locus using oligonucleotides OBB29 and OBB40.

References

1. **Antoniewski, C., B. Savelli, and P. Stragier.** 1990. The *spoIIJ* gene, which regulates early developmental steps in *Bacillus subtilis*, belongs to a class of environmentally responsive genes. J. Bacteriol. **172:**86-93.
2. **Burkholder, W. F., I. Kurtser, and A. D. Grossman.** 2001. Replication initiation proteins regulate a developmental checkpoint in *Bacillus subtilis*. Cell **104:**269-79.
3. **Gentleman, R. C., V. J. Carey, D. M. Bates, B. Bolstad, M. Dettling, S. Dudoit, B. Ellis, L. Gautier, Y. Ge, J. Gentry, K. Hornik, T. Hothorn, W. Huber, S. Iacus, R. Irizarry, F. Leisch, C. Li, M. Maechler, A. J. Rossini, G. Sawitzki, C. Smith, G. Smyth, L. Tierney, J. Y. Yang, and J. Zhang.** 2004. Bioconductor: open software development for computational biology and bioinformatics. Genome Biol **5:**R80.
4. **Guerout-Fleury, A. M., N. Frandsen, and P. Stragier.** 1996. Plasmids for ectopic integration in *Bacillus subtilis*. Gene **180:**57-61.
5. **Ritchie, M. E., J. Silver, A. Oshlack, M. Holmes, D. Diyagama, A. Holloway, and G. K. Smyth.** 2007. A comparison of background correction methods for two-colour microarrays. Bioinformatics **23:**2700-7.
6. **Ruvolo, M. V., K. E. Mach, and W. F. Burkholder.** 2006. Proteolysis of the replication checkpoint protein Sda is necessary for the efficient initiation of sporulation after transient replication stress in *Bacillus subtilis*. Mol. Microbiol. **60:**1490-508.
7. **Smyth, G. K.** 2004. Linear models and empirical bayes methods for assessing differential expression in microarray experiments. Stat Appl Genet Mol Biol **3:**Article3.
8. **Storey, J. D., and R. Tibshirani.** 2003. Statistical significance for genomewide studies. Proc Natl Acad Sci U S A **100:**9440-5.
9. **Wach, A.** 1996. PCR-synthesis of marker cassettes with long flanking homology regions for gene disruptions in *S. cerevisiae*. Yeast **12:**259-65.
10. **Wall, T., K. Bath, R. A. Britton, H. Jonsson, J. Versalovic, and S. Roos.** 2007. The early response to acid shock in *Lactobacillus reuteri* involves the ClpL chaperone and a putative cell wall-altering esterase. Appl. Environ. Microbiol. **73:**3924-35.

Figure legends

Fig. S1. Sporulation-specific gene expression is induced when cells enter stationary phase in LB supplemented with at least 1 μM $MgCl_2$.

Cells were grown in LB medium at 37ºC to an OD_{600} of 0.3-0.5 and diluted back to an OD_{600} of 0.02 into fresh, prewarmed LB medium or LB medium supplemented with 0.1, 1, 10, or 100 μM $MnCl_2$ (as indicated) and then grown until 3 hours after exit from exponential growth. Sporulation-specific gene expression was monitored using a *lacZ* transcriptional fusion to *spoIIE*. Symbols: squares, 0 μM Mn(II); diamonds, 0.1 μM Mn(II); triangles, 1 μM Mn(II); circles, 10 μM Mn(II); x, 100 μM Mn(II). Strains: BB825 (*sda*$^+$ *amyE*::P_{spoIIE}-*lacZ*); diamonds, BB827 (Δ*sda amyE*::P_{spoIIE}-*lacZ*).

Fig. S2. Supplementation of LB medium with L-malate had little or no effect on sporulation specific gene expression.

Cells were grown in LB medium at 37ºC to an OD_{600} of 0.3-0.5 and diluted back to an OD_{600} of 0.02 into fresh, prewarmed LB medium or LB medium supplemented with 15 mM L-malate, 15 mM L-malate and 15 mM KCl, 15 mM L-malate and 100 μM $MnCl_2$, or 100 μM $MnCl_2$ (as indicated) and then grown until 4.5 hours after exit from exponential growth. Sporulation-specific gene expression was monitored using a *lacZ* transcriptional fusion to *spoIIE*. Symbols: squares, LB; diamonds, LB with 15 mM L-malate; triangles, LB with 15 mM L-malate and 15 mM KCl; circles, LB with 15 mM L-malate and 100 μM Mn(II); x, LB with 100 μM Mn(II). Strains: BB825 (*sda*$^+$ *amyE*::P_{spoIIE}-*lacZ*); diamonds, BB827 (Δ*sda amyE*::P_{spoIIE}-*lacZ*).

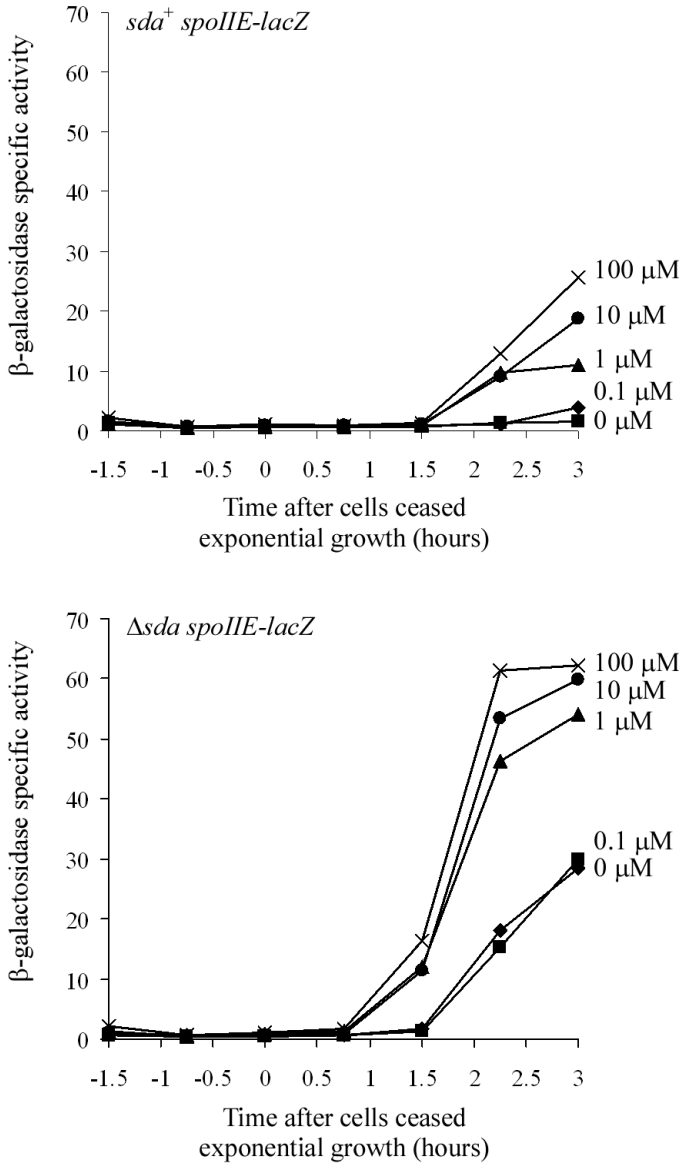
sda+ spoIIE-lacZ
β-galactosidase specific activity
70
60
50
40
30
20
10
0
-1.5
-1
-0.5
0
0.5
1
1.5
2
2.5
3
Time after cells ceased
exponential growth (hours)
100 μM
10 μM
1 μM
0.1 μM
0 μM
Δsda spoIIE-lacZ
β-galactosidase specific activity
Time after cells ceased
exponential growth (hours)
100 μM
10 μM
1 μM
0.1 μM
0 μM

Figure S1

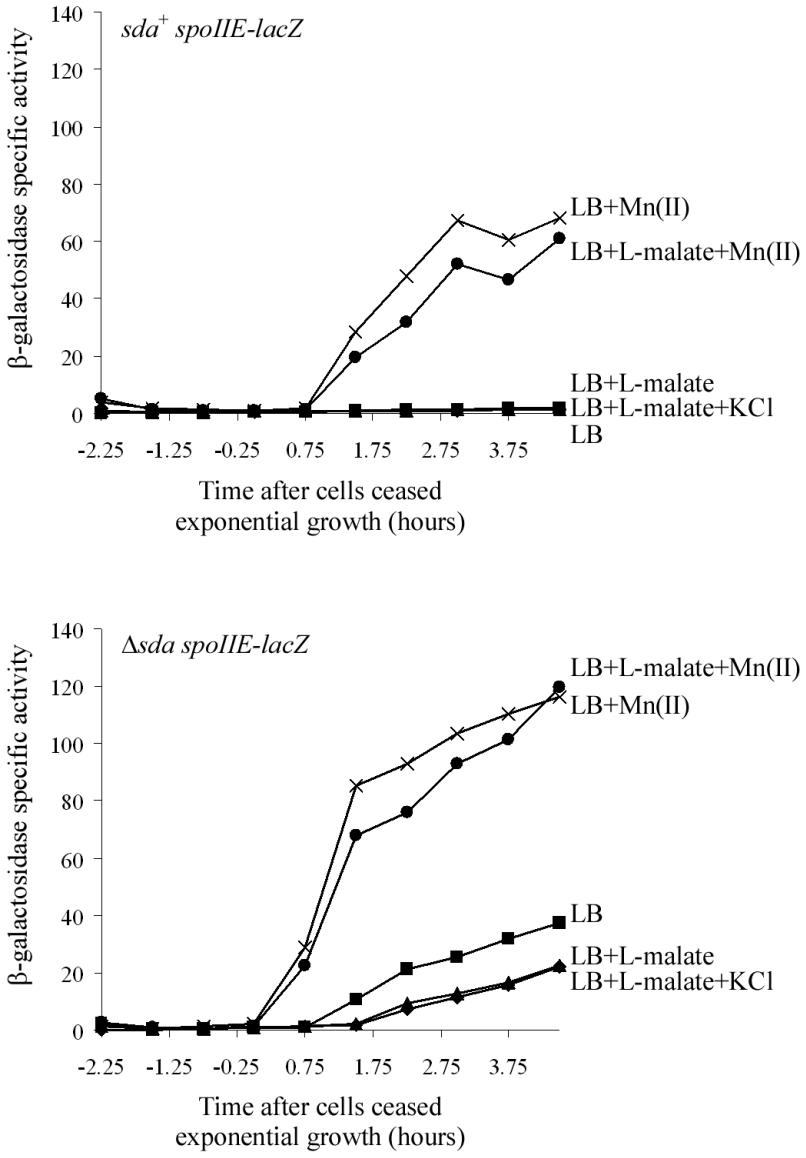
sda+ spoIIE-lacZ
β-galactosidase specific activity
140
120
100
80
60
40
20
0
-2.25
-1.25
-0.25
0.75
1.75
2.75
3.75
Time after cells ceased exponential growth (hours)
LB+Mn(II)
LB+L-malate+Mn(II)
LB+L-malate
LB+L-malate+KCl
LB
Δsda spoIIE-lacZ
β-galactosidase specific activity
Time after cells ceased exponential growth (hours)
LB+L-malate+Mn(II)
LB+Mn(II)
LB
LB+L-malate
LB+L-malate+KCl

Figure S2

Table S1. Plasmids used in this study.

Plasmid	Description	Source
pAM30	pDG1661 derived plasmid expressing P_{yneA}-*lacZ* at *amyE*. The promoter for *yneA* was amplified from JH642 by PCR using oligonucleotides OAM49 and OAM50 and ligated into pDG1661 following digestion of insert and plasmid with EcoRI and HindIII.	Burkholder lab (Allison Mo)
pBB73	pDG268 derived plasmid expressing P_{ywlC}-*lacZ* at *amyE*. The promoter for *ywlC* was amplified from JH642 by PCR using oligonucleotides OBB4 and OBB5 and ligated into pDG268 following digestion of insert and plasmid with EcoRI and BamHI.	
pBB153	pDG268 derived plasmid expressing P_{dnaA}-*lacZ* at *amyE*. The promoter for *dnaA* was amplified from JH642 by PCR using oligonucleotides OBB55 and OBB56 and ligated into pDG268 following digestion of insert and plasmid with HindIII and BamHI.	
pBB159	pDG268 derived plasmid expressing P_{sda}-*lacZ* at *amyE*. The promoter for *sda* was amplified from JH642 by PCR using oligonucleotides OBB61 and OBB65 and ligated into pDG268 following digestion of insert and plasmid with EcoRI and BamHI.	
pDG268	*amyE*::(*lacZ cat*); Amp^R	(1)
pDG1661	*Spc amyE*::(*lacZ cat*); Amp^R	(4)
pDG1663	*Spc thrC*::(*lacZ erm*); Amp^R	(4)
pDG1731	*Erm amyE* integration plasmid with *spc* marker; Amp^R	(4)
pEA18	*Spc amyE*::(P_{xylA}-*spoVG-gfp xylR cat*); Amp^R	Esther Angert
pKM32	pDG1731 derived plasmid with *gfp* inserted at *amyE*. The sequence for *gfp* was amplified from pEA18 by PCR using oligonucleotides OKM7 and OKM8 and ligated into pDG1731 following digestion of insert with BglII and BamHI and plasmid with BamHI.	Burkholder lab (Kathleen Mach)

pKM36	pKM32 derived plasmid expressing P_{spoIIE}-*gfp* at *amyE*. The promoter for *spoIIE* was amplified from JH642 by PCR using oligonucleotides OBB81 and OBB82 and ligated into pKM32 following digestion of insert and plasmid with EcoRI and BamHI.	Burkholder lab (Kathleen Mach)
pSB220	pDG1663 derived plasmid expressing P_{tagC}-*lacZ* at *thrC*. The promoter for *tagC* was amplified from JH642 by PCR using oligonucleotides OBB167 and OBB168 and ligated into pDG1663 following digestion of insert and plasmid with EcoRI and BamHI.	Burkholder lab (Steven Biller)
pSH53	pDG1661 derived plasmid expressing P_{katA}-*lacZ* at *amyE*. The promoter for *katA* was amplified from JH642 by PCR using oligonucleotides OSH84 and OSH85 and ligated into pDG1661 following digestion of insert and plasmid with EcoRI and BamHI.	
pSH57	pKM32 derived plasmid expressing P_{katA}-*gfp* at *amyE*. The promoter for *katA* was amplified from JH642 by PCR using oligonucleotides OSH84 and OSH85 and ligated into pKM32 following digestion of insert and plasmid with EcoRI and BamHI.	

All plasmids replicate in *E. coli* from pBR322-derived origins of replication. Amp^R confers ampicillin resistance in *E. coli.*

Table S2. Oligonucleotides used in this study.

