Open Access

In silico identification and experimental validation of PmrAB targets in *Salmonella typhimurium* by regulatory motif detection

Kathleen Marchal*, Sigrid De Keersmaecker†, Pieter Monsieurs*, Nadja van Boxel†, Karen Lemmens*, Gert Thijs*, Jos Vanderleyden† and Bart De Moor*

Addresses: *ESAT-SCD, Katholieke Universiteit Leuven, Kasteelpark Arenberg 10, 3001 Leuven-Heverlee, Belgium. †Centre of Microbial and Plant Genetics, Katholieke Universiteit Leuven, Kasteelpark Arenberg 20, 3001 Leuven-Heverlee, Belgium.

Correspondence: Kathleen Marchal. E-mail: Kathleen.Marchal@esat.kuleuven.ac.be

Abstract

Background: The PmrAB (BasSR) two-component regulatory system is required for *Salmonella typhimurium* virulence. PmrAB-controlled modifications of the lipopolysaccharide (LPS) layer confer resistance to cationic antibiotic polypeptides, which may allow bacteria to survive within macrophages. The PmrAB system also confers resistance to Fe^{3+}-mediated killing. New targets of the system have recently been discovered that seem not to have a role in the well-described functions of PmrAB, suggesting that the PmrAB-dependent regulon might contain additional, unidentified targets.

Results: We performed an *in silico* analysis of possible targets of the PmrAB system. Using a motif model of the PmrA binding site in DNA, genome-wide screening was carried out to detect PmrAB target genes. To increase confidence in the predictions, all putative targets were subjected to a cross-species comparison (phylogenetic footprinting) using a Gibbs sampling-based motif-detection procedure. As well as the known targets, we detected additional targets with unknown functions. Four of these were experimentally validated (*yibD*, *aroQ*, *mig-13* and *sseJ*). Site-directed mutagenesis of the PmrA-binding site (PmrA box) in *yibD* revealed specific sequence requirements.

Conclusions: We demonstrated the efficiency of our procedure by recovering most of the known PmrAB-dependent targets and by identifying unknown targets that we were able to validate experimentally. We also pinpointed directions for further research that could help elucidate the *S. typhimurium* virulence pathway.

Background

The PmrAB two-component regulatory system is part of a multicomponent feedback loop that acts as one of the key regulatory mechanisms of *Salmonella typhimurium* virulence [1-3]. The PmrAB regulatory system is itself responsive to Fe^{3+} and mild acid [4] and senses Mg^{2+} indirectly by communicating with the Mg^{2+}-sensitive PhoPQ system [5-8] via

PmrD [1,9]. PmrD is hypothesized to transduce the signal from the PhoPQ system to the PmrAB system via a posttranslational modification. The gene *pmrD* is transcriptionally activated by the PhoPQ system but repressed by the PmrAB system [1,9,10]. The PmrAB system is required for resistance to the cationic antibiotic polymyxin B [11] and to Fe^{3+}-mediated killing [4]. The Mg^{2+}-dependent regulation of PmrAB

was shown to be important for gene expression in an intracellular environment [12]. Fe^{3+}-dependent PmrAB regulation, on the other hand, has been hypothesized to be essential for survival in extracellular environments [13]. A region in DNA to which the PmrA protein binds has been identified by DNA footprinting analysis [14,15].

In contrast to *pmrD*, other known target genes of PmrAB in *S. typhimurium* are transcriptionally activated. One group of targets is involved in LPS modification. PmrAB-induced modifications include the addition of 4-amino-4-deoxy-L-arabinose (Ara4N) and phosphoethanolamine (pEtN) to lipid A [16]. Loci involved in the Ara4N modification of lipid A are *ugd* [6] and the *pmrHFIJKLM* loci, both of which are responsible for Ara4N biosynthesis [2,16-18] and incorporation of Ara4N into lipid A [19,20]. LPS modifications are hypothesized to allow bacterial survival within macrophages by lowering the affinity of the LPS for amphipathic cationic peptides with antimicrobial activity that are produced as a consequence of the innate immune response.

A second class of targets are directly dependent on PmrAB, but have as-yet-undefined functions. *pmrC* (co-transcribed with *pmrAB* [21]) and *pmrG* (located upstream of the *pmrHFIJKLM* operon) are both transcriptionally activated by PmrAB. Mutations in *pmrG* did not affect the resistance to polymyxin B [2]. Tamayo *et al.* recently identified two additional targets of PmrAB - *yibD* and *dgoA*. However, none of these was involved in resistance to polymyxin B or to high concentrations of Fe^{3+} [22]. These genes might therefore represent a group of as-yet-unidentified functions regulated by the PmrAB system [22]. Also, PmrAB-regulated genes involved in resistance to Fe^{3+} and pEtN addition to LPS remain to be identified [22]. Together with the recent indications of new PmrAB-dependent functions, this raises the possibility that not all PmrAB targets have yet been identified. Therefore, in this study we used an *in silico* approach to predict targets of the PmrAB regulatory system. Several methodologies exist for genome-wide screening using a motif model (or mathematical representation) of experimentally verified regulatory sites [23-27]. These assign to each possible motif position in the genome a score (the specifics of which depend on the methodology) that indicates how well the subsequence located at that position matches the motif model. Genome-wide screenings of this type have proved successful in detecting additional targets of the regulator being investigated. However, more reliable predictions for motifs in specific pathways have been obtained by incorporating cross-species comparisons (phylogenetic footprinting) [26,28-34]. Because evolutionary forces tend to preferentially retain functional DNA sequences, motifs that are conserved in the intergenic regions of orthologs derived from several related species are more likely to be biologically relevant [35,36].

In this study, we combine both approaches. Putative targets identified by a genome-wide screening were, whenever
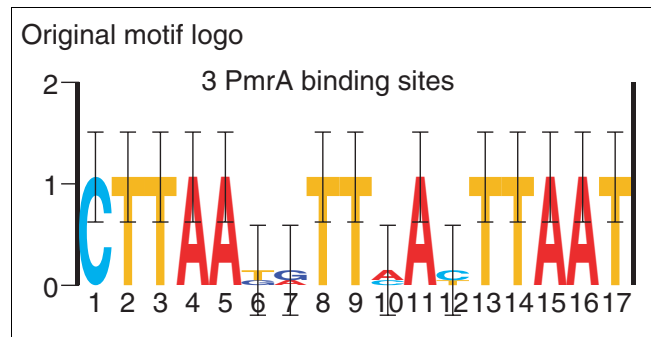
Figure 1
Consensus sequence of the PmrA box. Motif logo representing the initial motif model used to screen the *S. typhimurium* intergenic sequences.

possible, analyzed by phylogenetic footprinting based on Gibbs sampling [33,34,37]. Four interesting targets were validated by wet lab experiments and the PmrA box of a representative target was subjected to site-directed mutagenesis.

Results
Genome-wide screening using a PmrA motif model
Gibbs sampling was used to detect PmrA-binding motifs in the intergenic regions of three experimentally verified PmrAB targets (*ugd*, *pmrC*, *pmrG*). The logo of the statistically overrepresented motif detected is represented in Figure 1. This motif corresponded to the PmrA-binding site experimentally identified by Aguirre *et al.* [15] and partially overlapped the PmrA-binding site delineated by Wosten *et al.* [14]. They detected this site upstream of the transcription start of *pmrC*, in the intergenic region between *pmrG* and *pmrH*, and upstream of *ugd* (on the plus strand) [14,15]. We used the obtained motif model in a genome-wide screening of the *S. typhimurium* intergenic sequences [38]. Table 1 summarizes the results of our screening, using a threshold as described in Materials and methods. From experimentally verified examples, it appears that the PmrA motif can be biologically functional not only when present on the plus strand (as in the case of *pmrH*), but also when located on the minus strand (for example in *pmrG*) [14]. Therefore, both strands of the genome sequence were screened.

Identification of close homologs
We can expect to detect conserved biologically active PmrA motifs only in species that have a functional counterpart of the *S. typhimurium* PmrAB system. Of all the completely sequenced bacterial species, only the genomes of *S. typhimurium*, *S. typhi*, *Escherichia coli*, *Shigella flexneri* and *Yersinia pestis* contain the amino-acid motif that determines the specificity of the sensor protein PmrB (the amino acids suggested to be involved in binding Fe^{3+} [4]). Also, the protein domains involved in the binding of PmrA to DNA were almost perfectly conserved in the PmrA orthologs in the species above (PF00486 domain, see supplementary information on

Table 1

List of the putative PmrAB targets in *S. typhimurium*

Name	Description	Score	Instance	Alignment	Footprint	Distribution (COG)	Distribution [38]
Minus strand							
STM1273	Putative nitric oxide reductase	0.848436	CTTAATGTTT TCTTAAT	/	/	1000	All *Salmonella* only
STM2132	Pseudogene; frameshift; putative RBS for *STM2133*	0.814252	TTTTAGATTC ACTTAAT	/	/	1000	Some or all *Salmonella* only
STM4596	Paralog of *E. coli* ORF, hypothetical protein (AAC73478.1); BLAST hit to putative inner membrane protein	0.806962	TTTAATATTC ACTTAAA	/	/	1000	Some *Salmonella* only
STM3131	Putative cytoplasmic protein; putative RBS for *STM3130*; putative first gene of operon with *STM3130* (putative hypothetical protein)	0.801641	CTTAATTTTT ACTTATT	/	/	1000	All *Salmonella* only
STM1020	Gifsy-2 prophage	0.791616	CTTATTGTTA AGTCAAT	/	/	1000	Other distributions
stdA	*STM3029*; paralog of *E. coli* putative fimbrial-like protein (AAC73813.1); BLAST hit to putative fimbrial-like protein	0.788548	CAAAACATT AACTTAAT	/	/	1000	Subspecies I only?
ugd	*STM2080*; *S. typhimurium* UDP-glucose 6-dehydrogenase	0.781719	CTCAGAATT AACTTAAT	m	+	1100	All nine genomes
sinR	*STM0304*; *S. typhimurium* SINR protein. (SW:SINR_SALTY) transcriptional regulator	0.780204	CTTGATATCA TCTTAAT	/	/		Subspecies I only
STM3131	Putative cytoplasmic protein; putative RBS for *STM3130*; putative first gene of operon with *STM3130*; (putative hypothetical protein)	0.772846	CTTAATACTC ACATTAT	/	/	1000	Other distributions
STM4413	Putative imidazolonepropionase and related amidohydrolases; putative RBS for *STM4412*; first gene of operon with *STM4412* (D-galactonate transport)	0.771153	GTGAATGTT AAATTAAT	/	/	1000	Some or all *Salmonella* only
ybdO	*STM0606*; ortholog of *E. coli* putative transcriptional regulator LYSR-type (AAC73704.1); BLAST hit to putative transcriptional regulator, LysR family	0.769839	CTTAATGTA GAGTTTAT	m	+	1110	All *Salmonella* only
oraA	*STM2828*; ortholog of *E. coli* regulator, OraA protein (AAC75740.1); BLAST hit to regulator	0.766748	CTTGATGGT AATTTAAC	m	-	1110	All nine genomes
sdhC	*STM0732*; Ortholog of *E. coli* succinate dehydrogenase, cytochrome b556 (AAC73815.1); Putative RBS for *sdhD*; first gene of putative operon encoding succinate dehydrogenase	0.765950	CTTATTATTC CCTTAAG	/	/	1000	All nine genomes
ycaR	*STM0987*; Ortholog of *E. coli* ORF, hypothetical protein (AAC74003.1); BLAST hit to putative inner membrane protein; Putative RBS for *kdsB*; first gene of a putative operon with *ksdB* (CMP-3-deoxy-D-manno-octulosanate transferase)	0.765889	TTCAATATTA ACATAAT	/	/	1000	All nine genomes
lasT	*STM4600*; Ortholog of *E. coli* ORF, hypothetical protein (AAC77356.1); BLAST hit to putative tRNA*tRNA methyltransferase	0.765754	ATTTAGGATA ATTTAAT	nd	/	1110	All nine genomes
STM2137	Putative cytoplasmic protein	0.764036	TTTAACCTTA ATTTAAT	nd	/	1100	Some *Salmonella* only
STM1672	Putative cytoplasmic protein	0.762904	ATTAATAGTC ACTTATT	/	/	1000	Subspecies I only?

