Supporting Information

Figure S1. SACE_6965 encodes the putative phosphate utilization regulator PhoP in *S. erythraea.* **(a)** Genetic organization of *phoPR of S. coelicolor* and its homologous genes of *S. erythraea*. **(b)** Alignment of amino acid sequences of HTH domains of PhoP proteins in some actinomycetes species. **(c)** Phylogenetic analysis of some PhoP proteins.

Figure S2. Verification of *phoP*-overexpressed mutant ($phoP_O$) by PCR and real time quantitative PCR (RT-qPCR). **(a)** PCR of the integrated fragment spanning inserted *phoP* gene region and its downstream plasmid region; **(b)** Transcription analysis of *phoP* in WT and $phoP_O$ *by* RT-qPCR.

Figure S3. The plasmid-alone negative control for transcription analysis and phenotype analysis between WT and $phoP_O$. **(a)** Transcription analysis of *glnR* and *phoP* in WT and NULL mutant as the plasmid-alone negative control; **(b)** Ery A production in WT and NULL mutant.

Figure S4. Comparison of the binding activity between His-PhoP and His-$PhoP^{DBD}$.

Figure S5. Cell growth (a) and erythromycin product (b) of *S. erythraea* wild type (WT), *glnR*-deleted mutant (Δ*glnR*), *glnR* complementary strain ($glnR_C$), *phoP*-overexpressed strain ($phoP_O$), and *phoP*-overexpressed Δ*glnR* strain (Δ*glnR: phoP*$_O$). The growth was determined with OD_{600}. The erythromycin A was determined by HPLC.