Primer	Sequence
OAM49	5'-gcgggatccgaattcttttcgcacctcaaaacgtcg-3'
OAM50	5'-gcgaagcttaacctccaacaggaatgtttg-3'
OBB4	5'-cccggatcccacgccccgctttttttagcc-3'
OBB5	5'-ggaattcgcgtctggataagtgc-3'
OBB29	5'-ggcggatccgtcgaaaaaaatcgaacttgcg-3'
OBB40	5'-ctgaaaatagtagtaaagcgcgcagc-3'
OBB55	5'-gcgaagcttatttgcccctaaaatcacgc-3'
OBB56	5'-gcgggatcctttttcttagaaaatggcg-3'
OBB61	5'-gcgggatcccatttcggtggctttgaaataag-3'
OBB65	5'-ggcgaattcgtcgaaaaaaatcgaacttgcg-3'
OBB81	5'-gcggaattccgtacgggtcatcctaacaaatcg-3'
OBB82	5'-gcgggatccttcgttgcctgtcattatagcg-3'
OBB167	5'-gtattctgatgggaattcaagc-3'
OBB168	5'-gcgggatccacggttttgtctgctacacg-3'
OKM7	5'-cgggatccgggaaaaggtggtgaac-3'
OKM8	5'-gaagatcttatttgtatagttcatccatgcc-3'
OSH78	5'-gatcctaataaatttaaatatcaaaaag-3'
OSH79	5'-ctttaactctggcaaccctc-3'
OSH84	5'-gcggaattcgccaaccccgccttcaaaaaaaac-3'
OSH85	5'-gcgggatccgcgccccagctagttgtcag-3'
OSH99	5'-ggttgtttgtatcgggtgcggag-3'
OSH100	5'-ctttttgatatttaaatttattaggatccagctttttcatacacctctcccc-3'
OSH101	5'-gagggttgccagagttaaaggtggactggacaagagcctaata-3'
OSH102	5'-cgggcggaatttggcgtaatc-3'

Restriction sites used for cloning are underlined.

Hoover et al. (2010)

Table S3. Fold-differences in relative expression for genes in the DnaA regulon.

Numbers indicate fold-change (log10)
Brackets: Not significant; q > 0.05 or fold-change < log2 0.6 (= 1.5-fold)
No brackets: Significant; q ≤ 0.005 (asterisk) or q ≤ 0.05 (no asterisk) and fold-change ≥ log2 (0.6) (= 1.5-fold)

		Tm				T0				T3			
		Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator - Operon - Regulation		sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
DnaA	citZ-icd-mdh CcpA (-); CcpC (-); DnaA (+)												
citZ	Citrate synthase 2	[1.1]	[1.1]	[1.1]	[1.2]	[-1.3]	[-1.3]	[-1.1]	[-1.1]	[-1]	-2.3	[1.7]	[-1.4]
icd	Isocitrate dehydrogenase [NADP]	[1.2]	[-1.1]	[1]	[-1.2]	[-1.1]	[-1.5]	[1.5]	[1.1]	-2	-2.7 *	2	[1.5]
mdh	Malate dehydrogenase	[-1]	[1.2]	[-1.2]	[1.1]	[-1.6]	[-1.5]	[1.1]	[1.1]	-2.6	-3.1 *	[1.7]	[1.4]
DnaA	dhbACEBF DnaA (-) (Indirect?); Fur (-)												
dhbA	2,3-dihydro-2,3-dihydroxybenzoate	[-1.2]	[-1.3]	[1.1]	[-1]	-2 *	-2.4 *	[1.2]	[-1]	-2.5 *	-2.8 *	1.6	[1.5]
dhbC	Isochorismate synthase dhbC	[-1.1]	[-1.5]	[1.2]	[-1.2]	[-2.2]	-3.2	[1.4]	[-1.1]	[-1.2]	[1.1]	[1.3]	[1.8]
dhbE	2,3-dihydroxybenzoate-AMP ligase	[-1]	[-1.5]	[1.1]	[-1.3]	-1.8	-2.4 *	[1.2]	[-1.1]	[-1]	[1.3]	[-1.2]	[1.1]
dhbB	Isochorismatase	[-1]	[-1.4]	[1.1]	[-1.2]	-2	-2.6	[1.2]	[-1.1]	[1.1]	[1.2]	[1.1]	[1.3]
dhbF	Dimodular nonribosomal peptide	[-1.1]	[-1.3]	[1.1]	[-1.1]	[-1.4]	-1.9 *	[1.3]	[-1.1]	[-1.4]	[-1.4]	[1.5]	[1.4]
DnaA	dnaAN DnaA (-); Spo0A (-)												
dnaA	Chromosomal replication initiator	[1.5]	[1.2]	[1.1]	[-1.1]	2.1 *	1.8 *	[1.3]	[1]	-1.8 *	[-1.5]	1.6	2 *
dnaN	DNA polymerase III subunit beta	[1.1]	[1.2]	[1]	[1.1]	2	[1.6]	[1.2]	[1]	-1.9	-2.4 *	[1.6]	[1.2]
DnaA	dnaB-dnaI-ytxB DnaA (-); SigE (+)												
dnaB	Replication initiation and membrane	[-1.8]	[-1.5]	[-1.2]	[-1]	-1.9 *	-1.8 *	[1]	[1.1]	-2.8 *	-4 *	[1.3]	[-1.1]
dnaI	Primosomal protein dnaI	[-1.1]	[1.1]	[1]	[1.2]	[1.1]	[1.1]	[1.1]	[1.2]	[1]	[1.1]	[1]	[1.1]
ytxB	TVP38/TMEM64 family membrane	[-1.1]	[-1.1]	[-1.1]	[-1]	[1.1]	[1]	[-1.1]	[-1.1]	[-1.2]	[-1.1]	[-1.3]	[-1.2]

Table S3. Fold-differences in relative expression for genes in the DnaA regulon.

			Tm				T0				T3			
			Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator	Operon	Regulation	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
DnaA	fla-che	DnaA (-) (Indirect?); SigD (+); Spo0A (-)												
flgB		Flagellar basal-body rod protein flgB	[-1.1]	[1]	[1]	[1.1]	[1.1]	[-1.1]	[1.1]	[-1.1]	-1.9 *	-2.8 *	1.9	[1.3]
flgC		Flagellar basal-body rod protein flgC	[-1]	[-1]	[1.1]	[1.1]	[1.1]	[1]	[1.1]	[1]	-2	-2.7 *	2.2	[1.6]
fliE		Flagellar hook-basal body complex	[-1.4]	[-1]	[-1.2]	[1.2]	[-1.3]	[1]	[-1.2]	[1.1]	-5 *	-7.7 *	2.8 *	1.8
fliF		Flagellar M-ring protein	[-1]	[-1.1]	[1]	[-1]	[-1.1]	[-1.2]	[1]	[-1.1]	2.6 *	4.3 *	[-1.5]	[1.1]
fliG		Flagellar motor switch protein fliG	[1.1]	[-1.1]	[1.1]	[-1.1]	[1]	[-1.1]	[-1]	[-1.2]	[1.4]	[1.4]	[1]	[1]
fliH		Probable flagellar assembly protein fliH	[-1]	[-1]	[-1]	[1]	[-1.1]	[-1.1]	[1]	[-1]	-2.3 *	-1.8 *	[1.3]	[1.6]
fliI		Flagellum-specific ATP synthase	[-1.1]	[1.1]	[-1.2]	[-1]	[1.1]	[1.1]	[-1.1]	[-1.1]	-2.6 *	-2.8 *	1.6	[1.4]
fliJ		Flagellar fliJ protein	[-1]	[1]	[1]	[1.1]	[1]	[-1.1]	[1]	[-1.1]	2.8 *	7.4 *	-2.4 *	[1.1]
ylxF		FlaA locus 22.9 kDa protein	[-1.1]	[-1.3]	[-1]	[-1.2]	[1.3]	[1]	[1.4]	[1.1]	-5.1 *	-4.1 *	[1.1]	[1.4]
fliK		Probable flagellar hook-length control	[-1.1]	[1.1]	[-1.2]	[-1]	[-1.1]	[1]	[1]	[1.1]	-1.7 *	[-1.4]	[1.1]	[1.4]
ylxG		FlaA locus uncharacterized protein	[-1.1]	[1]	[-1.1]	[1]	[-1.1]	[1.2]	[-1.2]	[1.1]	-1.5	-1.8 *	2.2 *	1.9 *
flgG (flgE)		Flagellar basal-body rod protein flgG	[-1]	[-1.2]	[1.2]	[1]	[1.1]	[1.3]	[-1.2]	[-1]	-2.2 *	-2.9 *	[1.4]	[1]
fliL		Flagellar fliL protein	[1]	[-1]	[-1.1]	[-1.2]	[1.2]	[1.5]	[-1.3]	[-1]	[1.4]	2.3 *	[-1.5]	[1.1]
fliM		Flagellar motor switch protein fliM	[-1.1]	[-1.1]	[-1.2]	[-1.2]	[-1]	[1.2]	[-1.2]	[1]	[-1.3]	[1]	[1.1]	[1.4]
fliY		Flagellar motor switch phosphatase fliY	[-1.1]	[-1.3]	[1.2]	[-1]	[1.4]	[1.3]	[1.1]	[1.1]	-4.7 *	-6.6 *	2.1	[1.5]
cheY		Chemotaxis protein cheY homolog	[-1.2]	[-1.1]	[-1.1]	[-1]	[1]	[1]	[-1]	[-1]	[1.3]	[-1.1]	[1.3]	[-1]
fliZ		Flagellar biosynthetic protein fliZ	[-1]	[-1.1]	[1]	[-1]	[1.2]	[1.2]	[1.1]	[-1]	[-1.4]	-1.7	2.1	[1.7]
fliP		Flagellar biosynthetic protein fliP	[-1]	[-1]	[-1.1]	[-1.1]	[1.1]	[-1.2]	[1.4]	[1.1]	-1.6	[-1.5]	[1.3]	[1.4]
fliQ		Flagellar biosynthetic protein fliQ	[1]	[1]	[1]	[1]	[1.2]	[1.3]	[-1.1]	[-1]	[-1.2]	-1.8 *	[1.4]	[-1]
fliR		Flagellar biosynthetic protein fliR	[-1]	[-1]	[-1.3]	[-1.2]	[1.4]	[1.2]	[1.1]	[-1.1]	[1.3]	[-1.2]	[2]	[1.3]
flhB		Flagellar biosynthetic protein flhB	[-1]	[1]	[-1.1]	[-1.1]	[-1.1]	[1]	[-1.1]	[1]	[-1.1]	[1]	[1.1]	[1.3]
flhA		Flagellar biosynthesis protein flhA	[-1]	[-1]	[1]	[-1]	[-1.2]	[-1.3]	[-1]	[-1.1]	[-1.2]	[-1.3]	[1.3]	[1.1]
flhF		Flagellar biosynthesis protein flhF	[1.1]	[-1.1]	[1]	[-1.2]	[1.5]	[1.3]	[-1]	[-1.1]	-2.1	-2.1	[1]	[1]
ylxH		Uncharacterized protein ylxH	[-1.1]	[1.1]	[-1.2]	[-1.1]	[-1.1]	[1.2]	[-1.5]	[-1.2]	[-1]	[-1.2]	[1.3]	[1.1]
cheB		Chemotaxis response regulator	[1]	[-1]	[1.3]	[1.2]	[1.8]	2.1	[-1.4]	[-1.1]	[-1.3]	-1.7	[1.1]	[-1.2]
cheA		Chemotaxis protein cheA	[1]	[-1.2]	[-1.1]	[-1.3]	[1.2]	[1.1]	[1]	[-1.1]	-3.6 *	-3.5 *	[1.2]	[1.3]
cheW		Chemotaxis protein cheW	[-1.1]	[-1]	[-1.1]	[-1]	[1.3]	[1]	[1.2]	[-1]	[-1.4]	-1.9 *	1.8	[1.3]

Table S3. Fold-differences in relative expression for genes in the DnaA regulon.

			Tm				T0				T3			
			Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator	Operon	Regulation	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
cheC		CheY-P phosphatase cheC	[1.1]	[1.1]	[-1.4]	[-1.5]	[1.3]	[1.9]	[-1.4]	[-1]	-2	-2.7 *	[1.1]	[-1.2]
cheD		Chemoreceptor glutamine deamidase	[-1.1]	[-1.1]	[-1.1]	[-1.1]	[1.1]	[1.2]	[1]	[1.1]	-2.3 *	-2.1 *	[1.1]	[1.2]
sigD		RNA polymerase sigma-D factor	[1]	[1.1]	[-1.1]	[-1]	[1.4]	[1.3]	[1]	[-1.1]	[-1.3]	[-1.3]	[1.1]	[1.1]
swrB (ylxL)		Swarming motility protein swrB	[-1]	[-1.2]	[1.1]	[-1]	[-1]	[1]	[-1]	[1]	[1.2]	2 *	-1.8	[-1.1]
DnaA	kdgRKAT	CcpA (-); DnaA (-); KdgR (-)												
kdgR		HTH-type transcriptional regulator	[-1]	[-1]	[-1]	[1]	[1.1]	[-1.1]	[1.1]	[-1.1]	[1.2]	[1.4]	[-1.2]	[-1]
kdgK		2-dehydro-3-deoxygluconokinase	[-1]	[1.1]	[-1.2]	[-1]	[-1.6]	[-1.4]	[-1]	[1.1]	[-1.3]	[-1.1]	[-1]	[1.1]
kdgA		KHG/KDPG aldolase [Includes: 4-	[1.2]	[1.3]	[-1.3]	[-1.2]	[1.2]	[1.2]	[-1.1]	[-1.1]	[1.3]	2.1 *	[-1.5]	[1.1]
kdgT		2-keto-3-deoxygluconate permease	[-1.1]	[-1.1]	[-1.1]	[-1.1]	[-1.3]	[-1.1]	[-1.3]	[-1.1]	[-1.1]	[-1.2]	[-1]	[-1.1]
DnaA	lytABC	DnaA (-); LytR (-); SigD (+); YvrH (-)												
lytA		Membrane-bound protein lytA	[1]	[-1.1]	[1]	[-1.1]	[1.1]	[1.1]	[-1]	[-1]	[-1.3]	-1.9 *	1.8	[1.2]
lytB		Amidase enhancer	[-1]	[-1.4]	[1.3]	[-1.1]	[1]	[-1]	[1.1]	[1]	-3 *	-4.7 *	[2]	[1.3]
lytC		N-acetylmuramoyl-L-alanine amidase	[0]	[0]	[0]	[0]	[0]	[0]	[0]	[0]	[0]	[0]	[0]	[0]
DnaA	mraZ-mraW-ftsL-pbpB	DnaA (-) (Indirect?)												
mraZ (yllB)		Protein mraZ	[-1.5]	[-1.2]	[-1.2]	[-1]	[-1.2]	[1.3]	[-1.6]	[-1.1]	1.8	[1.3]	[1.4]	[1.1]
mraW (ylxA)		S-adenosyl-L-methionine-dependent	[-1.1]	[-1.1]	[1.1]	[1.1]	[-1.1]	[-1]	[-1.1]	[-1]	[1.3]	[1.2]	1.5	[1.4]
ftsL		Cell division protein ftsL homolog	[-1]	[-1]	[-1.2]	[-1.2]	[1.1]	[1.4]	[-1.1]	[1.2]	[1]	[1]	[1.3]	[1.4]
pbpB		Penicillin-binding protein 2B	[1.2]	[-1]	[1.1]	[-1]	[1.3]	1.8 *	[-1.3]	[1.1]	[1.3]	[1.3]	[1.3]	[1.3]
DnaA	nrdIEF-ymaB	DnaA (+) (Indirect?); ResD (+)												
nrdI (ymaA)		Protein nrdI	[-1.1]	[-1]	[-1.2]	[-1.1]	[1.2]	[1.1]	[1.2]	[1.2]	-2.1 *	-2.2 *	[1.1]	[1]
nrdE		Ribonucleoside-diphosphate reductase	[1]	[1.1]	[-1.2]	[-1.1]	[1.3]	[1.2]	[1]	[1]	-2 *	-2.2 *	[-1]	[-1.1]
nrdF		Ribonucleoside-diphosphate reductase	[-1.1]	[1.1]	[-1.1]	[1.1]	[1.1]	[1.3]	[1.1]	[1.3]	[-1.4]	[-1.4]	[1.1]	[1.1]
ymaB		Uncharacterized protein ymaB	[-1]	[1.1]	[-1.1]	[-1]	[1.3]	[-1.3]	[1.2]	[-1.4]	2.6 *	1.8	[1]	[-1.5]

Table S3. Fold-differences in relative expression for genes in the DnaA regulon.

