

**Table S1. List of primers used in this work.**

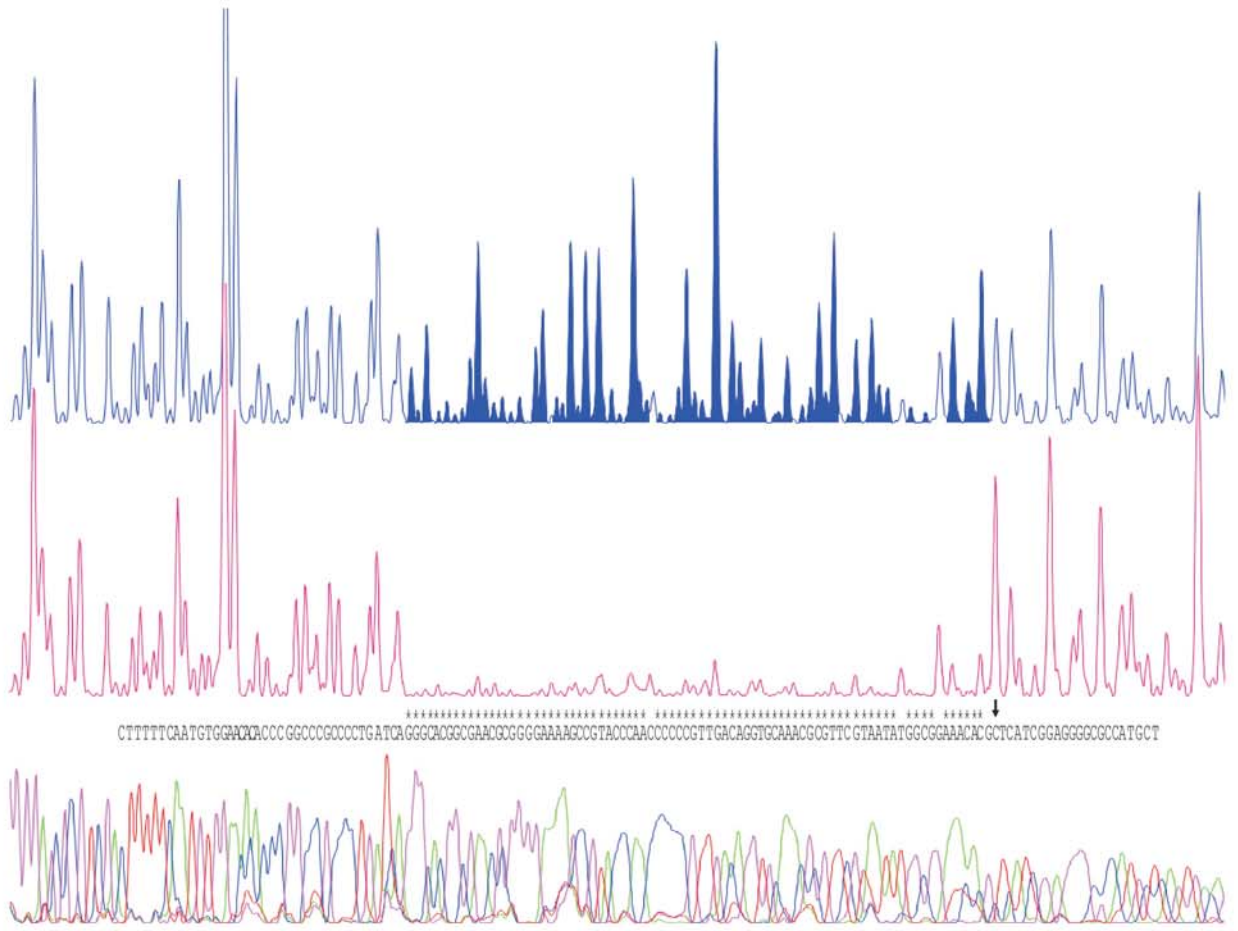
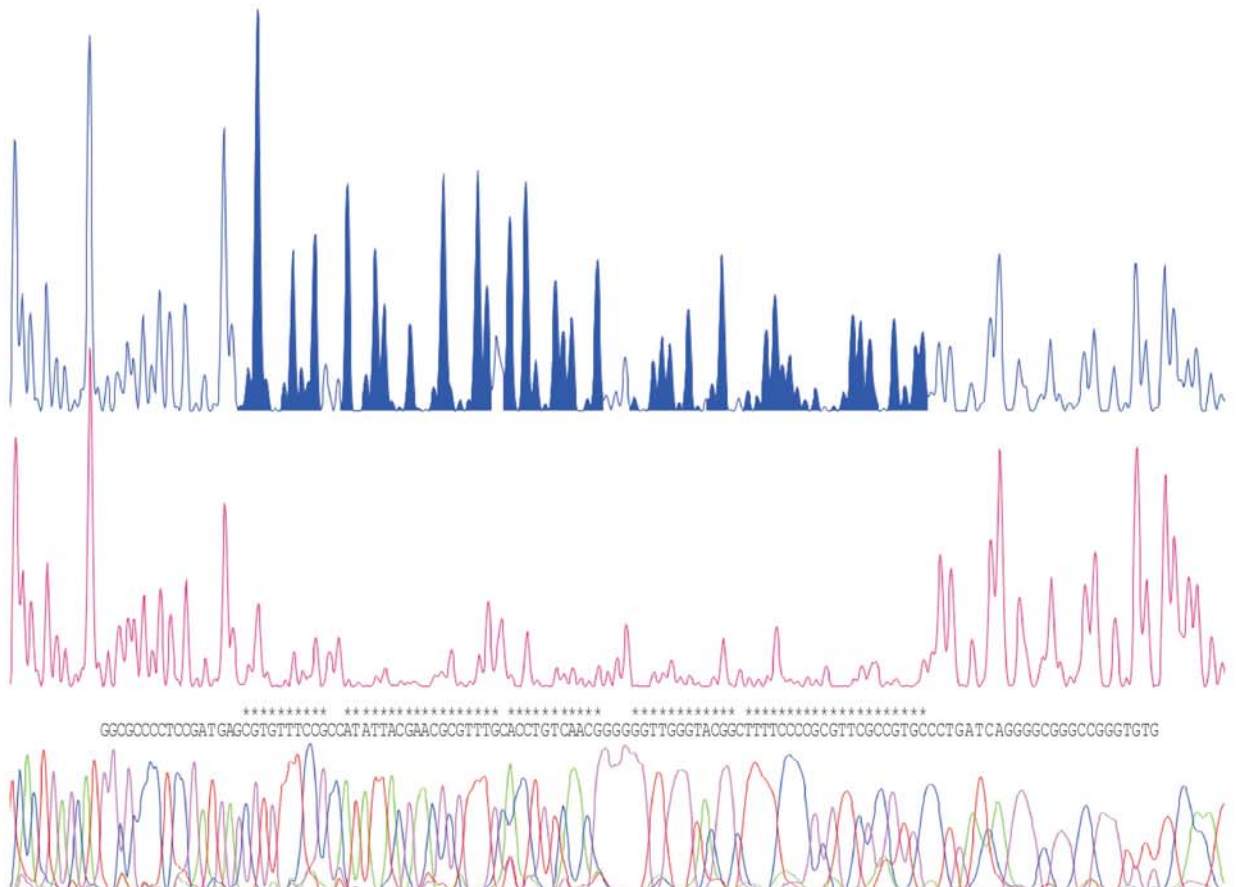
<b>Primer</b>	<b>Sequence<sup>1</sup></b>	<b>Promoter</b>
PHO-47	ATGGGTCCTCCAGGGTTCGA	SCO0255
PHO-48	CGCTGCCAGGAGTTGAGGAT	
PHO-49	GAGCATCACCGCTTCGGCAT	<i>ureA</i> (SCO1236)
PHO-50	CGTGCGGGGTCAGTTGCATT	
PHO-51	GGTCCGCCACCGTGTGAAGT	SCO2195
PHO-52	CCTGCATCGTGGAGGTCCCC	