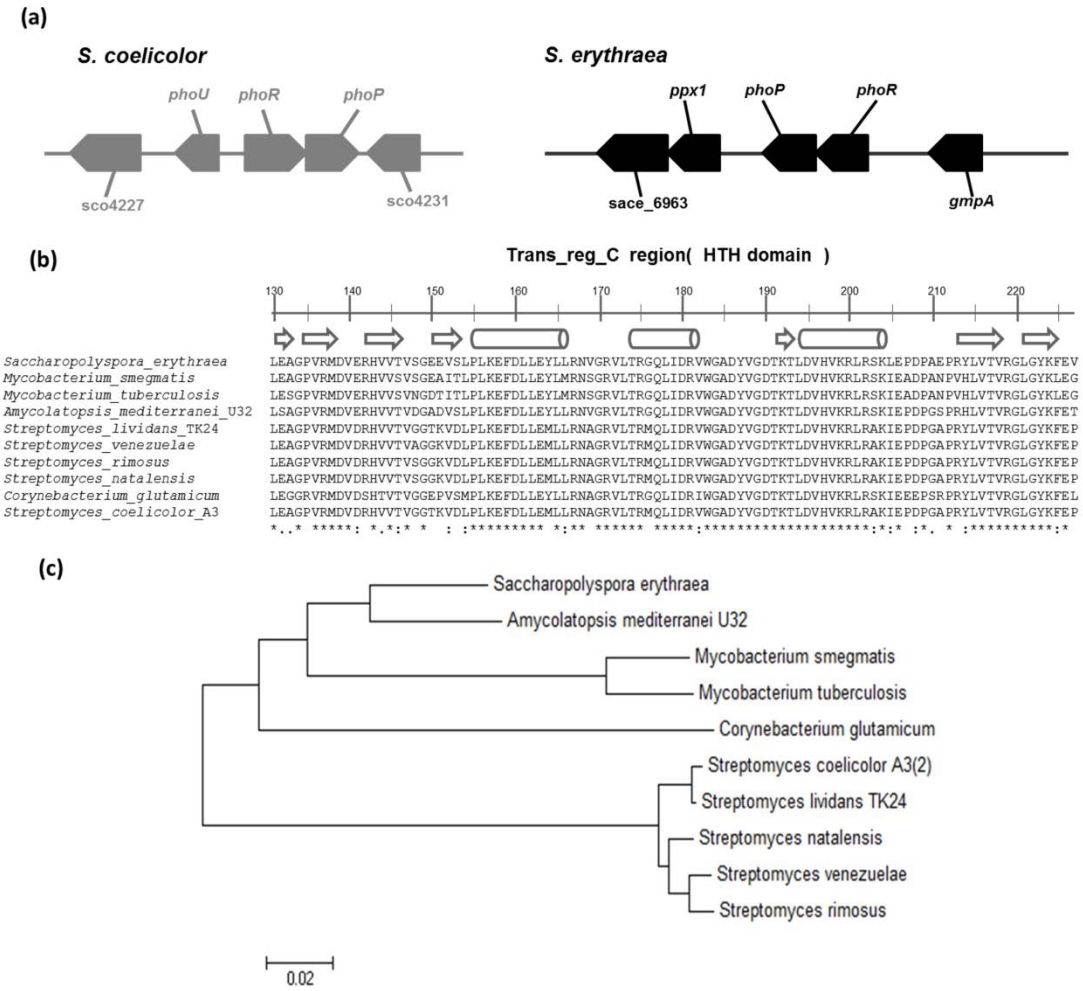

Figure S1. SACE_6965 encodes the putative phosphate utilization regulator PhoP in *S. erythraea.* **(a)** Genetic organization of *phoPR of S. coelicolor* and its homologous genes of *S. erythraea*. **(b)** Alignment of amino acid sequences of HTH domains of PhoP proteins in some actinomycetes species. **(c)** Phylogenetic analysis of some PhoP proteins.

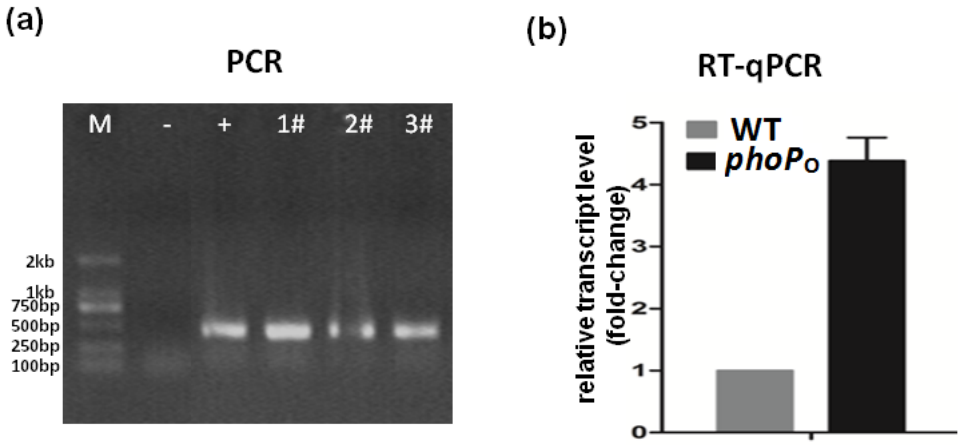

Figure S2. Verification of *phoP*-overexpressed mutant (*phoP*$_O$) by PCR and real time quantitative PCR (RT-qPCR). **(a)** PCR of the integrated fragment spanning inserted *phoP* gene region and its downstream plasmid region; **(b)** Transcription analysis of *phoP* in WT and *phoP*$_O$ *by* RT-qPCR.

