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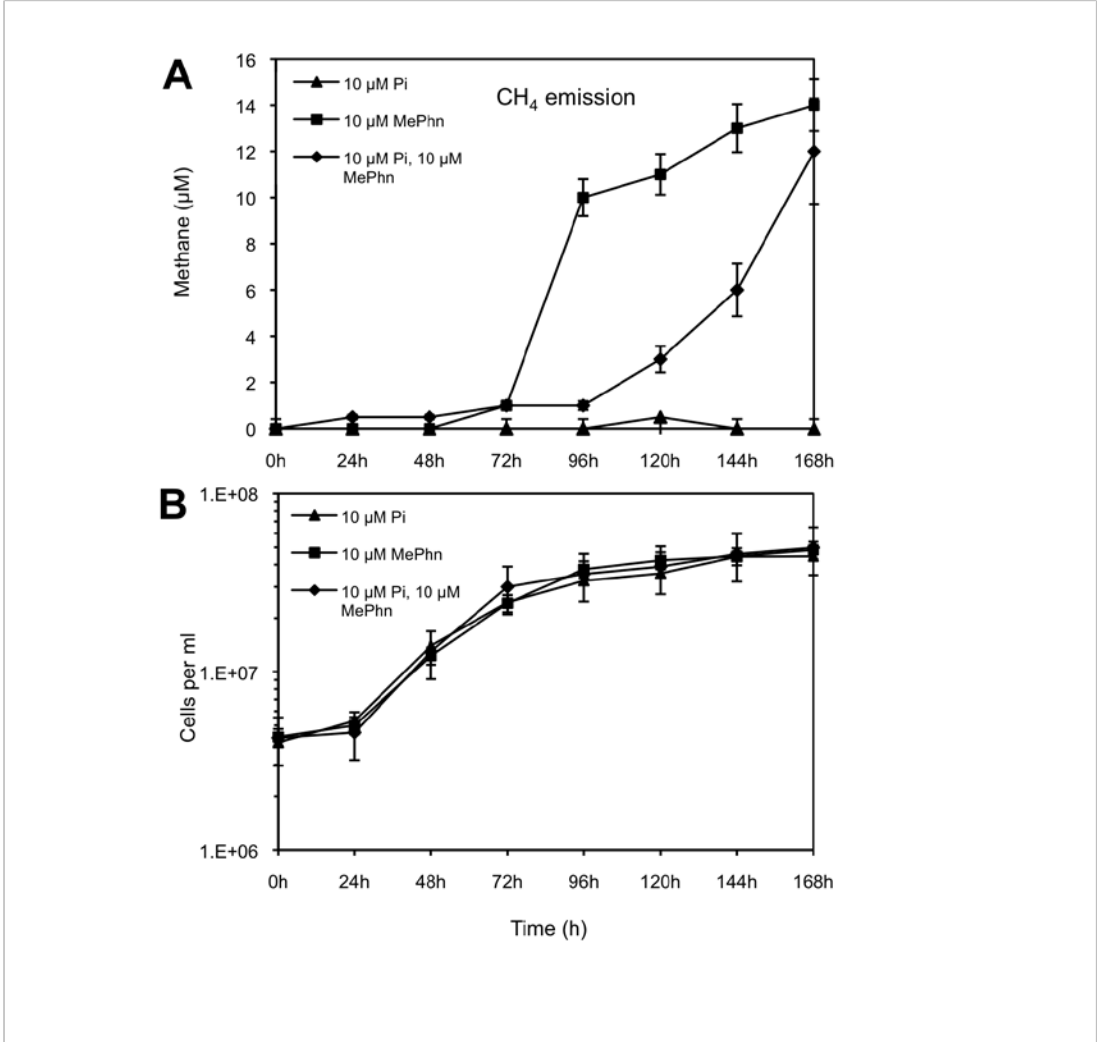
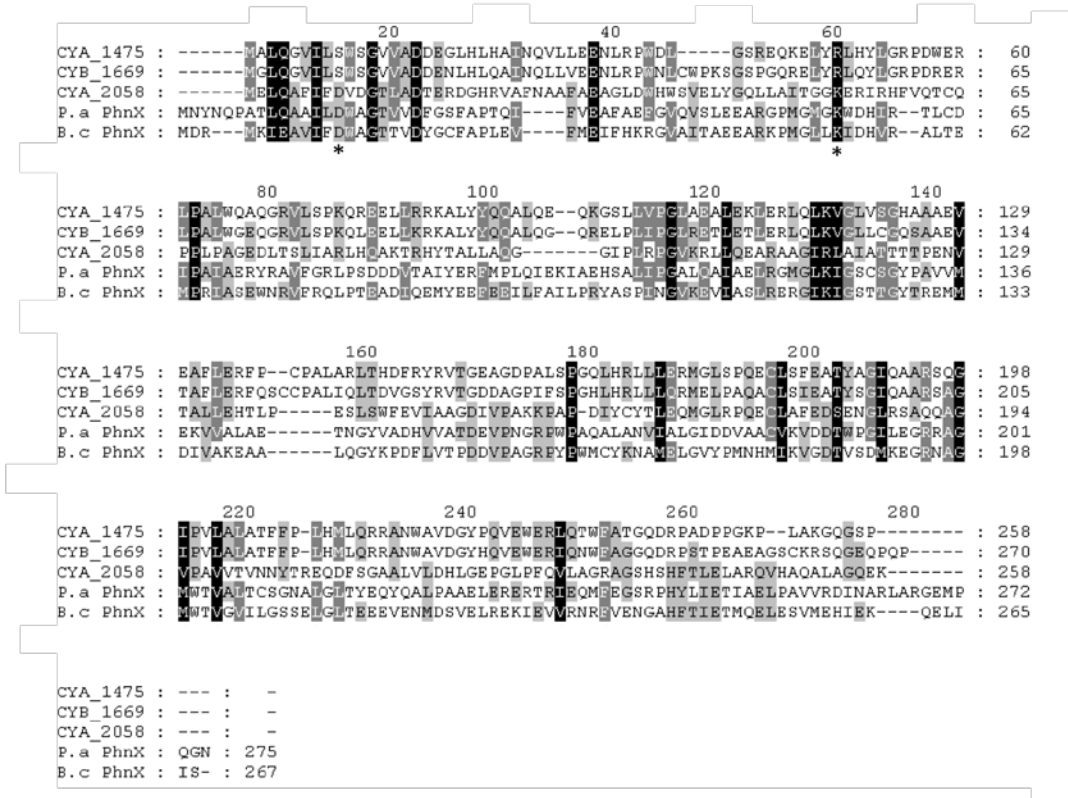