PHO-53	GGACGATCGATTTGCAGGTC	SCO1863
PHO-54	CGGATACTCGCACAAAGCAGA	
GLN-01	CGAAACAAATGGG <u>AA</u> ACGCCCGAGAAATCACC	<i>glnA</i> -M1
GLN-02	GGTGATTTCTCGGGCGT <u>TT</u> CCCATTTGTTTCG	
GLN-03	GGTAACTTCTGCGT <u>CA</u> CAAATGGGTCACG	<i>glnA</i> -M2
GLN-04	CGTGACCCATTTGT <u>GAC</u> GCAGAAGTTAACC	
GLN-05	GGAGGGAGCCGGT <u>TCG</u> CTTCTGCGAAAC	<i>glnA</i> -M5
GLN-06	GTTTCGCAGAAG <u>CGA</u> ACCGGCTCCCTCC	
GLN-07	GCGAAACAAATGGG <u>GA</u> ACGCCCGAGAAATCACC	<i>glnA</i> -M7
GLN-08	GGTGATTTCTCGGGCGT <u>TC</u> CCCATTTGTTTCGC	
GLN-09	GGAGGGAGCCGG <u>GAA</u> ACTTCTGCGAAAC	<i>glnA</i> -M8
GLN-10	GTTTCGCAGAAGT <u>TTCC</u> CGGCTCCCTCC	
GLN-11	GGTAACTTCTGCT <u>GAA</u> CAAATGGGTCACG	<i>glnA</i> -M9
GLN-12	CGTGACCCATTTGTT <u>CAG</u> CAGAAGTTAACC	
GLN-13	CGAAACAAATGGGT <u>CAAC</u> CGGCCGAGAAATCACC	<i>glnA</i> -M10
GLN-14	GGTGATTTCTCGGG <u>GT</u> TGACCCATTTGTTTCG	