			Tm				T0				T3			
			Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator	Operon	Regulation	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
DnaA	pyrRPBCAAABKDFE	DnaA (-); PurR (-); PyrR (-); PyrR (-); PyrR (-)												
pyrR		Bifunctional protein pyrR [Includes:	[1.1]	[1.1]	[-1.2]	[-1.1]	[1.2]	[1.3]	[-1.1]	[1]	[1]	[1.3]	[-1.2]	[1.1]
pyrP		Uracil permease	[1.2]	[1.6]	[-1.4]	[-1]	[1]	1.7	[-1.3]	[1.2]	[1.4]	[1.3]	[1.3]	[1.1]
pyrB		Aspartate carbamoyltransferase	[1.1]	[1.2]	[-1.1]	[-1.1]	[1.1]	[1.5]	[-1.3]	[1.1]	[-1.4]	[-1.4]	[1.2]	[1.2]
pyrC		Dihydroorotase	[1.5]	[1.4]	[1.1]	[-1]	[1.4]	[1.7]	[1.1]	[1.3]	[-1.4]	[-1.2]	[1.2]	[1.4]
pyrAA		Carbamoyl-phosphate synthase	[1.2]	[1]	[1.1]	[-1.1]	1.8	2	[-1.1]	[1]	-1.6	[-1.5]	[1.1]	[1.2]
pyrAB		Carbamoyl-phosphate synthase	[1.6]	[1.7]	[-1.4]	[-1.3]	[1.4]	[1.5]	[-1]	[1.1]	[-1.5]	[-1.1]	[1]	[1.4]
pyrK		Dihydroorotate dehydrogenase	[1.2]	[1.3]	[-1.1]	[-1]	[1.5]	[1.4]	[1.1]	[1]	[-1.3]	[-1.2]	[1.4]	[1.4]
pyrD		Dihydroorotate dehydrogenase,	[1.3]	[1.2]	[1.3]	[1.2]	[1.4]	[1.5]	[1.1]	[1.3]	[-1.3]	[-1.3]	[1.1]	[1.1]
pyrF		Orotidine 5'-phosphate decarboxylase	[-1]	[-1.1]	[1.1]	[1]	[1.1]	[-1]	[1.3]	[1.2]	-2.1 *	-1.9 *	[1]	[1.1]
pyrE		Orotate phosphoribosyltransferase	[-1]	[1.1]	[-1]	[1.1]	[1.1]	[1.2]	[1.1]	[1.2]	-2.2	-2.1	[1.1]	[1.2]
DnaA	rocABC	AhrC (+); DnaA (+) (Indirect?); RocR (+); SigL (+)												
rocA		1-pyrroline-5-carboxylate	[-1.2]	[-1.1]	[-1.1]	[1]	2.8 *	3.3 *	[-1.3]	[-1.1]	-4.3 *	-4 *	[1]	[1.1]
rocB		Protein rocB	[-1.1]	[-1.2]	[1.1]	[-1]	2	2.3 *	[-1.2]	[-1.1]	[-1.3]	-2 *	1.8	[1.1]
rocC		Amino-acid permease rocC	[1.4]	[1.1]	[1.1]	[-1.2]	[1.2]	2.1 *	[-1.3]	[1.5]	[1.2]	[-1.3]	[1.2]	[-1.3]
DnaA	rocDEF	AhrC (+); DnaA (+) (Indirect?); RocR (+); SigL (+); Spo0A (-)												
rocD		Ornithine aminotransferase	[-1.2]	[-1.1]	[1]	[1.2]	2.8 *	2.3 *	[1.3]	[1.1]	-2.9 *	-2.4 *	[1.6]	1.8
rocE		Amino-acid permease rocE	[-1.2]	[1]	[1.6]	[2]	4.4 *	3.4	[1.1]	[-1.2]	-6.6 *	-12.7 *	[1.8]	[-1]
rocF		Arginase	[-1]	[-1.2]	[1.4]	[1.2]	4 *	2.7	[1.2]	[-1.2]	-4.2 *	-4.6 *	[1.3]	[1.2]
DnaA	sda	DnaA (+); LexA (-)												
sda		Sporulation inhibitor sda	[-1.1]	[-1.1]	[1.2]	[1.2]	[-1.1]	-1.6	[2]	[1.3]	[-1.1]	[-1]	2 *	2.1 *
DnaA	soj-spo0J	DnaA (-); Spo0A (-)												
soj		Sporulation initiation inhibitor protein	[1]	[-1]	[-1]	[-1.1]	[-1]	[-1.4]	[1.4]	[1]	[-1.3]	[-1]	[1.1]	[1.3]
spo0J		Stage 0 sporulation protein J	[1.1]	[-1.1]	[1.1]	[-1]	[1]	[-1.4]	[1.4]	[1]	2.4 *	3.2 *	-1.6	[-1.2]
DnaA	sunA	DnaA (-) (Indirect?); Rok (-); YvrH (+)												
sunA		SPBc2 prophage-derived lantibiotic	[-1.2]	[-1.2]	[1.1]	[1.1]	[-1.1]	[-1.2]	[1.2]	[1.2]	[1.1]	[1.3]	[1.2]	[1.4]

Table S3. Fold-differences in relative expression for genes in the DnaA regulon.

			Tm				T0				T3			
			Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator	Operon	Regulation	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
DnaA	thdF-gidAB-yyaA	ComK (+); DnaA (-)												
mnmE (thdF)	tRNA modification GTPase mnmE		[1]	[1.1]	[-1.1]	[-1.1]	[1]	[-1]	[1.1]	[1.1]	[1]	[1]	[1.4]	[1.4]
mnmG (gidA)	tRNA uridine 5-		[1]	[-1.1]	[1]	[-1.1]	-1.8 *	-1.6	[-1]	[1]	-1.6	-1.5	[1.3]	[1.3]
rsmG (gidB)	Ribosomal RNA small subunit		[1.1]	[1.2]	[-1.1]	[1.1]	-1.8	[-1.6]	[1.1]	[1.2]	[-1.4]	[-1.2]	[1.1]	[1.3]
noc (yyaA)	Nucleoid occlusion protein		[1.3]	[1]	[1]	[-1.2]	[1.2]	[1.4]	[-1.1]	[1.1]	[1.4]	[-1.2]	[1.5]	[-1.1]
DnaA	yclNOPQ	DnaA (-); Fur (-)												
yclN	Uncharacterized ABC transporter		[-1]	[1.2]	[-1.4]	[-1.2]	[-1.5]	[-1.2]	[-1.3]	[-1]	-1.6	[-1.2]	[1.6]	2
yclO	Uncharacterized ABC transporter		[-1]	[1.2]	[-1.8]	[-1.5]	[1.1]	[1.1]	[-1.2]	[-1.1]	[-1.3]	[1.3]	[1.3]	2.1
yclP	Uncharacterized ABC transporter ATP-		[-1]	[-1.2]	[-1.2]	[-1.3]	[-1.3]	[-1.2]	[-1]	[1]	[-1.2]	[-1.1]	[1.6]	[1.7]
yclQ	Uncharacterized ABC transporter		[-1]	[-1.2]	[-1]	[-1.1]	[-1.3]	[-1.6]	[1.3]	[1.1]	[-1.2]	[1]	[1.8]	2.1
DnaA	ykuNOP	DnaA (-); Fur (-)												
ykuN	Probable flavodoxin-1		[-1.1]	[-1.2]	[1]	[-1.1]	[-1.8]	-1.9	[-1.1]	[-1.2]	[1.5]	[1.6]	[1.4]	[1.4]
ykuO	Uncharacterized protein ykuO		[-1.3]	[-1.8]	[1.2]	[-1.2]	[-1.9]	-3.5 *	[1.6]	[-1.1]	[-1.3]	[-1.1]	[1.2]	[1.5]
ykuP	Probable flavodoxin-2		[-1.3]	[-1.3]	[-1.3]	[-1.3]	-2.5 *	-2.2 *	[-1.1]	[-1]	[-1.4]	[1.1]	[1.1]	[1.6]
DnaA	ypvA	DnaA (+)												
ypvA	Probable ATP-dependent helicase		[-1]	[1.1]	[-1.1]	[-1]	[-1]	[-1.1]	[1.1]	[1.1]	[1.1]	1.8 *	-1.6	[-1]
DnaA	yqeGH-aroD-yqeI-nadD-yqeK	DnaA (-)												
yqeG	Uncharacterized protein yqeG		[1.2]	[1.2]	[-1.6]	[-1.6]	[1.2]	2	[-2]	[-1.2]	[-1.6]	-1.8	[-1]	[-1.1]
yqeH	Uncharacterized protein yqeH		[-1.1]	[-1]	[-1.5]	[-1.4]	[1.2]	2	[-2.2]	[-1.3]	[-1.7]	[-1.4]	[-1.2]	[1]
aroD	Shikimate dehydrogenase		[-1.1]	[-1]	[-1.3]	[-1.2]	[1.3]	[1.4]	[-1.3]	[-1.3]	-1.9 *	-1.8 *	[1.1]	[1.1]
yqeI	Probable RNA-binding protein yqeI		[1.1]	[1.1]	[-1.3]	[-1.4]	[1.1]	[1.6]	[-1.3]	[1.1]	[-1.1]	[1.2]	[-1.1]	[1.1]
nadD (yqeJ)	Nicotinate-nucleotide		[1.1]	[1]	[-1.1]	[-1.2]	[1.3]	[1.4]	[-1.3]	[-1.2]	[-1.3]	[-1.1]	[-1.1]	[1.1]
yqeK	Uncharacterized protein yqeK		[1]	[-1]	[-1.1]	[-1.1]	[1.1]	[1.2]	[-1.3]	[-1.2]	[-1.1]	1.6	[-1.6]	[1.1]

Table S3. Fold-differences in relative expression for genes in the DnaA regulon.

			Tm				T0				T3			
			Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator	Operon	Regulation	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
DnaA	yurY-yurX-csd-nifU-yurU	DnaA (+)												
sufC (yurY)	sulfur mobilizing ABC protein, ATPase		[-1.5]	[-1.5]	[1.1]	[1.1]	-2.7 *	-3.1 *	[1.1]	[-1.1]	-2 *	-2.1 *	[1]	[-1]
sufD (yurX)	FeS cluster assembly protein sufD		[-1.6]	[-1.6]	[1.1]	[1.1]	-2	-3.7 *	[1.4]	[-1.3]	-3.2 *	-2.8 *	[-1.1]	[1]
csd	Probable cysteine desulfurase		[-1.1]	[-1.5]	[1.2]	[-1.1]	-1.9	-2.6 *	[1.3]	[-1]	[-1.5]	[-1.3]	[-1.1]	[1]
nifU (yurV)	NifU-like protein		[-1.7]	[-1.5]	[1.1]	[1.3]	-2.5 *	-4 *	[1.2]	[-1.3]	-2.7 *	-3.4 *	[1]	[-1.2]
sufB (yurU)	FeS cluster assembly protein sufB		[-1.6]	[-1.6]	[1.4]	[1.5]	-2.4 *	-3 *	[1.1]	[-1.1]	-2.7 *	-3.4 *	[-1.1]	[-1.4]
DnaA	yvdCD	DnaA (+) (Indirect?)												
yvdC	Uncharacterized protein yvdC		[1]	[-1.1]	[-1]	[-1.2]	[-1.2]	[-1.1]	[-1]	[1]	-1.6	-1.7	[1.4]	[1.3]
yvdD	UPF0717 protein yvdD		[-1]	[-1]	[-1]	[-1]	[-1]	[-1.2]	[1.1]	[-1]	[-1.1]	[-1.1]	[1.2]	[1.2]
DnaA	ywlC	DnaA (-)												
ywlC	Uncharacterized protein ywlC		[-1.1]	[-1.2]	[1.1]	[-1.1]	[-1]	[-1.4]	[1.3]	[-1.1]	[1.1]	[1.4]	[-1.1]	[1.2]
DnaA	ywzC-ywfO-ywgA	DnaA (+)												
ywzC	UPF0741 protein ywzC		[1.2]	[1.2]	[-1.1]	[-1.1]	[1.2]	[1.1]	[1.2]	[1.1]	[1.1]	[-1]	[1.4]	[1.2]
ywfO	Uncharacterized protein ywfO		[1.3]	[1.4]	[-1.2]	[-1.1]	[-1]	[-1.2]	[1]	[-1.2]	-2	-2 *	[1.4]	[1.4]
ywgA	Uncharacterized protein ywgA		[1.1]	[1.2]	[-1.2]	[-1.1]	[1]	[-1.3]	[1.4]	[1]	-2.7 *	-2.3 *	[1.2]	[1.4]
DnaA	yydA	DnaA (-) (weak)												
rlmH (yydA)	Ribosomal RNA large subunit		[1]	[-1]	[1]	[-1.1]	[1]	[-1.1]	[1.2]	[1]	[1.2]	1.6 *	[1.1]	[1.5]

Numbers indicate fold-change (log10)
Brackets: Not significant; q > 0.05 or fold-change < log2 0.6 (= 1.5-fold)
No brackets: Significant; q ≤ 0.005 (asterisk) or q ≤ 0.05 (no asterisk)
and fold-change ≥ log2 (0.6) (= 1.5-fold)

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Table S4. Fold-differences in relative expression for genes in the Fur regulon.