Table 1 *(Continued)*

List of the putative PmrAB targets in *S. typhimurium*

gcvA	*STM2982*; Ortholog of *E. coli* positive regulator of *gcv* operon (AAC75850.1); first gene of putative operon (*gcvA, ygdD, ygdE* containing a SAM-dependent methyltransferase)	0.761166	CTTAATGTC GAATGAAT	m	+	1111	All nine genomes
ycgO	*STM1801*; Ortholog of *E. coli* ORF, hypothetical protein (AAC74275.1); BLAST hit to putative CPA1 family, Na:H transport protein	0.760685	TTTAACATTA ACATAAT	m	+	1110	All nine genomes?
STM2287	Paralog of *E. coli* putative sulfatase* phosphatase (AAC75329.1); BLAST hit to putative cytoplasmic protein	0.759519	CTTATTATTC ACATAAC	/	/	1000	Some or all *Salmonella* only?
yebW	*STM1852*; Ortholog of *E. coli* ORF, hypothetical protein (AAC74907.1); BLAST hit to putative inner membrane lipoprotein	0.754895	CTCAATGTTA ACTACTT	/	/	1000	All nine genomes?
STM0897	Hypothetical protein Fels-1 prophage	0.754468	CGTAAGGCT CTTTTAAT	/	/	1000	Some *Salmonella* only
lpfA	*STM3640*; *S. typhimurium* long polar fimbrial protein A precursor; first gene of a putative fimbriae synthesis operon	0.753228	ATTAAGAATA AATTAAT	/	/	1000	Other distributions
Plus strand							
*yjdB**	*STM4293*; *S. typhimurium* hypothetical 61.6 kDa protein in *basS*pmrA-adiY* intergenic region. (SW:YJDB_SALTY) putative integral membrane protein; Putative RBS for *basR*; first gene of the putative operon (*yjdB basR basS*)	0.930146	CTTAAGGTT CACTTAAT	m	+	1111	All nine genomes
ugd	*STM2080*; *S. typhimurium* UDP-glucose 6-dehydrogenase	0.913666	CTTAATATTA ACTTAAT	m	+	1100	All nine genomes
yfbE/ais	*STM2297*; Ortholog of *E. coli* putative enzyme (AAC75313.1); first gene of the *yfbE* operon; shared intergenic with *ais*	0.912660	CTTAATGTTA ATTTAAT	m	+	1111	All nine genomes?
STM1269/ STM1268*	Putative chorismate mutase; intergenic shared with *STM1268*	0.888478	CTTAATGTTA TCTTAAT	/	/	1000	All *Salmonella* only
STM0692	Paralog of *E. coli* nitrogen assimilation control protein (AAC75050.1); putative transcriptional regulator, LysR family	0.814773	CTTGATGTT GATTTAAT	/	/	1000	All *Salmonella* only
*ybjG/mdfA**	*STM0865*; Ortholog of *E. coli* orf, hypothetical protein (AAC73928.1); putative permease; intergenic shared with *mdfA* (multidrug translocase)	0.810981	CTTTAAGGTT AATTTAA	m	+	1111	All nine genomes
STM2901	Hypothetical protein putative cytoplasmic protein; located downstream of pathogenicity island 1	0.803712	CTTAATATCA ATATAAT	/	/	1000	Other distributions
yhjC/yhjB	*STM3607*; Ortholog of *E. coli* putative transcriptional regulator LysR-type (AAC76546.1); intergenic shared with *yhjB* (putative transcriptional regulator)	0.796967	TTGAATATTA ATTTAAT	nd	/	1110	All nine genomes?
yjbE/pgi	*STM4222*; Ortholog of *E. coli* orf, hypothetical protein (AAC76996.1); BLAST hit to putative outer membrane protein; first gene of the putative operon (*yjbE, yjbF, yjbG, yjbH*) consisting of putative outer membrane (lipo)proteins; intergenic shared with *pgi* (glucosephosphate isomerase)	0.791181	TTTAATTTTA ACTTATT	/	/	1000	All nine genomes?
*yibD**	*STM3707*; Ortholog of *E. coli* putative regulator (AAC76639.1); BLAST hit to putative glycosyltransferase	0.790879	CTTAATAGTT TCTTAAT	m	+	1100	Other distributions

Table 1 *(Continued)*

List of the putative PmrAB targets in *S. typhimurium*

STM1926/flhC	Putative cytoplasmic protein; Putative RBS for *STM1926*; first gene of a putative operon with *yecG* (putative universal stres protein); shared intergenic with *flhC* en *flhD* (flagellar transcriptional activator)	0.790699	CCTAATGTT CACTTTTT	/	/	1000	Some or all *Salmonella* only
STM0334/ STM0335	Putative cytoplasmic protein; shared intergenic with *STM0335*	0.789514	TTTCATATTC ATTTAAT	/	/	1000	Some *Salmonella* only
ybdN	*STM0605*; Ortholog of *E. coli* orf, hypothetical protein (AAC73703.1); BLAST hit to putative 3-phosphoadenosine 5-phosphosulfate sulfotransferase (PAPS reductase)*FAD synthetase Putative RBS for *ybdM*; first gene of a putative operon with *ybdM* (hypothetical transcriptional regulator)	0.788778	ATTAATATAA ATTTAAT	nd	/	1100	All nine genomes?
glgB	*STM3538*; Ortholog of *E. coli* 1,4-alpha-glucan branching enzyme (AAC76457.1); BLAST hit to 1,4-alpha-glucan branching enzyme; Putative RBS for *glgX*; putative first gene of operon involved in glycogen synthesis	0.779808	TTTAAGGGT AGCTTAAT	m	-	1111	All nine genomes
leuO	*STM0115*; *S. typhimurium* probable activator protein in leuabcd operon. (SW:LEUO_SALTY) putative transcriptional regulator (LysR family)	0.776490	ATTAATGTTA ACTTTTT	m	-	1111	All nine genomes
STM0343	Paralog of *E. coli* orf, hypothetical protein (AAC75237.1); BLAST hit to AAC75237.1 identity in aa 10 - 512 putative Diguanylate cyclase*phosphodiesterase domain	0.774271	ATTAATGTTA CTTTAGT	nd	/	1100	Subspecies 1 only
orf242	*STM1390 S. typhimurium* ORF242 (gi|4456866) putative regulatory proteins, *merR* family	0.773644	CTTAGTCTTC ATTTGAT	/	/	1000	Other distributions
STM1868A/ mig-3	Lytic enzyme; intergenic shared with *mig-3* (phage assembly protein)	0.773462	CTTAATGATT ATTTATT	/	/	1000	?
STM2763/ STM2726	Paralog of *E. coli* prophage CP4-57 integrase (AAC75670.1); BLAST hit to putative integrase; intergenic shared with *STM2726* (putative inner membrane)	0.772053	ATTAATGTCC ATTTAGT	/	/	1000	*S. typhimurium* only
pntA	*STM1479*; Ortholog of *E. coli* pyridine nucleotide transhydrogenase, alpha subunit (AAC74675.1); Blast hit to AAC74675.1 pyridine nucleotide transhydrogenase (proton pump), alpha subunit; Putative RBS for *pntB*; first gene of the putative operon (*pntA, pntB*)	0.770547	TTTAATGTTA ATTTCTT	m	-	1111	All nine genomes
STM0057/cit2	Putative citrate-sodium symport; intergenic shared with *citC2* (citrate lyase synthetase)	0.767968	CTCATGGTT CATTGAAT	nd	/	1110	Other distributions
yrbF	*STM3313*; Ortholog of *E. coli* putative ATP-binding component of a transport system (AAC76227.1); Blast hit to AAC76227.1 putative ABC superfamily (atp_bind) transport protein; Putative RBS for *yrbE*; RegulonDB:STMS1H003330; first gene of putative *yrb* operon (ABC transporter)	0.766758	CCTAATTTTG ACTTTAT	m	+	1111	All nine genomes
yejG	*STM2220*; Paralog of *E. coli* orf, hypothetical protein (AAC75242.1); Blast hit to putative cytoplasmic protein	0.767099	CTTTATGTTT ATTTTAT	m	+	1111	All nine genomes
slsA	*STM3761*; putative inner membrane protein	0.765418	CTTTATGTTA TTTAAAT	nd	/	1110	Other distributions
yhcN	*STM3361*; Ortholog of *E. coli* orf, hypothetical protein (AAC76270.1); Blast hit to putative outer membrane protein	0.764452	ATTAGTGTAT ACTTAAT	m	+	1111	All nine genomes?

Table 1 *(Continued)*

List of the putative PmrAB targets in *S. typhimurium*

yceP	*STM1161*; Ortholog of *E. coli orf*, hypothetical protein (AAC74144.1); Blast hit to putative cytoplasmic protein	0.764191	TTTATTGTTC ATATAAT	m	+	1100	All nine genomes
STM4098	putative arylsulfate sulfotransferase	0.763003	TCTAATATTT ATTTAAT	nd	/	1100	Subspecies 1 only?
stfA	*STM0195*; *S. typhimurium* major fimbrial subunit StfA	0.762241	ATCAATTTTA ATTTAAT	/	/	1000	Some *Salmonella* only
atpF	*STM3869*; Ortholog of *E. coli* membrane-bound ATP synthase, F0 sector, subunit b (AAC76759.1); Blast hit to imembrane-bound ATP synthase, F0 sector, subunit b; Putative RBS for *atpH*; first gene of a putative operon encoding putative ATP synthase	0.760841	CAGAAGGTT AACTAGAT	m	+	1111	All nine genomes
yegH/wza	*STM2119*; Ortholog of *E. coli* putative transport protein (AAC75124.1); Blast hit to putative inner membrane protein; intergenic shared with *wza* (putative polysaccharide export protein)	0.760004	ATTAATATTA AATGAAT	m	-	1111	All nine genomes
yjgD/argI	*STM4470*; *S. typhimurium* hypothetical protein in *argI-miaE* intergenic region (ORF15.6). (SW:YJGD_SALTY) putative cytoplasmic protein; Putative binding site for ArgR; shared intergenic regions with *argI* (arginine ornithine transferase); first gene of a putative operon with *miaE* (tRNA hydroxylase)	0.759514	ATTAAAATTC ACTTTAT	m	+	1111	All nine genomes
sseJ/ STM1630	*STM1631*; *S. typhimurium* secreted effector; regulated by SPI-2; shared intergenic with *STM1630* (putative inner membrane protein)	0.758303	CTTAAGAAAT ATTTAAT	/	/	1000	Some *Salmonella* only
csrA	*STM2826*; *S. typhimurium* carbon storage regulator	0.756990	CTTAGGTTTA ACAGAAT	m	+	1111	All nine genomes
dinP/yafK	*STM0313*; Ortholog of *E. coli* damage-inducible protein P; putative tRNA synthetase (AAC73335.1); Blast hit to AAC73335.1 DNA polymerase IV, devoid of proofreading, damage-inducible protein P; intergenic shared with *yafKJ* (periplasmic protein, putative amido transferase)	0.756938	CATACTGTA CACTTAAA	m	+	1111	All nine genomes
STM0346	Putative outer membrane protein; Homolog of *ail* and *ompX*	0.756369	CATTAGGTG CTCTTAAT	/	/	1000	Some *Salmonella* only
ybfA/STM0707	*STM0708*; Ortholog of *E. coli orf*, hypothetical protein (AAC73793.1); Blast hit to putative periplasmic protein; intergenic shared with *STM0707* (hypothetical protein)	0.754265	ATTAGTATTA ATTTAAC	m	+	1111	All nine genomes?
yncD/STM1587	*STM1587*; Ortholog of *E. coli* putative outer membrane receptor for iron transport (AAC74533.1); Blast hit to paral putative outer membrane receptor; intergenic shared with *STM1586* (putative receptor)	0.754063	CATTTTCTTA ACTTAAT	m	-	1100	All nine genomes

Table 1 (*Continued*)