CAR87	<u>ATTCGCATGC</u> ATGAAGCCAGCGTAAAG	SCO0888
CAR88	<u>ATTCACGCGT</u> CGGACAGACATGAGTAC	
CAR89	<u>ATTCGCATGCG</u> ACTTGACCAGCGGAAC	SCO7155
CAR90	<u>ATTCACGCGT</u> CGGTGTCGTAGCGCAAG	

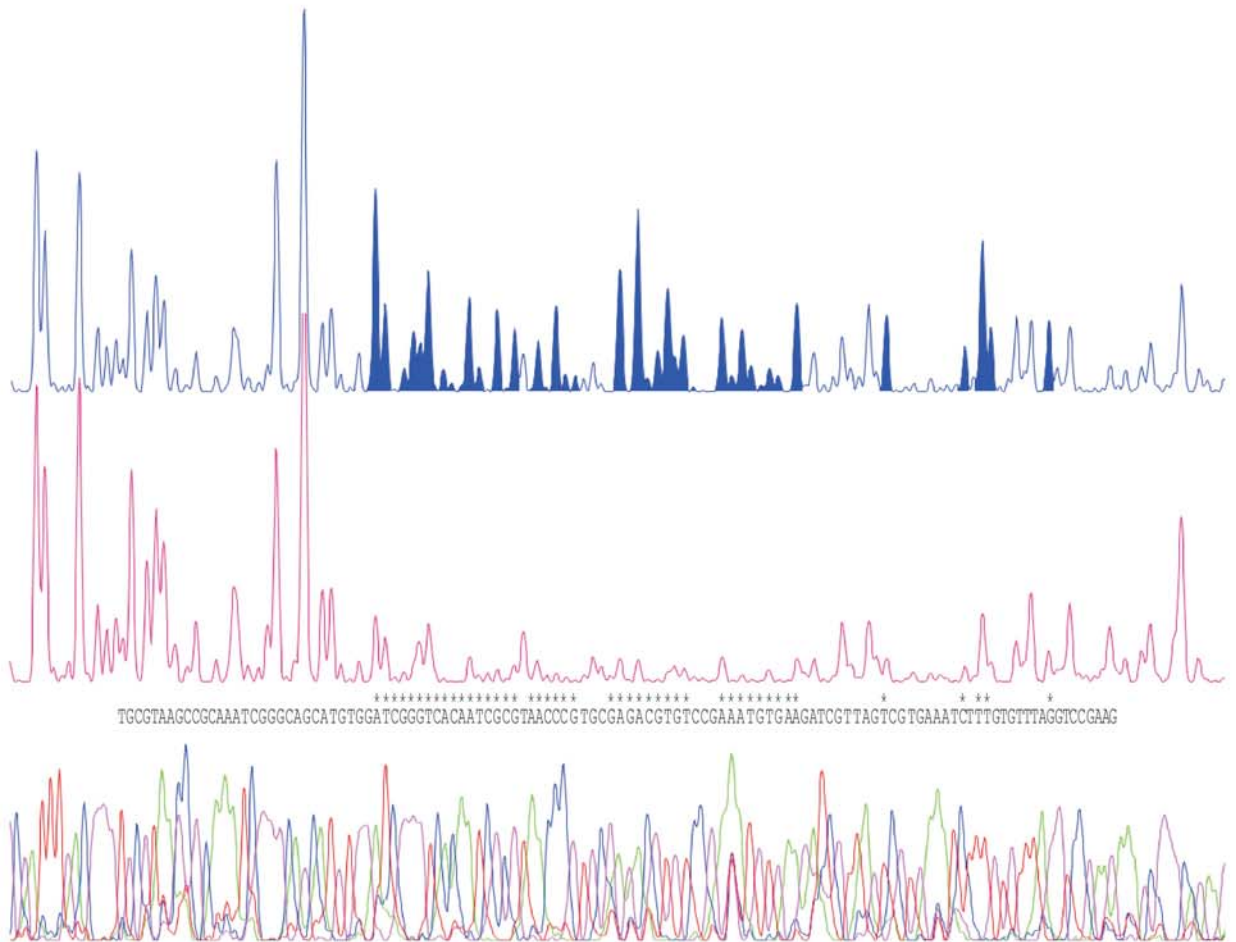
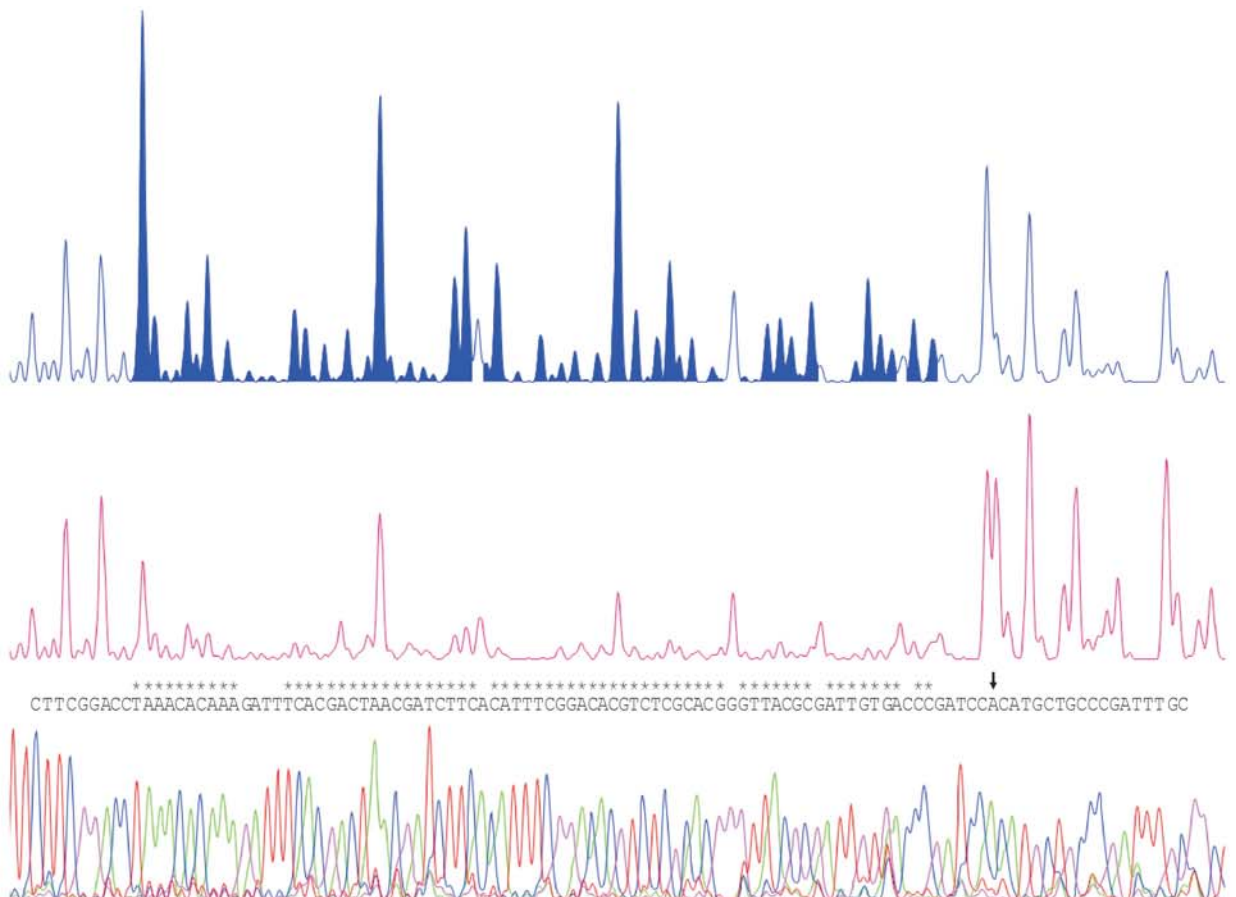
<sup>1</sup> Nucleotides changed for directed mutagenesis are shown with double underline. Restriction sites added to the sequences are underlined.