Numbers indicate fold-change (log10)
Brackets: Not significant; q > 0.05 or fold-change < log2 0.6 (= 1.5-fold)
No brackets: Significant; q ≤ 0.005 (asterisk) or q ≤ 0.05 (no asterisk) and fold-change ≥ log2 (0.6) (= 1.5-fold)

		Tm				T0				T3			
		Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator - Operon - Regulation		sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
Fur	dhbACEBF DnaA (-) (Indirect?); Fur (-)												
dhbA	2,3-dihydro-2,3-dihydroxybenzoate	[-1.2]	[-1.3]	[1.1]	[-1]	-2 *	-2.4 *	[1.2]	[-1]	-2.5 *	-2.8 *	1.6	[1.5]
dhbC	Isochorismate synthase dhbC	[-1.1]	[-1.5]	[1.2]	[-1.2]	[-2.2]	-3.2	[1.4]	[-1.1]	[-1.2]	[1.1]	[1.3]	[1.8]
dhbE	2,3-dihydroxybenzoate-AMP ligase	[-1]	[-1.5]	[1.1]	[-1.3]	-1.8	-2.4 *	[1.2]	[-1.1]	[-1]	[1.3]	[-1.2]	[1.1]
dhbB	Isochorismatase	[-1]	[-1.4]	[1.1]	[-1.2]	-2	-2.6	[1.2]	[-1.1]	[1.1]	[1.2]	[1.1]	[1.3]
dhbF	Dimodular nonribosomal peptide	[-1.1]	[-1.3]	[1.1]	[-1.1]	[-1.4]	-1.9 *	[1.3]	[-1.1]	[-1.4]	[-1.4]	[1.5]	[1.4]
Fur	feuABC-ybbA Fur (-); YbbB (+)												
feuA	Iron-uptake system-binding protein	[-1.3]	[-2.6]	[1.1]	[-1.8]	-3.3 *	-5 *	[1.4]	[-1.1]	[-1.7]	[-1.6]	[1.3]	[1.4]
feuB	Iron-uptake system permease protein	[-1.5]	[-1.2]	[-1.3]	[-1.1]	-2.3	[-2]	[-1.1]	[1]	-2.1	-2	[1.1]	[1.1]
feuC	Iron-uptake system permease protein	[-1.2]	[-1.6]	[-1.3]	[-1.7]	[-1.5]	[-1.5]	[-1.1]	[-1.1]	[-1.5]	-3 *	2.1	[1]
ybbA	Uncharacterized protein ybbA	[-1.2]	[-1.7]	[-1.2]	[-1.6]	[-1.9]	[-1.9]	[-1.1]	[-1.1]	[1.2]	2.8 *	-2.2	[1.1]
Fur	fhuD Fur (-)												
fhuD	Iron(3+)-hydroxamate-binding protein	[-1.1]	[-1.6]	[1.2]	[-1.2]	[-1.4]	-1.9	[1.3]	[-1]	-1.8	[1]	[1.4]	2.6 *
Fur	mrgC Fur (-)												
yybR	Uncharacterized HTH-type	[1.1]	[1]	[1]	[-1.1]	[-1.2]	[-1]	[-1.2]	[1]	[-1.1]	[-1.1]	[-1.2]	[-1.2]
Fur	nasBCDEF ArfM (+); Fur (-); GlnR (-); ResD (+); TnrA (+); TnrA (+); YhdE (-)												
nasB	Assimilatory nitrate reductase electron	[1.2]	[1.1]	[-1]	[-1.1]	[1.4]	[1.4]	[1]	[-1]	-1.5	-1.6	[1.3]	[1.2]
nasC	Assimilatory nitrate reductase catalytic	[1.1]	[-1.3]	[1.1]	[-1.2]	[1.2]	[1]	[1]	[-1.1]	[-1.2]	[-1.3]	[1.2]	[1.1]
nasD	Nitrite reductase [NAD(P)H]	[1]	[-1]	[1.3]	[1.2]	[1.8]	[2.3]	[-1]	[1.2]	[2.3]	3.7 *	[2]	3.2
nasE	Assimilatory nitrite reductase [NAD(P)	[-1.1]	[1]	[-1.2]	[-1.1]	[1.3]	[1.3]	[-1]	[-1.1]	[-1.1]	[1.2]	[1.1]	[1.3]
nasF	Uroporphyrinogen-III C-	[-1]	[1.1]	[-1.1]	[1.1]	[1.5]	1.8 *	[-1.2]	[1]	[-1.2]	[-1]	[-1.3]	[-1.1]
Fur	ybbB Fur (-)												
ybbB	Uncharacterized HTH-type	[1]	[-1.1]	[1.3]	[1.1]	[1.1]	[-1.1]	[1.2]	[-1]	[-1.3]	[1.2]	[-1.2]	[1.3]

Table S4. Fold-differences in relative expression for genes in the Fur regulon.

			Tm				T0				T3			
			Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator	Operon	Regulation	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
Fur	ycgT	Fur (-)												
ycgT		Ferredoxin--NADP reductase 1	[-1.2]	[-2]	[1.2]	[-1.4]	-1.7	-2.2 *	[1.2]	[1]	-1.5	[-1.2]	1.7	2.1 *
Fur	yclNOPQ	DnaA (-); Fur (-)												
yclN		Uncharacterized ABC transporter	[-1]	[1.2]	[-1.4]	[-1.2]	[-1.5]	[-1.2]	[-1.3]	[-1]	-1.6	[-1.2]	[1.6]	2
yclO		Uncharacterized ABC transporter	[-1]	[1.2]	[-1.8]	[-1.5]	[1.1]	[1.1]	[-1.2]	[-1.1]	[-1.3]	[1.3]	[1.3]	2.1
yclP		Uncharacterized ABC transporter ATP-	[-1]	[-1.2]	[-1.2]	[-1.3]	[-1.3]	[-1.2]	[-1]	[1]	[-1.2]	[-1.1]	[1.6]	[1.7]
yclQ		Uncharacterized ABC transporter	[-1]	[-1.2]	[-1]	[-1.1]	[-1.3]	[-1.6]	[1.3]	[1.1]	[-1.2]	[1]	[1.8]	2.1
Fur	ydbN	Fur (-)												
ydbN		Uncharacterized protein ydbN	[-1.1]	[-1.5]	[1.1]	[-1.2]	-3.3 *	-3.3 *	[1.2]	[1.2]	[1.6]	[1.4]	2.2	[2]
Fur	ydhU	Fur (-)												
			[1]	[-1.1]	[1]	[-1.1]	[1.1]	[1.1]	[-1]	[-1.1]	[1.2]	2 *	-1.7	[1]
Fur	yfhC	Fur (-)												
yfhC		Putative NAD(P)H nitroreductase yfhC	[-1.3]	[-1.6]	[1.1]	[-1.1]	[-1.5]	[-2]	[1.4]	[1.1]	[-1.1]	[-1.5]	[1.7]	[1.3]
Fur	yfiY	Fur (-)												
yfiY		Probable siderophore-binding	[-1.2]	[-1.2]	[1.1]	[1.1]	[-1.1]	[-1.6]	[1.5]	[1]	[-1.4]	[1.3]	[1.7]	3.2
Fur	yfiZ-yfhA	Fur (-)												
yfiZ		Probable siderophore transport system	[1]	[-1.1]	[-1.1]	[-1.2]	[-1.1]	[-1.1]	[1]	[1]	[-1.2]	[-1.4]	1.8	[1.5]
yfhA		Probable siderophore transport system	[-1.1]	[-1.1]	[1.1]	[-1]	[-1.1]	[-1.2]	[1.2]	[1]	[-1.1]	[1.2]	[-1.1]	[1.1]
Fur	yfkM	Fur (-)												
yfkM		General stress protein 18	[1.1]	[1]	[1.4]	[1.3]	[-1]	[1.2]	[-1.6]	[-1.4]	[1.2]	[1.1]	[-1.3]	[-1.4]
Fur	yfmCDEF	Fur (-)												
yfmC		Fe(3+)-citrate-binding protein yfmC	[-1]	[-1.2]	[-1.1]	[-1.3]	[-1]	[-1.5]	[1.3]	[-1.2]	[-1.5]	[1.1]	[1.4]	2.2
yfmD		Fe(3+)-citrate import system permease	[-1.3]	[-1.2]	[-1.3]	[-1.3]	[-1.1]	[1.2]	[-1.5]	[-1.1]	[-1]	[-1.1]	[-1.2]	[-1.3]
yfmE		Fe(3+)-citrate import system permease	[1.1]	[1.2]	[-1.2]	[-1.1]	[1.1]	[1.4]	[1.1]	[1.5]	[1.1]	[1.1]	[1.3]	[1.3]
yfmF		Fe(3+)-citrate import ATP-binding	[1]	[-1.2]	[-1.2]	[-1.5]	1.9 *	[1.1]	[1.8]	[1]	-3.3 *	-2.3 *	[-1]	[1.4]

Table S4. Fold-differences in relative expression for genes in the Fur regulon.

			Tm				T0				T3			
			Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator	Operon	Regulation	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
Fur	yhfQ	Fur (-)												
yhfQ		Putative ABC transporter substrate-	[-1]	[-1.1]	[-1.3]	[-1.4]	[-1.2]	[-1.7]	[1.2]	[-1.1]	[-1.5]	[1.1]	[1.6]	2.5 *
Fur	ykuNOP	DnaA (-); Fur (-)												
ykuN		Probable flavodoxin-1	[-1.1]	[-1.2]	[1]	[-1.1]	[-1.8]	-1.9	[-1.1]	[-1.2]	[1.5]	[1.6]	[1.4]	[1.4]
ykuO		Uncharacterized protein ykuO	[-1.3]	[-1.8]	[1.2]	[-1.2]	[-1.9]	-3.5 *	[1.6]	[-1.1]	[-1.3]	[-1.1]	[1.2]	[1.5]
ykuP		Probable flavodoxin-2	[-1.3]	[-1.3]	[-1.3]	[-1.3]	-2.5 *	-2.2 *	[-1.1]	[-1]	[-1.4]	[1.1]	[1.1]	[1.6]
Fur	yoaJ	Fur (-)												
yoaJ		Expansin-yoaJ	[1.1]	[-1]	[1]	[-1.1]	[-1.3]	[-1.2]	[1.2]	[1.3]	[-1.1]	[1.3]	[-1.1]	[1.2]
Fur	yuiI	Fur (-)												
besA (yuiI)		Ferri-bacillibactin esterase besA	[-1.7]	[-2.1]	[1.1]	[-1.1]	-2.4	-3.5 *	[1.3]	[-1.1]	[-1.4]	[-1.4]	2.2	2.3
Fur	yusV	Fur (-)												
yusV		Probable siderophore transport system	[-1.2]	[-1.5]	[1.1]	[-1.1]	-2.4	-2.6	[1.2]	[1.1]	[1.3]	[1.4]	[1.3]	[1.4]
Fur	ywbLMN	Fur (-); SigW (+); SigX (+)												
ywbL		Uncharacterized membrane protein	[-1.3]	[-1.3]	[-1.3]	[-1.2]	[-1.2]	[-1.4]	[1.5]	[1.2]	[-1.1]	[1]	[1.8]	2.1
ywbM		UPF0409 protein ywbM	[-1.2]	[-1.4]	[-1.1]	[-1.3]	[-1.4]	-2	[1.5]	[1]	[-1.3]	[-1.4]	2.5 *	2.4 *
ywbN		Putative peroxidase ywbN	[-1.3]	[-1.4]	[1]	[-1]	[-1.5]	-1.8	[1.1]	[-1.2]	[-1]	[-1]	[1.8]	[1.8]
Fur	ywjA	Fur (-)												
ywjA		Uncharacterized ABC transporter ATP-	[-1]	[-1.1]	[1]	[-1.1]	[-1.1]	[-1.1]	[-1.1]	[-1.1]	[1.1]	[-1.2]	[1.6]	[1.1]
Fur	yxeB	Fur (-)												
yxeB		Iron(3+)-hydroxamate-binding protein	[-1.8]	[-1.9]	[1.1]	[1.1]	[-1.6]	-2.7	[1.9]	[1.2]	-2.3	[-1]	[2]	4.5 *

Numbers indicate fold-change (log10)
Brackets: Not significant; q > 0.05 or fold-change < log2 0.6 (= 1.5-fold)
No brackets: Significant; q ≤ 0.005 (asterisk) or q ≤ 0.05 (no asterisk)
and fold-change ≥ log2 (0.6) (= 1.5-fold)

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Table S5. Operons with genes that are significantly repressed (q ≤ 0.005) at T3 in an *sda*-dependent manner in the absence of Mn(II).

Numbers indicate fold-change (log10)
Brackets: Not significant; q > 0.05 or fold-change < log2 0.6 (= 1.5-fold)
No brackets: Significant; q ≤ 0.005 (asterisk) or q ≤ 0.05 (no asterisk) and fold-change ≥ log2 (0.6) (= 1.5-fold)

		Tm				T0				T3			
		Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator - Operon - Regulation		sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
AbrB	aprE AbrB (-); DegU (+); Hpr (-); SinR (-); TenA (+)												
aprE	Subtilisin E	[-1.1]	[-1.2]	[1.4]	[1.2]	[1]	[-1.2]	[1]	[-1.2]	2.2 *	-1.7	[1.5]	-2.5 *
AbrB	skf AbrB (-); PhoP (+); Spo0A (+)												
skfA (ybcO)	Sporulation-killing factor skfA	[-1]	[-1.2]	[1.4]	[1.2]	[1.1]	[-1.2]	[1.2]	[-1.1]	[1.8]	2.5	[-1.9]	[-1.3]
skfB (ybcP)	Uncharacterized protein skfB	[-1.1]	[-1.1]	[1.1]	[1]	[-1.3]	[-1.1]	[-1.1]	[1.1]	1.9 *	[-1.2]	[1.3]	-1.7
skfC (ybcS)	Sporulation-killing factor biosynthesis	[1]	[-1.1]	[-1.1]	[-1.2]	[1.3]	[1.4]	[-1.4]	[-1.3]	3.9 *	[1.4]	[1]	-2.7 *
skfC (ybcS)	Sporulation-killing factor biosynthesis	[-1.1]	[-1.1]	[1]	[-1]	[-1.1]	[-1.1]	[1]	[-1]	2.1 *	[-1.3]	1.7 *	-1.6
skfE (ybdA)	SkfA peptide export ATP-binding	[-1]	[-1]	[1.2]	[1.2]	[-1.1]	[1.3]	[-1.9]	[-1.3]	5.6 *	[-1]	[1.7]	-3.3 *
skfF (ybdB)	Putative bacteriocin-skfA transport	[-1]	[1.3]	[-1.2]	[1.1]	[1.1]	[1.4]	[-1.2]	[1.1]	2.5 *	[-1.3]	[1.1]	-2.9 *
skfG (ybdD)	Uncharacterized protein skfG	[1]	[-1]	[1.1]	[1]	[-1.1]	[-1.2]	[-1.3]	[-1.3]	[1.2]	[-1.4]	[1.3]	[-1.3]
skfH (ybdE)	Thioredoxin-like protein skfH	[-1.4]	[-1.2]	[1.1]	[1.2]	-1.6	[-1.3]	[-1.4]	[-1.1]	3.2 *	[-1.2]	[1.1]	-3.4 *
DegU	aprE AbrB (-); DegU (+); Hpr (-); SinR (-); TenA (+)												
aprE	Subtilisin E	[-1.1]	[-1.2]	[1.4]	[1.2]	[1]	[-1.2]	[1]	[-1.2]	2.2 *	-1.7	[1.5]	-2.5 *
GerE	gerPABCDEF GerE (-); SigK (+)												
gerPA	Probable spore germination protein	[-1]	[-1.2]	[1.1]	[-1.1]	-3.1 *	-3.9 *	[1.1]	[-1.1]	3.4 *	3.1 *	-1.7	-1.9 *
gerPB	Probable spore germination protein	[1.2]	[-1.1]	[-1.1]	[-1.4]	[1.1]	[-1]	[-1.1]	[-1.2]	[1.1]	[1.3]	[-1.2]	[-1]
gerPC	Probable spore germination protein	[1.5]	[-1.1]	[1.3]	[-1.3]	[1.3]	[-1]	[1.1]	[-1.2]	3.5 *	[1.4]	[-1.1]	-2.7 *
gerPD	Probable spore germination protein	[-1.2]	[-1]	[-1.2]	[1]	-3.6 *	-3.9 *	[-1.1]	[-1.2]	1.6	[1.5]	[-1.4]	[-1.5]
gerPE	Probable spore germination protein	[1.1]	[1.1]	[1.2]	[1.2]	[1.2]	[-1.1]	[1.2]	[-1.2]	8.2 *	3.5 *	[-1.2]	-2.8 *
gerPF	Probable spore germination protein	[1.2]	[1]	[1.3]	[1.1]	[1]	[-1]	[-1.2]	[-1.3]	[1.4]	[-1.1]	[-1.1]	[-1.7]
Hpr	aprE AbrB (-); DegU (+); Hpr (-); SinR (-); TenA (+)												
aprE	Subtilisin E	[-1.1]	[-1.2]	[1.4]	[1.2]	[1]	[-1.2]	[1]	[-1.2]	2.2 *	-1.7	[1.5]	-2.5 *

Table S5. Operons with genes that are significantly repressed (q ≤ 0.005) at T3 in an *sda*-dependent manner in the absence of Mn(II).

