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| **List of most abundant OTUs related to oxygenic phototrophs in black beachrock and seawater a** | | | | |  |
| **OTU b** | **Best hit c** | **Top layer (0-2 mm)** | **Green layer (2-5 mm)** | **Seawater** | | |
| OTU\_019 | *Calothrix scopulorum* NIES-268 (100.0%) | 23.4 | 0.2 | 0.0 | | |
| OTU\_002 | *Rivularia* sp. PCC 7116 (99.5%) | 16.5 | 0.0 | 2.4 | | |
| OTU\_005 | *Halomicronema hongdechloris* C2206 (98.0%) | 9.8 | 79.9 | 0.0 | | |
| OTU\_013 | *Chroococcidiopsis* sp. CCMP1489 (98.0%) | 7.1 | 0.1 | 0.0 | | |
| OTU\_010 | *Cyanothece* sp. ATCC 51142 (93.6%) | 6.8 | 0.2 | 0.0 | | |
| OTU\_035 | *Gomphosphaeria aponina* SAG 52.96 (92.6%) | 4.5 | 0.0 | 0.0 | | |
| OTU\_015 | *Spirulina subsalsa* IAM M-223 (92.8%) | 3.7 | 0.0 | 0.0 | | |
| OTU\_073 | *Chroococcidiopsis* sp. QUCCCM26 (97.4%) | 2.9 | 0.1 | 0.0 | | |
| OTU\_081 | *Chroococcidiopsis* sp. QUCCCM26 (98.5%) | 2.4 | 0.0 | 0.0 | | |
| OTU\_033 | *Chroococcidiopsis* sp. CCMP3187 (99.0%) | 2.4 | 0.0 | 0.0 | | |
| OTU\_060 | *Microcoleus* sp. DAI (94.4%) | 2.4 | 0.0 | 0.0 | | |
| OTU\_179 | *Cyanothece* sp. HPC-11 (94.2%) | 1.9 | 0.0 | 0.0 | | |
| OTU\_117 | *Chroococcidiopsis* sp. CCMP3185 (97.4%) | 1.7 | 0.0 | 0.0 | | |
| OTU\_072 | *Chroococcidiopsis* sp. QUCCCM26 (98.5%) | 1.5 | 0.0 | 0.0 | | |
| OTU\_095 | *Hyella patelloides* LEGE 07179 (96.2%) | 1.3 | 0.0 | 0.0 | | |
| OTU\_080 | *Chroococcidiopsis* sp. CCMP3185 (96.9%) | 1.3 | 0.0 | 0.0 | | |
| OTU\_063 | *Dermocarpella incrassata* PCC 7326 (96.9%) | 1.1 | 0.0 | 0.0 | | |
| OTU\_003 | *Pseudocapsa* sp. Ryu8-6 (95.4%) | 0.0 | 10.2 | 0.0 | | |
| OTU\_006 | *Nodosilinea* sp. LEGE 06001 (93.1%) | 0.0 | 6.9 | 0.0 | | |
| OTU\_070 | *Cyanothece* sp. SKTU126 (94.4%) | 0.0 | 2.2 | 0.0 | | |
| Other cyanobacteria | - | 9.4 | 0.2 | 80.0 | | |
| Chloroplasts | - | 0 d | 0 d | 17.6 | | |

a The OTU included constitute at least 1% of all cyanobacterial-like sequences in either the top layer or the green layer. The abundance is shown as percentage of total cyanobacterial-like sequences; b The OTU sequences have been submitted to GenBank with accession numbers XXXXXXXX-XXXXXXXX; c Best hit to a cultured and named organism in the NCBI non-redundant database. Percentage sequence identity is shown in parenthesis; d No chloroplasts sequences were found.