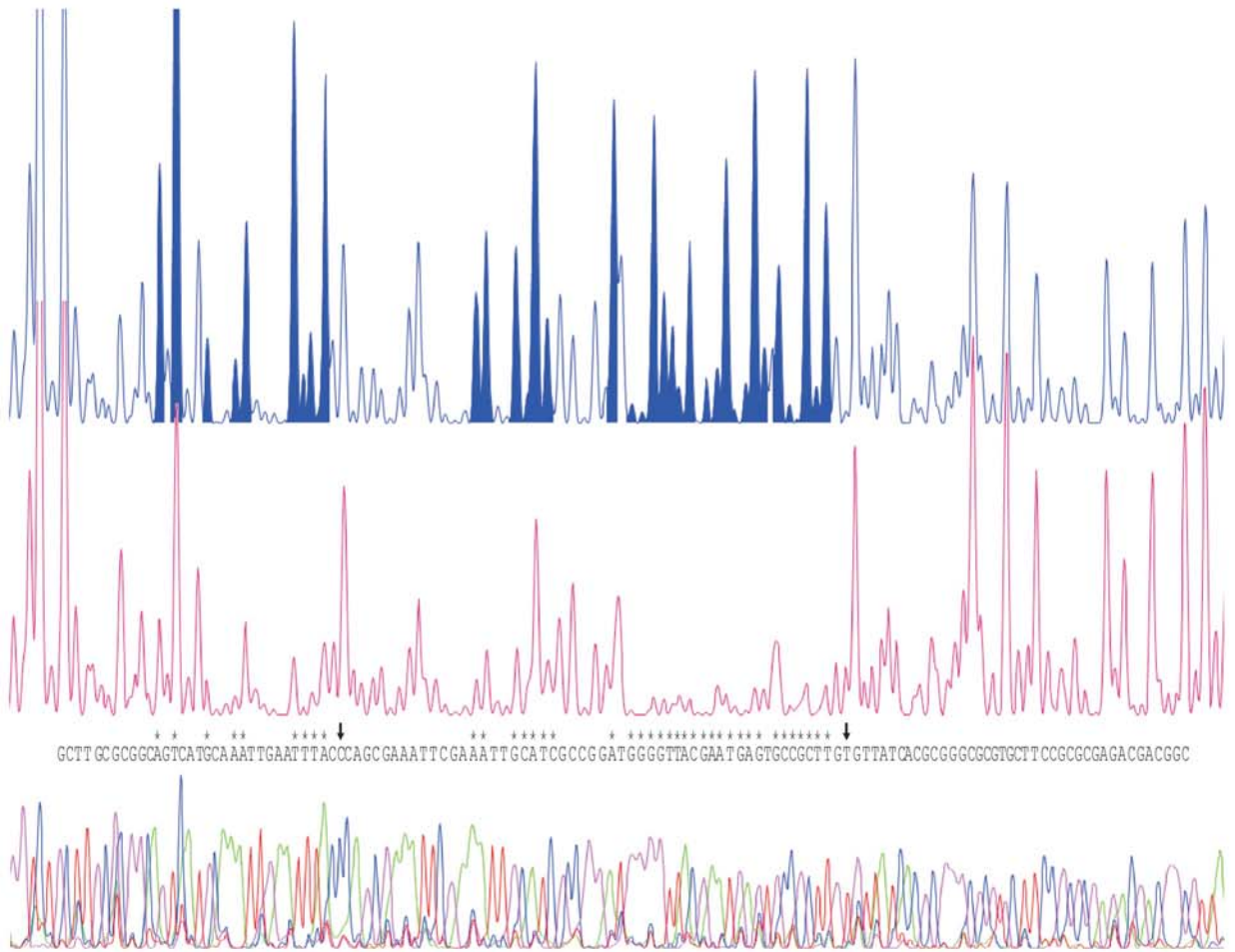
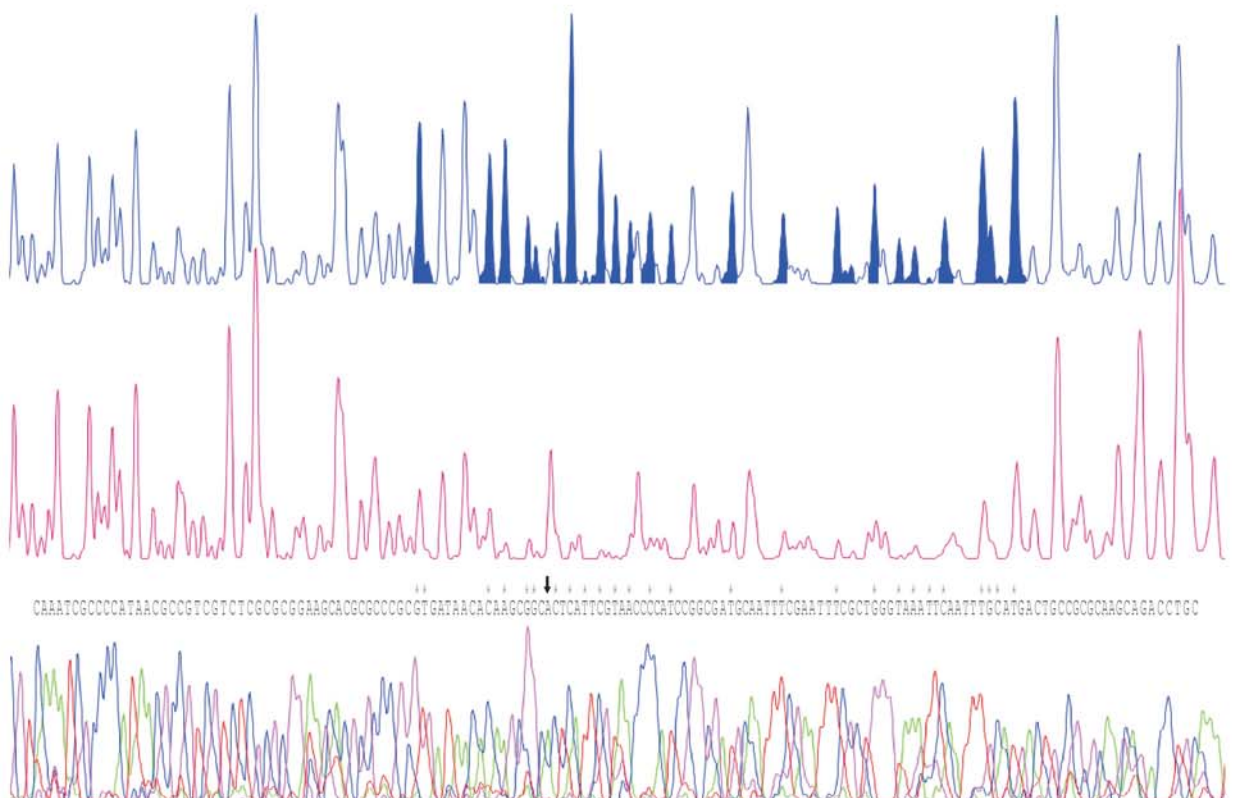
**Supplementary Figure S1.** DNase I footprints of the GST-PhoP<sup>DBD</sup> protein bound to the promoter regions of SCO0255 (A), SCO1863 (B, C), and *ureA* genes (D). Blue electropherograms are control reactions without protein; the red ones correspond to reactions containing 4  $\mu$ M of GST-PhoP<sup>DBD</sup>. The protected nucleotides are indicated by asterisks and the peak shadowed areas. Hypersensitive sites created by protein binding are