Figure S1

Figure S1. Suppression of methane production in *Syn* OS-B' cultures supplemented with a low concentration of Pi. (A) Measurements of methane concentrations in the headspace of acclimated cultures (three weeks growth in DH10–P medium supplemented with MePhn) transferred to DH10–P medium supplemented with 10 μM Pi, 10 μM MePhn, and 10 μM Pi plus 10 μM MePhn (as indicated). (B) Growth and density of the cell cultures (cells per ml) used for the measurements made in A. Note, the number of cells per ml on the y axis is presented on a log scale

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Figure S2

6 **Figure S2. Alignment of deduced Phnase polypeptides.** Putative Phnases from *Syn*

7 OS-A (CYA_1475, CYA_2058, CYA_2485), *Syn* OS-B' (CYB_1669, CYB_2092,

8 CYB_0748), phosphonoacetaldehyde phosphohydrolase from *B. cereus* (PhnX,

9 GenBank AAB 86434.1) and the Phnase of *P. aeruginosa* PAO1 (GeneBank

10 AAG04700.1). The alignment was generated using ClustalW and colored with Gene Doc

11 and is based on percentage of residues conserved, 100% conservancy (dark grey),

12 80% (grey) and 60% (light grey). Lys (K) 53 and Asp (D) 12 are marked with an asterisk

13 (see text for detail) in *B. cereus* and *P. aeruginosa* PhnX. The putative Lys/ Arg possibly

14 implied in the active core are marked with a rectangle in the figure.

1 **Table S1: Genes involved in P and Phn transport and metabolism in *Synechococcus* OS-A and OS_B'**