			Tm				T0				T3			
			Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator	Operon	Regulation	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
PhoP	skf	AbrB (-); PhoP (+); Spo0A (+)												
	skfA (ybcO)	Sporulation-killing factor skfA	[-1]	[-1.2]	[1.4]	[1.2]	[1.1]	[-1.2]	[1.2]	[-1.1]	[1.8]	2.5	[-1.9]	[-1.3]
	skfB (ybcP)	Uncharacterized protein skfB	[-1.1]	[-1.1]	[1.1]	[1]	[-1.3]	[-1.1]	[-1.1]	[1.1]	1.9 *	[-1.2]	[1.3]	-1.7
	skfC (ybcS)	Sporulation-killing factor biosynthesis	[1]	[-1.1]	[-1.1]	[-1.2]	[1.3]	[1.4]	[-1.4]	[-1.3]	3.9 *	[1.4]	[1]	-2.7 *
	skfC (ybcS)	Sporulation-killing factor biosynthesis	[-1.1]	[-1.1]	[1]	[-1]	[-1.1]	[-1.1]	[1]	[-1]	2.1 *	[-1.3]	1.7 *	-1.6
	skfE (ybdA)	SkfA peptide export ATP-binding	[-1]	[-1]	[1.2]	[1.2]	[-1.1]	[1.3]	[-1.9]	[-1.3]	5.6 *	[-1]	[1.7]	-3.3 *
	skfF (ybdB)	Putative bacteriocin-skfA transport	[-1]	[1.3]	[-1.2]	[1.1]	[1.1]	[1.4]	[-1.2]	[1.1]	2.5 *	[-1.3]	[1.1]	-2.9 *
	skfG (ybdD)	Uncharacterized protein skfG	[1]	[-1]	[1.1]	[1]	[-1.1]	[-1.2]	[-1.3]	[-1.3]	[1.2]	[-1.4]	[1.3]	[-1.3]
	skfH (ybdE)	Thioredoxin-like protein skfH	[-1.4]	[-1.2]	[1.1]	[1.2]	-1.6	[-1.3]	[-1.4]	[-1.1]	3.2 *	[-1.2]	[1.1]	-3.4 *
PhoP	ykzB-ykoL	PhoP (+); TnrA (+)												
	ykzB	Uncharacterized protein ykzB	[1]	[1.2]	[-1.3]	[-1.2]	[1.3]	1.7	[-1.3]	[-1]	4.3 *	4 *	-1.8	-1.9 *
	ykoL	Stress response protein ykoL	[-1]	[-1]	[-1.1]	[-1]	[1.2]	[1.1]	[-1.1]	[-1.2]	2.3 *	1.9 *	[-1]	[-1.2]
PhoP	yttP	PhoP (+); Spo0A (+)												
	yttP	Probable HTH-type transcriptional	[-1.2]	[-1.2]	[1.1]	[1.1]	[-1.1]	[-1.4]	[1.3]	[1]	6.4 *	1.9	[1]	-3.2 *
RsfA	rsfA	RsfA (-); SigF (+); SigG (+)												
	rsfA	Prespore-specific transcriptional	[-1.2]	[-1.2]	[1.6]	[1.6]	[-1.8]	-2.2	[1.3]	[1.1]	10.7 *	5.2 *	-1.9	-3.8 *
RsfA	spoIIGA-sigE-sigG	RsfA (+); SigF (+); SigG (+); Spo0A (+); SpoVT (-)												
	spoIIGA	Sporulation sigma-E factor-processing	[1.1]	[-1.2]	[1.4]	[1.1]	[1.2]	[-1.2]	[1.4]	[-1.1]	3.7 *	2.3 *	-1.9	-2.9 *
	sigE	RNA polymerase sigma-E factor	[1.1]	[1.2]	[-1]	[1.1]	[1]	[1.2]	[-1.1]	[1.1]	[1.5]	[1.4]	-1.5	-1.6
	sigG	RNA polymerase sigma-G factor	[1.2]	[1.5]	[1.2]	[1.5]	[1.4]	[1.4]	[-1]	[-1]	6.1 *	2.4 *	-2.4 *	-5.9 *
RsfA	spoIIR	RsfA (-); SigF (+)												
	spoIIR	Stage II sporulation protein R	[-1.1]	[1]	[-1.2]	[-1.1]	[1]	[-1.2]	[1.2]	[-1.1]	8.2 *	3.3 *	[-1.5]	-3.6 *
SigE	dacB-spmAB	SigE (+)												
	dacB	D-alanyl-D-alanine carboxypeptidase	[1]	[-1]	[1.1]	[-1]	[1.1]	[-1]	[1.3]	[1.1]	4.2 *	4.4 *	[-1.7]	[-1.6]
	spmA	Spore maturation protein A	[-1.1]	[-1]	[1.2]	[1.2]	[-1.2]	-1.6	[1.3]	[-1]	7.1 *	5.7 *	-1.8	-2.3 *
	spmB	Spore maturation protein B	[1.2]	[-1]	[1.2]	[-1]	[-1.2]	[-1.3]	[1.1]	[-1]	4.1 *	3.2 *	[-1.5]	-1.8

Table S5. Operons with genes that are significantly repressed (q ≤ 0.005) at T3 in an *sda*-dependent manner in the absence of Mn(II).

			Tm				T0				T3			
			Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator	Operon	Regulation	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
SigE	gerR	SigE (+)												
ylbO		Uncharacterized protein ylbO	[1.2]	[1.1]	[1.6]	[1.4]	[1.6]	[1.5]	[1.1]	[1]	12.1 *	8.8 *	-2.5	-3.5 *
SigE	glgBCDAP	SigE (+)												
glgB		1,4-alpha-glucan-branching enzyme	[-1.1]	[1]	[1.4]	[1.5]	[-1]	[-1.1]	[-1.2]	[-1.3]	4.7 *	2.6 *	-2.3	-4.1 *
glgC		Glucose-1-phosphate	[-1.1]	[1]	[1.1]	[1.3]	[-1.3]	[-1.5]	[1.2]	[1]	4.9 *	5 *	-2	[-2]
glgD		Glycogen biosynthesis protein glgD	[-1.4]	[-1]	[-1.3]	[1]	-3.1 *	-3.5 *	[1.1]	[-1]	3.2 *	2.3 *	-2	-2.7
glgA		Glycogen synthase	[-1.2]	[-1.5]	[1.4]	[1.1]	-3.2 *	-3.6 *	[1.2]	[1.1]	6.9 *	3.9 *	-2.1	-3.8 *
glgP		Glycogen phosphorylase	[-1]	[-1]	[1.1]	[1.1]	-1.7	-1.9	[1.3]	[1.2]	6.8 *	3.2 *	[-1.6]	-3.4 *
SigE	safA-coxA	SigE (+)												
safA		SpoIVD-associated factor A	[1]	[-1.3]	[2.3]	[1.7]	[1.3]	[-1.4]	[1.6]	[-1.1]	13.2 *	7 *	[-1.9]	-3.5 *
coxA		Sporulation cortex protein coxA	[1]	[-1.1]	[1.2]	[1.1]	[-1.2]	[1]	[1.2]	[1.4]	[1.1]	2.6 *	-2.6 *	[-1.1]
SigE	spoIVA	SigE (+); SpoIIID (-)												
spoIVA		Stage IV sporulation protein A	[-1.1]	[-1.1]	[1.3]	[1.3]	[-1.1]	[-1.4]	[1.2]	[-1]	18.5 *	4.3 *	[-1]	-4.4 *
SigE	spoIVFAB	SigE (+); SpoIIID (-)												
spoIVFA		Stage IV sporulation protein FA	[1]	[-1.1]	[1.4]	[1.2]	[-1]	[-1.1]	[1.1]	[1]	9 *	4.8 *	-1.6	-3 *
spoIVFB		Stage IV sporulation protein FB	[-1.1]	[-1.1]	[-1.1]	[-1]	-2.2 *	-2.2 *	[-1.2]	[-1.2]	2.5 *	2.8 *	[-1.5]	[-1.4]
SigE	spoVID-ysxE	SigE (+)												
spoVID		Stage VI sporulation protein D	[-1.5]	[-1.6]	[1.2]	[1.2]	-2.2	-2.3	[1.3]	[1.2]	20.6 *	7.8 *	[-1.5]	-3.9 *
ysxE		Uncharacterized protein ysxE	[-1.2]	[1]	[1.8]	[2.1]	[-1.1]	[-1.1]	[1.5]	[1.4]	12.5 *	9.5 *	-2.5	-3.3
SigE	spoVR	SigE (+)												
spoVR		Stage V sporulation protein R	[1.2]	[1.1]	[1.7]	[1.6]	[1.3]	[1.1]	[1.1]	[-1.1]	9.7 *	7.3 *	-2.3	-3 *
SigE	ydcC	SigE (+)												
ydcC		Sporulation protein ydcC	[-1.2]	[-1.2]	[1.7]	[1.7]	[1.1]	[-1.2]	[1.5]	[1.1]	12.6 *	8.3 *	-1.9	-2.9 *
SigE	ydhD	SigE (+)												
ydhD		Putative sporulation-specific	[1]	[1]	[1.1]	[1.1]	[1.1]	[-1.3]	[1.4]	[-1]	8 *	6.2 *	-1.6	-2.1 *

Table S5. Operons with genes that are significantly repressed (q ≤ 0.005) at T3 in an *sda*-dependent manner in the absence of Mn(II).

			Tm				T0				T3			
			Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator	Operon	Regulation	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
SigE	yhaX	SigE (+)												
yhaX		Stress response protein yhaX	[1]	[-1.1]	[1.2]	[1.1]	[-1]	[-1.1]	[1.4]	[1.3]	5.3 *	5.4 *	-2.7 *	-2.7 *
SigE	yjbX	SigE (+)												
cotO (yjbX)		Spore coat protein O	[-1]	[-1.1]	[1.8]	[1.6]	[1]	[-1.4]	[1.9]	[1.4]	14.8 *	7.1 *	[-1.9]	-4 *
SigE	ykvUV	SigE (+); SigG (+); SpoIIID (-)												
ykvU		Sporulation protein ykvU	[1.1]	[-1]	[1.3]	[1.2]	[1.1]	[1.2]	[1.1]	[1.2]	4.7 *	3.9 *	-2	-2.4 *
stoA (ykvV)		Sporulation thiol-disulfide	[-1]	[-1.1]	[1.3]	[1.1]	[1.5]	[1.2]	[1.3]	[1]	1.7	2.8 *	-2 *	[-1.2]
SigE	yngJIHGFE	SigE (+)												
yngJ		Probable acyl-CoA dehydrogenase	[1.1]	[-1]	[1.4]	[1.3]	[1.2]	[-1.1]	[1.7]	[1.3]	6.9 *	6.9 *	-3.2 *	-3.1 *
yngI		Putative acyl-CoA synthetase yngI	[1.2]	[1.3]	[1.2]	[1.3]	3	2.7	[-1.1]	[-1.1]	[1.3]	2.1	[-2]	[-1.2]
accC2 (yngH)		Biotin carboxylase 2	[-1]	[-1]	[1]	[1]	[-1.2]	[-1.2]	[1.1]	[1.1]	[1.1]	2.2 *	-1.8	[1.1]
yngG		Hydroxymethylglutaryl-CoA lyase yngG	[-1.2]	[-1.1]	[1.1]	[1.1]	[1]	[-1.1]	[1.1]	[-1]	1.8	4.5 *	-3.4 *	[-1.4]
yngF		Putative enoyl-CoA	[1.1]	[-1.2]	[1.4]	[1.1]	[1]	[1]	[1.1]	[1.1]	2.8 *	5.8 *	-4.1 *	-2
yngE		Uncharacterized carboxylase yngE	[1]	[-1.2]	[1.5]	[1.3]	[-1.5]	-1.9	[1.6]	[1.3]	4.9 *	5.1 *	-2.7 *	-2.5 *
SigE	yqhV-spoIIIAABCDEFGH	SigE (+); SigE (+); SpoIIID (-); SpoIIID (-); YlbO (-)												
yqhV		Uncharacterized protein yqhV	[-1]	[-1.1]	[1]	[1]	[1]	[-1.1]	[1.2]	[1.1]	1.7	2.3 *	[-1.6]	[-1.2]
spoIIIAA		Stage III sporulation protein AA	[1]	[-1.1]	[1.3]	[1.2]	[-1.1]	[-1.3]	[1.2]	[-1]	8.3 *	5.1 *	[-1.5]	-2.3 *
spoIIIAB		Stage III sporulation protein AB	[1.2]	[-1]	[1.2]	[1]	[1.4]	[1.2]	[1.1]	[1]	7.3 *	5.5 *	[-1.7]	-2.3
spoIIIAC		Stage III sporulation protein AC	[-1.2]	[-1]	[1.1]	[1.2]	-4.9 *	-5 *	[1]	[1]	4.4 *	4.2 *	[-1.5]	[-1.6]
spoIIIAD		Stage III sporulation protein AD	[1.3]	[-1.1]	[1.5]	[1.1]	[-1]	[-1.1]	[1.1]	[1.1]	8.2 *	4.8 *	[-1.5]	-2.6 *
spoIIIAE		Stage III sporulation protein AE	[1]	[1]	[1.1]	[1.1]	[-1.2]	[-1.2]	[1.2]	[1.2]	6.8 *	6.3 *	-2.1	-2.3
spoIIIAF		Stage III sporulation protein AF	[-1.1]	[-1.2]	[1.5]	[1.3]	-2.8 *	-4.2 *	[1.4]	[-1.1]	15.4 *	5.9 *	[-1.3]	-3.4 *
spoIIIAG		Stage III sporulation protein AG	[-1]	[-1.4]	[1.4]	[1.1]	-1.9	-2.3 *	[1.2]	[-1]	5.8 *	3.9 *	[-1.5]	-2.2
spoIIIAH		Stage III sporulation protein AH	[-1.2]	[-1.6]	[2.6]	[2]	[-1.4]	[-1.8]	[1.9]	[1.5]	20 *	5.1 *	[-1.2]	-4.7 *

Table S5. Operons with genes that are significantly repressed (q ≤ 0.005) at T3 in an *sda*-dependent manner in the absence of Mn(II).