highlighted by vertical arrows. The correspondence between fluorescence peaks and nucleotide bases was determined using the sequencing reactions shown below.

**Supplementary Figure S2.** Analysis by EMSA of the binding of PhoP and GlnR to the *phoRP* and *pstS* promoters. The conditions of binding reaction were those described previously for GlnR (24). P, probe without protein. Numbers indicate the protein concentration ( $\mu$ M). The film was overexposed to show that no bands are formed with the GlnR protein. PhoP shifted bands are indicated by arrows.

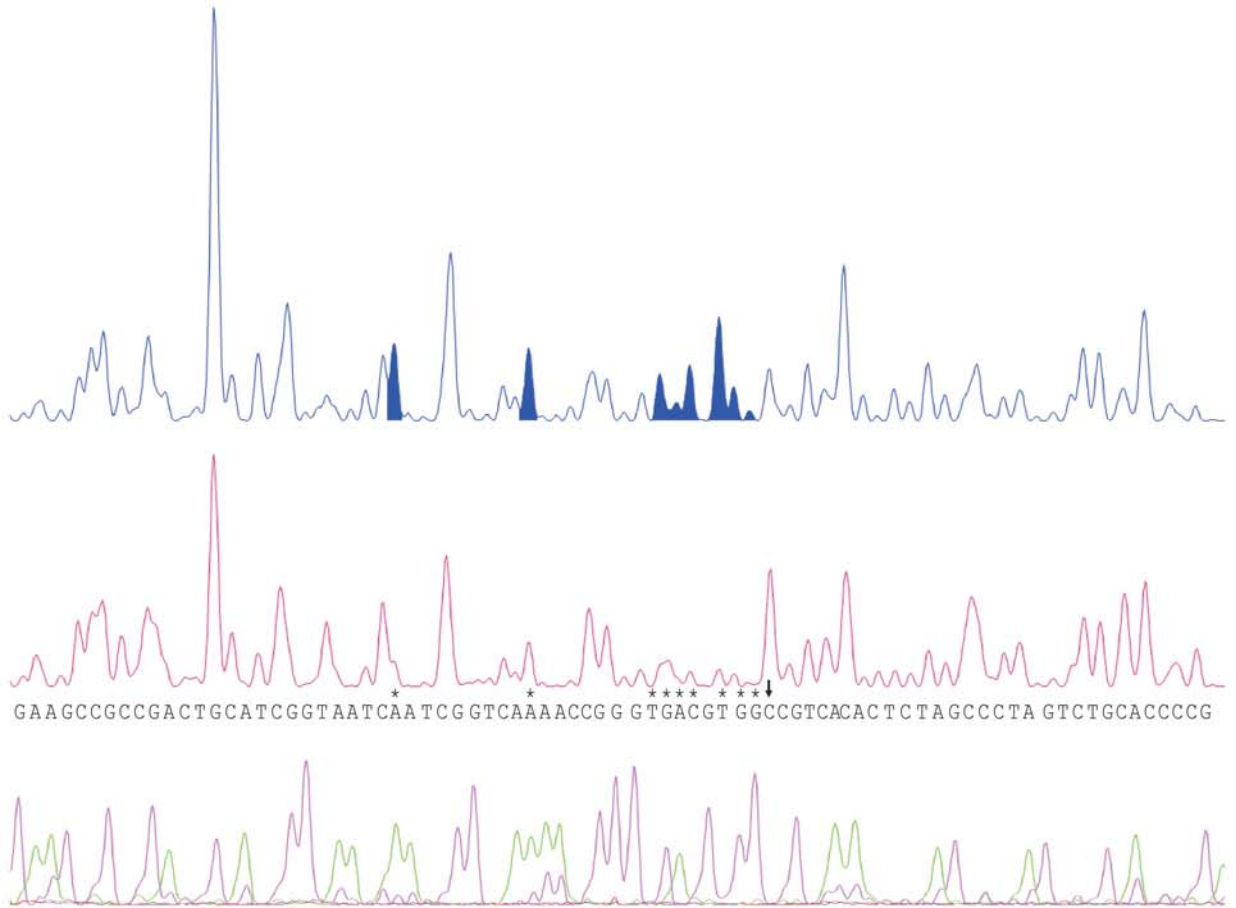
