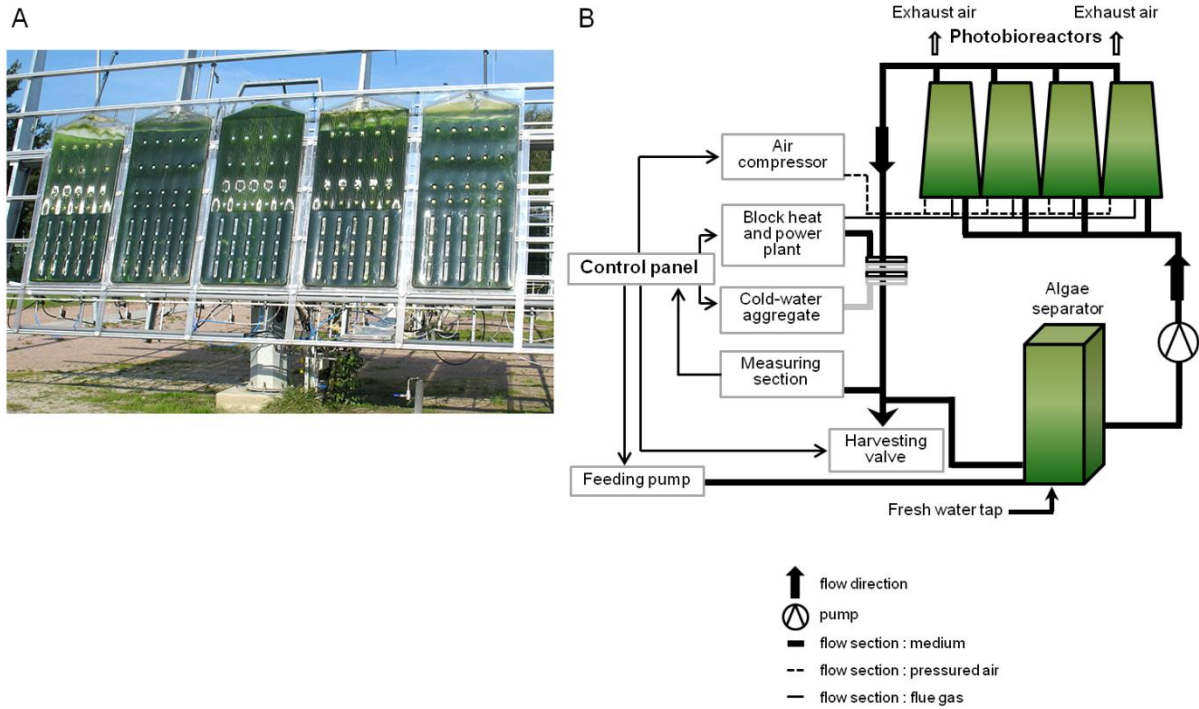


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**SUPPLEMENTAL FIGURES\_revised version**

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FIGURE S1, Krohn-Molt et al 2013,

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**FIGURE S1:** **A:** Photobioreactors mounted on a solar tracker. **B:** Flow chart of the microalgae pilot plant's function (modified from S. Hindersin, M. Leupold, M. Kerner, and D. Hanelt, "Irradiance optimization of outdoor microalgal cultures using solar tracked photobioreactors," *Bioprocess Biosyst. Eng.* 36:345-355, 2013, Fig. 2, with kind permission from Springer Science and Business Media [copyright 2013 Springer-Verlag]). For the duration of cultivation, part of the culture medium circulates through an external circuit. The algal biomass was harvesting continuously, which adjusts cell density to a constant value. The process parameters were monitored by measuring the temperature, turbidity, pH, O<sub>2</sub>, NH<sub>4</sub><sup>+</sup>, NO<sub>3</sub><sup>-</sup>, and K<sup>+</sup>. Above a set value, nutrients were added automatically. A heat exchanger within the circular flow allowed temperature control.

