

Supplementary Information

An Essential Regulatory System Originating from Polygenic Transcriptional Rewiring of PhoP-PhoQ of *Xanthomonas campestris*

Bao-Yu Peng,^{†, ‡, ¶} Yue Pan,^{†, ‡, ¶} Ru-Jiao Li,^{§, ¶} Jin-Wei Wei,^{†, ‡} Fang Liang,[§] Li Wang,[†]
Fang-Fang Wang,[†] and Wei Qian^{†,1}

[†] *State Key Laboratory of Plant Genomics, Institute of Microbiology, Chinese Academy of Sciences, Beijing 100101, China*

[‡] *School of Biological Sciences, University of Chinese Academy of Sciences, Beijing 100049, China*

[§] *Beijing Institute of Genomics, Chinese Academy of Sciences, Beijing 100101, China*

[¶] These authors contributed equally to this work.

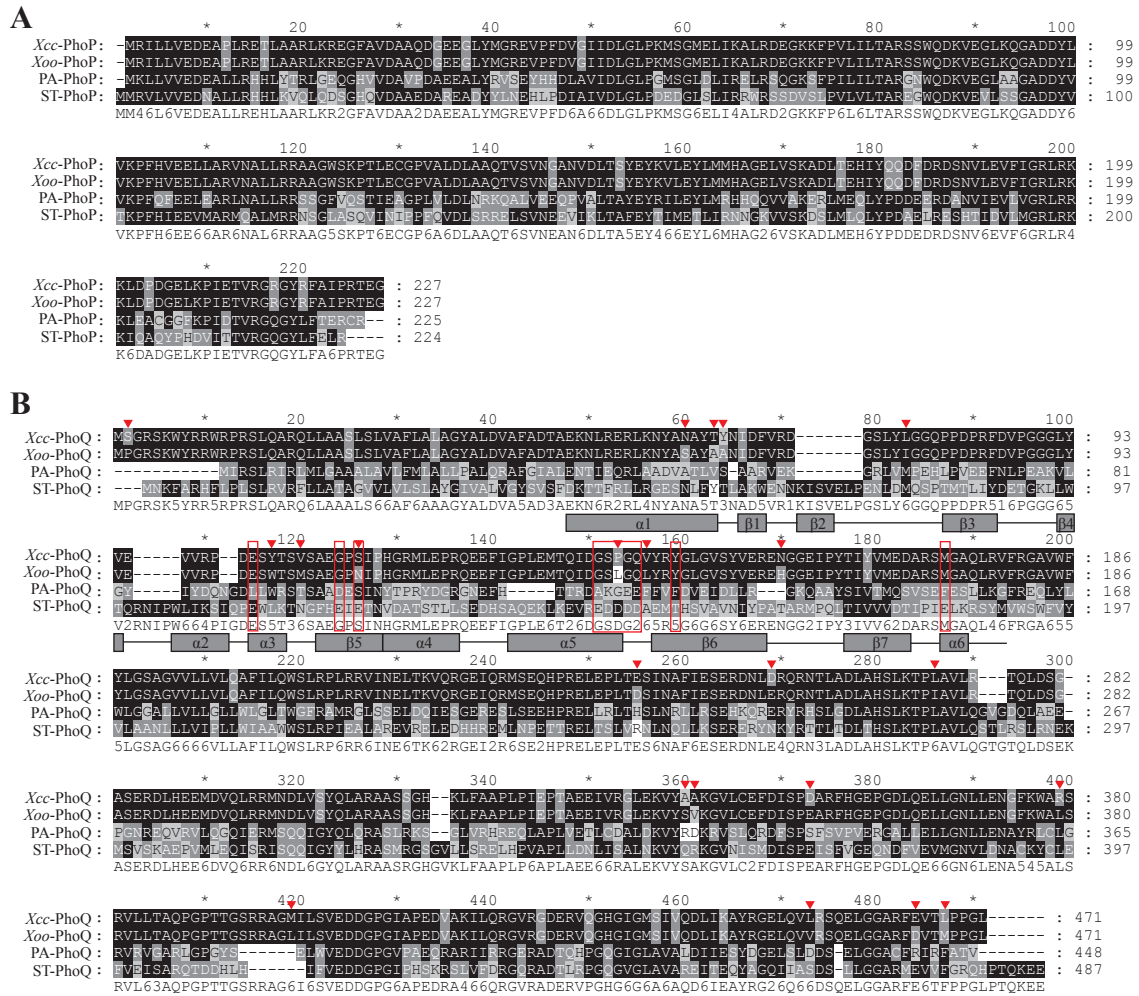


Figure S1 Genetic polymorphisms in PhoP-PhoQ orthologues. (A) Alignment of PhoP protein sequences. *Xcc*: *X. campestris* pv. *campestris*. *Xoo*: *X. oryzae* pv. *oryzae*. *ST*: *Salmonella enterica*. *PA*: *Pseudomonas aeruginosa*. (B) Alignments of PhoQ protein sequences. The secondary structure of the sensor domain from *ST*-PhoQ is depicted below the sequences, and the corresponding amino acid residue sites between *Xcc*-PhoQ and *Xoo*-PhoQ in each sequence are labelled with a small red triangle above the sequenCCces. Residues that make up the *ST*-PhoQ acidic patch are shown in red boxes.

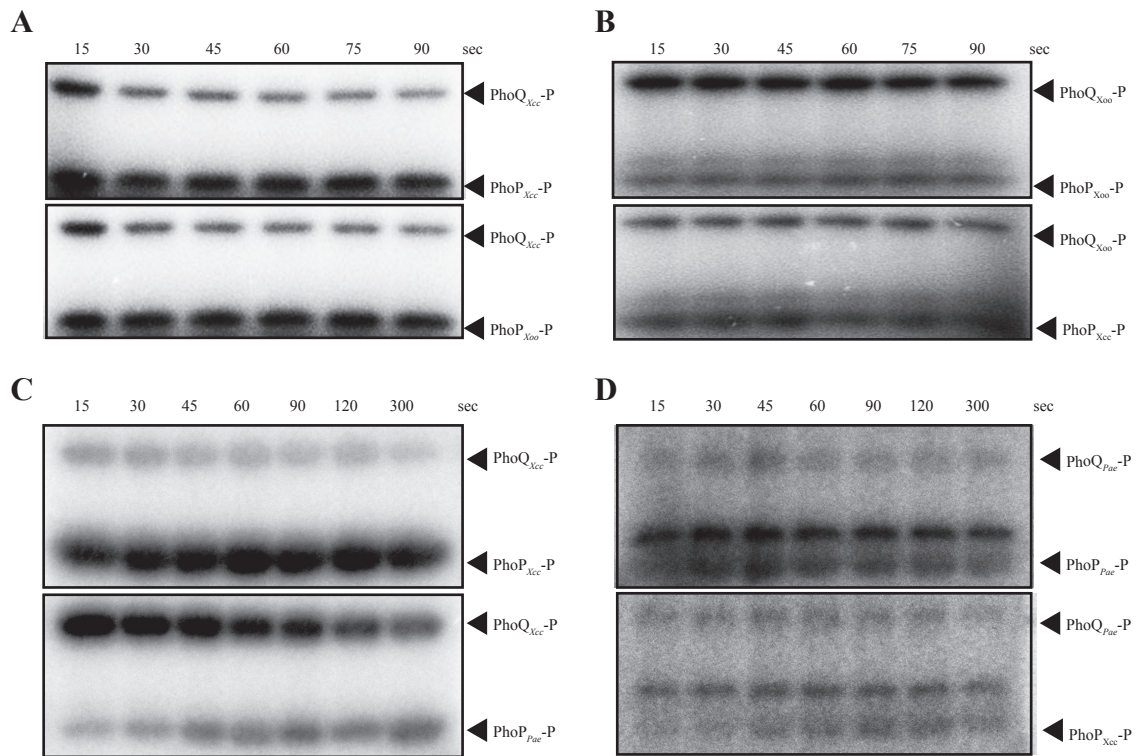


Figure S2 *in vitro* phosphorylation assay of PhoP-PhoQ from different bacteria. (A) Full-length PhoQ_{Xcc} phosphorylates PhoP_{Xcc} and PhoP_{Xoo}, respectively. (B) Full-length PhoQ_{Xoo} phosphorylates PhoP_{Xcc} and PhoP_{Xoo}, respectively. (C) Full-length PhoQ_{Xcc} phosphorylates PhoP_{Xcc} and PhoP_{Pae}, respectively. (D) Full-length PhoQ_{Pae} phosphorylates PhoP_{Pae} and PhoP_{Xcc}, respectively. In (A-D), inverted membrane vesicles (IMVs) of PhoQ (10 μ g) were co-incubated with [γ -³²P]ATP for 20 min, and 10 μ M PhoP was then added to the reaction mixtures. Aliquots were taken at the indicated times. The reactions were stopped by adding 5 μ l of 5 \times SDS PAGE loading buffer. The experiments were repeated three times and a representative is shown.

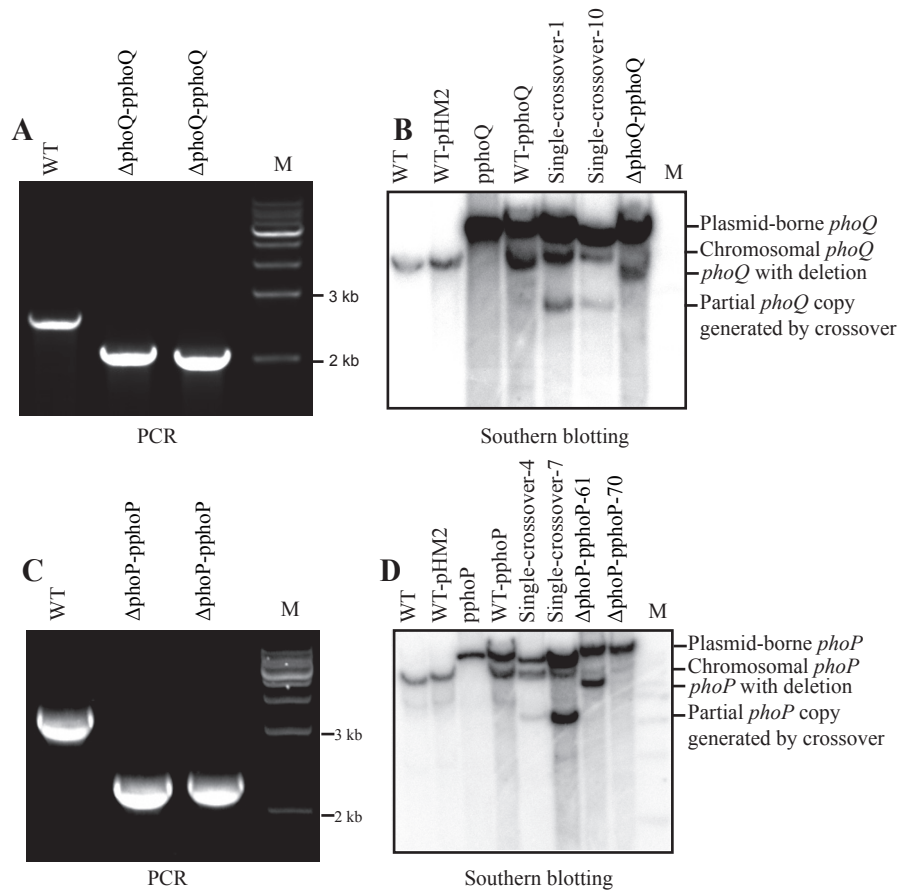


Figure S3 Genetic verification of *phoP*_{Xcc} and *phoQ*_{Xcc} mutants. (A) Verification of the *phoQ*_{Xcc} mutant by PCR. (B) Verification of the *phoQ*_{Xcc} mutant by Southern blotting. (C) Verification of the *phoP*_{Xcc} mutant by PCR. (D) Verification of the *phoP*_{Xcc} mutant by Southern blotting. WT: *X. campestris* pv. *campestris* 8004. Δ phoQ-pphoQ: the putative *phoQ*_{Xcc} in-frame deletion mutant. Δ phoP-pphoP-61 and Δ phoP-pphoP-70: putative *phoP*_{Xcc} in-frame deletion mutants. WT-pHM2: the wild-type strain containing an empty pHM2 vector. WT-pphoP: the wild-type strain containing a plasmid copy of *phoP*_{Xcc}. WT-pphoQ: the wild-type strain containing a plasmid copy of *phoQ*_{Xcc}. Single-crossover-4, -7, -1 and -10 are recombinant constructs obtained by the first round of homologous cross-over of *phoP*_{Xcc} and *phoQ*_{Xcc}. Note that the candidate for Δ phoP-pphoP-70 was a false positive construct, which was verified by Southern blotting in (D). The primer sequences in (A) and (C) are listed in Table S2. In (B) and (D), bacterial DNA was digested with *Kpn*I. The *phoP*_{Xcc} and *phoQ*_{Xcc} PCR products were labelled with [α -³²P]dCTP and used as probes. A 1-kb DNA marker was used to indicate the band size in both the PCR and Southern blotting assays.

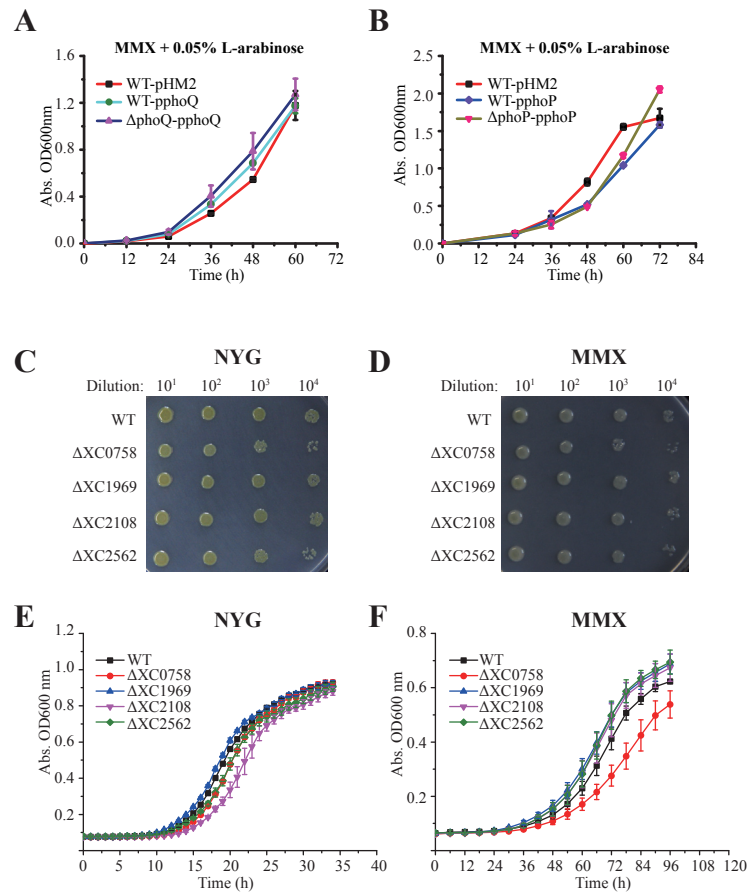


Figure S4. Bacterial growth in the MMX medium with L-arabinose. (A) Growth curve of the $phoP_{Xcc}$ mutant of *X. campestris* pv. *campestris* in MMX with 0.05% L-arabinose. (B) Growth curve of the $phoP_{Xcc}$ mutant in MMX with 0.05% L-arabinose. WT-pHM2: the wild-type strain containing an empty pHM2 vector. WT-pphoP and WT-pphoQ: the wild-type strains containing plasmid copies of $phoP_{Xcc}$ and $phoQ_{Xcc}$, respectively. ΔphoP-pphoP and ΔphoQ-pphoQ are in-frame deletion mutants of $phoP_{Xcc}$ and $phoQ_{Xcc}$, respectively. All bacterial strains were grown at 28°C. Error bars indicate the standard deviation ($n = 4$). (C) Morphology of bacterial strains grown on rich NYG agar. (D) Morphology of bacterial strains grown on minimal MMX agar. In (C and D) 1 μl of bacterial culture was inoculated on the agar plates and grown for 36-48 hours. (E) Growth curves of bacterial strains in rich NYG medium. (F) Growth curves of bacterial strains in minimal MMX medium. In (E and F), each data point is the average of 3 repeated experiments, and the vertical bars indicate standard deviation.