Gene(s) name	Putative encoded protein	Locus tag in <i>Syn</i> OS-B'	Locus tag in <i>Syn</i> -OSA	AA ID*
<i>phoR</i>	Sensor histidine kinase	CYB_0858	CYA_2352	87%
<i>phoB</i>	Response regulator	CYB_2856	CYA_1033	92%
<i>phoA</i>	Alkaline phosphatase	CYB_1198	CYA_0781	94%
<i>phoX</i>	Alkaline phosphatase	CYB_1988	CYA_1696	93%
<i>phoD</i>	Phosphodiesterase	CYB_0684	CYA_2506	95%
<i>phoH</i>	phoH family protein	CYB_2320	CYA_1201	93%
<i>npp</i>	5'-nucleotidase	CYB_0274	CYA_1059	91%
<i>nuch</i>	Putative nuclease	CYB_2765	CYA_0177	88%
<i>surE-1</i>	Acid phosphatase/ polyphosphatase	CYB_0884	CYA_0967	95%
<i>surE-2</i>	Acid phosphatase/polyphosphatase	CYB_1427	CYA_0017	92%
<i>ppx</i>	Exopolyphosphatase	CYB_1493	CYA_2432	91%
<i>ppk</i>	Polyphosphate kinase	CYB_2082	CYA_2477	94%
<i>pstS-1</i> , <i>pstC-1</i> , <i>pstA-1</i> , <i>pstB-1</i>	ABC type Pi transporter	CYB_1077-74	CYA_1558-55	86-89%
<i>pstS-2</i> , <i>pstC-2</i> , <i>pstA-2</i> , <i>pstB-2</i>	ABC type Pi transporter	CYB_1915-12	CYA_1735-32	97-99%
<i>phoU</i>	Regulatory protein	CYB_2526	CYA_0182	95%
<i>phnC-1</i> , <i>phnD-1</i> , <i>phnE-1</i>	Phn ABC-transporter	CYB_0159-61	none	
<i>phnG-phnM</i>	C-P lyase	CYB_0162-68	none	
<i>phnD</i> , <i>phnD-2</i> , <i>phnD-3</i> , <i>phnC-2</i> , <i>phnE-2</i> , <i>phnE-3</i>	Phn ABC-transporter	CYB_1464-69	none	
<i>phnE-4</i> , <i>phnD-4</i> , <i>phnC-3</i>	Phn ABC-transporter	CYB_0012-11, 09	none	
<i>ugpB</i> <i>ugpA</i>	glycerol-3-P transporter	CYB_2477-78	CYA_2785-86	94-95%
<i>phnX</i> like	HAD hydrolase,	CYB_0748	CYA_2058	90%
<i>phnX</i> like	Phosphonate	CYB_1669	CYA_1475	74%
<i>phnX</i> like	Phosphonate	CYB_2092	CYA_2485	98%
<i>phnY</i>	γ -aminobutyraldehyde	CYB_0745	CYA_0264	94%

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* Amino acid identity between *Synechococcus* OS-A and OS-B'.

¹No homologs were found in *Synechococcus* OS-B' or OS-A for PhnA (uncharacterized Zn-ribbon-containing protein involved in phosphonate metabolism in *Streptococcus equi* subsp. *zooepidemicus* MGCS10565_YP_002123256), PhnW (2-aminoethyl phosphonate: pyruvate aminotransferase from *Pseudomonas aeruginosa* PAO1, [AAG04699.1](#)), PhnZ (predicted HD phosphohydrolase in uncultured bacterium HF130_AEPn_1).

²CYB_2092 and CYA_1475 may have a periplasmic location according to the Signal_P prediction program.

³*PhnX* likes are based on homology to PhnX from *B. cereus* (YP_002450365), *phnY* is based on homology to HF130_AEPn_1 *phnY* (Martinez, A., Tyson, G.W. and Delong, E.F., 2009).

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Table S2. Primers used for RT-PCR and qPCR analysis of *Synechococcus* OS-A and *Synechococcus* OS-B' transcript levels

CYA_2058F	GAGCCAGCTCCAGAGTAAAGTG
CYA_2058R	CGTGGTGACAGTAAACAACACTATACG
CYA_1475F	GGTTTATCCAGCAGCTTTTGCT
CYA_1475R	TCGCTGCGCTTAGTGCAA
CYA_2485F	TCATAGTCGCTGCGCTTATGGTA
CYA_2485R	CAAACGGGATCCACCATCAT
CYB_1198R	AATCTCCTCATAGTCGCTGCGCTT
CYB_1198R	AATCTCCTCATAGTCGCTGCGCTT
CYB_0159F	AAACAAGGTTGCCCTAAGGGAGGT
CYB_0159R	TGGCCTTCATGGAGAGGAAGAGAA
CYB_1988F	ACGATGCCCGCTTTGAGTACATCT
CYB_1988R	CTTGGCCACATACAAGGTGCCATT
CYB_1669F	GCCCGCTTTGAGTACATCAAGA
CYB_1669R	ATAGTCGCTGCGCTTTCATAG
CYB_2092F	TTTATCCAGCAGCTTTTGCT
CYB_2092R	ACAAGGTTGCCCTAAGGGAGG
CYB_0748F	GGTGCAAACGGGATCCATCATT
CYB_0748R	AAACGGGATCCACCATCAT

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Table S3. In situ quantification of transcripts from the putative Phnases CYA_2458, CYA_1669, CYB_2092 and CYB_0748

Time (h)	RU			
	CYA_2458	CYA_1669	CYB_2092	CYB_0748
12:00	20±6	1	1	3±.3
14:00	22±4	3±.5	2±	4±.1
16:00	19±5	6±1	2±	3±.1
18:00	13±4	2±.5	1	5±.5
20:00	4±1	3±.5	2±.3	2±.5
22:00	4±1	26±3	3±.4	3±.5
0:00	3±1	6±1	4±	1
2:00	4±1	7±2	14±3	55±4
4:00	5±1	3±1	16±2	13±3
6:00	6±2	4±1	18±4	12±1
8:00	5±1	6±2	43±4	10±3
10:00	6±1	3±1	3±.5	5±2

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