List of the putative PmrAB targets in *S. typhimurium*

yafC/*STM0275*	*STM0256*; Ortholog of *E. coli* putative transcriptional regulator LysR-type (AAC73313.1); Blast hit to putative transcriptional regulator, LysR family; intergenic shared *STM0275* (drug efflux protein)	0.753257	CAAAATATC AATTTAAT	m	-	1111	Other distributions

Name: name of the gene in the *S. typhimurium* genome (NC_003197). For genes that are divergently transcribed and have a shared intergenic region, the gene for which the motif is detected on the plus strand is indicated first and the gene for which the motif is on the minus strand is indicated after the slash. Description: annotation of the encoded proteins and genome location of the genes (derived from GenBank and Sanger annotation). Score: normalized score assigned to the respective motifs by MotifLocator. Site: instance of the motif as detected in the respective intergenic sequence. Distribution (COG): distribution of the protein as determined by our analysis. The distribution is indicated by a binary profile that indicates the presence 1 versus absence 0 of the protein in species (serovars) of, respectively, *Salmonella*, *E. coli*, *Shigella* and *Yersinia* (for example, 1111 indicates protein present in all four species; 1000: protein present in *Salmonella* species only). Distribution: distribution of the protein encoded by the corresponding gene in nine bacterial genomes as determined by McClelland *et al.* [38]. Proteins having close homologs in at least one *Salmonella* strain but not in *E. coli* or *K. pneumoniae* are indicated by 'some *Salmonella* only'. Genes that contain close homologs in all genomes are indicated by 'all nine genomes'. Other combinations are indicated by 'other distributions'. ? indicates that the authors were not certain about the statement. Differences between the distribution as determined by McClelland *et al.* and the one determined by our analysis is due to the difference in selection criteria used to identify close homologs (see Materials and methods). Alignment: indicates whether the intergenic regions in the dataset could be locally aligned (nd, no local alignment detected that contained the original sequence of *S. typhimurium*; m, local alignment detected. If the dataset only contained homologs from *Salmonella* species, local alignments were considered noninformative (indicated by /)). Footprint: denotes whether the PmrA motif is conserved in the close homologs. +, the retrieved putative PmrA motif is conserved; -, the intergenic sequences of the orthologs could be locally aligned but the PmrA motif was not part of the conserved regions. Most promising PmrAB targets that contained a PmrA motif matching the PmrA consensus (Figure 4) are in bold face. PmrA motifs that are experimentally validated in this study are indicated by an asterisk.

our website [39]). Therefore, these γ-proteobacterial species were used to perform phylogenetic footprinting analysis. For each gene containing a potential hit of the PmrA motif in the *S. typhimurium* genome sequence, close homologs were selected as described in Materials and methods.

Phylogenetic footprinting using Gibbs sampling

For each dataset we aimed at constructing a local multiple alignment. We used Gibbs sampling to generate motifs that can be used as alignment seeds. Alignments were subsequently constructed based on the positions of these motif seeds. Potential seeds were selected using a heuristic described in the supplementary information on [39]. Such multiple alignments summarize the motifs in the intergenic sequences that are conserved between species. We used the alignments to verify whether the putative PmrA motifs retrieved by the genome-wide screening were conserved in other species. Table 1 gives an overview of the results of the genome-wide screening and the phylogenetic footprinting approach (individual alignments are displayed in the supplementary information at [39]).

Detailed analysis of the putative PmrAB targets

Putative PmrA motifs were detected in the intergenic regions of genes encoding transcriptional regulators, outer-membrane and secreted proteins, proteins with functions involved in flagella and fimbria synthesis, proteins with a function related to the modification of cellular components, putative transport proteins, proteins involved in amino-acid synthesis and also in phage remnants. As mentioned above, if the puta-

tive PmrAB-regulated genes contained close homologs in other species, the intergenic sequences of these close homologs were locally aligned to check whether putative PmrA motifs were conserved in these other species as well. For some of the datasets, however, no local alignment could be identified (no motif detected). Closer inspection showed that most of these datasets contained highly homologous paralogs of the original sequence. The intergenic sequences of these paralogs showed an overall low degree of conservation (for example, STM0057) with the original intergenic sequence in *S. typhimurium* (data not shown). In some of the datasets, a local alignment of the respective intergenic regions could be detected, but the putative PmrA motif was not present within the conserved parts of the alignment (for example, *leuO*). For these putative PmrAB targets, phylogenetic footprinting could not strengthen the confidence in the prediction of the PmrA motif. If such putative motifs are biologically active, their activity will be restricted to *Salmonella* serovars or *S. typhimurium*.

Our analysis revealed that PmrA motifs, present in the intergenic sequences of known PmrAB-dependent *S. typhimurium* genes, were also conserved in the intergenic sequences of the orthologs of these genes in related species (Figure 2). An overview of the alignments of these known targets is given below.

pmrH (the first gene of an operon that contains the genes *pmrHFIJKLM*; Table 1) is the only known PmrAB-regulated gene for which the PmrA motif is conserved in all genome

(a)

(b)

Figure 2 *(see legend on page after next)*

(c)

(d)
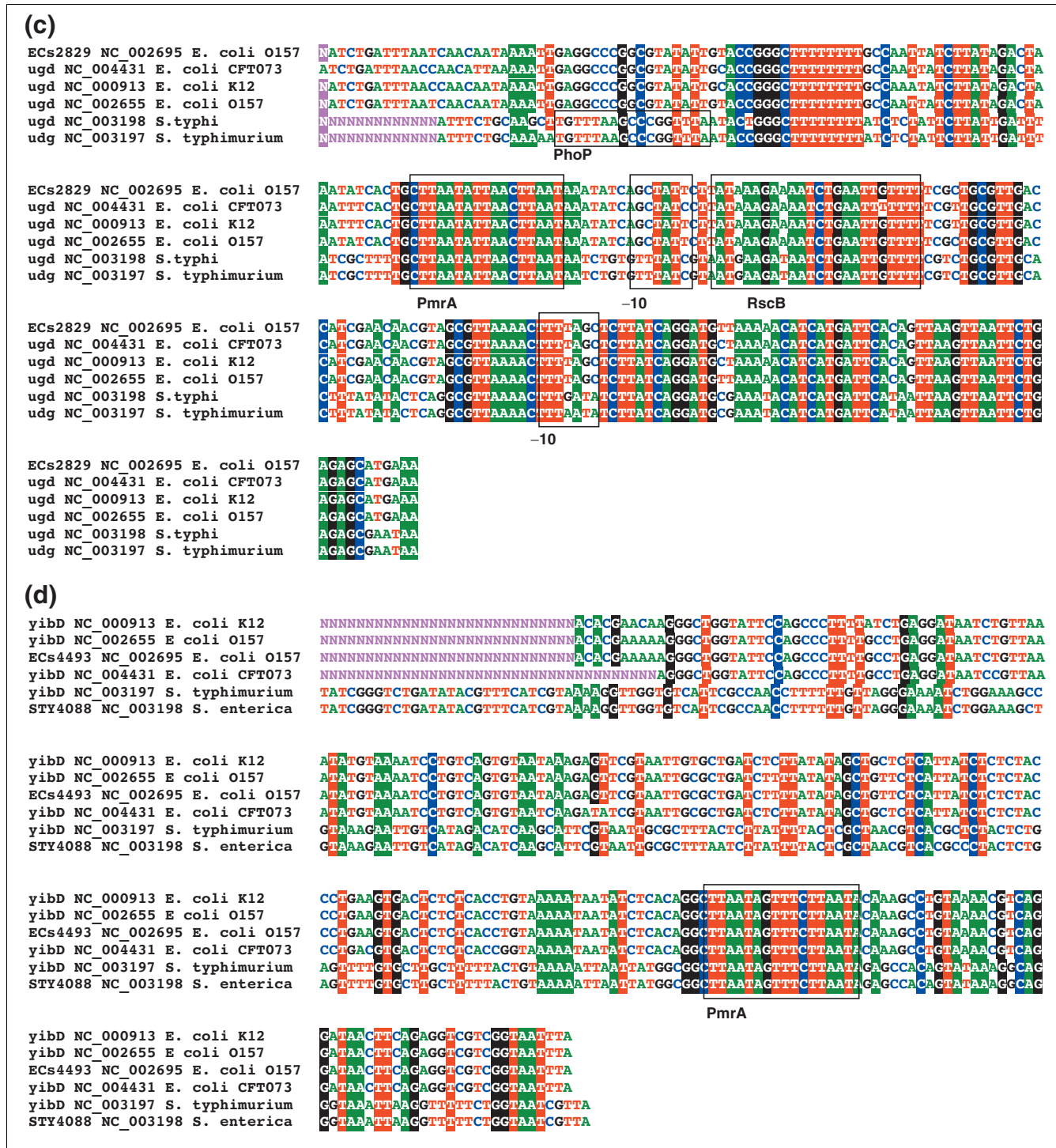
Figure 2 *(continued from the previous page, see legend on next page)*
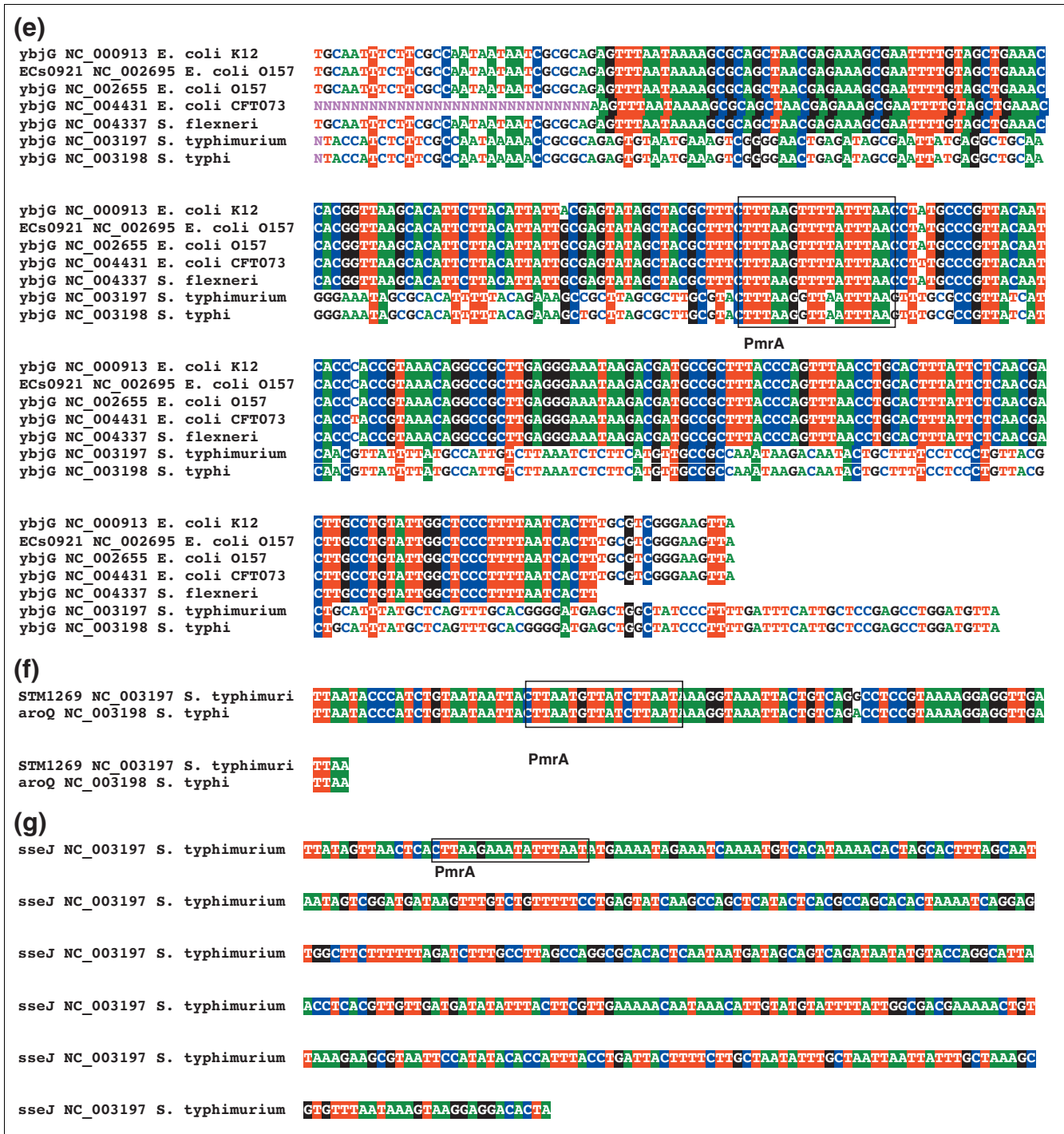
Figure 2 *(Continued from previous page)*
Local alignments of the most promising targets. Examples of local alignments obtained by phylogenetic footprinting of known PmrAB targets and of some promising potential targets. Known motifs or (putative) PmrA motifs are indicated by a box. **(a)** *yfbE* (*pmrH*); **(b)** *yjdB* (*pmrC*); **(c)** *ugd*; **(d)** *yibD*; **(e)** *ybjG* (*mig-13*); **(f)** *STM1269* (*aroQ*); **(g)** *sseJ*.