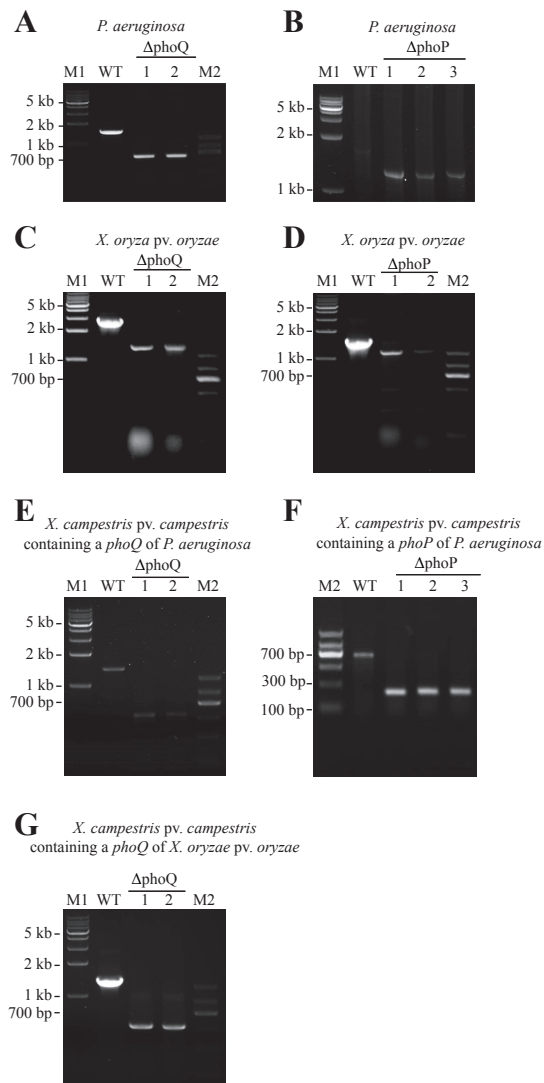


Figure S5. Verification of the *phoP* and *phoQ* in-frame deletion mutants of various bacteria. (A and B) Verification of the *phoP* and *phoQ* mutants of *P. aeruginosa* PAO1. (C and D) Verification of the *phoP* and *phoQ* mutants of *X. oryzae* pv. *oryzae* PXO99. An additional vector-borne copy of either *phoP* or *phoQ* was transformed into the wild-type strain before the deletion of the chromosomal copy. (E and F) *phoP* and *phoQ* of *P. aeruginosa* PAO1 are genetically equivalent to their orthologues in *X. campestris* pv. *campestris*. An additional vector-borne copy of either *phoP* or *phoQ* of *P. aeruginosa* PAO1 was transformed into wild-type strain of *X. campestris* pv. *campestris* before deletion of the chromosomal copy. (G) *phoQ* of *X. oryzae* pv. *oryzae* is genetically equivalent to its orthologues in *X. campestris* pv. *campestris*. An additional vector-borne copy of *phoQ* of *X. oryzae* pv. *oryzae* was transformed into the wild-type strain of *X. campestris* pv. *campestris* before the deletion of the chromosomal copy. In (A-G), 1, 2, and 3 indicate the recombinant strains obtained. PCR amplification of the *phoP* or *phoQ* gene of various bacterial strains was conducted to determine the correction of gene deletion. M1: 1 kb ladder. M2: 100 bp ladder.

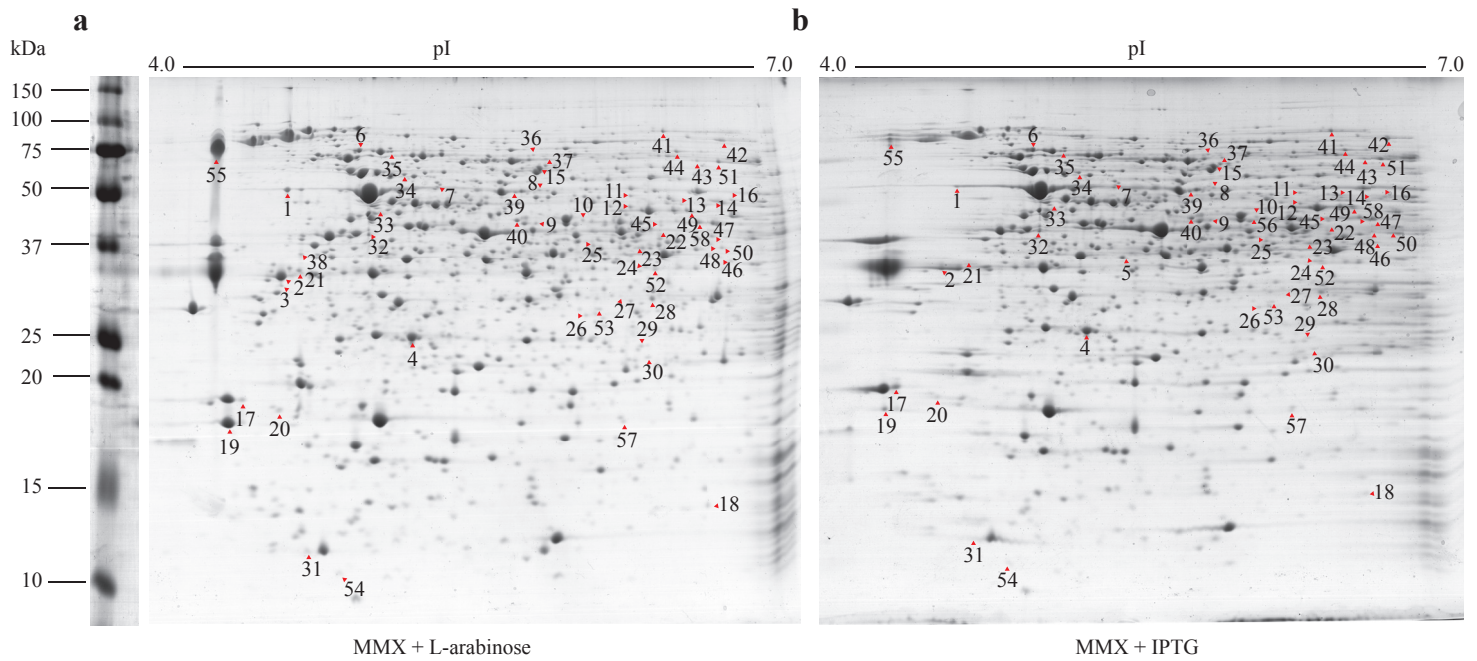


Figure S6. Two-dimension electrophoresis (2-DE) identified differently expressed proteins modulated by PhoP_{Xcc}. 2-DE analysis of total proteins of the Δ phoP-pphoP strain grown under the induced (A) and repressed (B) conditions. Total proteins were extracted from the Δ phoP-pphoP strain that was grown in MMX minimal medium with either 0.05% L-arabinose (A) or 2 mM IPTG (B) for 60 min, respectively. Coomassie brilliant blue was used to stain the proteins. The red triangles indicate protein spots identified by MALDI-TOF-MS/MS. Spot IDs are the same as those in Table S3. Each 2-DE analysis was repeated independently three times, with two technical replicates.

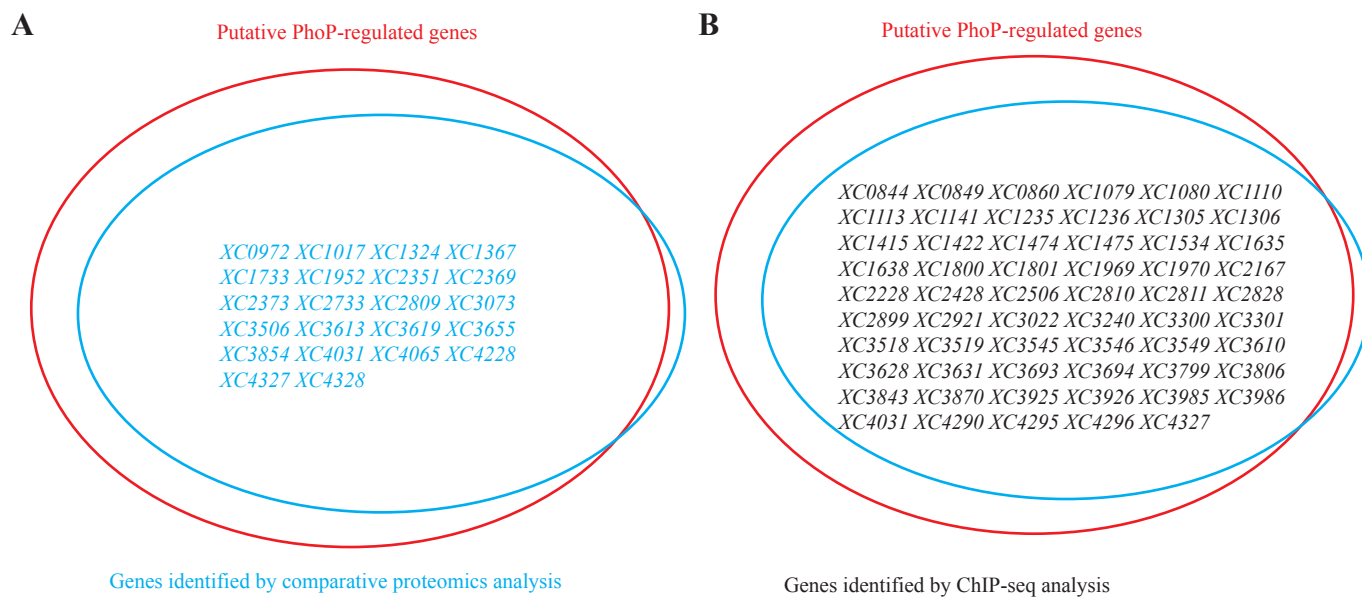


Figure S7 Venn diagram of PhoP-regulated genes of *X. campestris* pv. *campestris* identified by various approaches. (A) Genes with putative PhoP-binding motif in their promoter region. The listed genes encode differently expressed proteins that were identified by comparative proteomic analysis (Table S3). (B) Genes with putative PhoP-binding motif in their promoter region. The listed genes were identified by ChIP-seq analysis (Table S4). In both (A) and (B), results of proteomic and ChIP-seq analyses were compared to the predicted genes with PhoP-binding motif in their promoter region (Table S5).

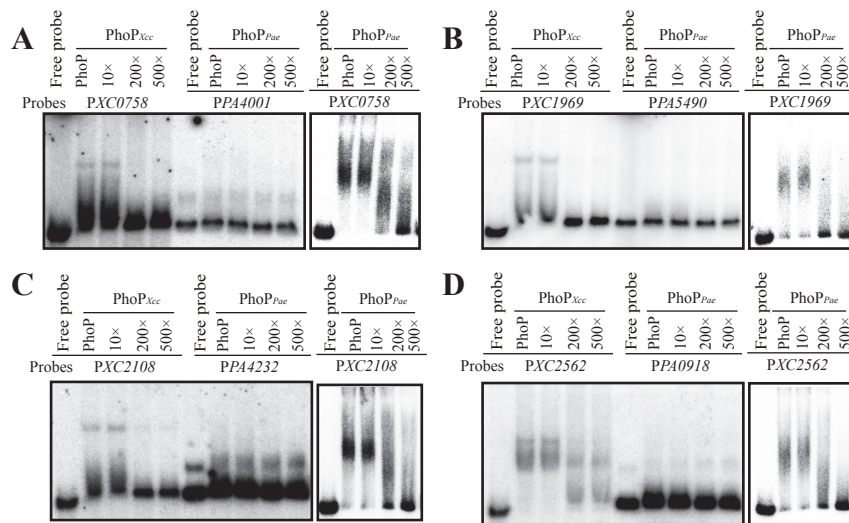


Figure S8. PhoP of *X. campestris* pv. *campestris* and *P. aeruginosa* differently control the transcriptions of downstream non-essential genes differently. (A–D) PhoP-promoter binding assay. EMSA analysis revealed that both PhoP_{Xcc} and PhoP_{Pae} bind directly to the promoter regions of four essential genes (*XC0758*, *XC1969*, *XC2108*, and *XC2562*) of *X. campestris* pv. *campestris*, but PhoP_{Pae} did not bind the promoter regions of their orthologues in *P. aeruginosa* (*PA4001*, *PA5490*, *PA4232*, and *PA0918*). The DNA probes were labelled with [γ -³²P]ATP. Increasing amounts of unlabelled probes were used as competitors. The experiments were repeated three times, and a representative is shown.