			Tm				T0				T3			
			Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator	Operon	Regulation	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
SigE	yqhV-spoIIIAABCDEFGH	SigE (+); SigE (+); SpoIIID (-); SpoIIID (-); YlbO (-)												
yqhV		Uncharacterized protein yqhV	[-1]	[-1.1]	[1]	[1]	[1]	[-1.1]	[1.2]	[1.1]	1.7	2.3 *	[-1.6]	[-1.2]
spoIIIAA		Stage III sporulation protein AA	[1]	[-1.1]	[1.3]	[1.2]	[-1.1]	[-1.3]	[1.2]	[-1]	8.3 *	5.1 *	[-1.5]	-2.3 *
spoIIIAB		Stage III sporulation protein AB	[1.2]	[-1]	[1.2]	[1]	[1.4]	[1.2]	[1.1]	[1]	7.3 *	5.5 *	[-1.7]	-2.3
spoIIIAC		Stage III sporulation protein AC	[-1.2]	[-1]	[1.1]	[1.2]	-4.9 *	-5 *	[1]	[1]	4.4 *	4.2 *	[-1.5]	[-1.6]
spoIIIAD		Stage III sporulation protein AD	[1.3]	[-1.1]	[1.5]	[1.1]	[-1]	[-1.1]	[1.1]	[1.1]	8.2 *	4.8 *	[-1.5]	-2.6 *
spoIIIAE		Stage III sporulation protein AE	[1]	[1]	[1.1]	[1.1]	[-1.2]	[-1.2]	[1.2]	[1.2]	6.8 *	6.3 *	-2.1	-2.3
spoIIIAF		Stage III sporulation protein AF	[-1.1]	[-1.2]	[1.5]	[1.3]	-2.8 *	-4.2 *	[1.4]	[-1.1]	15.4 *	5.9 *	[-1.3]	-3.4 *
spoIIIAG		Stage III sporulation protein AG	[-1]	[-1.4]	[1.4]	[1.1]	-1.9	-2.3 *	[1.2]	[-1]	5.8 *	3.9 *	[-1.5]	-2.2
spoIIIAH		Stage III sporulation protein AH	[-1.2]	[-1.6]	[2.6]	[2]	[-1.4]	[-1.8]	[1.9]	[1.5]	20 *	5.1 *	[-1.2]	-4.7 *
SigE	yyaD	SigE (+)												
yyaD		Uncharacterized protein yyaD	[1]	[1.1]	[-1.1]	[-1.1]	[1.1]	[1.3]	[-1.5]	[-1.3]	6.2 *	3.8 *	[-1.4]	-2.2 *
SigF	dacF-spoIIAAB-sigF	SigF (+); SigG (+); SigH (+); Spo0A (+); SpoVT (-)												
dacF		D-alanyl-D-alanine carboxypeptidase	[1.1]	[-1.1]	[1.3]	[1.1]	[1.2]	[-1.1]	[1.2]	[-1]	3 *	3.6 *	-1.9	[-1.6]
spoIIAA		Anti-sigma F factor antagonist	[-1.2]	[-1.1]	[1.6]	[1.8]	[1.1]	[1.1]	[1.1]	[1]	4.5 *	2.4 *	[-1.5]	-2.8
spoIIAB		Anti-sigma F factor	[-1.1]	[-1.2]	[1.8]	[1.5]	[-1.6]	[-1.6]	[-1.1]	[-1]	10.1 *	2.5 *	[-1.6]	-6.7 *
sigF		RNA polymerase sigma-F factor	[1.2]	[1.1]	[1.2]	[1.1]	[1.1]	[1.3]	[-1.1]	[1]	3.8 *	2.1 *	-1.7	-3.1 *
SigF	rsfA	RsfA (-); SigF (+); SigG (+)												
rsfA		Prespore-specific transcriptional	[-1.2]	[-1.2]	[1.6]	[1.6]	[-1.8]	-2.2	[1.3]	[1.1]	10.7 *	5.2 *	-1.9	-3.8 *
SigF	spoIIGA-sigE-sigG	RsfA (+); SigF (+); SigG (+); Spo0A (+); SpoVT (-)												
spoIIGA		Sporulation sigma-E factor-processing	[1.1]	[-1.2]	[1.4]	[1.1]	[1.2]	[-1.2]	[1.4]	[-1.1]	3.7 *	2.3 *	-1.9	-2.9 *
sigE		RNA polymerase sigma-E factor	[1.1]	[1.2]	[-1]	[1.1]	[1]	[1.2]	[-1.1]	[1.1]	[1.5]	[1.4]	-1.5	-1.6
sigG		RNA polymerase sigma-G factor	[1.2]	[1.5]	[1.2]	[1.5]	[1.4]	[1.4]	[-1]	[-1]	6.1 *	2.4 *	-2.4 *	-5.9 *
SigF	spoIIQ	SigF (+)												
spoIIQ		Stage II sporulation protein Q	[-1.2]	[-1]	[1.6]	[1.9]	[1.1]	[-1.5]	[1.3]	[-1.2]	21.2 *	3.8 *	[-1.1]	-6.1 *

Table S5. Operons with genes that are significantly repressed (q ≤ 0.005) at T3 in an *sda*-dependent manner in the absence of Mn(II).

			Tm				T0				T3			
			Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator	Operon	Regulation	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
SigF	spoIIR	RsfA (-); SigF (+)												
spoIIR		Stage II sporulation protein R	[-1.1]	[1]	[-1.2]	[-1.1]	[1]	[-1.2]	[1.2]	[-1.1]	8.2 *	3.3 *	[-1.5]	-3.6 *
SigF	yphA-seaA	SigF (+)												
yphA		Uncharacterized protein yphA	[1]	[1]	[-1.1]	[-1]	[-1.1]	[1.1]	[-1.2]	[1.1]	[-1.1]	[1.4]	[-1.4]	[1]
yphB (seaA)		Uncharacterized protein yphB	[1.1]	[1.1]	[1.1]	[1.1]	[1.1]	[1.1]	[-1.2]	[-1.2]	5.3 *	2 *	[-1.3]	-3.5 *
SigF	yuiC	SigF (+)												
yuiC		Uncharacterized protein yuiC	[1.3]	[-1]	[1.2]	[-1]	[1]	[-1.3]	[1.2]	[-1.1]	4.7 *	5.9 *	-3 *	-2.4 *
SigG	dacF-spoIIAAB-sigF	SigF (+); SigG (+); SigH (+); Spo0A (+); SpoVT (-)												
dacF		D-alanyl-D-alanine carboxypeptidase	[1.1]	[-1.1]	[1.3]	[1.1]	[1.2]	[-1.1]	[1.2]	[-1]	3 *	3.6 *	-1.9	[-1.6]
spoIIAA		Anti-sigma F factor antagonist	[-1.2]	[-1.1]	[1.6]	[1.8]	[1.1]	[1.1]	[1.1]	[1]	4.5 *	2.4 *	[-1.5]	-2.8
spoIIAB		Anti-sigma F factor	[-1.1]	[-1.2]	[1.8]	[1.5]	[-1.6]	[-1.6]	[-1.1]	[-1]	10.1 *	2.5 *	[-1.6]	-6.7 *
sigF		RNA polymerase sigma-F factor	[1.2]	[1.1]	[1.2]	[1.1]	[1.1]	[1.3]	[-1.1]	[1]	3.8 *	2.1 *	-1.7	-3.1 *
SigG	rsfA	RsfA (-); SigF (+); SigG (+)												
rsfA		Prespore-specific transcriptional	[-1.2]	[-1.2]	[1.6]	[1.6]	[-1.8]	-2.2	[1.3]	[1.1]	10.7 *	5.2 *	-1.9	-3.8 *
SigG	spoIIGA-sigE-sigG	RsfA (+); SigF (+); SigG (+); Spo0A (+); SpoVT (-)												
spoIIGA		Sporulation sigma-E factor-processing	[1.1]	[-1.2]	[1.4]	[1.1]	[1.2]	[-1.2]	[1.4]	[-1.1]	3.7 *	2.3 *	-1.9	-2.9 *
sigE		RNA polymerase sigma-E factor	[1.1]	[1.2]	[-1]	[1.1]	[1]	[1.2]	[-1.1]	[1.1]	[1.5]	[1.4]	-1.5	-1.6
sigG		RNA polymerase sigma-G factor	[1.2]	[1.5]	[1.2]	[1.5]	[1.4]	[1.4]	[-1]	[-1]	6.1 *	2.4 *	-2.4 *	-5.9 *
SigG	sspK	SigG (+)												
sspK		Small, acid-soluble spore protein K	[1.2]	[1.1]	[1]	[-1]	[1.3]	[1.2]	[1.3]	[1.2]	6 *	5.8 *	-1.7 *	-1.8 *
SigG	ykvUV	SigE (+); SigG (+); SpoIIID (-)												
ykvU		Sporulation protein ykvU	[1.1]	[-1]	[1.3]	[1.2]	[1.1]	[1.2]	[1.1]	[1.2]	4.7 *	3.9 *	-2	-2.4 *
stoA (ykvV)		Sporulation thiol-disulfide	[-1]	[-1.1]	[1.3]	[1.1]	[1.5]	[1.2]	[1.3]	[1]	1.7	2.8 *	-2 *	[-1.2]

Table S5. Operons with genes that are significantly repressed (q ≤ 0.005) at T3 in an *sda*-dependent manner in the absence of Mn(II).

			Tm				T0				T3			
			Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator	Operon	Regulation	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
SigH	dacF-spoIIAAB-sigF	SigF (+); SigG (+); SigH (+); Spo0A (+); SpoVT (-)												
dacF		D-alanyl-D-alanine carboxypeptidase	[1.1]	[-1.1]	[1.3]	[1.1]	[1.2]	[-1.1]	[1.2]	[-1]	3 *	3.6 *	-1.9	[-1.6]
spoIIAA		Anti-sigma F factor antagonist	[-1.2]	[-1.1]	[1.6]	[1.8]	[1.1]	[1.1]	[1.1]	[1]	4.5 *	2.4 *	[-1.5]	-2.8
spoIIAB		Anti-sigma F factor	[-1.1]	[-1.2]	[1.8]	[1.5]	[-1.6]	[-1.6]	[-1.1]	[-1]	10.1 *	2.5 *	[-1.6]	-6.7 *
sigF		RNA polymerase sigma-F factor	[1.2]	[1.1]	[1.2]	[1.1]	[1.1]	[1.3]	[-1.1]	[1]	3.8 *	2.1 *	-1.7	-3.1 *
SigH	racA	SigH (+); Spo0A (+)												
racA (ywkC)		Chromosome-anchoring protein racA	[-1.2]	[1.1]	[1]	[1.3]	[-1]	[1.1]	[-1.1]	[1]	8 *	2.6 *	[-1.2]	-3.6 *
SigK	gerPABCDEF	GerE (-); SigK (+)												
gerPA		Probable spore germination protein	[-1]	[-1.2]	[1.1]	[-1.1]	-3.1 *	-3.9 *	[1.1]	[-1.1]	3.4 *	3.1 *	-1.7	-1.9 *
gerPB		Probable spore germination protein	[1.2]	[-1.1]	[-1.1]	[-1.4]	[1.1]	[-1]	[-1.1]	[-1.2]	[1.1]	[1.3]	[-1.2]	[-1]
gerPC		Probable spore germination protein	[1.5]	[-1.1]	[1.3]	[-1.3]	[1.3]	[-1]	[1.1]	[-1.2]	3.5 *	[1.4]	[-1.1]	-2.7 *
gerPD		Probable spore germination protein	[-1.2]	[-1]	[-1.2]	[1]	-3.6 *	-3.9 *	[-1.1]	[-1.2]	1.6	[1.5]	[-1.4]	[-1.5]
gerPE		Probable spore germination protein	[1.1]	[1.1]	[1.2]	[1.2]	[1.2]	[-1.1]	[1.2]	[-1.2]	8.2 *	3.5 *	[-1.2]	-2.8 *
gerPF		Probable spore germination protein	[1.2]	[1]	[1.3]	[1.1]	[1]	[-1]	[-1.2]	[-1.3]	[1.4]	[-1.1]	[-1.1]	[-1.7]
SigK	sps	SigK (+)												
spsA		Spore coat polysaccharide	[-1]	[1]	[-1.3]	[-1.2]	[-1.5]	[-1.4]	[-1.1]	[-1]	2.1 *	2.2 *	[-1.4]	[-1.3]
spsB		Spore coat polysaccharide	[-1]	[-1.1]	[-1.1]	[-1.2]	-1.8	-1.8	[-1]	[-1]	1.6	1.8 *	[-1.3]	[-1.1]
spsC		Spore coat polysaccharide	[-1]	[1]	[-1.2]	[-1.1]	[-1.4]	-1.9	[1.3]	[-1]	1.6	2.1 *	-1.7	[-1.3]
spsD		Spore coat polysaccharide	[-1.1]	[-1.1]	[-1]	[-1.1]	[-1.4]	[-1.6]	[1.2]	[1]	[1.2]	[1.2]	[-1]	[-1]
spsE		Spore coat polysaccharide	[1.1]	[1]	[1.3]	[1.2]	[1.3]	[1]	[1.2]	[-1.1]	12.2 *	9.6 *	-2.5 *	-3.1 *
spsF		Spore coat polysaccharide	[-1.1]	[1]	[-1.2]	[-1.1]	[-1.5]	-1.6	[-1]	[-1.1]	[1.2]	[-1.3]	2.2 *	[1.4]
spsG		Spore coat polysaccharide	[1.2]	[-1.1]	[1.2]	[-1.1]	[1]	[1.2]	[-1.2]	[1]	[1.2]	1.6	[-1.2]	[1.1]
spsI		Spore coat polysaccharide	[-1.1]	[-1.1]	[1]	[-1]	-1.9	-1.9	[1]	[1]	[-1.2]	[-1.1]	[1.1]	[1.2]
spsJ		Spore coat polysaccharide	[1.1]	[-1.2]	[1.2]	[-1.1]	[1]	[1.1]	[-1]	[1.1]	1.8	4.1 *	-2.5 *	[-1]
spsK		Spore coat polysaccharide	[1.1]	[-1.1]	[1.2]	[-1.1]	[1.2]	[1.1]	[1.3]	[1.2]	2.3 *	3.6 *	[-1.7]	[-1.1]
spsL		Spore coat polysaccharide	[1.2]	[1.1]	[1.1]	[1.1]	1.6	1.5	[1.1]	[-1]	[1.5]	1.8 *	[-1.2]	[-1]

Table S5. Operons with genes that are significantly repressed (q ≤ 0.005) at T3 in an *sda*-dependent manner in the absence of Mn(II).