sequences analyzed (including that of *Y. pestis*). In *pmrC*, encoding a gene with unknown function [15,22], the PmrA motif is conserved in the intergenic regions of its orthologs in *E. coli* strains, *Salmonella* species and *Shigella*. *ugd* encodes a UDP-D-glucose dehydrogenase required for the synthesis of

Ara4N. Three two-component systems are involved in its regulation (PmrAB, PhoPQ and RcsCB) [12,15] and this is reflected in the presence of the corresponding motifs: *ugd* contains PmrA, PhoP and RcsB motifs. The experimentally confirmed PmrA motif on the plus strand and part of the -10

sequence as determined by Aguirre *et al.* have been conserved in *S. typhimurium*, *S. typhi* and *E. coli* [15]. The promoter of *ugd* also has a hit of the PmrA motif on the minus strand. This was, however, not confirmed by DNA footprint analysis [15] and might represent a false positive. The PhoP motif on the plus strand in *ugd* of *Salmonella*, although occurring as a dyad, is not conserved in close orthologs and was recently demonstrated to be non-functional [12]. The recognition site for the RcsB protein [12] is also conserved in *E. coli*. Lastly, *yibD* encodes a putative glycosyltransferase. The PmrA motif is conserved in *E. coli*. *yibD* has recently been identified as a PmrAB target by a genome-wide mutagenesis study. Its actual function is still unknown [22].

Experimental validation by expression analysis

Our *in silico* predictions pointed towards putative targets of the PmrAB regulatory system. Some of these have functions that were previously not associated with the PmrAB system. To prove the strength of our *in silico* approach, four potential targets were selected for biological validation: *yibD* (novel at the time of our analysis), *aroQ* (STM1269), *mig-13* and *sseJ*. *aroQ* and *yibD* were selected because a perfect repeat of the previously described PmrA half-site (CTTAAT [15]) was detected in their respective intergenic regions. *mig-13* (Figure 2) was chosen because it has previously been reported as a gene selectively induced in macrophages, but with further unknown regulation [40]. *sseJ* (Figure 2) was further analyzed because although PmrAB-regulated genes have been implicated in animal virulence [2], no direct link between SPI-2 (*Salmonella* pathogenicity island 2) gene regulation and PmrAB has been demonstrated yet.

For each of these targets, green fluorescent protein (GFP) reporter fusions were constructed and their expression was determined by fluorescence-activated cell sorter (FACS) analysis in wild-type *S. typhimurium* and a *pmrA*::Tn*10*d mutant. Because the PmrAB system is sensitive to Mg^{2+} and Fe^{3+} concentration, we tested the effect of these signals on the expression of the fusions [22] (Table 2). All experiments were performed at pH 5.8 and pH 7.7. All fusions tested exhibited the same PmrAB-dependent expression behavior at both pH levels. In all experiments, *pmrC* was used as a positive control.

The *pmrC* fusion showed a clear induction by either Mg^{2+} deprivation or Fe^{3+} excess. The observed level of induction was higher for the Fe^{3+}-dependent signal than for the Mg^{2+}-dependent signal and the combination of both signals seemed to act synergistically. For both signals, induction was abrogated in a *pmrA*::Tn*10*d background, indicating that induction by Mg^{2+} and Fe^{3+} is solely PmrAB dependent. For the *mig-13* fusion, similar observations were made, although induction by low Mg^{2+} and the synergistic effect of both signals were less pronounced. *mig-13* also exhibited a considerable background expression level both in a *pmrA*::Tn*10*d mutant and in the uninduced state in a wild-type background.

aroQ was strongly induced by low Mg^{2+} and induction was abrogated in a *pmrA*::Tn*10*d background. The influence of Fe^{3+} was less pronounced. In the case of *yibD*, the opposite was found: the *yibD* gene was barely induced by low Mg^{2+} but Fe^{3+} excess resulted in a large induction. For the *yibD* fusion, although Fe^{3+} excess, but not Mg^{2+} deprivation, seemed to be a sufficient signal to trigger expression, both signals acted synergistically. Also, induction of *yibD* was abrogated in a *pmrA*::Tn*10*d background. Compared to the other fusions, the observed expression levels of the *sseJ* fusion were rather low in the test conditions. Because *sseJ* showed a higher overall expression level at pH 5.8, these data were considered most representative (see Table 2). Results show an upregulation of *sseJ* expression in elevated Fe^{3+} concentrations that was absent in the *pmrA*::Tn*10*d background. As observed for *mig-13*, *sseJ* was expressed at a background level in the mutant *pmrA*::Tn*10*d. Interestingly, even at low concentrations, Mg^{2+} seemed to counteract the Fe^{3+}-dependent induction.

Site-directed mutagenesis of the PmrA box

We constructed a set of mutant PmrA box sequences by site-directed mutagenesis of the PmrA box of *yibD*. AT → GC and GC → AT substitutions were introduced in the first half-site of the PmrA box (Figure 3a). We focused on the first half-site, as in the experimentally verified target *pmrC*, the second half-site overlaps with the -35 promoter site [14]. Expression was compared in different mutagenized fusions and the nonmutated fusion in the wild type and in the *pmrA*::Tn*10*d strain in all conditions mentioned above. For simplicity, only the expression values for two inducing conditions are displayed in Figure 3b. One is induction by the combined action of high Fe^{3+} and low Mg^{2+} concentrations and the other is the induction by raised Fe^{3+} levels in the presence of high Mg^{2+}. Observations under all other conditions allowed us to draw similar conclusions. Substitutions in the third and fifth positions of the motif box completely abrogated PmrAB-dependent expression. Mutations of the first, second, fourth or sixth position reduced PmrAB-dependent induction. Note that for the mutation in the second position, expression was very low but not completely abrogated. Results from this site-directed mutagenesis experiment of one representative PmrAB target allowed us to demonstrate unequivocally that the PmrA box we identified was responsible for PmrAB-dependent transcriptional activation. It also allowed us to further delineate the sequence requirements of the PmrA consensus.

Other promising PmrAB targets

On the basis of the instances of the PmrA motif in experimentally verified PmrAB targets of *Salmonella* (verified previously or validated in this study), a PmrA consensus was built (Figure 4). The motif consensus of PmrA was converted into a regular expression (A/C)(C/T)T(A/T)A(T/G/A) N_5NTT(A/T)A(T/A/G). To construct this regular expression we only considered the two conserved half-sites, because the PmrA motif is believed to be a dyad [15]. We preferred the part

Table 2

Expression analysis of the GFP reporter fusions

Fusion	Strain	10 mM MgCl$_2$	10 μM MgCl$_2$	100 μM FeCl$_3$	10 mM MgCl$_2$ 100 μM FeCl$_3$	10 μM MgCl$_2$ 100 μM FeCl$_3$
pmrC::GFP	**WT**	6.06 (0.18)	16.8 (1.42)	70.53 (3.84)	27.39 (4.41)	83.2 (3.21)
	pmrA⁻	1.00 (0.01)	1.02 (0.02)	1.08 (0.03)	1.03 (0.03)	1.16 (0.12)
mig-13::GFP	**WT**	6.17 (1.55)	13.50 (2.02)	35.81 (4.67)	17.86 (5.04)	49.23 (5.43)
	pmrA⁻	2.69 (0.11)	4.32 (0.48)	5.2 (0.09)	2.67 (0.16)	9.64 (1.19)
aroQ::GFP	**WT**	2.32 (0.22)	20.39 (1.54)	19.39 (0.53)	4.38 (0.19)	19.48 (2.07)
	pmrA⁻	1.06 (0.02)	1.09 (0.02)	1.71 (0.09)	1.02 (0.01)	1.09 (0.03)
yibD::GFP	**WT**	1.25 (0.02)	1.67 (0.26)	33.35 (7.01)	27.52 (5.64)	52.46 (8.98)
	pmrA⁻	1.26 (0.02)	1.21 (0.06)	1.30 (0.02)	1.14 (0.02)	1.81 (0.44)
sseJ::GFP	**WT**	7.68 (1.55)	11.25(1.46)	22.58 (1.01)	3.80 (1.13)	8.03 (1.27)
	pmrA⁻	5.64 (0.72)	8.72 (1.05)	7.35 (1.55)	2.99 (0.43)	6.47 (1.36)

All experiments were performed twice. Values indicate the average mean peak fluorescence measurements of at least three samples for the populations grown under the conditions indicated for one representative experiment. Values in parentheses represent standard deviations. All values are expressed in arbitrary units. Strains used: WT = ATCC14028s and *pmrA*⁻ = *pmrA*::Tn*10*d. For *pmrC*, *aroQ*, *mig-13* and *yibD*, values represented in the table correspond to experiments performed at pH 7.7. Similar results were obtained at pH 5.8 (data not shown). For *sseJ*, values correspond to experiments performed at pH 5.8 because at this pH the overall measured expression was higher. The constitutive *gfp* fusion (pFPV25.1) varied less than 10% between the conditions tested.

between the conserved half-sites of the regular expression to be represented as degenerate (that is, N$_5$). Indeed, the observed degree of conservation in the intermediate part of the motif model (Figure 4b) is probably related to the restricted sample size of the training set rather than being an intrinsic property of the motif. Promising motifs (indicated in bold in Table 1) are, therefore, motifs that match this regular expression and thus contain nucleotides that occur in the conserved half-sites of one of the experimentally verified examples. Promising targets for which the putative PmrA motif was also conserved in species other than *Salmonella* were *mig-13*, *yrbF*, *yjgD*, *ybdO*, *yejG*, *lasT* and *ybdN*. Promising targets only present in *S. typhimurium* and/or *S. typhi* were *STM1269* (*aroQ*), *STM1273*, *sseJ* and *lpfA*. Note that this listing is just based on an arbitrary selection criterion, that is, a preliminary PmrA motif consensus that will be improved as more PmrAB targets become experimentally validated. As well as the targets mentioned above, Table 1 contains other targets that are of interest because their annotation relates to the PmrAB system (such as *yncD*).

Discussion

Putative PmrAB targets were detected by genome-wide screening of *S. typhimurium* intergenic sequences using a PmrA motif model. If possible, the confidence in the predicted motifs was strengthened by a cross-species comparison: we tested whether the PmrA motif was conserved in the intergenic regions of close homologs in related species. To this end, we developed a two-step procedure for phylogenetic footprinting. In the first step, a motif-detection procedure

based on Gibbs sampling was performed to generate a list of motifs. In the second step, these motifs were used as seeds to generate local multiple alignments. Eventually, the biological relevance of the obtained alignments was assessed.