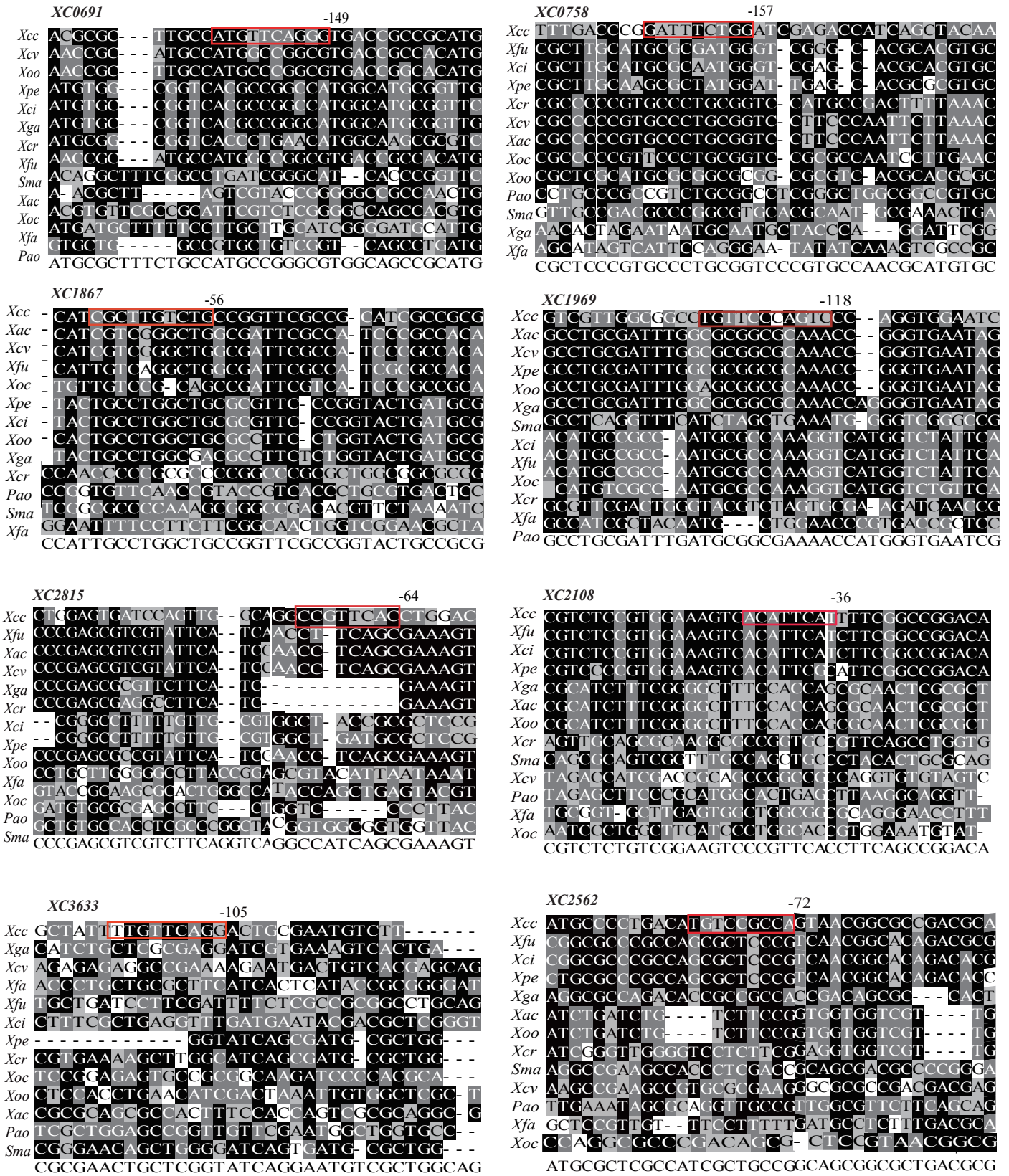


Figure S9 Genetic polymorphism of the promoter regions of PhoP-regulated genes in *Xanthomonas* spp. and close-relatives. Sequences were aligned by Clustal X. The PhoP-binding motif is indicated by red frame. *Xcc*, *Xanthomonas campestris* pv. *campestris* 8004. *Pao*, *Pseudomonas aeruginosa* PAO1. *Xfu*, *Xanthomonas fuscans* subsp. *aurantifolii* FDC 1609. *Xcr*, *Xanthomonas campestris raphani* 756C. *Xoc*, *Xanthomonas oryzae oryzicola* BLS256. *Xac*, *Xanthomonas axonopodis* pv. *citrumelo* F1. *Xcv*, *Xanthomonas campestris vesicatoria* 85-10. *Xpe*, *Xanthomonas perforans* 91-118. *Xci*, *Xanthomonas citri* subsp. *citri* LH201. *Xga*, *Xanthomonas gardneri* strain JS749-3. *Xoo*, *Xanthomonas oryzae* pv. *oryzae* PAO99A. *Sma*, *Stenotrophomonas maltophilia* K279a. *Xfa*, *Xylella fastidiosa* M12

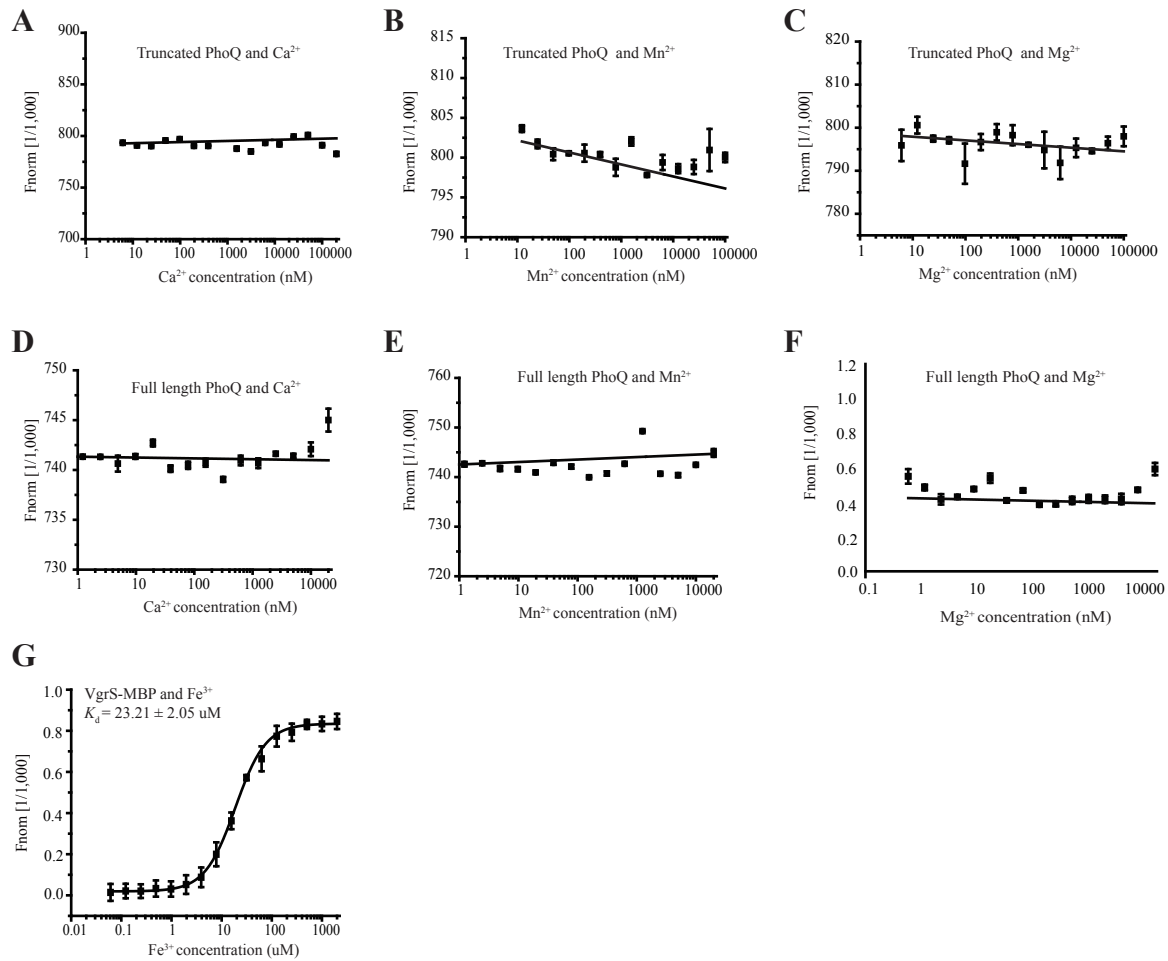


Figure S10. PhoQ_{Xcc} of *X. campestris* pv. *campestris* did not bind to metal ions. Microscale thermophoresis was used to measure the binding affinity between metal ions and PhoQ_{Xcc}. (A-C) Truncated, soluble PhoQ_{Xcc} did not bind to Ca²⁺, Mn²⁺ or Mg²⁺. Truncated PhoQ_{Xcc} containing the cytoplasmic region was used in the analysis. (D-E) Full-length PhoQ_{Xcc} embedded in the inverted membrane vesicle did not bind to Ca²⁺, Mn²⁺ or Mg²⁺. (G) Full-length histidine kinase VgrS_{Xcc} embedded in the inverted membrane vesicle binds to Fe³⁺, which is used as a positive control. The concentrations of metal ions were gradually increased from 0.01 μM to 1.0 mM. K_d = dissociation constant. The assay was repeated independently three times.

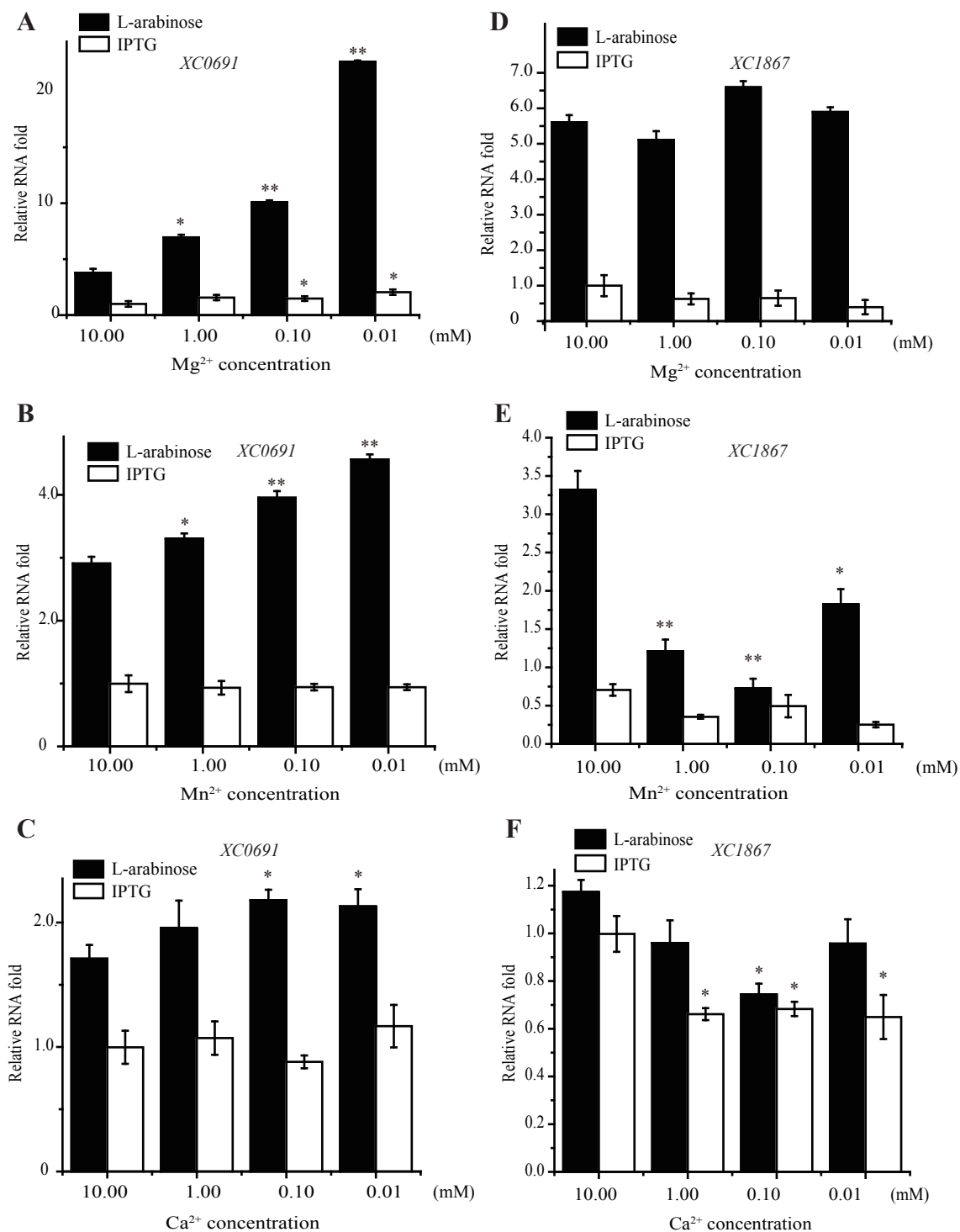


Figure S11 Transcription levels of PhoP regulated genes under various metal stimulation. (A-C) mRNA levels of *XC0691*; (D-F) mRNA levels of *XC1867*. qRT-PCR was used to quantify the amount of mRNA in the *phoP* mutant of *X. campestris* pv. *campestris*. L-arabinose and IPTG were used to activate or repress the transcription of *phoP* gene. Different concentrations of Mg^{2+} ($MgSO_4$), Mn^{2+} ($MnCl_2$) and Ca^{2+} ($CaCl_2$) were used to treat bacteria before extraction of total RNA. Amplification of the cDNA of tmRNA was used as internal control. The experiment was repeated biologically for three times, and the result of a representative one was shown. * indicates significant difference compared with the samples treated by 10 mM metal.

Table S1. Bacterial strains and plasmids used in this study.

Strain or plasmid	Genotype or description ^a	Reference or source
Strains		
<i>X. campestris</i> pv. <i>campestris</i> 8004	Wild-type strain (WT), Rif ^r	Laboratory collection
<i>Pseudomonas aeruginosa</i> PAO1	Wild-type strain, Cb ^r	Laboratory collection
<i>X. oryzae</i> pv. <i>oryzae</i> PXO99 ^A	Wild-type strain	Laboratory collection
<i>E. coli</i> DH5 α	Bacterial host for gene cloning	Laboratory collection
<i>E. coli</i> BL21(DE3) M0050	Bacterial host for protein expression WT-pHM2, wild-type of <i>X. campestris</i> pv. <i>campestris</i> 8004 containing a blank pHM2 plasmid, Rif ^r , Sp ^r	Novagen This study
M0051	WT-pphoP, wild-type of <i>X. campestris</i> pv. <i>campestris</i> 8004 containing a pBAD- <i>araC-phoP_{Xcc}</i> insert supplemented by pHM2 vector, Rif ^r , Sp ^r	This study
M0052	WT-pphoQ, wild-type of <i>X. campestris</i> pv. <i>campestris</i> 8004 containing a pBAD- <i>araC-phoQ_{Xcc}</i> insert supplemented by pHM2 vector, Rif ^r , Sp ^r	This study
M0053	Δ phoP-pphoP, chromosomal <i>phoP_{Xcc}</i> in-frame deletion mutant of <i>X. campestris</i> pv. <i>campestris</i> 8004, containing a vector-borne pBAD- <i>araC-phoP_{Xcc}</i> , Rif ^r , Sp ^r	This study
M0054	Δ phoQ-pphoQ, chromosomal <i>phoQ_{Xcc}</i> in-frame deletion mutant of <i>X. campestris</i> pv. <i>campestris</i> 8004, containing a vector-borne pBAD- <i>araC-phoQ_{Xcc}</i> , Rif ^r , Sp ^r	This study
M0055	Δ phoP*-GFP, Δ phoP* strain of <i>X. campestris</i> pv. <i>campestris</i> 8004 containing a chromosomal <i>PnptIII</i> -GFP fusion that was inserted into the genomic region between <i>XC_1972</i> and <i>XC_1973</i> , Rif ^r , Sp ^r , Kan ^r	This study
M0056	Δ phoQ*-GFP, Δ phoP* strain of <i>X. campestris</i> pv. <i>campestris</i> 8004 containing a chromosomal <i>PnptIII</i> -GFP fusion that was inserted into the genomic region between <i>XC_1972</i> and <i>XC_1973</i> , Rif ^r , Sp ^r , Kan ^r	This study
M0057	Δ phoQ*-phoP-his ₆ , Δ phoQ* strain of <i>X. campestris</i> pv. <i>campestris</i> 8004 containing a His ₆ coding sequence-tagged <i>phoP_{Xcc}</i> , Rif ^r , Sp ^r . For chromatin-immunoprecipitation.	This study
M0058	Δ phoP _{Pae} , Markerless deletion mutant of <i>phoP_{Pae}</i> of <i>P. aeruginosa</i> , Cb ^r	This study
M0060	Δ phoP _{Pae} -phoP _{Pae} , genetic complementary strain of M0058	This study
M0061	Δ phoQ _{Pae} , Markerless deletion mutant of <i>phoQ_{Pae}</i> of <i>P. aeruginosa</i> , Cb ^r	This study
M0062	Δ phoQ _{Pae} -phoQ _{Pae} , genetic complementary strain of M0061	This study
M0063	Δ phoP*-phoP _{Pae} , chromosomal <i>phoP_{Xcc}</i> in-frame deletion mutant, containing a vector-borne pHM1- <i>phoP_{Pae}</i> of <i>P. aeruginosa</i> , Rif ^r , Sp ^r	This study