			Tm				T0				T3			
			Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator	Operon	Regulation	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
SigK	ytaA	SigK (+)												
	cotI (ytaA)	Spore coat protein I	[1.1]	[-1.1]	[1.2]	[-1]	[-1]	[-1.2]	[1]	[-1.1]	2.9 *	[1.3]	[-1.2]	-2.7 *
SinR	aprE	AbrB (-); DegU (+); Hpr (-); SinR (-); TenA (+)												
	aprE	Subtilisin E	[-1.1]	[-1.2]	[1.4]	[1.2]	[1]	[-1.2]	[1]	[-1.2]	2.2 *	-1.7	[1.5]	-2.5 *
Spo0A	dacF-spoIIAAB-sigF	SigF (+); SigG (+); SigH (+); Spo0A (+); SpoVT (-)												
	dacF	D-alanyl-D-alanine carboxypeptidase	[1.1]	[-1.1]	[1.3]	[1.1]	[1.2]	[-1.1]	[1.2]	[-1]	3 *	3.6 *	-1.9	[-1.6]
	spoIIAA	Anti-sigma F factor antagonist	[-1.2]	[-1.1]	[1.6]	[1.8]	[1.1]	[1.1]	[1.1]	[1]	4.5 *	2.4 *	[-1.5]	-2.8
	spoIIAB	Anti-sigma F factor	[-1.1]	[-1.2]	[1.8]	[1.5]	[-1.6]	[-1.6]	[-1.1]	[-1]	10.1 *	2.5 *	[-1.6]	-6.7 *
	sigF	RNA polymerase sigma-F factor	[1.2]	[1.1]	[1.2]	[1.1]	[1.1]	[1.3]	[-1.1]	[1]	3.8 *	2.1 *	-1.7	-3.1 *
Spo0A	racA	SigH (+); Spo0A (+)												
	racA (ywkC)	Chromosome-anchoring protein racA	[-1.2]	[1.1]	[1]	[1.3]	[-1]	[1.1]	[-1.1]	[1]	8 *	2.6 *	[-1.2]	-3.6 *
Spo0A	skf	AbrB (-); PhoP (+); Spo0A (+)												
	skfA (ybcO)	Sporulation-killing factor skfA	[-1]	[-1.2]	[1.4]	[1.2]	[1.1]	[-1.2]	[1.2]	[-1.1]	[1.8]	2.5	[-1.9]	[-1.3]
	skfB (ybcP)	Uncharacterized protein skfB	[-1.1]	[-1.1]	[1.1]	[1]	[-1.3]	[-1.1]	[-1.1]	[1.1]	1.9 *	[-1.2]	[1.3]	-1.7
	skfC (ybcS)	Sporulation-killing factor biosynthesis	[1]	[-1.1]	[-1.1]	[-1.2]	[1.3]	[1.4]	[-1.4]	[-1.3]	3.9 *	[1.4]	[1]	-2.7 *
	skfC (ybcS)	Sporulation-killing factor biosynthesis	[-1.1]	[-1.1]	[1]	[-1]	[-1.1]	[-1.1]	[1]	[-1]	2.1 *	[-1.3]	1.7 *	-1.6
	skfE (ybdA)	SkfA peptide export ATP-binding	[-1]	[-1]	[1.2]	[1.2]	[-1.1]	[1.3]	[-1.9]	[-1.3]	5.6 *	[-1]	[1.7]	-3.3 *
	skfF (ybdB)	Putative bacteriocin-skfA transport	[-1]	[1.3]	[-1.2]	[1.1]	[1.1]	[1.4]	[-1.2]	[1.1]	2.5 *	[-1.3]	[1.1]	-2.9 *
	skfG (ybdD)	Uncharacterized protein skfG	[1]	[-1]	[1.1]	[1]	[-1.1]	[-1.2]	[-1.3]	[-1.3]	[1.2]	[-1.4]	[1.3]	[-1.3]
	skfH (ybdE)	Thioredoxin-like protein skfH	[-1.4]	[-1.2]	[1.1]	[1.2]	-1.6	[-1.3]	[-1.4]	[-1.1]	3.2 *	[-1.2]	[1.1]	-3.4 *
Spo0A	spoIIE	Spo0A (+)												
	spoIIE	Stage II sporulation protein E	[1]	[1.1]	[1]	[1.1]	[1]	[-1.2]	[1.1]	[-1.1]	3.4 *	1.7	-2.2 *	-4.5 *
Spo0A	spoIIGA-sigE-sigG	RsfA (+); SigF (+); SigG (+); Spo0A (+); SpoVT (-)												
	spoIIGA	Sporulation sigma-E factor-processing	[1.1]	[-1.2]	[1.4]	[1.1]	[1.2]	[-1.2]	[1.4]	[-1.1]	3.7 *	2.3 *	-1.9	-2.9 *
	sigE	RNA polymerase sigma-E factor	[1.1]	[1.2]	[-1]	[1.1]	[1]	[1.2]	[-1.1]	[1.1]	[1.5]	[1.4]	-1.5	-1.6
	sigG	RNA polymerase sigma-G factor	[1.2]	[1.5]	[1.2]	[1.5]	[1.4]	[1.4]	[-1]	[-1]	6.1 *	2.4 *	-2.4 *	-5.9 *

Table S5. Operons with genes that are significantly repressed (q ≤ 0.005) at T3 in an *sda*-dependent manner in the absence of Mn(II).

			Tm				T0				T3			
			Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator	Operon	Regulation	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
Spo0A	yneEF	Spo0A (+)												
sirA (yneE)		Sporulation inhibitor of replication	[-1.1]	[-1.1]	[-1]	[-1]	[-1.2]	[-1.2]	[-1.1]	[-1.1]	1.9 *	1.6 *	-1.6	-1.9 *
yneF		UPF0154 protein yneF	[1]	[1.2]	[-1.2]	[1]	[-1]	[1.2]	[-1.3]	[1]	[1.4]	[-1.1]	[1.3]	[-1.1]
Spo0A	yppDE	Spo0A (+)												
yppD		Uncharacterized protein yppD	[1.1]	[1.1]	[1.1]	[1.1]	[1]	[1]	[-1.1]	[-1.1]	2.7 *	1.8 *	[-1.5]	-2.2 *
yppE		Uncharacterized protein yppE	[-1.3]	[-1.2]	[-1]	[1]	-1.7	[-1.5]	[1]	[1.2]	2.9 *	[1.1]	[-1.1]	-2.9 *
Spo0A	yttP	PhoP (+); Spo0A (+)												
yttP		Probable HTH-type transcriptional	[-1.2]	[-1.2]	[1.1]	[1.1]	[-1.1]	[-1.4]	[1.3]	[1]	6.4 *	1.9	[1]	-3.2 *
Spo0A	yusED	Spo0A (+)												
yusE		Thioredoxin-like protein yusE	[1]	[1]	[-1.1]	[-1.1]	[-1.2]	[-1.2]	[1.1]	[1.1]	[-1.1]	[-1]	[1.3]	[1.3]
yusD		Uncharacterized protein yusD	[1]	[1.1]	[1.1]	[1.2]	[-1.4]	[-1.3]	[1]	[1.1]	2.9 *	[1.4]	[-1.1]	-2.3 *
SpoIIID	spoIVA	SigE (+); SpoIIID (-)												
spoIVA		Stage IV sporulation protein A	[-1.1]	[-1.1]	[1.3]	[1.3]	[-1.1]	[-1.4]	[1.2]	[-1]	18.5 *	4.3 *	[-1]	-4.4 *
SpoIIID	spoIVFAB	SigE (+); SpoIIID (-)												
spoIVFA		Stage IV sporulation protein FA	[1]	[-1.1]	[1.4]	[1.2]	[-1]	[-1.1]	[1.1]	[1]	9 *	4.8 *	-1.6	-3 *
spoIVFB		Stage IV sporulation protein FB	[-1.1]	[-1.1]	[-1.1]	[-1]	-2.2 *	-2.2 *	[-1.2]	[-1.2]	2.5 *	2.8 *	[-1.5]	[-1.4]
SpoIIID	ykvUV	SigE (+); SigG (+); SpoIIID (-)												
ykvU		Sporulation protein ykvU	[1.1]	[-1]	[1.3]	[1.2]	[1.1]	[1.2]	[1.1]	[1.2]	4.7 *	3.9 *	-2	-2.4 *
stoA (ykvV)		Sporulation thiol-disulfide	[-1]	[-1.1]	[1.3]	[1.1]	[1.5]	[1.2]	[1.3]	[1]	1.7	2.8 *	-2 *	[-1.2]

Table S5. Operons with genes that are significantly repressed (q ≤ 0.005) at T3 in an *sda*-dependent manner in the absence of Mn(II).

			Tm				T0				T3			
			Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator	Operon	Regulation	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
SpoIIID	yqhV-spoIIIAABCDEFGH	SigE (+); SigE (+); SpoIIID (-); SpoIIID (-); YlbO (-)												
yqhV	Uncharacterized protein yqhV		[-1]	[-1.1]	[1]	[1]	[1]	[-1.1]	[1.2]	[1.1]	1.7	2.3 *	[-1.6]	[-1.2]
spoIIIAA	Stage III sporulation protein AA		[1]	[-1.1]	[1.3]	[1.2]	[-1.1]	[-1.3]	[1.2]	[-1]	8.3 *	5.1 *	[-1.5]	-2.3 *
spoIIIAB	Stage III sporulation protein AB		[1.2]	[-1]	[1.2]	[1]	[1.4]	[1.2]	[1.1]	[1]	7.3 *	5.5 *	[-1.7]	-2.3
spoIIIAC	Stage III sporulation protein AC		[-1.2]	[-1]	[1.1]	[1.2]	-4.9 *	-5 *	[1]	[1]	4.4 *	4.2 *	[-1.5]	[-1.6]
spoIIIAD	Stage III sporulation protein AD		[1.3]	[-1.1]	[1.5]	[1.1]	[-1]	[-1.1]	[1.1]	[1.1]	8.2 *	4.8 *	[-1.5]	-2.6 *
spoIIIAE	Stage III sporulation protein AE		[1]	[1]	[1.1]	[1.1]	[-1.2]	[-1.2]	[1.2]	[1.2]	6.8 *	6.3 *	-2.1	-2.3
spoIIIAF	Stage III sporulation protein AF		[-1.1]	[-1.2]	[1.5]	[1.3]	-2.8 *	-4.2 *	[1.4]	[-1.1]	15.4 *	5.9 *	[-1.3]	-3.4 *
spoIIIAG	Stage III sporulation protein AG		[-1]	[-1.4]	[1.4]	[1.1]	-1.9	-2.3 *	[1.2]	[-1]	5.8 *	3.9 *	[-1.5]	-2.2
spoIIIAH	Stage III sporulation protein AH		[-1.2]	[-1.6]	[2.6]	[2]	[-1.4]	[-1.8]	[1.9]	[1.5]	20 *	5.1 *	[-1.2]	-4.7 *
SpoIIID	yqhV-spoIIIAABCDEFGH	SigE (+); SigE (+); SpoIIID (-); SpoIIID (-); YlbO (-)												
yqhV	Uncharacterized protein yqhV		[-1]	[-1.1]	[1]	[1]	[1]	[-1.1]	[1.2]	[1.1]	1.7	2.3 *	[-1.6]	[-1.2]
spoIIIAA	Stage III sporulation protein AA		[1]	[-1.1]	[1.3]	[1.2]	[-1.1]	[-1.3]	[1.2]	[-1]	8.3 *	5.1 *	[-1.5]	-2.3 *
spoIIIAB	Stage III sporulation protein AB		[1.2]	[-1]	[1.2]	[1]	[1.4]	[1.2]	[1.1]	[1]	7.3 *	5.5 *	[-1.7]	-2.3
spoIIIAC	Stage III sporulation protein AC		[-1.2]	[-1]	[1.1]	[1.2]	-4.9 *	-5 *	[1]	[1]	4.4 *	4.2 *	[-1.5]	[-1.6]
spoIIIAD	Stage III sporulation protein AD		[1.3]	[-1.1]	[1.5]	[1.1]	[-1]	[-1.1]	[1.1]	[1.1]	8.2 *	4.8 *	[-1.5]	-2.6 *
spoIIIAE	Stage III sporulation protein AE		[1]	[1]	[1.1]	[1.1]	[-1.2]	[-1.2]	[1.2]	[1.2]	6.8 *	6.3 *	-2.1	-2.3
spoIIIAF	Stage III sporulation protein AF		[-1.1]	[-1.2]	[1.5]	[1.3]	-2.8 *	-4.2 *	[1.4]	[-1.1]	15.4 *	5.9 *	[-1.3]	-3.4 *
spoIIIAG	Stage III sporulation protein AG		[-1]	[-1.4]	[1.4]	[1.1]	-1.9	-2.3 *	[1.2]	[-1]	5.8 *	3.9 *	[-1.5]	-2.2
spoIIIAH	Stage III sporulation protein AH		[-1.2]	[-1.6]	[2.6]	[2]	[-1.4]	[-1.8]	[1.9]	[1.5]	20 *	5.1 *	[-1.2]	-4.7 *
SpoVT	dacF-spoIIAAB-sigF	SigF (+); SigG (+); SigH (+); Spo0A (+); SpoVT (-)												
dacF	D-alanyl-D-alanine carboxypeptidase		[1.1]	[-1.1]	[1.3]	[1.1]	[1.2]	[-1.1]	[1.2]	[-1]	3 *	3.6 *	-1.9	[-1.6]
spoIIAA	Anti-sigma F factor antagonist		[-1.2]	[-1.1]	[1.6]	[1.8]	[1.1]	[1.1]	[1.1]	[1]	4.5 *	2.4 *	[-1.5]	-2.8
spoIIAB	Anti-sigma F factor		[-1.1]	[-1.2]	[1.8]	[1.5]	[-1.6]	[-1.6]	[-1.1]	[-1]	10.1 *	2.5 *	[-1.6]	-6.7 *
sigF	RNA polymerase sigma-F factor		[1.2]	[1.1]	[1.2]	[1.1]	[1.1]	[1.3]	[-1.1]	[1]	3.8 *	2.1 *	-1.7	-3.1 *

Table S5. Operons with genes that are significantly repressed (q ≤ 0.005) at T3 in an *sda*-dependent manner in the absence of Mn(II).