We used the alignments rather than a listing of the high-scoring motifs obtained by Gibbs sampling for the following reasons. First, we observed, as also reported by McCue *et al.*, a high overall similarity in intergenic regions of the selected species [34]. In general, the overall degree in conservation between the intergenic sequences of close homologs is about 93.56% for the sequenced representatives of *Escherichia* and *Shigella* species, 69.21% for *Shigella* and *Salmonella* and 53.31% for *Salmonella* and *Yersinia*. As a result of this property (high correlation in the data), not only the motif itself turns out to be conserved, but also its local neighborhood. Moreover, the degree of conservation between the aligned sequences in a biologically relevant alignment will reflect, in most cases, the phylogenetic relatedness of the species from which the sequences are derived (see Figure 2 for examples). By selecting the most promising alignment seeds (based on the appropriate heuristics for the scores) and constructing a local alignment with these seeds, we could also evaluate the local neighborhood of the seed. If this one seemed to be conserved as well, we could be more confident in the obtained alignment and in the motifs contained within the conserved parts. Therefore, the use of local alignments allows a better judgment on the reliability of the motifs.
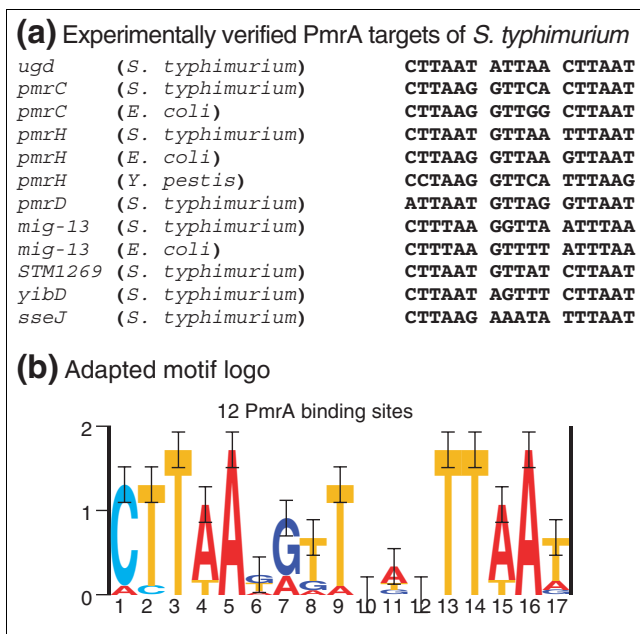
Second, Gibbs sampling is a stochastic procedure. The algorithm has to be run repeatedly on the same dataset, each time
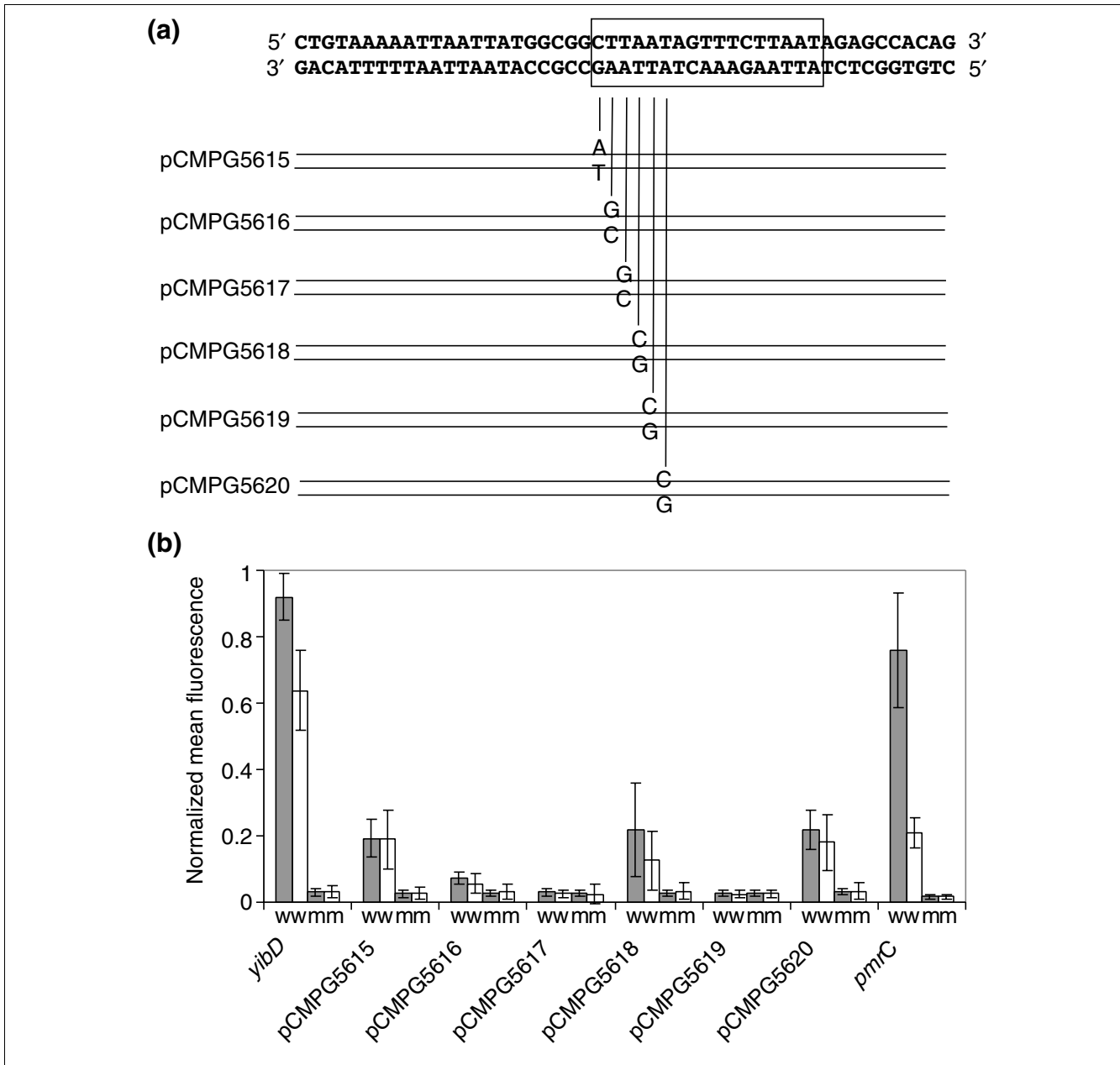
Figure 3
Site-directed mutagenesis of the PmrA box in *yibD*. **(a)** Construction of six species of the *yibD* promoter mutant, designated pCMPG5615 to pCMPG5620, each with a single base substitution (T → G or A → C) in the PmrA box. Promoters were fused to GFP and promoter activity was assessed by FACS analysis. **(b)** Plot of the normalized expression values of the six mutant fusions and the wild-type fusion measured in two distinct conditions in the wild type and *pmrA*::Tn*10*d mutant background. Gray bars represent condition 1 (pH 7.7, 100 μM FeCl$_3$ + 10 μM MgCl$_2$), white bars correspond to the expression values observed in condition 2 (pH 7.7, 100 μM FeCl$_3$ + 10 mM MgCl$_2$). w, wild-type background; m, *pmrA*::Tn*10*d mutant background. The *pmrC*::*GFP* fusion was included as a positive control. Bars represent the standard deviations of three independent measurements.

generating potentially different motifs. As a consequence, the output of a motif-detection approach can be simultaneously redundant and non-exhaustive: some statistically strong motifs are detected repeatedly in different runs. On the other hand, some motifs might never be detected. Indeed, because Gibbs sampling was originally designed for unrelated sequences and because of the high correlation in the data, the

number of possible equally scoring motifs (local optima) might be so high that many runs have to be performed before all motifs have been covered. All these local optima coincide with motifs that, when used as seeds, will result in a similar alignment. The same alignment can thus be obtained by several motifs, but there is no guarantee that all possible motifs that result in the same alignment will be detected by Gibbs

(a) Experimentally verified PmrA targets of *S. typhimurium*

ugd	(*S. typhimurium*)	CTTAAT ATTAA CTTAAT
pmrC	(*S. typhimurium*)	CTTAAG GTTCA CTTAAT
pmrC	(*E. coli*)	CTTAAG GTTGG CTTAAT
pmrH	(*S. typhimurium*)	CTTAAT GTTAA TTTAAT
pmrH	(*E. coli*)	CTTAAG GTTAA GTTAAT
pmrH	(*Y. pestis*)	CCTAAG GTTCA TTTAAG
pmrD	(*S. typhimurium*)	ATTAAT GTTAG GTTAAT
mig-13	(*S. typhimurium*)	CTTTAA GGTTA ATTTAA
mig-13	(*E. coli*)	CTTTAA GTTTT ATTTAA
STM1269	(*S. typhimurium*)	CTTAAT GTTAT CTTAAT
yibD	(*S. typhimurium*)	CTTAAT AGTTT CTTAAT
sseJ	(*S. typhimurium*)	CTTAAG AAATA TTTAAT

(b) Adapted motif logo

Figure 4
Refined consensus of the PmrA box. **(a)** Alignment of all experimentally verified PmrA sites ([15] or this work) in *S. typhimurium* [1]. PmrA sites in the orthologs of these respective experimentally verified genes are also displayed if these PmrA motif instances deviated from the PmrA motif in *S. typhimurium*. **(b)** An adapted motif model of the PmrA site was built (represented by its logo) on the basis of the sequences represented in (a).

sampling. Therefore, an alignment is a better summary of the degree of conservation between the intergenic regions than a listing of the highest-scoring motifs.

Moreover, regulatory systems such as PmrAB might have acquired some very species-specific targets. For such highly specialized regulatory systems, motifs are likely to be present in the intergenic sequences of a selected subset of orthologs only. Because such motifs occur in a restricted number of sequences of the dataset, they will not necessarily correspond to the highest-scoring motifs. Thus, they might be overlooked when selecting on high-scoring motifs by, for instance, setting a threshold on the score. Once a reliable local alignment of a set of intergenic sequences is obtained, one can judge the degree of confidence to put on the prediction of the motif of interest not only by checking in which subset of species the motif is conserved, but also by taking into consideration other factors, such as the functional annotation of the putative target. The motifs that we select on the basis of our heuristic will result in a biologically relevant alignment that includes the maximal number of species. As such, our heuristic tries to overcome the fact that Gibbs sampling is intrinsically unable to cope with correlated data. Note that the motif of interest (PmrA motif) does not necessarily have to correspond to the motif used to produce the alignment.

We showed that our *in silico* phylogenetic footprinting approach can be used to confirm targets detected by genome-wide screening. So far, it can only be used for species that show a high degree of conservation in their intergenic regions, similar to the conservation observed in this study. As more complete genomic data become available, the approach might be extended to other species.

As suggested previously [34], the high observed similarity in intergenic sequences might be due to the small phylogenetic distance between the species we analyzed. However, it cannot be excluded that because of the small size of the intergenic regions in bacteria and the very similar habitat and mechanism of regulation among the γ-proteobacterial species used in this study, a large part of the complete intergenic region is functional and therefore conserved. This hypothesis was also put forward by Rajewsky *et al.* [41]. The alignment of the intergenic region of the well-characterized *ugd* indeed points in that direction. Large parts of the conserved regions of the alignments correspond to experimentally verified motifs.

Remarkably, most potential PmrAB-regulated genes exhibited a footprint of the PmrA motif in *E. coli* only, and several target genes had no counterpart at all in organisms other than *Salmonella* species. This indicates a high degree of specialization of the PmrAB two-component system in *Salmonella*. Such specialization could also explain the considerable differences between PmrAB-dependent regulons in related species. For instance, in both *Y. pestis* and *S. typhimurium* the attenuated virulence of *phoP* mutants is ascribed to a defect in LPS modification, a process shown to be PmrAB-dependent [42]. So far, two *S. typhimurium* loci have been postulated to be involved in this LPS remodeling: *pmrHFIJKLM* and *ugd*. Only for *pmrH* did we detect an ortholog in *Y. pestis* and a conserved footprint of the PmrA motif in the promoter region of this ortholog. The Ugd protein does not even have a functional counterpart in *Y. pestis*. This low similarity in PmrAB regulon composition indicates that a different network of genes must be responsible for a similar phenotype in distinct species. This is not completely unexpected in view of the very different LPS composition of *Salmonella* and *Y. pestis* [42].