M0064	Δ phoQ*-phoP _{Pae} , chromosomal <i>phoQ</i> _{Xcc} in-frame deletion mutant, containing a vector-borne pHM1- <i>phoQ</i> _{Pae} of <i>P. aeruginosa</i> , Rif ^r , Sp ^r	This study
M0065	Δ phoQ*-phoQ _{Xoo} , chromosomal <i>phoQ</i> _{Xcc} in-frame deletion mutant, containing a vector-borne pBAD- <i>araC-phoQ</i> _{Xoo} of <i>X. oryzae</i> pv. <i>oryzae</i> PXO99 ^A , Rif ^r , Sp ^r	This study
M0066	Δ phoP* _{Xoo} , chromosomal <i>phoP</i> _{Xoo} in-frame deletion mutant, containing a vector-borne pBAD- <i>araC-phoP</i> _{Xoo} , Rif ^r , Sp ^r	This study
M0067	Δ phoQ* _{Xoo} , chromosomal <i>phoQ</i> _{Xoo} in-frame deletion mutant <i>X. oryzae</i> pv. <i>oryzae</i> PXO99 ^A , containing a vector-borne pBAD- <i>araC-phoQ</i> _{Xoo} , Rif ^r , Sp ^r	This study
M0068	Δ XC0691*, in-frame deletion mutant of essential gene <i>XC0691</i> , which contains a pHM1:: <i>XC0691</i> as a prerequisite to delete the chromosomal copy. Rif ^r , Sp ^r	This study
M0069	Δ XC1867*, in-frame deletion mutant of essential gene <i>XC1867</i> , which contains a pHM1:: <i>XC1867</i> as a prerequisite to delete the chromosomal copy. Rif ^r , Sp ^r	This study
M0070	Δ XC2815*, in-frame deletion mutant of essential gene <i>XC2815</i> , which contains a pHM1:: <i>XC2815</i> as a prerequisite to delete the chromosomal copy. Rif ^r , Sp ^r	This study
M0071	Δ XC3633*, in-frame deletion mutant of essential gene <i>XC3633</i> , which contains a pHM1:: <i>XC3633</i> as a prerequisite to delete the chromosomal copy. Rif ^r , Sp ^r	This study
M0072	Δ XC0758, insertional mutant of non-essential gene <i>XC0758</i> , Kan ^r , Sp ^r	This study
M0073	Δ XC1969, insertional mutant of non-essential gene <i>XC1969</i> , Kan ^r , Sp ^r	This study
M0074	Δ XC2108, insertional mutant of non-essential gene <i>XC2108</i> , Kan ^r , Sp ^r	This study
M0075	Δ XC2562, insertional mutant of non-essential gene <i>XC2562</i> , Kan ^r , Sp ^r	This study
Plasmids		
pGEM-T Easy	Cloning vector for PCR products, Amp ^r .	Promega
pET30a	Protein expression vector with a T7 promoter, Kan ^r .	Novagen
pK18mobsacB	<i>sacB</i> marker containing mobilizable suicide vector, Kan ^r . For gene in-frame deletion.	Schäfer et al. (1994)
pEX18Gm	<i>sacB</i> marker-containing mobilizable suicide vector, Gm ^r . For in-frame deletion of genes in <i>P. aeruginosa</i> PAO1.	Hoang et al., (1998)
pHM1	<i>lacZ</i> promoter driving broad-host-range plasmid, Sp ^r . For gene complementation.	Laboratory collection
pHM2	Promoterless broad-host-range plasmid, Sp ^r .	Laboratory collection
pphoP _{Xcc}	pHM2::pBAD- <i>araC-phoP</i> _{Xcc} , Sp ^r .	This study
pphoQ _{Xcc}	pHM2::pBAD- <i>araC-phoQ</i> _{Xcc} , Sp ^r .	This study

pK-phoP _{Xcc}	pK18mobsacB derivate which contains part of <i>phoP_{Xcc}</i> gene. For constructing in-frame deletion mutant of <i>phoP_{Xcc}</i> gene, Kan ^r	This study
pK-phoQ _{Xcc}	pK18mobsacB derivate which contains part of <i>phoQ_{Xcc}</i> gene. For constructing in-frame deletion mutant of <i>phoQ_{Xcc}</i> gene, Kan ^r	This study
pK-phoP _{Xoo}	pK18mobsacB derivate which contains part of <i>phoP_{Xoo}</i> gene. For constructing in-frame deletion mutant of <i>phoP_{Xoo}</i> gene, Kan ^r	This study
pK-phoQ _{Xoo}	pK18mobsacB derivate which contains part of <i>phoQ_{Xoo}</i> gene. For constructing in-frame deletion mutant of <i>phoQ_{Xoo}</i> gene, Kan ^r	This study
Gm-phoP _{Pae}	pEX18Gm derivate which contains part of <i>phoP_{Pae}</i> gene. For constructing in-frame deletion mutant of <i>phoP_{Pae}</i> gene, Gm ^r	This study
Gm-phoQ _{Pae}	pEX18Gm derivate which contains part of <i>phoQ_{Pae}</i> gene. For constructing in-frame deletion mutant of <i>phoQ_{Pae}</i> gene, Gm ^r	This study
pK-XC0691	pK18mobsacB derivate which contains part of <i>XC0691</i> gene. For constructing in-frame deletion mutant of <i>XC0691</i> , Kan ^r	This study
pK-XC1867	pK18mobsacB derivate which contains part of <i>XC1867</i> gene. For constructing in-frame deletion mutant of <i>XC1867</i> , Kan ^r	This study
pK-XC2815	pK18mobsacB derivate which contains part of <i>XC2815</i> gene. For constructing in-frame deletion mutant of <i>XC2815</i> , Kan ^r	This study
pK-XC3633	pK18mobsacB derivate which contains part of <i>XC3633</i> gene. For constructing in-frame deletion mutant of <i>XC3633</i> , Kan ^r	This study
ii-XC0758	pK18mobsacB derivate which contains part of <i>XC0758</i> gene. For constructing insert inactivation mutant of <i>XC0758</i> gene, Kan ^r	This study
ii-XC1969	pk18mobsacB derivate which contains part of <i>XC1969</i> gene. For constructing insert inactivation mutant of <i>XC1969</i> , Kan ^r	This study
ii-XC2108	pK18mobsacB derivate which contains part of <i>XC2108</i> gene. For constructing insert inactivation mutant of <i>XC2108</i> , Kan ^r	This study
ii-XC2562	pK18mobsacB derivate which contains part of <i>XC2562</i> gene. For constructing insert inactivation mutant of <i>XC2562</i> , Kan ^r	This study
pET-phoP _{Xcc}	pET30a:: <i>phoP_{Xcc}</i> , for expression of full-length PhoP _{Xcc} , Kan ^r	This study
pET-phoQ _{Xcc}	pET30a:: <i>phoQ_{Xcc}</i> , for expression of full-length PhoQ _{Xcc} , Kan ^r	This study
pET-phoP _{Xoo}	pET30a:: <i>PXO_02836</i> , for expression of full-length PhoP _{Xoo} . Kan ^r	This study
pET-phoQ _{Xoo}	pET30a:: <i>PXO_02837</i> , for expression of full-length PhoP _{Xoo} . Kan ^r	This study
pET-phoP _{Pae}	pET30a::PA1179, for expression of full-length PhoP _{Pae} , Kan ^r	This study
pET-phoQ _{Pae}	pET30a::PA1180, for expression of full-length PhoQ _{Pae} , Kan ^r	This study
pHM-XC0691	pHM1:: <i>XC0691</i> , Sp ^r .	This study
pHM-XC1867	pHM1:: <i>XC1867</i> , Sp ^r .	This study
pHM-XC2815	pHM1:: <i>XC2815</i> , Sp ^r .	This study
pHM-XC3633	pHM1:: <i>XC3633</i> , Sp ^r .	This study

^a Antibiotic resistance: Rif^r, Kan^r, Amp^r, Gm^r, Cb^r and Sp^r, represent resistant to rifampicin, kanamycin, ampicillin, gentamicin, carbenicillin and spectinomycin, respectively.

Table S2. Primers used in this study.

Primer name	Sequence (forward/reverse)	Length & description
P1	CGGCATGATTCTGTCCGGTGG	487 bp;
P2	TTGCAGTTGCTGCGGTGTCG	For operon verification
P3	GAGCAAGCCGACCCTGGAAT	525 bp;
P4	GGCGTTGGCGTAGTTCCTCAGC	For operon verification
P5	TTTGGCGATAGCCGGCTGAC	321 bp;
P6	AACAGCAAAGCCTTCGCGCT	For operon verification
P7	GGTTGGGAGCTGGTGGAACA	413 bp;
P8	AGACGACGGGACGTGTGGAA	For operon verification
P9	TGTTGTTCCGCCCTTCGGACG	401 bp;
P10	ATTTCCGTGTACAGCCGCGC	For operon verification
phoQ-F	GGACGTTCCAAGTGGTATCG	224 bp;
phoQ-R	CCGAGATACAGCGAGCCATC	as positive control For operon verification
4031-up-F	TCTAGATGTTCCGTTTGGCGATAGC	353 bp;
4031-up-R	GAATTCCTTCTTCGCCGTCTGTGC	For Δ phoP _{Xcc} * construction
4031-down-F	GAATTCGTGCTGGAAGTGTTCATCGG	444 bp;
4031-down-R	CTGCAGCGTCAGGTCGACCACTTC	For Δ phoP _{Xcc} * construction
4030-up-F	GAATTCGTGCTGGAAGTGTTCATCGG	444 bp;
4030-up-R	GGATCCGTCAGGTCGACCACTTC	For Δ phoQ _{Xcc} * construction
4030-down-F	GATCCGCCGGCATGATTCTGTCCGGTGG	444 bp;
4030-down-R	GTCGACTTGCAGTTGCTGCGGTGTGC	For Δ phoQ _{Xcc} * construction
His-PhoP-Xcc-F	CATATGCGTATCCTTTTGGTCTGA	681 bp;
His-PhoP-Xcc-R	CTCGAGGCCTTCCGTACGCGGGA	For PhoP _{Xcc} protein expression
His-PhoQ-Xcc-F	CATATGGTGTCTGGGACGTTCCAAGTGG	1413 bp;
His-PhoQ-Xcc-R	CTCGAGCAAGCCTGGCGGCAGGGTGA	For PhoQ _{Xcc} protein expression
phoP-F	GTCGACCATATGCGTATCCTTTTGGTCTGA	684 bp;
phoP-R	GGTACCCTCGAGGCCTTCCGTACGCGGGA	For pphoP _{Xcc} plasmid construction
phoQ-F	GCGTGCACATGTCTGGGACGTTCCAAGTGG	1416 bp;
phoQ-R	CGGGGTACCTTACAAGCCTGGCGGCAGGGTGA	For pphoQ _{Xcc} plasmid construction
XC4030-F	GGATCCGGCGAGATCCCGTACACCATT	801 bp;
XC4030-R	AAGCTTACGCACACCGCGCTGCAGGA	For <i>phoQ</i> _{Xcc} insertion inactive mutant construction
XC4031-F	AGGTCTCTACATGGGCCGTGAA	524 bp;
XC4031-R	TCGGCTTCAACTACCATCCGGGTCAAG	For <i>phoP</i> _{Xcc} insertion inactive mutant construction
pBAD-F	GAATTCACTCCAGAAAGGCCACCAAC	1371 bp;
pBAD-R	GTCGACCCCAAAAAACGGGTATGGA	For pBAD- <i>araC</i> promoter fragment PCR
p-F	ATTGGTGTGACACGGTGCCG	1577 bp;
p-R	ATGCGGCCATGCGGAATGCT	For Δ phoP _{Xcc} mutant PCR verification

q-F	GAGCAAGCCGACCCTGGAAT	2135 bp;
q-R	GGCAACGCTGCATCGTCGCT	For Δ phoQ _{Xcc} mutant PCR verification
c-F	AACGCGGCCGCGTGCATATC	200 bp; For EMSA probe
c-R	GCACTCTCCCTACTTACGTT	
q-phoP-F	GCCAATGTGGATCTGACCAG	120 bp; For qRT-PCR
q-phoP-R	GCGGTCGAAATCCTGCTGAT	
q-phoQ-F	GGCATGTGATCGTGCAGGA	100 bp; For qRT-PCR
q-phoQ-R	GCAGGGTGACTTCGAAGCGT	
tmRNA-F	GGGGGTGCACTGGTTTCG	113 bp; For qRT-PCR internal reference
tmRNA-R	CCGTAGTTGTCGTCGTTGGC	
4031-up -F	TCTAGATGTTCCGTTTGGCGATAGC	931 bp;
P2-6his-R	TCAGTGGTGGTGGTGGTGGTGGCCTTCCGTA CGCGGGAT	For <i>phoP</i> _{Xcc} -His ₆ epitope construction
P3-6his-F	CACCACCACCACCACCCTGAGTCAGCACA GCGGCG	344 bp; For <i>phoP</i> _{Xcc} -His ₆ epitope construction
4031-down-R	CTGCAGCGTCAGGTCGACCACTTC	314 bp;
ftsA-F	AAATTTTCGAGATGGTGCAG	For <i>ftsA</i> _{Xcc} qRT-PCR assay
ftsA-R	GCGATACCAGTTCTTCAATT	200 bp;
ftsA-Xccp-F	GGAATTCACAACGTCCGATCGCGCGCG	For <i>Xcc-ftsA</i> promoter fragment PCR
ftsA-Xccp-R	CGCGGATCCAGCCGGAATAGCGAATGGG	
ftsA-Xoop-F	GAATTCAGCTGGCCGATCCGCAGCG	200 bp;
ftsA-Xoop-R	GGATCCTTAAAGCCGGGAGTCGGGAG	For <i>Xoo-ftsA</i> promoter fragment PCR
PftsA-F	GGATCCTGCGCGCGCACGCCTGCAGC	300 bp;
PftsA -R	AAGCTTCAGTCCAACGATGAGGGA	For <i>ftsA</i> _{Xcc} footprinting assay
PphoP -F	GGATCCTTTGGCGATAGCCGGCTGACGC	280 bp;
PphoP -R	AAGCTTCGCGCAGCGGAGCTTCGT	For <i>phoP</i> _{Xcc} footprinting assay
Poar -F	CACACAGCATTGCTCGAACGA	202 bp;
Poar -R	ACGGACACTGCAGACGTGGGAC	For <i>oar</i> _{Xcc} footprinting assay
A28nt-F	CGCACGCGCTGGTCCTTAATTCTCTGCG	28 bp; as <i>ftsA</i> -Wt
A28nt-R	CGCAGAGAATTAAGGACCAGCGCGTGCG	For motif EMSA and MST test
P28nt-F	ACTTCTGCGTTTCAGTGACATAAATCCCC	28 bp; as <i>phoP</i> _{Xcc} -Wt
P28nt-R	GGGGATTTATGTCACTGAACGCAGAAGT	For motif MST test
Oar25nt-F:	CCGTTTCAGGTTGTTTCAGGCGATCCC	25 bp; as <i>Oar</i> _{Xcc} -Wt2
Oar25nt-R:	GGGATCGCCTGAACAACCTGAACGG	For motif MST test
7273-up-F	GAGCTCGGTACCCGGGGAT CCACCAAAGACGGCTGACG GTTG	319 bp; For <i>ftsZ</i> _{Xcc} -eGFP construction
7273-up-R	CTGAGCTGTTACAGCCTGACCCGTCCTGACT GTCCTCAAGAT	
Npt-rbs-F	GTCAGGCTGTAACAGCTCAGA	386 bp; For <i>ftsZ</i> _{Xcc} -eGFP construction
Npt-rbs-R	AGTTCAAATGTGCCATATGTTTTTCCTCCTT	