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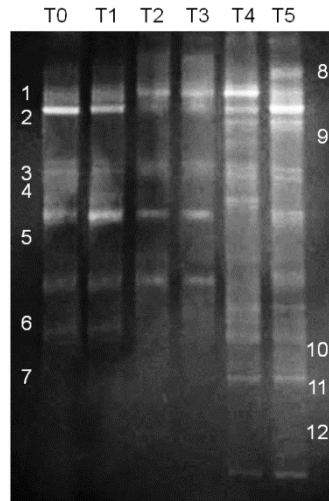
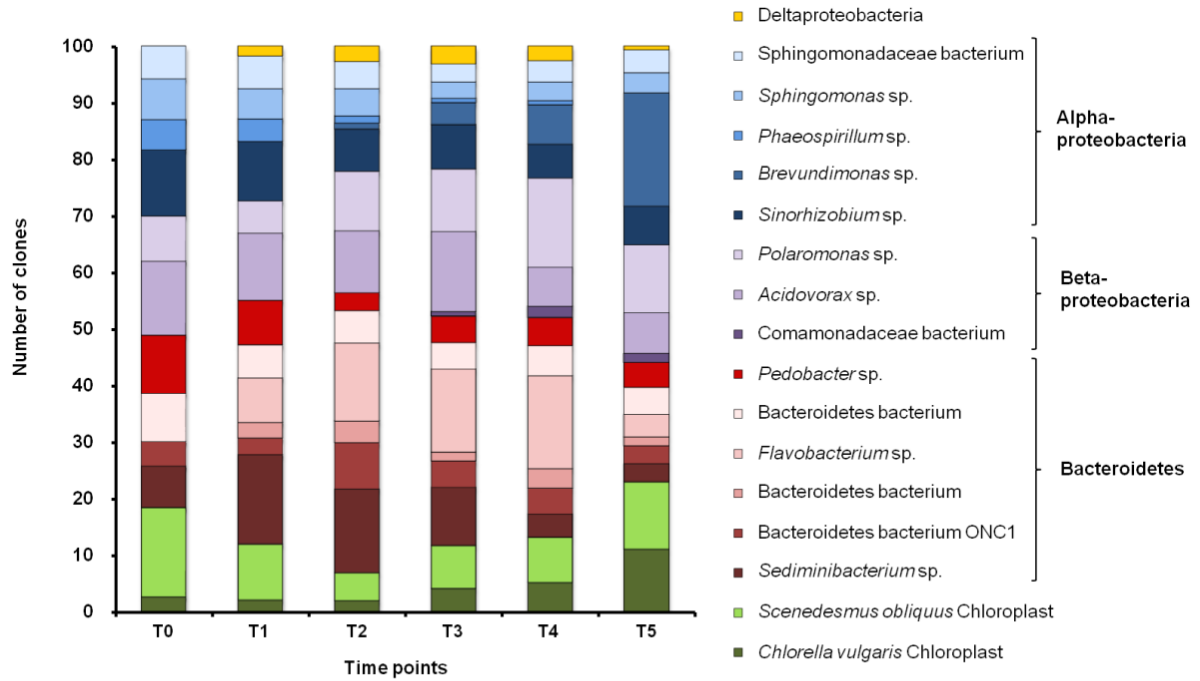


FIGURE S2, Krohn-Molt et al 2013

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17 **FIGURE S2:** DGGE analysis of PCR-amplified 16S rRNA gene fragments obtained  
 18 from six biofilm samples. Lanes 1-6 represent the different time points (T0-T5) of  
 19 sampling, which were taken in 14 day intervals. The different DGGE bands (1-13)  
 20 represent the 16S rRNA fragments of associated microorganisms, which could be  
 21 assigned to sequences stored in the NCBI database. **(1)** *Pedobacter* sp.  
 22 (EU585748.1), **(2)** *Flavobacterium* sp. (JX827624.1), **(3)** *Acidovorax* sp.  
 23 (KC464816.1), **(4)** *Rhodobacter* sp. (KC157045.1), **(5)** plastid gene of *Nitzschia*  
 24 *frustulum* (AY221721.1), **(6)** chloroplast of *Scenedesmus obliquus* (DQ396875.1),  
 25 **(7)** chloroplast of *Chlorella vulgaris* (AB001684.1), **(8)** Bacteroidetes bacterium  
 26 (HM205113.1), **(9)** *Sinorhizobium* sp. (JQ316267.1), **(10)** *Caulobacter* sp.  
 27 (EF020225.1), **(11)** uncultured Bacteroidetes bacterium (DQ463716.2),  
 28 **(12)** uncultured Bacteroidetes bacterium (AY874003.1), **(13)** Gemmatimonadetes  
 29 bacterium (JQ177808.1).