For most of the known experimentally verified targets, clear phylogenetic footprints of the PmrA motif could be detected in the intergenic regions of close homologs. In the intergenic region of *pmrD* we could recover the consensus sequence only partially (that is, one half-site) because the second half-site overlaps with the coding region (data not shown) and this was not included in the current analysis. Another PhoPQ-dependent gene that contributes to resistance to antimicrobial peptides is *mig-14* [10]. However, we could not find the presence of a clear PmrA consensus in the promoter of *mig-14*. Neither could we detect a PmrA motif in *dgoA*, which was previously shown to be regulated by PmrAB [22]. This would indicate that both targets are only indirectly dependent on

PmrAB. It can, however, not be excluded that they represent false negatives of our screening.

As well as the known targets, several putative new predictions could be made. Some of these predictions are consistent with previously published observations. Indeed, the PmrAB system is part of a complex regulatory cascade acting downstream of the pleiotropic PhoPQ system. The PhoPQ regulon is responsible for intracellular survival of bacteria and genes dependent on PhoPQ are induced in bacteria inside macrophages. Part of the PhoPQ regulon has been discovered to be dependent only indirectly on PhoPQ, via PmrAB. This PmrAB-dependent subset is known to confer resistance to cationic peptides by encoding genes involved in LPS modification and genes contributing to resistance to raised Fe^{3+} concentration. Genes encoding proteins involved in modification of membrane components and outer-membrane proteins are therefore sensible additional putative PmrAB targets. Another target worth mentioning in view of the Fe^{3+}-sensitivity of the PmrAB system is *yncD*, which encodes a putative outer-membrane receptor for iron transport.

Phage remnants, such as *mig-3*, have been described as macrophage inducible, PhoPQ-dependent genes [40], and thus can be PmrAB-dependent. This might explain the PmrA motif in the intergenic region between *STM1868A* and *mig-3*. Detweiler *et al.* showed that two genes, *virK* and *somA*, both coexpressed with the SPI-2 system, confer resistance to cationic peptides and their expression is PhoPQ-dependent. Also, four fimbrial operons had genes that were coexpressed with SPI-2 [43]. Predictions of the PmrAB-dependence of *sseJ*, which encodes a secreted effector of the SPI-2 system, or of genes that are involved in fimbrial synthesis (such as in *lpfA*, encoding the *S. typhimurium* long polar fimbria A precursor), could therefore be in agreement with these findings. Recently, the study of Kim *et al.* related PmrAB-dependent regulation to swarming motility functions in *S. typhimurium* [44]. This could explain why we detected a putative PmrA motif in the intergenic region of *flhC*, which encodes a master transcriptional activator of flagellar genes.

To confirm the predictive power of our methodology further, four putative PmrAB targets were validated biologically. Expression analysis clearly demonstrated PmrAB-dependence of *yibD*, which confirms the recent observations of Tamayo *et al.* [22]. The observed PmrA-dependence of *mig-13* accords with its being upregulated in macrophages in *in vivo* conditions [40]. The clear PmrAB-dependence of *aroQ*, which encodes a periplasmic chorismate mutase, is striking. In general, chorismate mutases are involved in the synthesis of tyrosine and phenylalanine and are key to the synthesis of a plethora of secondary metabolites [45]. The function of periplasmic chorismate mutases, which differ from the cytoplasmic chorismate mutases in their long carboxy-terminal extension [46], is still unclear. Periplasmic AroQ proteins have also been detected in *Y. pestis*, *Pseudomonas aerugi-*

nosa, *Mycobacterium* species, *Erwinia herbicola* and in the phytoparasitic nematode *Meloidogyne javanica* [46]. Strikingly, all these organisms containing AroQ interact with a eukaryotic host. This observation, together with the fact that AroQ is dependent on the key virulence regulator PmrAB in *S. typhimurium*, suggests that the as-yet-unknown function of AroQ might be involved in bacteria-host interactions.

Despite its low expression level in our *in vitro* conditions, the *sseJ* fusion showed a clear PmrAB-dependent induction by Fe^{3+} excess. SseJ is a secreted effector protein that is translocated across the membrane of the *Salmonella*-containing vacuole (SCV) by SPI-2. From recent evidence it was speculated that the putative acyltransferase activity of SseJ would be involved in modifying the lipid composition of the SCV [47,48], thereby interfering with the trafficking and maturation properties of the SCV in infected cells. The PmrA-dependence of *sseJ* would therefore link expression of genes involved in bacterial LPS modification with those involved in regulating the lipid composition of the SCV membrane.

Further experimental analysis will shed light on how these previously undescribed PmrAB-dependent proteins, with unknown functions, relate to the known part of the PmrAB-dependent regulon.

The extent to which each of the tested strains reacted to the signals Fe^{3+} or/and Mg^{2+} varied considerably. This is not surprising in view of the complex regulatory system that integrates both these signals. Indeed, both signals are transduced via the PhoPQ, PmrD, PmrAB multicomponent system, which includes a posttranslational signal transduction and a transcriptional feedback loop [1]. Depending on the affinities between the interacting components of such dynamic systems, small changes in the initial concentrations of the components might result in large differences in the observed expression levels [49]. A more detailed study of the dynamics of this system might reveal how such systems can integrate signals so differently.

Site-directed mutagenesis of the PmrA box in the *yibD* promoter indicated a crucial role for the T at position 3 and the A at position 5 of the first half-site of the motif. As can be deduced from the consensus site in Figure 4, no degeneracy is allowed at positions 3 and 5. This observation allows us to extrapolate to a certain extent the sequence requirements of the PmrA box in *yibD* to other PmrAB targets. Some positions seem essential, whereas it appears that the specific choice of nucleotide at the other positions affects the level of induction. By altering the nucleotides, the binding affinities of the regulatory protein to the box can be modified, allowing specific fine-tuning of gene expression in a cell.

Conclusions

We conclusively demonstrate that our *in silico* approach reliably identifies additional PmrAB-dependent targets. Although false positives will still be present among these predicted targets, the method offers an interesting approach for further elucidation of genetic networks involved in the expression of *S. typhimurium* virulence genes. We predicted the PmrAB-dependent regulation of four additional targets: *yibD*, *aroQ*, *mig-13* and *sseJ*. Our approach might become extendable to other species when more genome sequences become available.

Materials and methods
Selection of intergenic sequences

Genome sequences were obtained from GenBank [50]. All intergenic regions used in this study were extracted using the modules of INCLUSive [51] to automatically parse GenBank entries [52]. Here, we define an intergenic sequence as a region that contains the noncoding sequence between two coding regions. No overlap with coding regions is allowed. Intergenic regions with lengths smaller than 10 base-pairs (bp) were discarded because of computational reasons.

Construction of motif models

A motif model (a probabilistic representation of the consensus DNA pattern that is recognized by the respective regulatory protein) for PmrA was constructed using MotifSampler [53]. The PmrA training set consisted of the promoter regions of three known PmrAB-regulated genes (*ugd* [7,15,17], *pmrH* [7,14,17,19] and *pmrC* [2,14]) for which the binding of the PmrA protein to the promoter regions was verified by DNA footprint analysis [14,15].

Genome-wide screening

The intergenic regions of the complete genome of *S. typhimurium* LT2 (NC_003197 [38]) were screened using MotifLocator [54,55]. The scoring scheme used by MotifLocator is extensively described in Thijs *et al.* [55] and uses an extension of the classical position-weight matrix scoring scheme [56]. Given the motif model θ and the background model B_m a score $W(x)$ is computed for each window x of length l in the sequence S. $W(x)$ compares the score of the subsequence within the window being generated by the motif model to the score of the subsequence within the window being generated by the background model. b_j: nucleotide at position j in the segment.

$$W(x) = \log\left(\frac{P(x \mid \theta)}{P(x \mid S, B_m)}\right) = \sum_{j=1}^{l}[\log(\theta_j^{b_j}) - \log(P(b_j \mid S, B_m))]$$

Both the plus and minus strand were screened using a background model of order 3. The higher-order background allows implicit compensation for motifs that are located in a context highly resembling the global nucleotide composition of the genome. To apply a threshold on the scores, the scores of different motifs were normalized such that their values ranged between 0 and 1. The normalized scores $\overline{W}(x)$ are displayed in Table 1.

$$\overline{W}(x) = \frac{W(x) - W_{\min}}{W_{\max} - W_{\min}} \text{ with } W_{\min} = \min_{x} W(x) \text{ and } W_{\max} = \max_{x} W(x).$$

Hits with a score above 0.75 were retained (corresponding to a selection of the 0.003% top-scoring hits of the total number of possible motif positions in the genome. Possible positions are identified as overlapping windows of length *l*). To give a rough assessment of the number of hits with a score similar to the chosen threshold that could be expected from the specific nucleotide composition of the genome, we generated 100 random sets of intergenic sequences using a third-order background model. These random sets were scored with the same PmrA motif model. From these results it appeared that the true set contained three times more hits with a score above the threshold than an average random genome.

Identification of datasets

Highly similar homologs of the putative PmrAB-regulated genes were identified in the genome sequences of *S. typhimurium* (NC_003197), *S. typhi* (NC_003198), *S. flexneri* (NC_004337), *E. coli* O157:H7 (NC_002695), *E. coli* O157:H7 EDL933 (NC_002655), *E. coli* K12 (NC_000913), *Y. pestis* CO92 (NC_003143) and *Y. pestis* KIM (NC_004088). In general, only true orthologs are likely to have retained a similar function and therefore a similar mechanism of regulation [35]. However, ortholog identification is a difficult problem and discriminating between true orthologs and paralogs is not always straightforward. Because our motif-detection algorithm is, to some extent, robust against the presence of noise and allows for the presence of sequences that do not contain the motif [57], we did not make an *a priori* distinction between true orthologs and paralogs if both appeared highly similar to the original protein. This motivated us to use the principle of clusters of orthologs for dataset construction [58]. The pairwise BLAST scores obtained by mutually aligning the whole-genome sequences using BlastP [59] were used as input of the cluster program TRIBE-MCL [60]. Stringent criteria were applied to retain only closely related orthologs and paralogs (cut-off of the BLAST hit was an E-value of 1e-80). For those proteins that, when BLASTed against themselves, gave rise to an E-value higher than 1e-80 (*yjbE*, *STM1926*, *STM0344*, *yhcN*, *STM1868A*, *yceP*, *atpF*, *yjgD*, *csrA*, *ybfA*) the threshold was relaxed (E-value 1e-20). The choice of the stringent threshold was essential to maximally reduce the noise in the datasets.

Phylogenetic footprinting by Gibbs sampling

We used a two-step procedure for phylogenetic footprinting. In the first step, Gibbs sampling is performed to generate a list of motifs. Subsequently, local alignments are generated by

selecting motifs that can be used as alignment seeds and by assessing the relevance of the alignments by a test statistic.

Motif detection by Gibbs sampling
An advanced Gibbs sampling procedure for motif detection was used (MotifSampler). MotifSampler allows us to search for overrepresented motifs in each dataset. The motif length, the maximal number of different motifs and the background model are user-defined parameter settings of the algorithm described in Thijs *et al.* [53]. A recent extension of the algorithm allows to automatically determine the number of instances of a certain motif per sequence [55] and requires a predefined indication on the prior probability of expecting at least one motif per sequence. For each dataset, 100 runs of the MotifSampler were performed under the following conditions: motif lengths varying from 6, 8, 10, 12; background order 0; prior probability default value 0.7. Because Gibbs sampling is a stochastic procedure, each run can give rise to different motifs. To summarize the results from the 100 runs, all detected motifs were mutually compared and similar motifs were grouped. The information content was used as a similarity measure to compare motifs. For each dataset, therefore, a list of different potential motifs was obtained. Motifs in this list were ranked according to their log-likelihood score (LL-score) [53].

Generating reliable local alignments using the detected motifs
From the obtained list, motifs that could be used as seeds to generate a biologically relevant alignment were selected using a heuristic [61]. Motifs with a high LL-score that occurred preferentially once in each sequence were chosen (starting with those motifs that had the highest consensus score). Moreover, we preferentially selected motifs that occurred in the maximal number of species. For each dataset, multiple alignments were constructed using the position of these retrieved motifs as alignment initializations (seeds) until a reliable alignment was obtained. The alignment was considered biologically relevant if within a window of 100 bp around the motif it exhibited a degree of conservation that reflected the overall observed homology between intergenic sequences of the selected species (interspecies homology).