	CTGCAGAT	
ftsZ-F	ATGGCACATTTTGAAGCTGATCGA	1128bp; For ftsZ _{Xcc} -eGFP
ftsZ-R	TCGCCCTTGCTCACCATGTCGGCCTGGCGGC GCAGGAA	construction
Egfp-F	ATGGTGAGCAAGGGCGAGGAGCT	720 bp; For ftsZ _{Xcc} -eGFP
Egfp-R	CTGCCGTCTTCCCTAACGATCATTACTTGTAC AGCTCGTCCATGCCGA	construction
7273-down-F	TGATCGTTAGGGAAGACGGCAGGGC	427 bp; For ftsZ _{Xcc} -eGFP
7273-down-R	GCATGCCTGCAGGTCTACTCTAGAGGCCGGT TGGCTGACGAAAGTTGA	construction
PAOP-up-F	gaattcACAAGCTGGGCTCCCTGGACCT	300 bp
PAOP-up-R	ggatccGTCGATCACCGCCAGGTCGTGGT	For <i>phoP</i> _{Pae} mutant construction
PAOP-down-F	ggatccGACGAGGAGCGCGACGCCAAC	301 bp
PAOP-down-R	aagcttCCCTTCTCCACCCGCGCCGCCGA	For <i>phoP</i> _{Pae} mutant construction
PAOQ-up-F	gaattcGCGCAAGCTGGAGGCCTGCGGCGGCT	261 bp
PAOQ-up-R	ggatccGCCCTTCTCCACCCGCGCCGCCGA	For <i>phoQ</i> _{Pae} mutant construction
PAOQ-down-F	ggatccGGGCCGGGTTACTCGGAGCTGTGGGT	360 bp
PAOQ-down-R	aagcttAGCCCCTGTCGTCGGTTTTGCCACT	For <i>phoQ</i> _{Pae} mutant construction
CPAO1-P-F:	GTCGACatgaaactgctgtagtgaaga	678 bp
CPAO1-P-R:	GGTACCtaccggcagcgctcggtga	For pHM1- <i>phoP</i> _{Pae} construction
CPAO1-Q-F:	GTCGAC gtagccttccctgcatcctg	1347 bp
CPAO1-Q-R:	GGTACCttagactgtagcgaacgtatg	For pHM1- <i>phoQ</i> _{Pae} construction
PAO1-P-His6-F:	CATATGatgaaactgctgtagtgaaga	678 bp
PAO1-P-His6-R:	CTCGAGcggcagcgctcggtgaacagga	For <i>PhoP</i> _{Pae} protein expression
PAO1-Q-his6-F:	CATATGGtagccttccctgcatcctg	1347 bp
PAO1-Q-his6-R:	CTCGAGgactgtagcgaacgtatgcggaag	For <i>PhoQ</i> _{Pae} protein expression
P-XC0691-F	AAAGGTTAACGGCTGCGGCC	200 bp
P-XC0691-R	CGAGGGAGTCGTTCTTGAAG	For EMSA probe
P-XC1867-F	CAATGCCTGCCAGGCCAGCA	200 bp
P-XC1867-R	CTTGGCGAGGGTAACTGCGC	For EMSA probe
P-XC2815-F	AACCTTGATTGCGCTGTGCT	200 bp
P-XC2815-R	GAGGTCTCTCCAGGGATTCA	For EMSA probe
P-XC3633-F	GACCCGGAATATGCGCGAGCCATT	200 bp
P-XC3633-R	CGTTGCTACCTCTGAAATAGTCA	For EMSA probe
P-XC0758-F	CCTTTCTCTCTCCAGAAGGATTTT	200 bp
P-XC0758-R	GTGCGCCTGTCACGCGCTGCATAGG	For EMSA probe
P-XC1969-F	ACGAAACCATGCGCCCGCAGCCG	200 bp
P-XC1969-R	GCCGTGGCAGCCCTGGCAGGTG	For EMSA probe
P-XC2108-F	GGTGGACTCAACACCGAATCC	200 bp
P-XC2108-R	AGTTGGACTACCTTCCAGGCGAAT	For EMSA probe
P-XC2562-F	GCACATATCCGTGCACGTTTAC	200 bp
P-XC2562-R	GCCCGCGCGGTGGTCGCCGACGG	For EMSA probe
P-PA4418-F	GGCGCCATGCGTTATATAAG	200 bp
P-PA4418-R	GGGAAAGAAACCCTAGGCCGA	For EMSA probe
P-PA1795-F	ACATCAACGCCGACTCCCT	200 bp

P-PA1795-R	TTCCTCAGCCCTGTCCCA	For EMSA probe
P-PA0973-F	GCCCAATGGCACCATGCTAATCT	200 bp
P-PA0973-R	CATGTAACCTCCTAATGAACCCCA	For EMSA probe
P-PA5451-F	CAAGGCATGGCCAGGGTC	200 bp
P-PA5451-R	CAGACCACCTGCCGTAC	For EMSA probe
P-PA4001-F	GCCGGTGGCATCACCATGACG	200 bp
P-PA4001-R	TCTTGGTCTCAAACCTGGGCGATC	For EMSA probe
P-PA5490-F	ACCATGCCGCCTGGGAGCCGCGG	200 bp
P-PA5490-R	CAGCTAATCCAATTACGGCTAAG	For EMSA probe
P-PA4232-F	CCTGCCGCTCGCGCCCGCGCGC	200 bp
P-PA4232-R	GACGTTCTCCTAAGGTTACGCATC	For EMSA probe
P-PA0918-F	CCAGGCCATCCGCGACCGCGAG	200 bp
P-PA0918-R	CACGGTTCCTTCTTTCGGCTCTCG	For EMSA probe
q-XC0691-F	TTCAAGAACTCCGCGGCATGT	89 bp
q-XC0691-R	ATGCCTTGTCCGCGCACGTA	For qRT-PCR
q-XC1867-F	ATGAGCCTGCGCCTGCACAA	119 bp
q-XC1867-R	CCGATATGCGCATAGTTGTAGACCG	For qRT-PCR
q-XC2815-F	GTCACCCGCATCGATGAGGTTG	137 bp
q-XC2815-R	ACGTTCTTGTTGCCCTTGCTGC	For qRT-PCR
q-XC3633-F	GACATGATTCGGTCCGTATGGGC	104 bp
q-XC3633-R	ATCCACAAGGCGCCGAGCTT	For qRT-PCR
q-XC0758-F	GCCGCGCCACATTCCTCAA	87 bp
q-XC0758-R	GGCGAAAACAGCGGCGAAAC	For qRT-PCR
q-XC1969-F	ACGGCGTGACCGGCTACAAGAA	99 bp
q-XC1969-R	GGTATTCGGTCAGTGCCTGGGTCA	For qRT-PCR
q-XC2108-F	TGAAAGTGCAGATCATGAGTTCCGC	129 bp
q-XC2108-R	TGAACGGCAGTGGGAAATCGC	For qRT-PCR
q-XC2562-F	ATGCGTGTCTGCACTGGCTGA	108 bp
q-XC2562-R	TTCCAGCAACCACTGCCGCA	For qRT-PCR
q-tmRNA-F	AGGGGGCAGCTTTCCTCGTTAAT	90 bp
q-tmRNA-R	AATTAAGCGGCGATAGCGAAGTCC	For qRT-PCR
q-PA4481-F	ATTGCGTGGCATGTTTTCCAGC	112 bp
q-PA4481-R	AATGGCGACCACGGACGGTT	For qRT-PCR
q-PA1795-F	GTGCTGCAGATCTACAACACGCTGA	92 bp
q-PA1795-R	GTCATGCCGCACACGTACATGC	For qRT-PCR
q-PA0973-F	GGCAAATTTGCTGCGCTGGCT	89 bp
q-PA0973-R	CCATTGGCACCTTCACCGGAAG	For qRT-PCR
q-PA5451-F	ATGCTTCTTGCTTGTCTCGTTCCT	138 bp
q-PA5451-R	GATCATCGACAGCGGATTGAGCA	For qRT-PCR
q-PA4001-F	AATGCAAGTACTGCGTACATGGGCG	132 bp
q-PA4001-R	TCGCTGACGAACTCGGCCACTT	For qRT-PCR
q-PA5490-F	CTTCTCGTGAGTCTGCTGTTGACCC	146 bp
q-PA5490-R	AGTTTCGGGAAGTTCGGCGC	For qRT-PCR
q-PA4232-F	ATGGCCCGTGGGGTTAACAAAG	106 bp
q-PA4232-R	TGGCGAGGGTGATGTTGGTCAC	For qRT-PCR

q-PA0918-F	ATGAGCTGGAAAAACACCGAATCCC	117 bp
q-PA0918-R	GGGGAAATTGCCCTTCAGTTCGATA	For qRT-PCR
q-PAssrA-F	GCCAGCTCTCCGCTATCGGTTCTA	94 bp
q-PAssrA-R	ATACAGCTCGCTCCAAGCACCTG	For qRT-PCR
XC0691-up-F	gaattcAaaggttaacggctgcggccggc	380 bp
XC0691-up-R	ggatccggcctccgcaccgacggcagccac	For <i>XC0691</i> mutant construction
XC0691-down-F	ggatccCtgcgcgacctggaccgctgat	230 bp
XC0691-down-R	aagcttgggagcgcacatgaaacggcgcagg	For <i>XC0691</i> mutant construction
XC1867-up-F	gaattcGagacctgggctgaacgcagccc	310 bp
XC1867-up-R	ggatccgatgttgctgctgtagcgcagcgc	For <i>XC1867</i> mutant construction
XC1867-down-F	ggatccGcggcgaaaaaagccaagatttc	220 bp
XC1867-down-R	aagcttgcgggtggcttcgccttacctc	For <i>XC1867</i> mutant construction
XC2815-up-F	gaattcttaagcctggagtgatccagttg	250 bp
XC2815-up-R	ggatccggcccaatccacgcagcggttc	For <i>XC2815</i> mutant construction
XC2815-down-F	ggatccGccgcgtgatcatggtcaaccag	490 bp
XC2815-down-R	aagcttgatgcggtagatcgaccgatccgc	For <i>XC2815</i> mutant construction
XC3633-up-F	gaattcTctggtcctgttgctggaag	480 bp
XC3633-up-R	ggatccaggcaactttgctgccaggacctc	For <i>XC3633</i> mutant construction
XC3633-down-F	ggatccggggacttctttacggcgctgc	220 bp
XC3633-down-R	aagcttttcagaccaaacccagctggccgc	For <i>XC3633</i> mutant construction
PA4481-up-F	GAATTCGatgccgcggtgcggcgtcta	224 bp
PA4481-up-R	GGATCCaccaggtcgatcgacagatcgct	For <i>PA4481</i> mutant construction
PA4481-down-F	GGATCCGctcggatatacgcgagcgcg	450 bp
PA4481-down-R	AAGCTTatcagctcgctacggctgctgaa	For <i>PA4481</i> mutant construction
PA1795-up-F	GAATTCcggctgtcgcgccgagccgctc	230 bp
PA1795-up-R	GGATCCgccgaccagcggcgtgaagac	For <i>PA1795</i> mutant construction
PA1795-down-F	GGATCCCtgcaggcggcgccgagggca	480 bp
PA1795-down-R	AAGCTTgtggtgctgctgccggcaa	For <i>PA1795</i> mutant construction
PA0973-up-F	GAATTCtctacccaccgccagcaggac	240 bp
PA0973-up-R	GGATCCcacagccacagccatggcca	For <i>PA0973</i> mutant construction
PA0973-down-F	GGATCCGaaggccacaccgacgaacg	500 bp
PA0973-down-R	AAGCTTttgagctgctggatctggtt	For <i>PA0973</i> mutant construction
PA5451-up-F	GAATTCcaatggcagtgccgcgcggct	390 bp
PA5451-up-R	GGATCCgtaggccaggccctcgtcga	For <i>PA5451</i> mutant construction
PA5451-down-F	GGATCCctcaaccgatgaccgcgct	270 bp
PA5451-down-R	AAGCTTggcgcggagggtgaaaggca	For <i>PA5451</i> mutant construction
in-XC0691-F	gaattcAACTCCGCGCATGTTCT	304 bp
in-XC0691-R	aagcttAGGAAGCGCGACTTGTGCAC	For insert inactivation mutant construction of <i>XC0691</i>
in-XC1867-F	gaattcATGAGCCTGCGCCTGCACAA	346 bp
in-XC1867-R	aagcttTTGCCTCCGGCTCGATATCC	For insert inactivation mutant construction of <i>XC1867</i>
in-XC2815-F	gaattcATGAAGACCCGACTGCTC	347 bp
in-XC2815-R	aagcttTTGTTCTGGATCGCGTTG	For insert inactivation mutant construction of <i>XC2815</i>