			Tm				T0				T3			
			Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator	Operon	Regulation	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
SpoVT	spoIIGA-sigE-sigG	RsfA (+); SigF (+); SigG (+); Spo0A (+); SpoVT (-)												
spoIIGA		Sporulation sigma-E factor-processing	[1.1]	[-1.2]	[1.4]	[1.1]	[1.2]	[-1.2]	[1.4]	[-1.1]	3.7 *	2.3 *	-1.9	-2.9 *
sigE		RNA polymerase sigma-E factor	[1.1]	[1.2]	[-1]	[1.1]	[1]	[1.2]	[-1.1]	[1.1]	[1.5]	[1.4]	-1.5	-1.6
sigG		RNA polymerase sigma-G factor	[1.2]	[1.5]	[1.2]	[1.5]	[1.4]	[1.4]	[-1]	[-1]	6.1 *	2.4 *	-2.4 *	-5.9 *
TenA	aprE	AbrB (-); DegU (+); Hpr (-); SinR (-); TenA (+)												
aprE		Subtilisin E	[-1.1]	[-1.2]	[1.4]	[1.2]	[1]	[-1.2]	[1]	[-1.2]	2.2 *	-1.7	[1.5]	-2.5 *
TnrA	glnQHMP	TnrA (+)												
glnQ		Glutamine transport ATP-binding	[1.1]	[-1.2]	[1.5]	[1.2]	[1.1]	[-1.4]	[1.7]	[1.1]	3.3 *	7.4 *	-3.3 *	[-1.5]
glnH		ABC transporter glutamine-binding	[-1.2]	[1]	[1.4]	[1.6]	[-1.1]	[1.4]	[-3.4]	[-2.1]	5.8 *	2.7 *	[-1.6]	-3.3 *
glnM		Probable glutamine ABC transporter	[-1.3]	[-1.7]	[1.1]	[-1.2]	-2.1	-2.2	[1.1]	[1]	[1.2]	2.8 *	-2.1	[1.1]
glnP		Probable glutamine ABC transporter	[-1.1]	[-1.1]	[1.1]	[1]	[-1.1]	[-1.3]	[-1.3]	[-1.5]	[1.4]	[1.4]	-1.8 *	-1.9 *
TnrA	ykzB-ykoL	PhoP (+); TnrA (+)												
ykzB		Uncharacterized protein ykzB	[1]	[1.2]	[-1.3]	[-1.2]	[1.3]	1.7	[-1.3]	[-1]	4.3 *	4 *	-1.8	-1.9 *
ykoL		Stress response protein ykoL	[-1]	[-1]	[-1.1]	[-1]	[1.2]	[1.1]	[-1.1]	[-1.2]	2.3 *	1.9 *	[-1]	[-1.2]
YlbO	yqhV-spoIIIAABCDEFGH	SigE (+); SigE (+); SpoIIID (-); SpoIIID (-); YlbO (-)												
yqhV		Uncharacterized protein yqhV	[-1]	[-1.1]	[1]	[1]	[1]	[-1.1]	[1.2]	[1.1]	1.7	2.3 *	[-1.6]	[-1.2]
spoIIIAA		Stage III sporulation protein AA	[1]	[-1.1]	[1.3]	[1.2]	[-1.1]	[-1.3]	[1.2]	[-1]	8.3 *	5.1 *	[-1.5]	-2.3 *
spoIIIAB		Stage III sporulation protein AB	[1.2]	[-1]	[1.2]	[1]	[1.4]	[1.2]	[1.1]	[1]	7.3 *	5.5 *	[-1.7]	-2.3
spoIIIAC		Stage III sporulation protein AC	[-1.2]	[-1]	[1.1]	[1.2]	-4.9 *	-5 *	[1]	[1]	4.4 *	4.2 *	[-1.5]	[-1.6]
spoIIIAD		Stage III sporulation protein AD	[1.3]	[-1.1]	[1.5]	[1.1]	[-1]	[-1.1]	[1.1]	[1.1]	8.2 *	4.8 *	[-1.5]	-2.6 *
spoIIIAE		Stage III sporulation protein AE	[1]	[1]	[1.1]	[1.1]	[-1.2]	[-1.2]	[1.2]	[1.2]	6.8 *	6.3 *	-2.1	-2.3
spoIIIAF		Stage III sporulation protein AF	[-1.1]	[-1.2]	[1.5]	[1.3]	-2.8 *	-4.2 *	[1.4]	[-1.1]	15.4 *	5.9 *	[-1.3]	-3.4 *
spoIIIAG		Stage III sporulation protein AG	[-1]	[-1.4]	[1.4]	[1.1]	-1.9	-2.3 *	[1.2]	[-1]	5.8 *	3.9 *	[-1.5]	-2.2
spoIIIAH		Stage III sporulation protein AH	[-1.2]	[-1.6]	[2.6]	[2]	[-1.4]	[-1.8]	[1.9]	[1.5]	20 *	5.1 *	[-1.2]	-4.7 *

Numbers indicate fold-change (log10)
Brackets: Not significant; q > 0.05 or fold-change < log2 0.6 (= 1.5-fold)
No brackets: Significant; q ≤ 0.005 (asterisk) or q ≤ 0.05 (no asterisk)
and fold-change ≥ log2 (0.6) (= 1.5-fold)

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Table S6. Genes with significant changes in expression (q ≤ 0.05) at the mid-exponential time point.

		Tm				T0				T3			
		Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Gene		sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
aadK	Aminoglycoside 6-adenylyltransferase	-2.5	-2.4	[-1]	[1]	-2.4 *	-2.6 *	[1.1]	[1.1]	-2.7 *	-2.8 *	[1.1]	[1]
immR	HTH-type transcriptional regulator immR	[1.2]	[-1.4]	3.7	[2.1]	[1]	[-1.3]	[2.5]	[1.8]	[-1]	1.8	[1.4]	2.5
katA	Vegetative catalase	[-3]	-7.5 *	[1.9]	[-1.3]	-13.8 *	-17.9 *	[1.5]	[1.1]	-6 *	-10.9 *	[1.2]	[-1.5]
mntA	Manganese-binding lipoprotein mntA	[-2.6]	-6.6	[2.8]	[1.1]	-7.2 *	-17.9 *	[2.2]	[-1.1]	-11.1 *	-27.2 *	[2.2]	[-1.1]
mntB	Manganese transport system ATP-	-15.3 *	-19.9 *	[1.9]	[1.4]	-28 *	-57.4 *	[2.1]	[1]	-28.6 *	-11.8 *	[-1.5]	[1.6]
mntC	Manganese transport system membrane	-4.2	-7.6 *	[2.1]	[1.2]	-7.7 *	-14.3 *	[1.6]	[-1.2]	-16.1 *	-10.4 *	[-1.1]	[1.4]
mntD	Manganese transport system membrane	[-2.9]	-6.9	[2.2]	[-1]	-6.5 *	-14.4 *	[2.1]	[-1]	-11 *	-19.3 *	[1.6]	[-1.1]
mntH	Manganese transport protein mntH	-13 *	-11.7 *	[1.3]	[1.4]	-28.9 *	-32.6 *	[1.2]	[1]	-32.4 *	-29.9 *	[1.1]	[1.2]
pksB	Probable polyketide biosynthesis zinc-	-4.2 *	-4.7 *	[1.1]	[-1]	-2.7 *	-3.7 *	[1.3]	[-1]	-2.7 *	-4.2 *	[1.5]	[-1]
slp	Pal-related lipoprotein	[1.6]	2.4 *	[-1.4]	[1]	1.5	1.7	[-1.2]	[-1.1]	[1.2]	[1.2]	[-1.5]	-1.5
ydzA	Uncharacterized membrane protein ydzA	[-2.2]	-3.3	[1.5]	[-1]	-4.1 *	-6.4 *	[1.4]	[-1.1]	-3.8 *	-6.4 *	[1.2]	[-1.4]
yknV	Uncharacterized ABC transporter ATP-	-11.6 *	-13.7 *	[1.4]	[1.2]	-6.6 *	-16.6 *	[2.9]	[1.1]	-25.5 *	-8.8 *	-2.6	[1.1]
yqbK	Uncharacterized protein yqbK	-2.5 *	-3.1 *	[1.1]	[-1.1]	-2.3 *	-2.7 *	[1.2]	[1]	-2.1 *	-2.7 *	[1.4]	[1.1]

Brackets: Not significant; q > 0.05 or fold-change < log2 0.6 (= 1.5-fold)
No brackets: Significant; q ≤ 0.005 (asterisk) or q ≤ 0.05 (no asterisk)
and fold-change ≥ log2 (0.6) (= 1.5-fold)

Hoover et al. (2010)

Table S7. Fold-differences in relative expression for genes in the PerR regulon.

Numbers indicate fold-change (log10)
Brackets: Not significant; q > 0.05 or fold-change < log2 0.6 (= 1.5-fold)
No brackets: Significant; q ≤ 0.005 (asterisk) or q ≤ 0.05 (no asterisk) and fold-change ≥ log2 (0.6) (= 1.5-fold)

		Tm				T0				T3			
		Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator - Operon - Regulation		sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
PerR	ahpCF PerR (-)												
ahpC	Alkyl hydroperoxide reductase subunit	[-1.5]	[-1.8]	[-1.3]	[-1.5]	[-1.3]	[-1.2]	[1]	[1.1]	-2.1	-1.6	[-1.2]	[1.1]
ahpF	NADH dehydrogenase	[-3.5]	[-1.9]	[-1.3]	[1.4]	-3.2	[-2.3]	[-1.1]	[1.3]	-6.4 *	-3.7 *	[-1.5]	[1.1]
PerR	fur PerR (-)												
fur	Ferric uptake regulation protein	[1.1]	[-1.4]	[1.4]	[-1.1]	[-1.5]	[-1.4]	[1.1]	[1.1]	[1.2]	[-1.2]	[-1.1]	[-1.6]
PerR	hemAXCDBL PerR (-)												
hemA	Glutamyl-tRNA reductase	[-1]	[-1.5]	[1.6]	[1.1]	[-1.3]	[-1.4]	[-1.4]	[-1.5]	[-1]	-2.3 *	[1.3]	[-1.7]
hemX	Protein hemX	[-1]	[-1.1]	[1]	[-1.1]	-1.9	-1.6	[-1.2]	[-1]	[-1.4]	-1.6	[-1.1]	[-1.2]
hemC	Porphobilinogen deaminase	[-1.1]	[-1.3]	[1.3]	[1]	[1.1]	[1]	[-1.1]	[-1.1]	[-1.3]	-1.8	[1.1]	[-1.2]
hemD	Uroporphyrinogen-III synthase	[-1.4]	[-1.5]	[1]	[-1]	[-1.4]	[-1.3]	[-1.2]	[-1.1]	-2.2 *	-2.5 *	[-1.1]	[-1.2]
hemB	Delta-aminolevulinic acid dehydratase	[-1.3]	[-1.3]	[1.1]	[1.1]	[-1.2]	[-1.5]	[1.2]	[-1.1]	-1.7	-2 *	[1.1]	[-1]
hemL	Glutamate-1-semialdehyde 2,1-	[-1.5]	[-1.6]	[-1]	[-1.1]	[-1.3]	[-1.4]	[1]	[-1.1]	-2 *	-3.3 *	[1.3]	[-1.2]
PerR	katA PerR (-)												
katA	Vegetative catalase	[-3]	-7.5 *	[1.9]	[-1.3]	-13.8 *	-17.9 *	[1.5]	[1.1]	-6 *	-10.9 *	[1.2]	[-1.5]
PerR	mrgA PerR (-)												
mrgA	Metalloregulation DNA-binding stress	[1.2]	[1.1]	[1.3]	[1.2]	[1]	[-1.3]	[1]	[-1.3]	[-1]	-1.8 *	[-1.2]	-2.1 *
PerR	perR PerR (-)												
perR	Peroxide operon regulator	[-1.7]	[-1.5]	[-1.1]	[1.1]	-2.1 *	-2.3 *	[1.1]	[1]	-2.9 *	-4 *	[1.2]	[-1.2]

Table S7. Fold-differences in relative expression for genes in the PerR regulon.

			Tm				T0				T3			
			Mn +/-		sda +/-		Mn +/-		sda +/-		Mn +/-		sda +/-	
Regulator	Operon	Regulation	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-	sda+	sda-	Mn+	Mn-
PerR	srfAA-srfAB-comS-srfAC-srfAD	CodY (-); ComA (+); PerR (+); Spx (+)												
srfAA		Surfactin synthetase subunit 1	[1.2]	[1.4]	[-1]	[1.1]	1.8 *	2.3 *	[-1.1]	[1.1]	[1.3]	-1.7 *	2.8 *	[1.3]
srfAB		Surfactin synthetase subunit 2	[1]	[1]	[1]	[1]	2	[1.3]	[1.6]	[1]	[1]	[1.1]	[1.5]	[1.6]
comS		Competence protein S	[1.4]	[1.3]	[-1.2]	[-1.2]	2.8 *	2.5 *	[1.2]	[1]	[1.3]	[-1.4]	1.9	[1]
srfAC		Surfactin synthetase subunit 3	[1.2]	[1.2]	[1.1]	[1]	1.8 *	1.8 *	[1.1]	[1.1]	[1.1]	[-1.2]	2 *	[1.4]
srfAD		Surfactin synthetase thioesterase	[1.1]	[1.2]	[-1.1]	[1]	1.8	2 *	[-1.1]	[-1]	[-1.2]	-2.1 *	1.9 *	[1.1]
PerR	yjbCD	PerR (-); SigB (+); SigM (+); SigW (+); SigX (+); YodB (-)												
yjbC		Putative acetyltransferase yjbC	[-1.2]	[-1.5]	[1]	[-1.2]	[-1.3]	[-1.7]	[1.2]	[-1.1]	2.1	2.4	[-1.6]	[-1.3]
spxA (yjbD)		Regulatory protein spx	[-1.3]	[-1.7]	[1]	[-1.2]	-2.4	-3	[1.4]	[1.1]	[-1.2]	[-1.6]	[-1.2]	[-1.6]
PerR	ykvW	PerR (-)												
zosA (ykvW)		Zinc-transporting ATPase	[1.1]	[-1.2]	[1]	[-1.2]	[-1.3]	[-1.2]	[1]	[1.1]	[-1.4]	-2 *	[-1.1]	[-1.5]

Numbers indicate fold-change (log10)
Brackets: Not significant; q > 0.05 or fold-change < log2 0.6 (= 1.5-fold)
No brackets: Significant; q ≤ 0.005 (asterisk) or q ≤ 0.05 (no asterisk)
and fold-change ≥ log2 (0.6) (= 1.5-fold)