To assign a more quantitative criterion to the alignment, a *p*-value was assigned to each alignment that was calculated as follows: for each window of 100 bp around the motif, the largest conserved block not overlapping with the core motif was identified (using the consensus score of minimal 0.7 as minimal similarity measure). This *p*-value expresses the probability of observing a conserved block of the same length in a randomly aligned dataset of similar composition. Distributions of conserved blocks in randomly aligned sequences were constructed [62]. These random datasets take into account the observed high pairwise sequence homology between intergenic sequences derived from similar species (serovars) (homology between *E. coli* sequences, homology between *Salmonella* sequences, homology between *Y. pestis* sequences),

but not the interspecies homology between intergenic regions (for example, between *E. coli* and *Salmonella*). All alignments with a *p*-value less than 0.15 (the *p*-value of *ugd*) were considered as relevant (indicated in Table 1 with 'm'). Because the obtained alignments are local, they are gapless. In some cases, more than one alignment might be essential to cover the complete intergenic region.

Selected alignments are displayed in the supplementary information at [39]. Sequence editing was done in BioEdit [63].

Functional annotation
Functional annotation was derived from the National Center for Biotechnology Information (NCBI) [38,52] and from the Sanger annotation of *S. typhi* [64]. Specific genomic context was derived from NCBI [38,52]. The distribution of the putative targets (unique for *Salmonella* species versus more widely distributed), as derived from our clusters of orthologous groups (COGs), was verified by comparison to the analysis of McClelland *et al.* [38], who included, in addition to the species we used, several subspecies of *Salmonella* (six genomes), and species more distantly related to *Salmonella* (*Klebsiella pneumoniae*).

Bacterial strains and growth conditions
The bacterial strains and plasmids used in this study are listed in Table 3. Bacteria were grown overnight at 37°C with aeration in Luria-Bertani (LB) broth or in the nitrogen minimal medium of Nelson and Kennedy [65] with modifications as previously described [66]. The pH of the medium was buffered with 100 mM Tris-HCl, adjusted to pH 7.4 or pH 5.8. $MgCl_2$ was added at a final concentration of 10 μM or 10 mM. $FeCl_3$ was used at a final concentration of 100 μM from a freshly prepared 10 mM stock. Antibiotics were used, when appropriate, at the following concentrations: tetracycline, 30 μg/ml; and ampicillin, 100 μg/ml.

Molecular methods
Plasmid DNA, after passage through *S. typhimurium* LB5010 [67], was introduced into bacterial strains by electroporation. Polymerase chain reaction (PCR) was carried out in a Personal Mastercycler (Eppendorf, Hamburg, Germany) with *Pfx* DNA polymerase, using the manufacturer's instructions. The constructs containing the putative promoter regions of *yibD*, *mig-13*, *aroQ*, *sseJ* and *pmrC* and the site-directed mutated *yibD* promoter fragments were all verified by sequence analysis.

Construction of plasmids
To construct the *gfp* reporter fusions of *yibD*, *mig-13*, *aroQ*, *sseJ* and *pmrC*, the primers listed in Table 4 were used in a PCR reaction (as described above) to amplify the respective promoter regions from the ATCC14028s genome. Restriction sites in the primers are indicated in bold face in Table 4. The promoter fragments were digested with *Eco*RI and *Bam*HI

Table 3

Bacterial strains

Strain or plasmid		Relevant genotype	Reference or source
Salmonella	ATCC 14028s	Wild type	ATCC
	JSG421	*pmrA*::Tn*10*d	[21] kind gift of J.S. Gunn
	LB5010	*metA22 metE551 ilv-452 leu-3121 trp∆2 xyl-404 galE856 hsdLT6 hsdSA29 hsdSB121 rpsL120*	[67]
E. coli	DH5α	Fφ80∆*lac*ZM15 ∆(*lacZYAargF*)U169 *deoP recA1 endA1 hsdR17* (r$_k^-$m$_k^-$)	Gibco BRL
Plasmids	pCRII-TOPO	Cloning vector, Amp^R	Invitrogen
	pFPV25	ColE1 *mob bla* promoterless *gfp*mut3, Amp^R	[40] kind gift of R. Valdivia and S. Falkow
	pFPV25.1	Constitutive *rpsM* promoter in pFPV25, Amp^R	[40] kind gift of R. Valdivia and S. Falkow
	pCMPG5611	pFPV25 with *yibD* promoter	This work
	pCMPG5612	pFPV25 with *ybjG* promoter	This work
	pCMPG5613	pFPV25 with *STM1269* promoter	This work
	pCMPG5614	pFPV25 with *yjdB* promoter	This work
	pCMPG5621	pFPV25 with *sseJ* promoter	This work
	pCMPG5615	pCMPG5611 with point mutated putative PmrA motif C→A	This work
	pCMPG5616	pCMPG5611 with point mutated putative PmrA motif T→G	This work
	pCMPG5617	pCMPG5611 with point mutated putative PmrA motif T→G	This work
	pCMPG5618	pCMPG5611 with point mutated putative PmrA motif A→C	This work
	pCMPG5619	pCMPG5611 with point mutated putative PmrA motif A→C	This work
	pCMPG5620	pCMPG5611 with point mutated putative PmrA motif T→C	This work

and cloned into pCRII-TOPO that had been digested with *Eco*RI and *Bam*HI. The promoter fragments were subcloned as *Eco*RI/*Bam*HI fragments into the corresponding sites of pFPV25 [40], resulting in the pCMPG plasmids listed in Table 3. These plasmids were electroporated into ATCC14028s and JSG421 [21] after propagation through LB5010, as described above. Cloning steps were carried out in *E. coli* DH5α.

The single base-pair substitutions in the putative PmrA motif occurring in the *yibD* promoter sequence were introduced via a PCR approach using the QuickChange Site-Directed mutagenesis kit (Stratagene, La Jolla, CA), according to the manufacturer's instructions. The *yibD* promoter sequence introduced into pCRII-TOPO was used as the parent plasmid and appropriate primers were applied (sequences not

Table 4

Primers used to construct the GFP promoter fusions

Name	Sequence 5' to 3'	Description
Amplification of promoter regions		
Pro-115	**CCGAATTC**TAATTCGAGTTGCTTAAAGGCGGC	Amplification of *yibD* promoter region
Pro-116	**CCGGATCC**GCTCCCGCATTATATAACGGG	Amplification of *yibD* promoter region
Pro-117	**CCGAATTC**GCCAATAAAAACCGCGCAGAGTG	Amplification of *mig-13* promoter region
Pro-118	**CCGGATCC**AGCGAGTTGTTAAGGTTTTCCAGC	Amplification of *mig-13*promoter region
Pro-119	**CCGAATTC**GAAGATTCCGCAGAATCAACGGCC	Amplification of *aroQ* promoter region
Pro-120	**CCGGATCC**GGTGCTGCACATCAATAAAGAACAAAG	Amplification of *aroQ* promoter region
Pro-121	**CCGAATTC**GTATTGCATCTGGGCGGTCATCG	Amplification of *pmrC* promoter region
Pro-122	**CCGGATCC**AGGCGATTTGCCCAAGAACAGG	Amplification of *pmrC* promoter region
Pro-224	**ATGAATTC**GCTTCCCCATCCCAAACCACC	Amplification of *sseJ* promoter region
Pro-225	**ATGGATCC**GGAAGGCGTGCGCTTTCTTTTATC	Amplification of *sseJ* promoter region

Restriction sites in the primers are indicated in bold type.

shown). The site-directed mutated *yibD* promoter fragments were subcloned into pFPV25 (*Eco*RI/*Bam*HI), resulting in plasmids pCMPG5615 → pCMPG5620, as listed in Table 3. These reporter plasmids were electroporated into ATCC14028s and JSG421.

Fluorescence-activated cell sorter-based expression analysis

Bacterial strains harboring the reporter constructs were grown overnight in nitrogen (N)-minimal medium pH 7.4 plus 10 mM MgCl$_2$, harvested, washed in N-minimal medium pH 7.4 without MgCl$_2$, and diluted 1:100 in N-minimal medium pH 7.4 plus 10 mM MgCl$_2$. Mid-log-phase bacteria were then inoculated into the indicated media and grown for 3 h to allow expression of GFP. Bacteria were diluted into PBS and analyzed by flow cytometry with a Becton Dickinson FACSCalibur and CellQuest acquisition and analysis software [40] with gates set to forward and side scatters characteristic of the bacteria.

Nomenclature

As the gene names used in the annotation of the *S. typhimurium* genome sequence do not always match the 'common' names used in the PmrAB literature, we give a summary of the synonyms below. *STM1269* (*aroQ*); *ybjG* (*mig-13*); *pmrAB* (*basSR*); *ugd* (*udg*, *pagA*, *pmrE*); *pmrHFIJKLM* (*yfbE*, *pmrF*, *yfbG*, *STM2300*, *pqa*, *STM2302*, *STM2303*); *pmrC* (*yjdB*); *pmrG* (*ais*); *pbgP* (*yfbE,pmrH*).

Availability of data

All additional information of our analysis is available on our supplementary website [39].