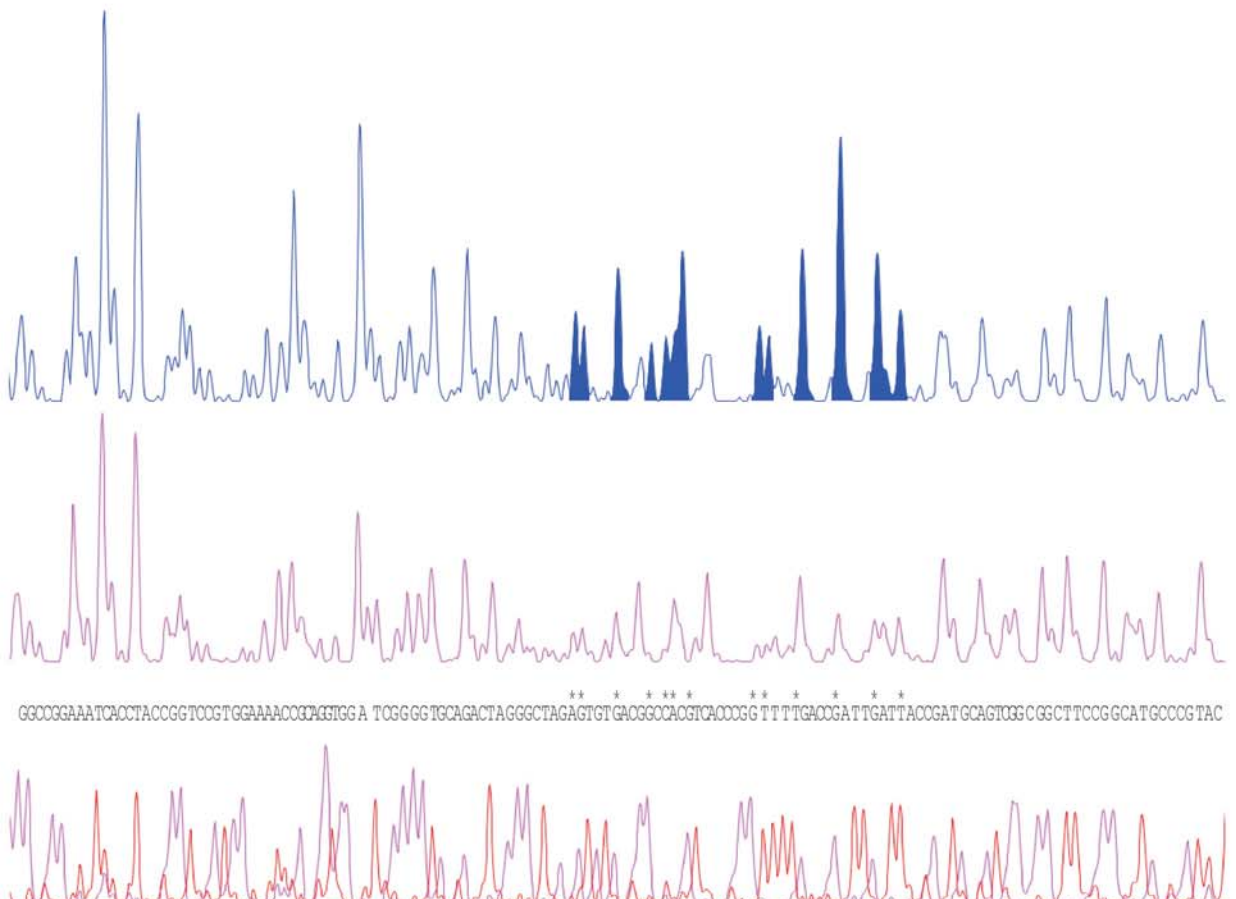
**Supplementary Figure S3.** Analysis by EMSA of binding of PhoP and GlnR to the *glnA* promoter. Lanes 1 and 6, probe without proteins; lanes 2-5 increasing concentrations of GlnR protein (from 0.125 to 1  $\mu$ M); lanes 7-10, increasing concentrations of GST-PhoP<sup>DBD</sup> protein (from 0.125 to 1  $\mu$ M). Shifted bands are shown by arrows. Note that the most retarded band by GlnR has a similar size to that retarded by PhoP.