in-XC3633-F	gaattcGACATGATTCGGTCCGTA	316 bp	
in-XC3633-R	aagcttGTGGAAACGCCTGCTTTT	For insert inactivation mutant construction of <i>XC3633</i>	
in-XC0758-F	gaattcGCCGCGCCACATTCCTCAA	311 bp	
in-XC0758-R	aagcttTACCGCTGCAGAAAGCCCTG	For insert inactivation mutant construction of <i>XC0758</i>	
in-XC1969-F	gaattcCGCTTGTCTCGCTCTGGTCGTCTT	311 bp	
in-XC1969-R	aagcttTTTGCGCCTGTGCCTGCATG	For insert inactivation mutant construction of <i>XC1969</i>	
in-XC2108-F	gaattcATGAAAGTGCAGATCATGA	206 bp	
in-XC2108-R	aagcttTTGTTCTGCAACGACTTG	For insert inactivation mutant construction of <i>XC2108</i>	
in-XC2562-F	gaattcATGCGTGTCCCTGCACTGGCT	302 bp	
in-XC2562-R	aagcttTAAGCGTTGCTCAGCGACC	For insert inactivation mutant construction of <i>XC2562</i>	
C-XC0691-F	AAGCTTATGTTCAAGAACTCCGCGG	1047 bp	
C-XC0691-R	GAATTCTCACTCCGGCGCGAAGAACT	For <i>XC0691</i> complementation	
C-XC1867-F	AAGCTTATGCCGATGAGCCTGCGCCT	1374 bp	
C-XC1867-R	GAATTCTCATGCGCGCTTCCAGCGCA	For <i>XC1867</i> complementation	
C-XC2815-F	AAGCTTATGAAGACCCGACTGCTCGT	480 bp	
C-XC2815-R	GAATTCGCGCAGCACGACCTTGCCGT	For <i>XC2815</i> complementation	
C-XC3633-F	AAGCTTTTGGACATGATTCGGTCCGT	792 bp	
C-XC3633-R	GAATTCTCATAGCGCATCCACCATTT	For <i>XC3633</i> complementation	
C-PA4481-F	AAGCTTATGTTCAAAAAATTGCGTGG	1038 bp	
C-PA4481-R	GAATTCTTACTCGGTGGAGAGCAGGT	For <i>PA4481</i> complementation	
C-PA1795-F	AAGCTTGTGCTGCAGATCTACAACA	1383 bp	
C-PA1795-R	GAATTCTCAGTCGGCCAGGCGCCA	For <i>PA1795</i> complementation	
C-PA0973-F	AAGCTTATGGAAATGCTGAAATTCGG	507 bp	
C-PA0973-R	GAATTCTTACTTCTTCAGCTCGACGC	For <i>PA0973</i> complementation	
C-PA5451-F	AAGCTTATGCTTCTTGGCTTGTCT	798 bp	
C-PA5451-R	GAATTCTCAGAGTTCATCCACCAT	For <i>PA5451</i> complementation	

Table S3. List of proteins (>1.2-fold) in the Δ phoP* mutant strain that were differentially expressed (>1.2-fold) between the induced and repressed conditions.

Spot No.	Protein code ^a	Protein name	Length (aa)	Protein annotation or description	Theoretical MW (kDa)	pI	Score ^b	Sequence coverage	Ratio ^c (ara ^d /IPTG)
Amino acid biosynthesis and metabolism									
33	XC0194		469	Glutamine synthetase	52.0	5.20	201	39%	2.20
12	XC1255		460	L-serine dehydratase	50.2	5.93	210	52%	-2.13
24	XC1367	PyrB	315	Aspartate carbamoyltransferase	34.0	5.94	137	52%	-2.54
11	XC1733		498	L-lysine 6-aminotransferase	53.9	5.89	163	40%	-2.07
45	XC2351		410	Valine-pyruvate aminotransferase	44.6	5.82	97	40%	1.96
10	XC2653	Hut1	401	Imidazolonepropionase	46.1	5.77	135	28%	-3.15
48	XC2809		387	Glutaryl-CoA dehydrogenase	41.9	5.94	156	36%	1.58
13	XC3313		478	Family II 2-keto-3-deoxy-D-arabino-heptulosonate 7-phosphate synthase	53.6	5.90	301	59%	-2.37
23	XC3655		367	Cysteine synthase	40.2	5.96	124	47%	-2.12
Carbohydrate metabolism									
49	XC0944		429	Citrate synthase	47.9	5.88	104	40%	1.46
46	XC0972		333	Glyceraldehyde-3-phosphate dehydrogenase	36.2	6.04	124	42%	1.39
6	XC1952	PpsA	792	Phosphoenolpyruvate synthase	86.5	5.12	76	10%	2.73
29	XC2369	MtnB	217	Sugar aldolase	24.4	5.92	217	34%	-2.02
9	XC2733		448	UDP-glucose dehydrogenase	49.0	5.79	94	21%	2.62
5	XC3613		351	dTDP-glucose-4,6-dehydratase	38.7	5.47	145	54%	$-\infty$
14	XC3674	GlmU	454	UDP-N-acetylglucosamine pyrophosphorylase	48.2	6.23	177	44%	-2.39
58	XC3769		398	UDP-galactopyranose mutase	45.9	5.94	159	58%	-1.3
36	XC3854		743	Isocitrate dehydrogenase	80.2	5.50	138	40%	1.74
16	XC4065		521	Beta-xylosidase	58.5	6.28	62	16%	2.82
Energy metabolism and detoxification									

26	XC0333		295	Oxidoreductase	30.0	5.73	52	24%	-2.43
3	XC0796		279	Glutaredoxin-like protein	29.9	4.59	198	51%	∞
42	XC1595		744	NADH-ubiquinone oxidoreductase NQO3 subunit	79.9	6.15	158	44%	1.53
0	XC3073		366	Xenobiotic flavin oxidoreductase A	39.6	6.06	50	20%	1.52
7	XC3397		529	Aalkyl hydroperoxide reductase subunit F	57.2	5.28	182	41%	2.96
15	XC3689		213	Dihydrolipoamide dehydrogenase	21.5	5.35	78	44%	-2.11
2	XC3754		299	Mn-containing catalase	32.4	4.70	301	49%	1.34
Fatty acid metabolism									
1	XC1017		594	Outer membrane lipase/esterase	61.9	4.76	114	18%	1.75
53	XC1516		291	Geranyltranstransferase; farnesyl-diphosphate synthase	30.3	5.65	88	36%	1.62
47	XC2980		393	Acyl-CoA dehydrogenase	42.6	5.96	202	62%	1.34
Nucleic acid and protein metabolism									
41	XC0004	GyrB	814	DNA gyrase subunit B	89.5	5.70	130	25%	1.51
21	XC1324	PurM	341	Phosphoribosylformylglycinamide cyclo-ligase	36.0	4.73	63	25%	2.43
39	XC1429	GltX	467	Glutamyl-tRNA synthetase	52.1	5.39	225	54%	1.56
37	XC1628		673	Excinuclease ABC subunit B	75.8	5.43	77	15%	1.84
44	XC2534	PyrG	554	CTP synthetase	62.8	5.95	60	20%	1.33
52	XC3619		309	Acetyl transferase/isomerase	33.5	5.80	73	52%	1.91
22	XC3943		419	DNA/pantothenate metabolism flavoprotein	43.7	6.01	139	56%	-2.02
40	XC4328	TrmE	446	Thiophene and furan oxidation protein	47.7	5.39	113	45%	1.92
Ribosome, protein biosynthesis and refolding									
55	XC0535	GroEL	546	60 kDa chaperonin	57.1	5.01	322	65%	-1.31
28	XC1492		301	Peptidyl-prolyl cis-trans isomerase	33.1	6.24	107	39%	2.06
56	XC3342	TufI	396	Elongation factor Tu	43.4	5.45	255	56%	$-\infty$
Signal transduction									
34	XC1691	FixL	540	Sensor histidine kinase	59.1	5.24	105	42%	1.39
4	XC4031	PhoP	227	two-component system regulatory protein	25.4	5.19	441	66%	2.19

Cell division										
25	XC3506	FtsA	411	Cell division protein	44.4	5.78	183	41%	-3.15	
Transportation										
32	XC0017		446	Outer membrane protein	47.1	5.18	575	62%	1.65	
35	XC1091		626	Outer membrane receptor for transport of vitamin B	68.2	5.22	259	52%	1.55	
54	XC4327	Oar	1006	Oar protein	10.6	4.68	263	45%	1.48	
Function unknown protein										
17 ^e	XC0215		198	Conserved hypothetical protein	21.8	4.60	76	47%	-2.38	
51	XC1374		451	Conserved hypothetical protein	49.9	6.15	157	45%	1.33	
43	XC2373		554	Conserved hypothetical protein	60.3	5.97	54	24%	1.56	
18	XC3095		134	Conserved hypothetical protein	14.9	6.28	134	51%	-2.15	
27	XC3393		265	Conserved hypothetical protein	28.9	6.55	59	30%	-2.01	
20	XC3882		165	Conserved hypothetical protein	16.7	4.82	89	43%	2.11	
30	XC4228		222	Conserved hypothetical protein	24.1	6.08	98	46%	2.08	

^a Names and codes of identified proteins are according to genomic annotation of *X. campestris* pv. *campestris* 8004.

^b Scores are based of Mascot search. Scores greater than 49 are significant ($p < 0.05$).

^c The ratio is the relative expression level of a protein under arabinose stimulation vs. IPTG stimulation. Fragments of these proteins were identified from different sites of the gels.

^d ara represent L-arabinose treated condition.

^e XC0215 was identified in another point, with a relative expression level of -2.01 (Mascot search score = 316)

Table S4. ChIP-seq analysis identified genes with promoter regions bound by PhoP in *X. campestris*. pv. *campestris*

No	Growth condition	Gene	Annotation ^a	Strand ^b	Peak Z-score	Peak start:end	Peak position	Classification
1 ^c	L-arabinose	XC0017	Outer membrane protein	-	5.69	20741: 21207	20982	Transportation
2	L-arabinose	XC0018	Conserved hypothetical protein	+	5.69	20741: 21207	20982	Function unknown protein
3	L-arabinose	XC0136	RhsD protein	+	2.00	165044: 167218	166891	Stress response
4	L-arabinose	XC0215	Conserved hypothetical protein	-	4.77	263259: 263668	263464	Function unknown protein
5	L-arabinose	XC0220	Conserved hypothetical protein	-	8.82	266928: 267479	267123	Function unknown protein
6	L-arabinose	XC0627	D-serine/D-alanine/glycine transporter	+	1.71	746367: 746782	746682	Transportation
7	L-arabinose	XC0758	Soluble lytic murein transglycosylase	-	6.12	910043: 910498	910266	Cell division
8	L-arabinose	XC0759	TonB-dependent receptor	+	6.12	910043: 910498	910266	Transportation
9	L-arabinose	XC0849	TonB-dependent receptor	+	1.71	1025496: 1025737	1025611	Transportation
10	L-arabinose	XC0860	Conserved hypothetical protein	-	2.23	1039352: 1040196	1039611	Function unknown protein
11	L-arabinose	XC0866	Conserved hypothetical protein	-	1.97	1045215: 1045653	1045367	Function unknown protein
12	L-arabinose	XC1022	Regulatory protein bphR	-	2.38	1235858: 1236983	1236550	Signal transduction

13	L-arabinose	XC1030	Conserved hypothetical protein	+	1.73	1245629: 1245874	1245675	Function unknown protein
14	L-arabinose	XC1079	Ferric enterobactin receptor	-	2.43	1303499: 1303819	1303627	Transportation
15	L-arabinose	XC1110	Cation:proton antiporter	-	2.48	1341738: 1342118	1341930	Transportation
16	L-arabinose	XC1113	Ferric enterobactin receptor	-	2.91	1349297: 1349693	1349515	Transportation
17	L-arabinose	XC1235	beta-lactamase	-	6.84	1511442: 1511866	1511670	Stress response
18	L-arabinose	XC1236	Conserved hypothetical protein	+	6.84	1511442: 1511866	1511670	Function unknown protein
19	L-arabinose	XC1305	Conserved hypothetical protein	-	8.31	1597236: 1597678	1597441	Function unknown protein
20	L-arabinose	XC1306	Phosphotransferase system HPr enzyme	-	8.31	1597236: 1597678	1597441	Carbohydrate metabolism
21	L-arabinose	XC1415	Conserved hypothetical protein	-	7.72	1707914: 1708353	1708175	Function unknown protein
22	L-arabinose	XC1422	Cysteine protease	-	2.25	1718240: 1718512	1718358	Proteolysis
23	L-arabinose	XC1474	RNA polymerase ECF-type sigma factor	-	5.28	1773368: 1773850	1773613	Signal transduction
24	L-arabinose	XC1475	ATP-dependent RNA helicase	+	5.28	1773368: 1773850	1773613	Macromolecule metabolism
25	L-arabinose	XC1546	TonB-dependent receptor	-	4.36	1863561: 1863967	1863767	Transportation
26	L-arabinose	XC1635	VirB11 protein	+	2.06	1961161: 1961920	1961334	Secretion system

27	L-arabinose	XC1638	VirB3 protein	+	2.25	1963675: 1964396	1963906	Secretion system
28	L-arabinose	XC1800	3-methyladenine DNA glycosylase	-	5.16	2189141: 2189544	2189333	Macromolecule metabolism
29	L-arabinose	XC1801	Chemotaxis protein	+	5.16	2189141: 2189544	2189333	Stress response
30	L-arabinose	XC1867	CysteinyI-tRNA synthetase	-	11.92	2261976: 2262432	2262219	Macromolecule metabolism
31	L-arabinose	XC1868	Conserved hypothetical protein	+	11.92	2261976: 2262432	2262219	Function unknown protein
32	L-arabinose	XC1969	Cytochrome C4	-	3.03	2375920: 2376285	2376097	Energy metabolism
33	L-arabinose	XC1970	Cation efflux system protein	+	3.03	2375920: 2376285	2376097	Transportation
34	L-arabinose	XC2167	Conserved hypothetical protein	-	2.95	2612885: 2613234	2613059	Function unknown protein
35	L-arabinose	XC2319	Conserved hypothetical protein	+	2.75	2801540: 2801857	2801667	Function unknown protein
36	L-arabinose	XC2428	Ankyrin repeat protein	-	1.69	2942759: 2943042	2942913	Signal transduction
37	L-arabinose	XC2506	Carbon storage regulator,CsrA	-	2.64	3035495: 3035905	3035778	Trnstransduction
38	L-arabinose	XC2535	Conserved hypothetical protein	-	3.25	3066045: 3066478	3066270	Function unknown protein
39	L-arabinose	XC2536	Topoisomerase IV subunit B	+	3.25	3066045: 3066478	3066270	Macromolecule metabolism
40	L-arabinose	XC2607	Conserved hypothetical protein	-	2.23	3148508: 3148818	3148667	Function unknown protein