References

1. Kato A, Latifi T, Groisman EA: **Closing the loop: the PmrA/PmrB two-component system negatively controls expression of its posttranscriptional activator PmrD.** *Proc Natl Acad Sci USA* 2003, **100:**4706-4711.
2. Gunn JS, Ryan SS, Van Velkinburgh JC, Ernst RK, Miller SI: **Genetic and functional analysis of a PmrA-PmrB-regulated locus necessary for lipopolysaccharide modification, antimicrobial peptide resistance, and oral virulence of *Salmonella enterica* serovar *typhimurium*.** *Infect Immun* 2000, **68:**6139-6146.
3. Zhao Y, Jansen R, Gaastra W, Arkesteijn G, van der Zeijst BA, van Putten JP: **Identification of genes affecting *Salmonella enterica* serovar *enteritidis* infection of chicken macrophages.** *Infect Immun* 2002, **70:**5319-5321.
4. Wosten MM, Kox LF, Chamnongpol S, Soncini FC, Groisman EA: **A signal transduction system that responds to extracellular iron.** *Cell* 2000, **103:**113-125.
5. Garcia Vescovi E, Soncini FC, Groisman EA: **Mg²⁺ as an extracellular signal: environmental regulation of *Salmonella* virulence.** *Cell* 1996, **84:**165-174.
6. Soncini FC, Groisman EA: **Two-component regulatory systems can interact to process multiple environmental signals.** *J Bacteriol* 1996, **178:**6796-6801.
7. Soncini FC, Garcia Vescovi E, Solomon F, Groisman EA: **Molecular basis of the magnesium deprivation response in *Salmonella typhimurium*: identification of PhoP-regulated genes.** *J Bacteriol* 1996, **178:**5092-5099.
8. Groisman EA: **The pleiotropic two-component regulatory system PhoP-PhoQ.** *J Bacteriol* 2001, **183:**1835-1842.
9. Kox LF, Wosten MM, Groisman EA: **A small protein that mediates the activation of a two-component system by another two-component system.** *EMBO J* 2000, **19:**1861-1872.
10. Brodsky IE, Ernst RK, Miller SI, Falkow S: ***mig-14* is a *Salmonella* gene that plays a role in bacterial resistance to antimicrobial peptides.** *J Bacteriol* 2002, **184:**3203-3213.
11. Roland KL, Martin LE, Esther CR, Spitznagel JK: **Spontaneous *pmrA* mutants of *Salmonella typhimurium* LT2 define a new two-component regulatory system with a possible role in virulence.** *J Bacteriol* 1993, **175:**4154-4164.
12. Mouslim C, Groisman EA: **Control of the *Salmonella ugd* gene by three two-component regulatory systems.** *Mol Microbiol* 2003, **47:**335-344.
13. Chamnongpol S, Dodson W, Cromie MJ, Harris ZL, Groisman EA: **Fe(III)-mediated cellular toxicity.** *Mol Microbiol* 2002, **45:**711-719.
14. Wosten MM, Groisman EA: **Molecular characterization of the PmrA regulon.** *J Biol Chem* 1999, **274:**27185-27190.
15. Aguirre A, Lejona S, Vescovi EG, Soncini FC: **Phosphorylated PmrA interacts with the promoter region of *ugd* in *Salmonella enterica* serovar *typhimurium*.** *J Bacteriol* 2000, **182:**3874-3876.
16. Zhou Z, Ribeiro AA, Lin S, Cotter RJ, Miller SI, Raetz CR: **Lipid A modifications in polymyxin-resistant *Salmonella typhimurium*: PmrA-dependent 4-amino-4-deoxy-L-arabinose, and phosphoethanolamine incorporation.** *J Biol Chem* 2001, **276:**43111-43121.
17. Gunn JS, Lim KB, Krueger J, Kim K, Guo L, Hackett M, Miller SI: **PmrA-PmrB-regulated genes necessary for 4-aminoarabinose lipid A modification and polymyxin resistance.** *Mol Microbiol* 1998, **27:**1171-1182.
18. Breazeale SD, Ribeiro AA, Raetz CR: **Oxidative decarboxylation of UDP-glucuronic acid in extracts of polymyxin-resistant *Escherichia coli*. Origin of lipid A species modified with 4-amino-4-deoxy-L-arabinose.** *J Biol Chem* 2002, **277:**2886-2896.
19. Trent MS, Ribeiro AA, Lin S, Cotter RJ, Raetz CR: **An inner membrane enzyme in *Salmonella and Escherichia coli* that transfers 4-amino-4-deoxy-L-arabinose to lipid A: induction on polymyxin-resistant mutants and role of a novel lipid-linked donor.** *J Biol Chem* 2001, **276:**43122-43131.
20. Trent MS, Ribeiro AA, Doerrler WT, Lin S, Cotter RJ, Raetz CR: **Accumulation of a polyisoprene-linked amino sugar in polymyxin-resistant *Salmonella typhimurium* and *Escherichia coli*: structural characterization and transfer to lipid A in the periplasm.** *J Biol Chem* 2001, **276:**43132-43144.
21. Gunn JS, Miller SI: **PhoP-PhoQ activates transcription of *pmrAB*, encoding a two-component regulatory system involved in *Salmonella typhimurium* antimicrobial peptide resistance.** *J Bacteriol* 1996, **178:**6857-6864.
22. Tamayo R, Ryan SS, McCoy AJ, Gunn JS: **Identification and genetic characterization of PmrA-regulated genes and genes involved in polymyxin B resistance in *Salmonella enterica* serovar Typhimurium.** *Infect Immun* 2002, **70:**6770-6778.
23. Staden R: **Methods for calculating the probabilities of finding patterns in sequences.** *Comput Appl Biosci* 1989, **5:**89-96.
24. van Helden J, Andre B, Collado-Vides J: **A web site for the computational analysis of yeast regulatory sequences.** *Yeast* 2000, **16:**177-187.
25. Hertz GZ, Stormo GD: **Identifying DNA and protein patterns with statistically significant alignments of multiple sequences.** *Bioinformatics* 1999, **15:**563-577.
26. Panina EM, Mironov AA, Gelfand MS: **Comparative analysis of FUR regulons in gamma-proteobacteria.** *Nucleic Acids Res* 2001, **29:**5195-5206.
27. Aerts S, Thijs G, Coessens B, Staes M, Moreau Y, De Moor B: **Tou-

can: deciphering the *cis*-regulatory logic of coregulated genes. *Nucleic Acids Res* 2003, **31**:1753-1764.

28. Gelfand MS, Koonin EV, Mironov AA: **Prediction of transcription regulatory sites in Archaea by a comparative genomic approach.** *Nucleic Acids Res* 2000, **28**:695-705.

29. Laikova ON, Mironov AA, Gelfand MS: **Computational analysis of the transcriptional regulation of pentose utilization systems in the gamma subdivision of Proteobacteria.** *FEMS Microbiol Lett* 2001, **205**:315-322.

30. Rodionov DA, Gelfand MS, Mironov AA, Rakhmaninova AB: **Comparative approach to analysis of regulation in complete genomes: multidrug resistance systems in gamma-proteobacteria.** *J Mol Microbiol Biotechnol* 2001, **3**:319-324.

31. Tan K, Moreno-Hagelsieb G, Collado-Vides J, Stormo GD: **A comparative genomics approach to prediction of new members of regulons.** *Genome Res* 2001, **11**:566-584.

32. Dombrecht B, Marchal K, Vanderleyden J, Michiels J: **Prediction and overview of the RpoN-regulon in closely related species of the Rhizobiales.** *Genome Biol* 2002, **3**:research0076.1-0076.11.

33. McCue L, Thompson W, Carmack C, Ryan MP, Liu JS, Derbyshire V, Lawrence CE: **Phylogenetic footprinting of transcription factor binding sites in proteobacterial genomes.** *Nucleic Acids Res* 2001, **29**:774-782.

34. McCue LA, Thompson W, Carmack CS, Lawrence CE: **Factors influencing the identification of transcription factor binding sites by cross-species comparison.** *Genome Res* 2002, **12**:1523-1532.

35. Frazer KA, Elnitski L, Church DM, Dubchak I, Hardison RC: **Cross-species sequence comparisons: a review of methods and available resources.** *Genome Res* 2003, **13**:1-12.

36. Gelfand MS: **Recognition of regulatory sites by genomic comparison.** *Res Microbiol* 1999, **150**:755-771.

37. McGuire AM, Hughes JD, Church GM: **Conservation of DNA regulatory motifs and discovery of new motifs in microbial genomes.** *Genome Res* 2000, **10**:744-757.

38. McClelland M, Sanderson KE, Spieth J, Clifton SW, Latreille P, Courtney L, Porwollik S, Ali J, Dante M, Du F *et al.*: **Complete genome sequence of *Salmonella enterica* serovar *Typhimurium* LT2.** *Nature* 2001, **413**:852-856.

39. **Supplementary information** [http://www.esat.kuleuven.ac.be/~kmarchal/ Supplementary_Information_GenBiol_2004/PmrAwebsite.html]

40. Valdivia RH, Falkow S: **Fluorescence-based isolation of bacterial genes expressed within host cells.** *Science* 1997, **277**:2007-2011.

41. Rajewsky N, Socci ND, Zapotocky M, Siggia ED: **The evolution of DNA regulatory regions for proteo-gamma bacteria by interspecies comparisons.** *Genome Res* 2002, **12**:298-308.

42. Hitchen PG, Prior JL, Oyston PC, Panico M, Wren BW, Titball RW, Morris HR, Dell A: **Structural characterization of lipo-oligosaccharide (LOS) from *Yersinia pestis*: regulation of LOS structure by the PhoPQ system.** *Mol Microbiol* 2002, **44**:1637-1650.

43. Detweiler CS, Monack DM, Brodsky IE, Mathew H, Falkow S: ***virK, somA* and *rcsC* are important for systemic *Salmonella enterica* serovar *Typhimurium* infection and cationic peptide resistance.** *Mol Microbiol* 2003, **48**:385-400.

44. Kim W, Killam T, Sood V, Surette MG: **Swarm-cell differentiation in *Salmonella enterica* serovar *Typhimurium* results in elevated resistance to multiple antibiotics.** *J Bacteriol* 2003, **185**:3111-3117.

45. Dosselaere F, Vanderleyden J: **A metabolic node in action: chorismate-utilizing enzymes in microorganisms.** *Crit Rev Microbiol* 2001, **27**:75-131.

46. Calhoun DH, Bonner CA, Gu W, Xie G, Jensen RA: **The emerging periplasm-localized subclass of AroQ chorismate mutases, exemplified by those from *Salmonella typhimurium* and *Pseudomonas aeruginosa*.** *Genome Biol* 2001, **2**:research0030.1-0030.16.

47. Ruiz-Albert J, Yu XJ, Beuzon CR, Blakey AN, Galyov EE, Holden DW: **Complementary activities of SseJ and SifA regulate dynamics of the *Salmonella typhimurium* vacuolar membrane.** *Mol Microbiol* 2002, **44**:645-661.

48. Freeman JA, Ohl ME, Miller SI: **The *Salmonella enterica* serovar *typhimurium* translocated effectors SseJ and SifB are targeted to the *Salmonella*-containing vacuole.** *Infect Immun* 2003, **71**:418-427.

49. Shen-Orr SS, Milo R, Mangan S, Alon U: **Network motifs in the transcriptional regulation network of *Escherichia coli*.** *Nat Genet* 2002, **31**:64-68.

50. **GenBank** [http://www.ncbi.nih.gov/genomes/MICROBES/Complete.html]

51. Thijs G, Moreau Y, De Smet F, Mathys J, Lescot M, Rombauts S, Rouze P, De Moor B, Marchal K: **INCLUSive: INtegrated Clustering, Upstream sequence retrieval and motif Sampling.** *Bioinformatics* 2002, **18**:331-332.

52. Benson DA, Karsch-Mizrachi I, Lipman DJ, Ostell J, Rapp BA, Wheeler DL: **GenBank.** *Nucleic Acids Res* 2002, **30**:17-20.

53. Thijs G, Marchal K, Lescot M, Rombauts S, De Moor B, Rouze P, Moreau Y: **A Gibbs sampling method to detect overrepresented motifs in the upstream regions of coexpressed genes.** *J Comput Biol* 2002, **9**:447-464.

54. **Biol@Sista Software: MotifLocator** [http://www.esat.kuleuven.ac.be/~dna/Biol/Software.html]

55. Thijs G: **Probabilistic methods to search for regulatory elements in sets of coregulated genes.** *PhD thesis* Katholieke Universiteit Leuven, Faculty of Applied Sciences; 2003.

56. Schneider T, Stormo G, Gold L, Ehrenfeucht J: **Information content of binding sites on nucleotide sequences.** *J Mol Biol* 1986, **188**:415-431.

57. Marchal K, Thijs G, De Keersmaecker S, Monsieurs P, De Moor B, Vanderleyden J: **Genome-specific higher-order background models to improve motif detection.** *Trends Microbiol* 2003, **11**:61-66.

58. Tatusov RL, Galperin MY, Natale DA, Koonin EV: **The COG database: a tool for genome-scale analysis of protein functions and evolution.** *Nucleic Acids Res* 2000, **28**:33-36.

59. Altschul SF, Madden TL, Schaffer AA, Zhang J, Zhang Z, Miller W, Lipman DJ: **Gapped BLAST and PSI-BLAST: a new generation of protein database search programs.** *Nucleic Acids Res* 1997, **25**:3389-3402.

60. Enright AJ, Van Dongen S, Ouzounis CA: **An efficient algorithm for large-scale detection of protein families.** *Nucleic Acids Res* 2002, **30**:1575-1584.

61. **Development of a heuristic for the selection of alignment seeds from a list of motifs generated by Gibbs sampling** [ftp://www.esat.kuleuven.ac.be/pub/sista/marchal/ Supplementary_information_GenBiol_2004/website/reports/ heuristic.pdf]

62. **Methodology to identify conserved sequence blocks in an alignment of intergenic sequences** [ftp://www.esat.kuleuven.ac.be/pub/sista/marchal/ Supplementary_information_GenBiol_2004/website/reports/ Validation_Alignments_221003.pdf]

63. Hall TA: **BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT.** *Nuceicl Acids Symp* 1999, **41**:95-98.

64. **The Sanger Institute** [http://www.sanger.ac.uk/Info/Intro]

65. Nelson DL, Kennedy EP: **Magnesium transport in *Escherichia coli*. Inhibition by cobaltous ion.** *J Biol Chem* 1971, **246**:3042-3049.

66. Snavely MD, Miller CG, Maguire ME: **The *mgtB* Mg^{2+} transport locus of *Salmonella typhimurium* encodes a P-type ATPase.** *J Biol Chem* 1991, **266**:815-823.

67. Bullas LR, Ryu JI: ***Salmonella typhimurium* LT2 strains which are r- m+ for all three chromosomally located systems of DNA restriction and modification.** *J Bacteriol* 1983, **156**:471-474.