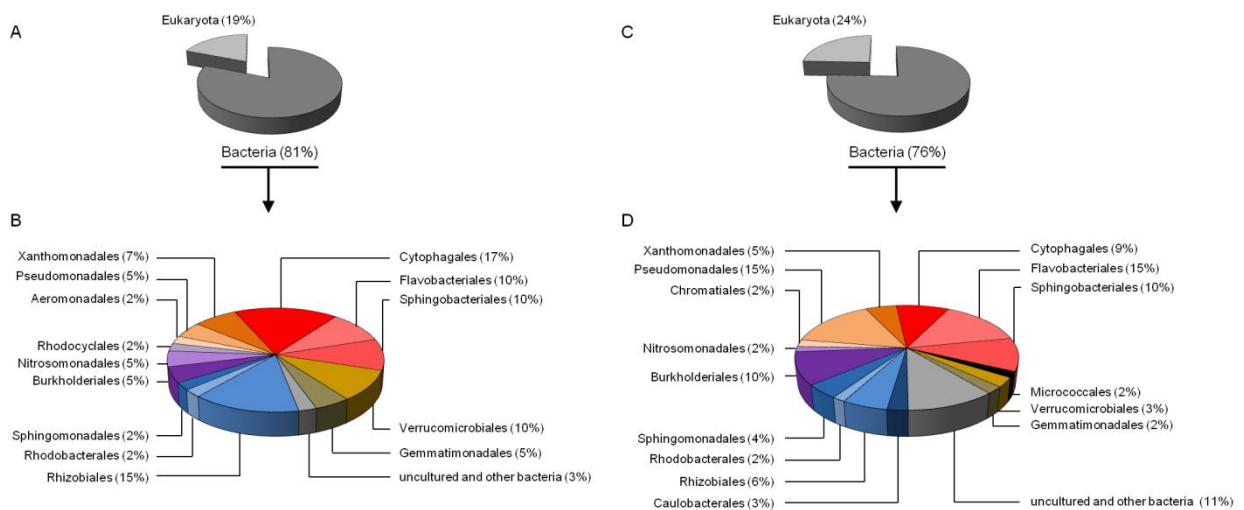
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31 FIGURE S3, Krohn-Molt et al 2013

32 **FIGURE S3:** Assignment of phylogenetic classes and orders of 16S rRNA sequences  
 33 from the RFLP analysis. Per sample (T0-T5), 100 clones were analysed.

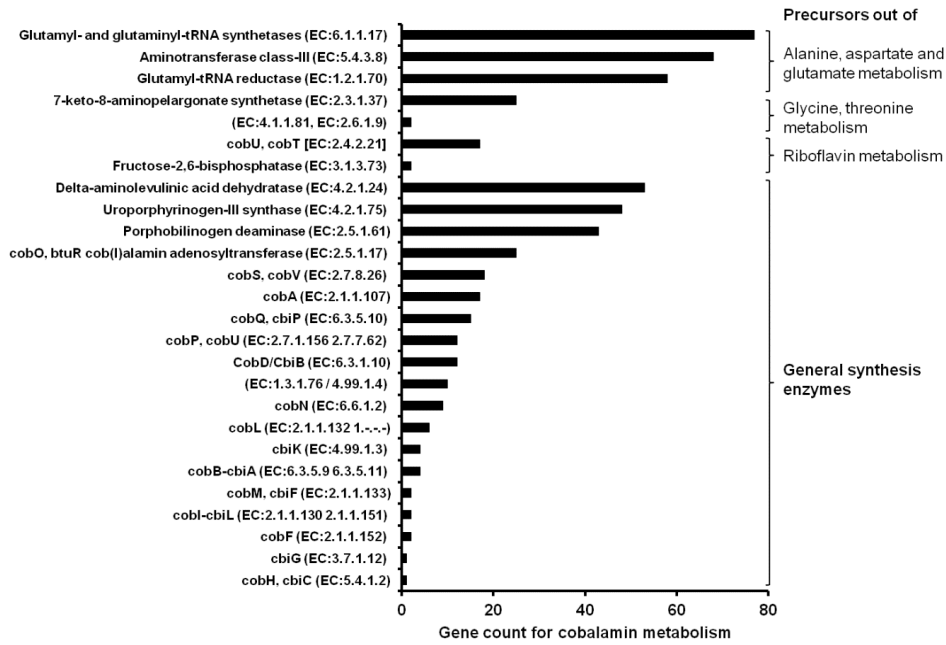
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35 FIGURE S4, Krohn-Molt et al 2013