41	L-arabinose	XC2705	Hypothetical protein	-	2.71	3250675: 3250990	3250850	Function unknown protein
42	L-arabinose	XC2810	Conserved hypothetical protein	-	3.67	3383766: 3384176	3383999	Function unknown protein
43	L-arabinose	XC2811	Conserved hypothetical protein	+	3.67	3383766: 3384176	3383999	Function unknown protein
44	L-arabinose	XC2828	Conserved hypothetical protein	-	2.06	3401130: 3401410	3401273	Function unknown protein
45	L-arabinose	XC2899	TonB-dependent receptor	+	3.62	3481926: 3482320	3482121	Transportation
46	L-arabinose	XC2921	Conserved hypothetical protein	-	2.96	3507165: 3507504	3507345	Function unknown protein
47	L-arabinose	XC2991	beta-glucosidase	-	1.67	3586406: 3586945	3586548	Virulence
48	L-arabinose	XC2994	Conserved hypothetical protein	-	2.12	3590975: 3591543	3591158	Function unknown protein
49	L-arabinose	XC3004	HrpB8 protein	-	1.51	3600612: 3600880	3600721	Secretion system
50	L-arabinose	XC3022	HpaB protein	+	2.08	3613348: 3613680	3613530	Secretion system
51	L-arabinose	XC3029	Alcohol dehydrogenase	-	1.53	3624113: 3624554	3624214	Carbohydrate metabolism
52	L-arabinose	XC3032	Tryptophan 2,3-dioxygenase	-	1.97	3627455: 3627937	3627568	Macromolecule metabolism
53	L-arabinose	XC3127	Conserved hypothetical protein	+	5.00	3731556: 3734825	3733079	Function unknown protein
54	L-arabinose	XC3240	Outer membrane protein Slp	+	9.46	3885409: 3885854	3885631	Stress response

55	L-arabinose	XC3300	Outer membrane protein	-	2.98	3952097: 3952633	3952309	Transportation
56	L-arabinose	XC3301	Oxidoreductase	+	2.98	3952097: 3952633	3952309	Energy metabolism
57	L-arabinose	XC3326	30S ribosomal protein S8	-	1.83	3978308: 3978515	3978408	Macromolecule metabolism
58	L-arabinose	XC3379	Extracellular protease	-	3.72	4030111: 4030541	4030310	Virulence
59	L-arabinose	XC3452	PgrR	-	10.43	4099239: 4101139	4100778	Signal transduction
60	L-arabinose	XC3518	Conserved hypothetical protein	-	2.97	4180281: 4180614	4180449	Function unknown protein
61	L-arabinose	XC3519	Conserved hypothetical protein	+	2.97	4180281: 4180614	4180449	Function unknown protein
62	L-arabinose	XC3545	conserved hypothetical protein	-	4.40	4208346: 4208795	4208590	Function unknown protein
63	L-arabinose	XC3546	ABC transporter ATP-binding protein	+	4.40	4208346: 4208795	4208590	Transportation
64	L-arabinose	XC3549	Conserved hypothetical protein	+	3.20	4212221: 4212577	4212396	Function unknown protein
65	L-arabinose	XC3576	Outer membrane protein	-	1.94	4250643: 4250903	4250748	Transportation
66	L-arabinose	XC3610	dTDP-4-dehydrorhamnose reductase	-	1.85	4292861: 4293130	4293016	Energy metabolism
67	L-arabinose	XC3621	Conserved hypothetical protein	+	2.25	4301008: 4302788	4302535	Function unknown protein
68	L-arabinose	XC3631	Putative kinase WxcB	-	1.79	4311956: 4312972	4312553	Carbohydrate metabolism

69	L-arabinose	XC3799	Transcriptional regulator	-	1.82	4493133: 4493466	4493304	Signal transduction
70	L-arabinose	XC3806	RNA polymerase sigma-70 factor	-	4.72	4501460: 4501882	4501683	Transcription
71	L-arabinose	XC3843	RNA polymerase sigma-32 factor	-	2.01	4541520: 4541780	4541685	Transcription
72	L-arabinose	XC3870	Conserved hypothetical protein	-	2.09	4575636: 4575974	4575854	Function unknown protein
73	L-arabinose	XC3925	Tyrosyl-tRNA synthetase	-	4.67	4639315: 4639706	4639513	Macromolecule metabolism
74	L-arabinose	XC3926	Conserved hypothetical protein	+	4.67	4639315: 4639706	4639513	Function unknown protein
75	L-arabinose	XC3973	Conserved hypothetical protein	-	2.39	4692449: 4692923	4692620	Function unknown protein
76	L-arabinose	XC3974	Hypothetical protein	-	2.39	4692449: 4692923	4692620	Function unknown protein
77	L-arabinose	XC3975	Conserved hypothetical protein	+	2.39	4692449: 4692923	4692620	Function unknown protein
78	L-arabinose	XC3985	Histone H1	-	3.78	4701326: 4701712	4701496	Signal transduction
79	L-arabinose	XC3986	Protease Do	+	3.78	4701326: 4701712	4701496	Proteolysis
80	L-arabinose	XC4031	PhoP	-	36.13	4747193: 4748123	4747401	Signal transduction
81	L-arabinose	XC4290	Hemagglutinin	-	2.64	5094677: 5094999	5094873	Virulence
82	L-arabinose	XC4295	Conserved hypothetical protein	-	2.99	5097596: 5097983	5097786	Function unknown protein

83	L-arabinose	XC4296	Toluene tolerance protein	+	2.99	5097596: 5097983	5097786	Stress response
84	L-arabinose	XC4327	Oar protein	+	14.88	5138422: 5138919	5138660	Transportation
1	IPTG	XC0017	Outer membrane protein	-	4.70	20756: 21196	20998	Transportation
2	IPTG	XC0018	Conserved hypothetical protein	+	4.70	20756: 21196	20998	Function unknown protein
3	IPTG	XC0131	Conserved hypothetical protein	+	1.66	160874: 161140	161071	Function unknown protein
4	IPTG	XC0215	Conserved hypothetical protein	-	4.27	263275: 263688	263506	Function unknown protein
5	IPTG	XC0220	Conserved hypothetical protein	-	6.50	266937: 267477	267125	Function unknown protein
6	IPTG	XC0758	Soluble lytic murein transglycosylase	-	5.49	910062: 910483	610276	Stress response
7	IPTG	XC0759	TonB-dependent receptor	+	5.49	910062: 910483	910276	Transportation
8	IPTG	XC0844	Prolyl oligopeptidase family protein	-	2.33	1019073: 1019460	1019288	Proteolysis
9	IPTG	XC0860	Conserved hypothetical protein	-	1.71	1039781: 1040149	1040012	Function unknown protein
10	IPTG	XC0866	Conserved hypothetical protein	-	1.55	1045282: 1045522	1045397	Function unknown protein
11	IPTG	XC1079	Ferric enterobactin receptor	-	2.44	1303508: 1303847	1303650	Transportation
12	IPTG	XC1080	Conserved hypothetical protein	+	2.44	1303508:	1303650	Function unknown protein

						1303847		
13	IPTG	XC1113	Ferric enterobactin receptor	-	2.86	1349310: 1349736	1349479	Function unknown protein
14	IPTG	XC1141	TolB protein	+	1.86	1382994: 1383388	1383259	Function unknown protein
15	IPTG	XC1235	beta-lactamase	-	6.06	1511440: 1511866	1511651	Stress response
16	IPTG	XC1236	Conserved hypothetical protein	+	6.06	1511440: 1511866	1511651	Function unknown protein
17	IPTG	XC1305	Phosphotransferase system HPr enzyme	-	6.31	1597228: 1597670	1597457	Carbohydrate metabolism
18	IPTG	XC1306	Conserved hypothetical protein	-	6.31	1597228: 1597670	1597457	Function unknown protein
19	IPTG	XC1415	Conserved hypothetical protein	-	7.61	1707905: 1708350	1708122	Function unknown protein
20	IPTG	XC1474	RNA polymerase ECF-type sigma factor	-	3.82	1773373: 1773853	1773623	Transcription
21	IPTG	XC1475	ATP-dependent RNA helicase	+	3.82	1773373: 1773853	1773623	Macromolecule metabolism
22	IPTG	XC1534	Conserved hypothetical protein	-	2.01	1843394: 1843696	1843580	Function unknown protein
23	IPTG	XC1546	TonB-dependent receptor	-	4.54	1863582: 1863997	1863788	Transportation
24	IPTG	XC1635	VirB11 protein	+	1.81	1961345: 1961652	1961440	Secretion system
25	IPTG	XC1800	3-methyladenine DNA glycosylase	-	4.51	2189143: 2189553	2189329	Macromolecule metabolism
26	IPTG	XC1801	Chemotaxis protein	+	4.51	2189143:	2189329	Stress response

						2189553		
27	IPTG	XC1867	CysteinyI-tRNA synthetase	-	10.00	2261975: 2262443	2262233	Macromolecule metabolism
28	IPTG	XC1868	Conserved hypothetical protein	+	10.00	2261975: 2262443	2262233	Function unknown protein
29	IPTG	XC1969	Cytochrome C4	-	2.89	2375906: 2376234	2376071	Energy metabolism
30	IPTG	XC1970	Cation efflux system protein	+	2.89	2375906: 2376234	2376071	Transportation
31	IPTG	XC2018	Conserved hypothetical protein	+	1.93	2432061: 2432300	2432195	Function unknown protein
32	IPTG	XC2228	c-di-GMP phosphodiesterase A	+	3.66	2684448: 2688647	2687666	Signal transduction
33	IPTG	XC2506	Carbon storage regulator	-	2.33	3035555: 3035905	3035769	Signal transduction
34	IPTG	XC2535	Conserved hypothetical protein	-	3.07	3066064: 3066466	3066303	Function unknown protein
35	IPTG	XC2536	Topoisomerase IV subunit B	+	3.07	3066064: 3066466	3066303	Macromolecule metabolism
36	IPTG	XC2607	Conserved hypothetical protein	-	2.27	3148422: 3148844	3148664	Function unknown protein
37	IPTG	XC2705	Hypothetical protein	-	2.34	3250670: 3251008	3250814	Function unknown protein
38	IPTG	XC2811	Conserved hypothetical protein	+	2.96	3383802: 3384159	3383956	Function unknown protein
39	IPTG	XC2899	TonB-dependent receptor	+	2.93	3481929: 3482294	3482114	Transportation
40	IPTG	XC2921	Conserved hypothetical protein	-	2.82	3507161:	3507316	Function unknown protein

						3507457		
41	IPTG	XC2994	Conserved hypothetical protein	-	1.67	3591247: 3591586	3591413	Function unknown protein
42	IPTG	XC3127	Conserved hypothetical protein	+	5.11	3731486: 3734859	3733093	Function unknown protein
43	IPTG	XC3136	Hypothetical protein	-	1.57	3749147: 3749347	3749194	Function unknown protein
44	IPTG	XC3240	Outer membrane protein Slp	+	6.81	3885418: 3885858	3885652	Stress response
45	IPTG	XC3257	Conserved hypothetical protein	-	2.25	3899542: 3899897	3899727	Function unknown protein
46	IPTG	XC3300	Outer membrane protein	-	2.30	3952150: 3952568	3952345	Transportation
47	IPTG	XC3326	30S ribosomal protein S8	-	1.80	3978303: 3978503	3978394	Macromolecule metabolism
48	IPTG	XC3379	Extracellular protease	-	2.90	4030103: 4030481	4030269	Virulence
49	IPTG	XC3452	PgrR	-	8.13	4099219: 4101185	4100779	Signal transduction
50	IPTG	XC3518	Conserved hypothetical protein	-	3.18	4180246: 4180622	4180417	Function unknown protein
51	IPTG	XC3519	Conserved hypothetical protein	+	3.18	4180246: 4180622	4180417	Function unknown protein
52	IPTG	XC3545	Conserved hypothetical protein	-	3.67	4208392: 4208790	4208581	Function unknown protein
53	IPTG	XC3546	ABC transporter ATP-binding protein	+	3.67	4208392: 4208790	4208581	Transportation
54	IPTG	XC3549	Conserved hypothetical protein	+	2.96	4212222:	4212396	Function unknown protein

						4212572		
55	IPTG	XC3576	Outer membrane protein	-	2.12	4250683: 4250943	4250800	Transportation
56	IPTG	XC3585	Leucyl aminopeptidase	+	4.16	4261331: 4261970	4261535	Proteolysis
57	IPTG	XC3620	Sugar translocase	+	1.69	4300375: 4300829	4300604	Transportation
58	IPTG	XC3628	Membrane protein WxcE	-	1.62	4308487: 4308919	4308685	Carbohydrate metabolism
59	IPTG	XC3693	Conserved hypothetical protein	-	3.10	4381037: 4381439	4381230	Function unknown protein
60	IPTG	XC3694	Outer membrane protein	+	3.10	4381037: 4381439	4381230	Transportation
61	IPTG	XC3806	RNA polymerase sigma-70 factor	-	3.98	4501480: 4501877	4501683	Transcription
62	IPTG	XC3870	Conserved hypothetical protein	-	1.94	4575682: 4575973	4575817	Function unknown protein
63	IPTG	XC3926	Conserved hypothetical protein	+	4.36	4639312: 4639693	4639501	Function unknown protein
64	IPTG	XC3974	Hypothetical protein	-	2.19	4692486: 4692917	4692682	Function unknown protein
65	IPTG	XC3975	Conserved hypothetical protein	+	2.19	4692486: 4692917	4692682	Function unknown protein
66	IPTG	XC3985	Histone H1	-	2.97	4701342: 4701731	4701510	Signal transduction
67	IPTG	XC3986	Protease Do	+	2.97	4701342: 4701731	4701510	Proteolysis
68	IPTG	XC4031	PhoP	-	32.33	4747175:	4747399	Signal transduction

						4748105		
69	IPTG	XC4295	Conserved hypothetical protein	-	3.02	5097569: 5097979	5097795	Function unknown protein
70	IPTG	XC4296	Toluene tolerance protein	+	3.02	5097569: 5097979	5097795	Stress response
71	IPTG	XC4327	Oar protein	+	12.92	5138441: 5138932	5138658	Transportation

^a Names and codes of identified genes are according to genomic annotation of *X. campestris* pv. *campestris* 8004.

^b “-” represents anti-sense strand; “+” represents sense strand.

^c Yellow highlight genes that were retrieved from both IPTG and L-arabinose treated bacterial samples.

Table S5. Theoretical prediction identified bacterial genes with a PhoP binding motif in the promoter region.