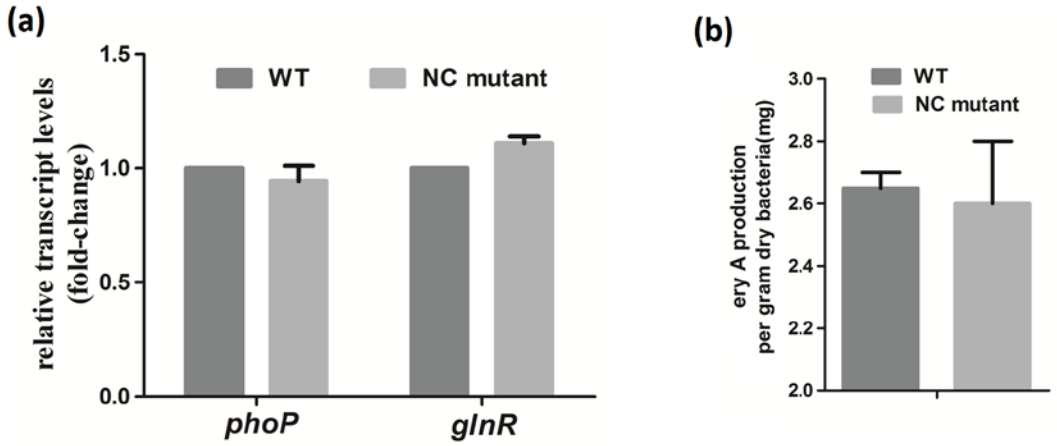

Figure S3. The plasmid-alone negative control for transcription analysis and phenotype analysis between WT and *phoP*$_O$. **(a)** Transcription analysis of *glnR* and *phoP* in WT and NULL mutant as the plasmid-alone negative control; **(b)** Ery A production in WT and NULL mutant.

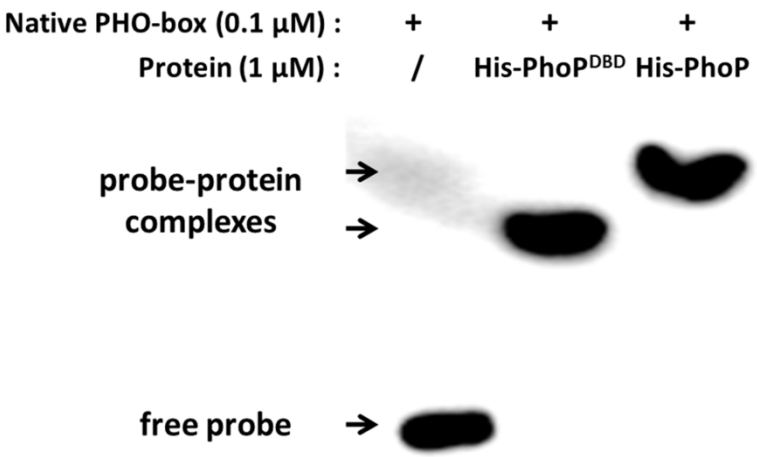

Figure S4. Comparison of the binding activity between His-PhoP and His-PhoP^{DBD}.

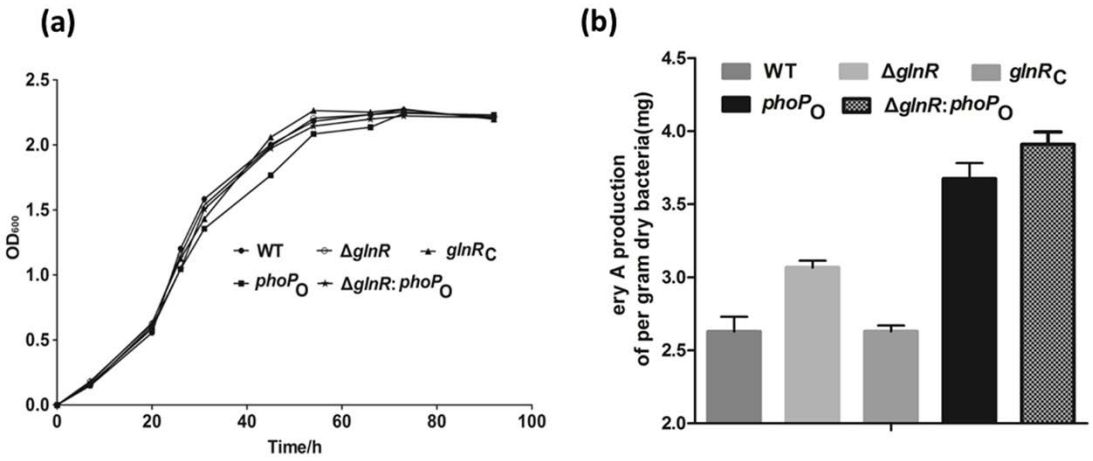

Figure S5. Cell growth (a) and erythromycin product (b) of *S. erythraea* wild type (WT), *glnR*-deleted mutant (Δ*glnR*), *glnR* complementary strain (*glnR*$_C$), *phoP*-overexpressed strain (*phoP*$_O$), and *phoP*-overexpressed Δ*glnR* strain (Δ*glnR: phoP*$_O$). The growth was determined with OD_{600}. The erythromycin A was determined by HPLC.