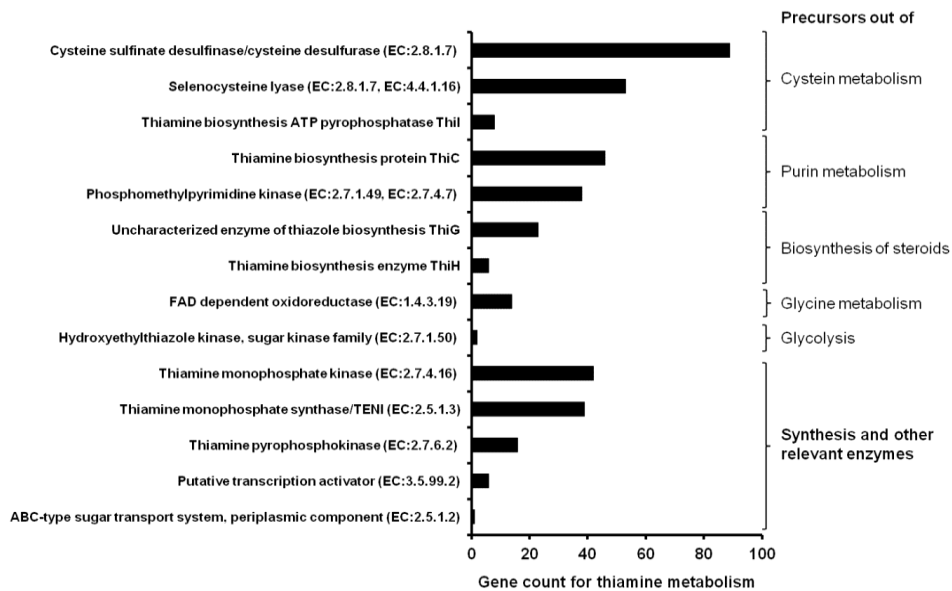
36 **FIGURE S4.** Distribution of phylogenetic classes and orders of the metagenome-  
 37 derived sequences in the PBR biofilm community. **A:** Overall diversity of 226  
 38 sequences from the FLX 454 dataset (Eukaryota 19%, Bacteria 81%),

39 **B:** Phylogenetic classification of the V6 region of the 16S rRNA from the FLX 454  
40 dataset (41 sequences). Alphaproteobacteria are represented by Sphingomonadales  
41 (2%), Rhodobacterales (2%), and Rhizobiales (15%). Betaproteobacteria were  
42 composed of Rhodocyclales (2%), Nitrosomonadales (5%), and Burkholderiales  
43 (5%). Gammaproteobacteria consisted of Xanthomonadales (7%), Pseudomonadales  
44 (5%), and Aeromonadales (2%). Bacteroidetes included Cytophagales (17%),  
45 Flavobacteriales (10%), and Sphingobacteriales (10%). 10% could be assigned to  
46 Verrucomicrobia (Verrucomicrobiales), and 5% could be classified as  
47 Gemmatimonadetes (Gemmatimonadales). **C:** Overall diversity of 137,506  
48 sequences from the Illumina dataset (Eukaryota 24%, Bacteria 76%),  
49 **D:** Phylogenetic classification of the V6 region of the 16S rRNA from the Illumina  
50 dataset (558 sequences). Alphaproteobacteria are represented by  
51 Sphingomonadales (4%), Rhodobacterales (2%), Rhizobiales (6%), and  
52 Caulobacterales (3%). Betaproteobacteria were composed of Nitrosomonadales (2%),  
53 and Burkholderiales (10%). Gammaproteobacteria consisted of Xanthomonadales  
54 (5%), Pseudomonadales (15%), and Chromatiales (2%). Bacteroidetes included  
55 Cytophagales (9%), Flavobacteriales (15%), and Sphingobacteriales (10%). 2% were  
56 represented by Actinobacteria (Micrococcales). 3% could be assigned to  
57 Verrucomicrobia (Verrucomicrobiales), and 2% could be classified as  
58 Gemmatimonadetes (Gemmatimonadales). Phylogenetic groups accounting for <1%  
59 of the sequences and sequences which were not assigned to a specific taxonomic  
60 group were summarized in the artificial groups “uncultured and other bacteria”.