**A****SCO0255 promoter, coding strand****SCO0255 promoter, complementary strand**

**B****SCO1863 promoter, coding strand, main protected region****SCO1863 promoter, complementary strand, main protected region**

**C****SCO1863 promoter, coding strand, second region****SCO1863 promoter, complementary strand, second region**



**D*****ureA* promoter, coding strand*****ureA* promoter, complementary strand**

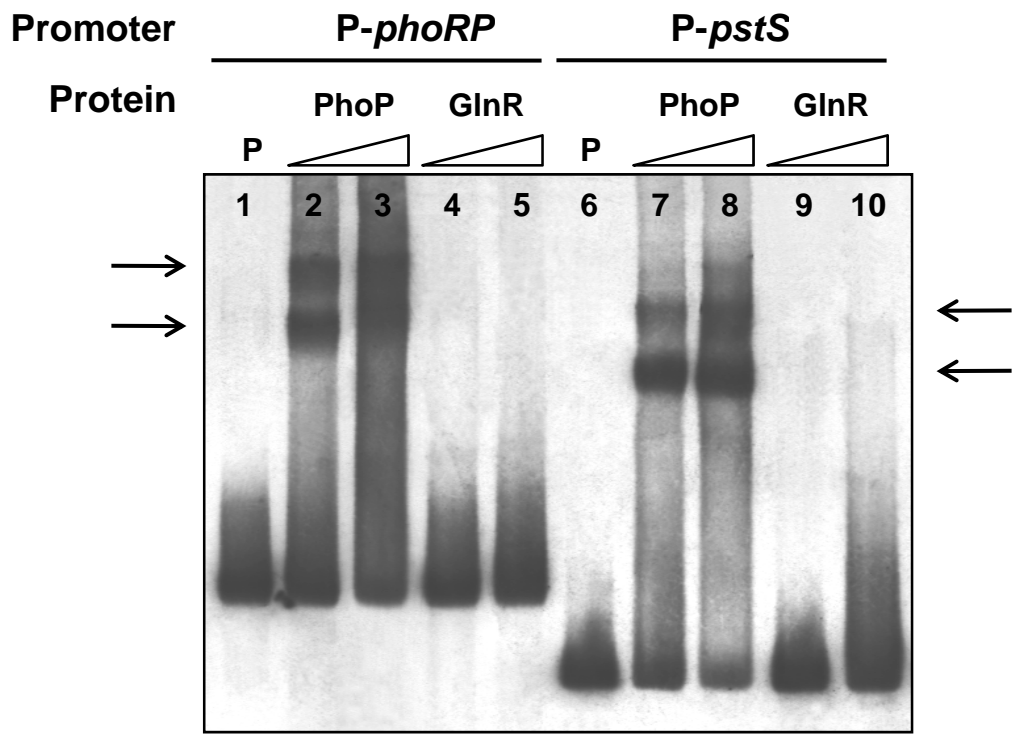


Figure S2. Sola-Landa *et al.*

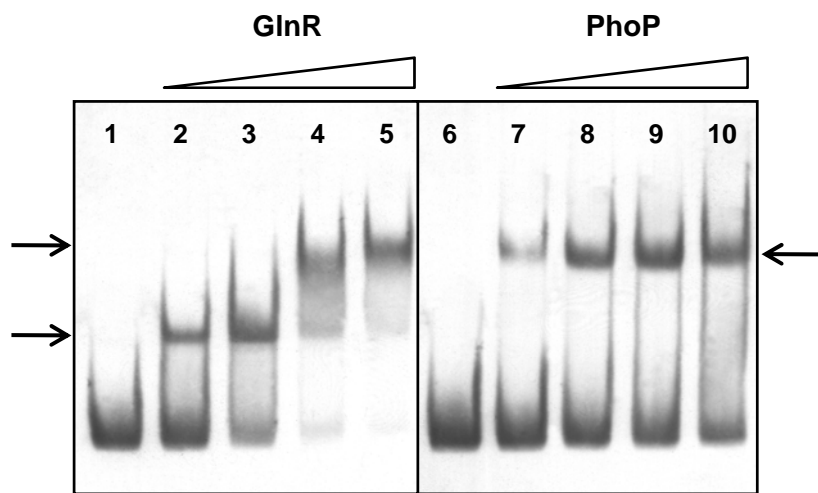


Figure S3. Sola-Landa *et al.*