No.	PID	Gene name	Gene function	Motif_sequence
<i>Xanthomonas campestris</i> pv. <i>campestris</i> 8004				
1	66571713	XC_0029	alcohol dehydrogenase	CCATTCACG
2	66571804	XC_0123	TonB-dependent receptor	TTGTTCATG
3		XC_0145		CTGTTACAG
4	66571863	XC_0186	cardiolipin synthase	ACGTTCATT
5	66571922	XC_0245	transcriptional regulator araC family	CTGTTACACC
6	66571951	XC_0274	organic hydroperoxide resistance protein	TCATTCATT
7	66571956	XC_0280	quinone oxidoreductase	CCATTCACT
8	66572013	XC_0338	conserved hypothetical protein	TCATTCAGC
9	66572020	XC_0345	xanthomonadin biosynthesis related protein 1	TCATTCATG
10	66572031	XC_0356	dihydroxy-acid dehydratase	CTGTTACACC
11	66572039	XC_0364	conserved hypothetical protein	ACGTTCAGT
12	66572066	XC_0391	threonine dehydratase	ATGTTCATT
13	66572101	XC_0427	glycogen debranching enzyme	TCGTTACACC
14	66572106	XC_0432	outer membrane protein	TTGTTCATG
15	66572234	XC_0563	conserved hypothetical protein	CTGTTCATT
16	66572312	XC_0642	ferripyoverdine receptor	ATATTCATT
17	66572317	XC_0647	two-component system sensor protein	CTGTTCATG
18	66572360	XC_0691	rod shape-determining protein	ATGTTCAGG
19	66572373	XC_0705	endopolygalacturonase	CCATTCACC
20	66572377	XC_0709	conserved hypothetical protein	ATGTTACAG
21	66572384	XC_0716	transcriptional regulator	TCATTCATG

22	66572396	XC_0728	two-component system sensor protein	CCATTCAGC		
23	66572410	XC_0742	type II secretion system protein G	TCG TTCACC		
24	66572444	XC_0776	conserved hypothetical protein	CCG TTCATC		
25	66572477	XC_0812	two-component system regulatory protein	CTATTCACG		
26	66572484	XC_0819	polyphosphate-selective porin O	CTG TTCATT		
27	66572486	XC_0821	NADP-dependent malic enzyme	TTG TTCAGG		
28	66572509	XC_0844	prolyl oligopeptidase family protein	TCG TTCAGC		
29	66572516	XC_0851	inorganic pyrophosphatase	CTATTCAGT		
30	66572519	XC_0854	conserved hypothetical protein	ATG TTCATG		
31	66572520	XC_0855	conserved hypothetical protein	TCG TTCACC		
32	66572580	XC_0916	transcriptional regulator blaI family	ATG TTCAGT		
33	66572587	XC_0923	transcriptional regulator	CCG TTCACT		
34	66572635	XC_0971	conserved hypothetical protein	ATATTCACG		
35	66572639	XC_0975	conserved hypothetical protein	TCG TTCATG		
36	66572656	XC_0992	NADPH-sulfite reductase flavoprotein subunit	TCG TTCATC		
37	66572681	XC_1017	lipase/esterase	ATG TTCATG		
38	66572699	XC_1038	conserved hypothetical protein	TTATTCAGC		
39	66572720	XC_1060	pilus biogenesis protein	CTATTCAGT		
40	66572733	XC_1073	conserved hypothetical protein	CCATTCATT		
41	66572740	XC_1080	conserved hypothetical protein	TTG TTCAGG		
42	66572778	XC_1118	transcriptional activator ampR family	ACG TTCACC		
43	66572788	XC_1128	aspartyl-tRNA synthetase	CTATTCAGC		
44	66572801	XC_1141	TolB protein	TCG TTCATG	3834475	TTG TTCAGC
45	66572844	XC_1184	PilH protein	CCATTCACC		

46	66572886	XC_1227	sulfite synthesis pathway protein	CTG TTCATT
47	66572894	XC_1235	beta-lactamase	CCATTCATC
48	66572930	XC_1271	conserved hypothetical protein	CTG TTCACC
49	66572951	XC_1292	endoproteinase Arg-C	ATATTCAGC
50	66572965	XC_1306	conserved hypothetical protein	CCATTCATT
51	66572966	XC_1307	conserved hypothetical protein	ATG TTCATC
52	66572974	XC_1315	conserved hypothetical protein	ACATTCACG
53	66572979	XC_1320	conserved hypothetical protein	ACG TTCACC
54	66572981	XC_1322	5'-phosphoribosylglycinamide transformylase	TCG TTCATG
55	66572988	XC_1329	conserved hypothetical protein	CTG TTCAGC
56	66573021	XC_1362	conserved hypothetical protein	ACATTCAGG
57	66573037	XC_1378	single-stranded DNA binding protein	ACATTCATC
58	66573043	XC_1384	alcohol dehydrogenase	TTG TTCACG
59	66573075	XC_1417	conserved hypothetical protein	TCATTCACG
60	66573119	XC_1461	conserved hypothetical protein	ACATTCAGG
61	66573132	XC_1474	RNA polymerase ECF-type sigma factor	TTG TTCAGG
62	66573156	XC_1498	lipoprotein	CCG TTCACG
63	66573163	XC_1505	outer membrane protein	ATATTCATC
64	66573168	XC_1510	TldD protein	ACG TTCAGC
65	66573169	XC_1511	conserved hypothetical protein	CCG TTCATG
66	66573190	XC_1534	conserved hypothetical protein	TTATTCAGG
67	66573227	XC_1571	conserved hypothetical protein	ACG TTCAGT
68	66573295	XC_1639	VirB4 protein	CTATTCAGG
69	66573298	XC_1642	alpha-glucosidase	CTATTCATG

70	66573366	XC_1710	conserved hypothetical protein	ACG TTC ACC		
71	66573388	XC_1733	L-lysine 6-aminotransferase	CC ATT CATT		
72	66573394	XC_1739	protein-export membrane protein	AT GTT CACC		
73	66573454	XC_1801	chemotaxis protein	AC ATT CAGG	2189514	AC GTT CACT
74	66573460	XC_1807	conserved hypothetical protein	CC GTT CACG		
75	66573487	XC_1834	ABC transporter ATP-binding protein	TC GTT CATG		
76	66573495	XC_1842	conserved hypothetical protein	TC GTT CATG		
77	66573510	XC_1857	peptidase	CC GTT CACC		
78	66573558	XC_1905	conserved hypothetical protein	CT GTT CACT		
79	66573562	XC_1909	transcriptional regulator lacI family	TT ATT CACG		
80	66573575	XC_1922	50S ribosomal protein L36	TC ATT CAGG		
81	66573605	XC_1952	phosphoenolpyruvate synthase	CC ATT CAGC		
82	66573623	XC_1970	cation efflux system protein	CT GTT CACG		
83	66573687	XC_2036	conserved hypothetical protein	AT GTT CATC		
84	66573700	XC_2049	plasmid-related protein	TC ATT CATC		
85	66573705	XC_2055	conserved hypothetical protein	CC GTT CACC		
86	66573742	XC_2096	transcriptional regulator luxR/uhpA family	TT ATT CACG		
87	66573745	XC_2099	pseudouridylate synthase	AT GTT CAGC		
88	66573754	XC_2108	single-stranded DNA binding protein	AC ATT CATT		
89	66573810	XC_2164	conserved hypothetical protein	CC GTT CACT		
90	66573856	XC_2211	outer-membrane lipoproteins carrier protein precursor	CC ATT CATC		
91	66573876	XC_2231	flagellar protein	TC GTT CAGG		
92	66573877	XC_2232	flagellar protein	AC GTT CACG		
93	66573890	XC_2245	flagellar protein	TT ATT CATC		

94	66573912	XC_2267	flagellar protein	CTG TTC ACC
95	66573944	XC_2300	chemotaxis protein	CCATTCATG
96	66573950	XC_2306	chemotaxis protein	ACG TTC AGT
97	66573969	XC_2326	aconitate hydratase 2	ACATTCACT
98	66573975	XC_2332	RpfF protein	ACG TTC AGT
99	66573999	XC_2356	enoyl-CoA hydratase	CCATTCATG
100	66574010	XC_2367	cationic amino acid transporter	CCATTCATG
101	66574019	XC_2376	phosphoribosylformimino-5-aminoimidazole carboxam	CTG TTC ACC
102	66574028	XC_2385	conserved hypothetical protein	ACG TTC AGC
103	66574069	XC_2429	conserved hypothetical protein	CTG TTC ACC
104	66574077	XC_2437	hypothetical protein - Escherichia coli plasmid ColIa (fragment) gi	CTG TTC ACT
105	66574113	XC_2473	conserved hypothetical protein	ACG TTC ACT
106	66574146	XC_2506	carbon storage regulator	TCATTCAGG
107	66574162	XC_2522	lipoprotein	CCG TTC ATC
108	66574184	XC_2544	general stress protein	TTG TTC ACC
109	66574188	XC_2548	conserved hypothetical protein	CCG TTC ATG
110	66574198	XC_2558	glycosyl transferase	CTG TTC ACT
111	66574202	XC_2562	cytochrome like B561	ACG TTC ACC
112	66574205	XC_2565	conserved hypothetical protein	CCG TTC ACC
113	66574218	XC_2578	response regulator	CCATTCAGG
114	66574220	XC_2580	endonuclease precursor	CCATTCACT
115	66574264	XC_2625	IS1404 transposase	CTG TTC ACC
116	66574312	XC_2673	asparaginyl-tRNA synthetase	CTG TTC AGG
117	66574349	XC_2710	ABC transporter phosphate permease	TTG TTC ATC

118	66574374	XC_2735	ABC transporter vitamin B12 uptake permease	CTG TTCATG
119	66574376	XC_2737	ABC transporter ATP-binding protein	ATG TTCATG
120	66574407	XC_2768	outer membrane protein	CCG TTCATT
121	66574409	XC_2770	conserved hypothetical protein	TTG TTCAGG
122	66574419	XC_2780	phage-related integrase	ATG TTCAGT
123	66574449	XC_2810	conserved hypothetical protein	TTG TTCAGG
124	66574454	XC_2815	peptidoglycan-associated outer membrane lipoprotein	CCG TTCACC
125	66574466	XC_2827	transcriptional regulator marR family	CCATTCAGT
126	66574468	XC_2829	conserved hypothetical protein	TTG TTCATG
127	66574479	XC_2840	transcriptional regulator marR family	TTATTCATT
128	66574526	XC_2888	conserved hypothetical protein	ACG TTCATG
129	66574538	XC_2900	methionyl-tRNA synthetase	ATG TTCACG
130	66574547	XC_2909	conserved hypothetical protein	CCG TTCATC
131	66574552	XC_2914	conserved hypothetical protein	ACG TTCATC
132	66574558	XC_2920	conserved hypothetical protein	TTG TTCAGG
133	66574559	XC_2921	conserved hypothetical protein	ATG TTCATG
134	66574576	XC_2938	conserved hypothetical protein	TTATTCACG
135	66574602	XC_2964	RNA methyltransferase	ATG TTCATG
136	66574661	XC_3023	HrpW protein	CCATTCATC
137	66574708	XC_3072	positive regulator of sigma-B	ACG TTCAGC
138	66574749	XC_3113	conserved hypothetical protein	TCG TTCACG
139	66574795	XC_3161	excinuclease ABC subunit A	CTG TTCAGC
140	66574804	XC_3170	oxidoreductase	TCG TTCACC
141	66574808	XC_3174	conserved hypothetical protein	CCG TTCACG

142	66574834	XC_3200	peroxiredoxin	ATG TTCATG	3834475	TTG TTCAGC
143	66574869	XC_3235	conserved hypothetical protein	CCATTCACC		
144	66574881	XC_3247	molybdenum cofactor biosynthesis protein C	CCG TTCACC		
145	66574901	XC_3267	conserved hypothetical protein	TCATTCACC		
146	66574918	XC_3284	conserved hypothetical protein	TCATTCAGG		
147	66574929	XC_3295	ABC transporter sulfate binding protein	CTG TTCAGG		
148	66574939	XC_3305	conserved hypothetical protein	CCATTCAGC		
149	66574942	XC_3308	peptidyl-prolyl cis-trans isomerase	CCATTCAGG		
150	66574985	XC_3351	50S ribosomal protein L11	TTG TTCAGG		
151	66574989	XC_3355	GTP-binding protein	CCATTCACT		
152	66574995	XC_3361	conserved hypothetical protein	CCATTCAGG	4011473	TTG TTCAGT
153	66575053	XC_3419	transcriptional regulator marR family	CCG TTCATG		
154	66575063	XC_3429	conserved hypothetical protein	CTG TTCACC		
155	66575095	XC_3461	conserved hypothetical protein	ACG TTCACC		
156	66575102	XC_3468	ribokinase	ACG TTCATG		
157	66575105	XC_3471	methionine adenosyltransferase	CCG TTCAGG		
158	66575138	XC_3505	cell division protein FtsZ	CCATTCACG		
159	66575139	XC_3506	cell division protein FtsA	CCTTAATT		
160	66575155	XC_3522	conserved hypothetical protein	TTG TTCATT		
161	66575167	XC_3534	conserved hypothetical protein	ACG TTCACC		
162	66575179	XC_3546	ABC transporter ATP-binding protein	CCATTCAGG		
163	66575236	XC_3604	flavoprotein-ubiquinone oxidoreductase	ATG TTCATG		
164	66575242	XC_3610	dTDP-4-dehydrorhamnose reductase	TTG TTCAGC		
165	66575258	XC_3627	putative GDP-mannose 4,6-dehydratase	CCG TTCACC		

166	66575264	XC_3633	membrane subunit of LPS efflux transporter	TTGTTCAGG
167	66575265	XC_3634	glycosyltransferase	CTGTTCACC
168	66575266	XC_3635	cystathionine gamma-lyase-like protein	CCATTCAGG
169	66575272	XC_3641	maleylacetoacetate isomerase	CCGTTCATG
170	66575283	XC_3652	beta-ketoacyl-[ACP] synthase I	ATGTTCACT
171	66575323	XC_3693	conserved hypothetical protein	TTGTTCAGG
172	66575342	XC_3712	L-sorbose dehydrogenase	CTGTTCAGG
173	66575343	XC_3713	conserved hypothetical protein	TCGTTCACG
174	66575365	XC_3735	DNA polymerase related protein	ATGTTCAGC
175	66575410	XC_3780	oxidoreductase	CTGTTCATG
176	66575439	XC_3809	phosphinothricin acetyltransferase	TTGTTCATC
177	66575471	XC_3841	NADH dehydrogenase	ACATTCATT
178	66575480	XC_3850	transcription termination factor Rho	CCGTTCATT
179	66575481	XC_3851	conserved hypothetical protein	TTGTTCATG
180	66575500	XC_3870	conserved hypothetical protein	ACGTTCATT
181	66575554	XC_3925	tyrosyl-tRNA synthetase	CTGTTCATT
182	66575614	XC_3985	histone H1	ACATTCAGC
183	66575615	XC_3986	protease Do	TCGTTCAGC
184	66575641	XC_4012	conserved hypothetical protein	CCGTTCATC
185	66575649	XC_4020	thymidylate kinase	TTGTTCAGT
186	66575661	XC_4032	conserved hypothetical protein	ATGTTCATT
187	66575682	XC_4053	TonB-dependent receptor	TTGTTCATT
188	66575716	XC_4087	beta-ketoacyl-[ACP] synthase II	ACGTTCAGT
189	66575762	XC_4133	transglycosylase associated protein	CCGTTCAGC

190	66575769	XC_4140	conserved hypothetical protein	CCG TTCAGT		
191	66575850	XC_4222	transcriptional regulator lacI family	TCATTCATG		
192	66575862	XC_4234	XmnI methyltransferase	ATG TTCAGC		
193	66575918	XC_4293	microcystin dependent protein	CCATTCACC		
194	66575921	XC_4296	toluene tolerance protein	ATG TTCAGC		
195	66575924	XC_4299	toluene tolerance protein	ATG TTCAGT		
196	66575935	XC_4310	conserved hypothetical protein	CTG TTCAGC		
197	66575952	XC_4327	Oar protein	CCG TTCAGG	5138751	TTG TTCAGG
198		XC_4352	Cys tRNA	CCG TTCACT		