61 FIGURE S5, Krohn-Molt et al 2013

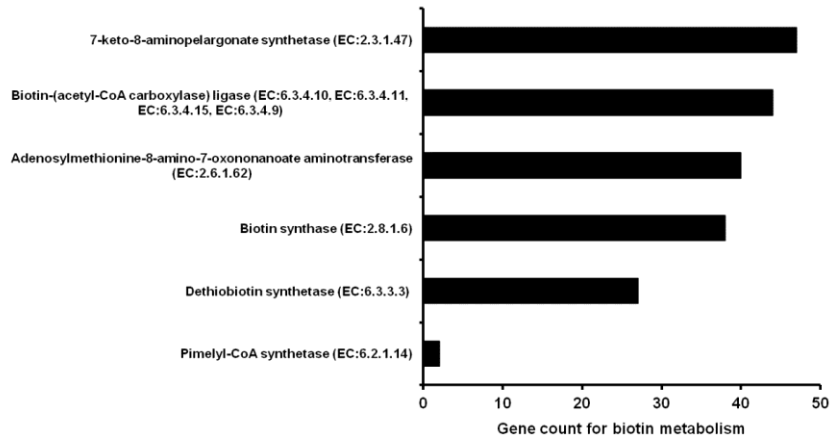
62 **FIGURE S5.** Gene count for cobalamin metabolism. Analysis of the metagenome-  
 63 derived sequences was done using the KEGG database. In total 533 sequences  
 64 were assigned to the metabolism of cobalamin.



65 FIGURE S6, Krohn-Molt et al 2013

66 **FIGURE S6:** Gene count for thiamine metabolism. Analysis of the metagenome-  
 67 derived sequences was done using the KEGG database. In total 383 sequences  
 68 were assigned to the metabolism of thiamine.

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FIGURE S7, Krohn-Molt et al 2013

71 **FIGURE S7:** Gene count for biotin metabolism. Analysis of the metagenome-derived  
72 sequences was done using the KEGG database. In total 198 sequences were  
73 assigned to the various biosynthesis steps of the vitamer biotin.

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**SUPPLEMENTAL TABLES**

85 **TABLE S1.** Phylogenetic analysis of 171 16S rRNA clones sequences derived from  
 86 the biofilm's fully established microbial community (T5).

| Phyla/Class         | Sequence count | Order/Family                        | Sequence count |
|---------------------|----------------|-------------------------------------|----------------|
| Alphaproteobacteria | 48             | Sphingomonadales                    | 12             |
|                     |                | Rhodobacterales                     | 7              |
|                     |                | Rhodospirillales                    | 3              |
|                     |                | Rhizobiales                         | 15             |
|                     |                | Caulobacterales                     | 11             |
| Betaproteobacteria  | 26             | Burkholderiales                     | 15             |
|                     |                | uncultured<br>Comamonadaceae        | 11             |
| Deltaproteobacteria | 6              | Desulfovibrionales                  | 3              |
|                     |                | uncultured<br>Deltaproteobacteria   | 3              |
| Gammaproteobacteria | 19             | Xanthomonadales                     | 16             |
|                     |                | uncultured<br>Gammaproteobacteria   | 3              |
|                     |                | Flavobacteriales                    | 10             |
|                     |                | Cytophagales                        | 5              |
|                     |                | uncultured<br>Bacteroidetes         | 13             |
| Actinobacteria      | 9              | Acidimicrobiales                    | 2              |
|                     |                | Actinomycetales                     | 3              |
|                     |                | uncultured<br>Actinobacteria        | 4              |
| Planctomycetes      | 7              | Planctomycetales                    | 7              |
| Verrucomicrobia     | 5              | uncultured<br>Verrucomicrobia       | 5              |
| Chloroflexi         | 3              | uncultured<br>Chloroflexi bacterium | 3              |

|                  |   |                                      |   |
|------------------|---|--------------------------------------|---|
| unknown Bacteria | 4 | Candidate division<br>OP10 bacterium | 2 |
|                  |   | uncultured<br>TM7 bacterium          | 2 |

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88 **TABLE S2.** Bacteria cultivated from the PBR microbial community on solid media.

| Bacterial Isolate | Closest relatives  | 16S rRNA gene identity (%) |
|-------------------|--|----------------------------|
| A                 | <i>Brevundimonas</i> sp. (JQ661035.1)                            | 94                         |
| B                 | <i>Paracoccus</i> sp. (JQ404485.1)                               | 96                         |
| C                 | <i>Chryseobacterium taichungense</i> (JQ071521.1)                | 99                         |
| D                 | <i>Brevibacterium</i> sp. / <i>Arthrobacter</i> sp. (GQ199748.1) | 99                         |
| E                 | uncultivated / <i>Roseomonas</i> sp. (HQ588850.1)                | 78                         |
| F                 | uncultivated CFB affiliated bacterium (AJ583211.1)               | 96                         |
| G                 | <i>Xanthomonas</i> sp. (EU887990.1)                              | 99                         |
| H                 | <i>Rhodococcus</i> sp. (EU041710.1)                              | 99                         |

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