Data from the molecular diversity studies in the proposed ASPA in parts of Western Sør Rondane Mountains, Dronning Maud Land, East Antarctica

This document is presented in support of the Working Paper 47

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Summary

Belgium has introduced a draft Management plan for a proposed ASPA in parts of Western Sør Rondane Mountains, Dronning Maud Land, East Antarctica. This draft Management Plan is included as Appendix C to Working Paper 47, which presents the Subsidiary Group on Management Plans’ report of activities during the intersessional period 2022-2023. This proposed ASPA includes seven sites. This IP presents an overview of the data on the biodiversity of biological communities in these seven different sites.

Background

The study of the biological diversity in the Western Sør Rondane Mountains has mainly started since 2007, due to the construction of the Belgian station Princess Elisabeth on the Utsteinen Ridge (CEE, 2007). The only classical list of species identified by morphology is the list of lichen species published by Ertz et al. (2014) who mainly collected samples on the Utsteinen Ridge and Nunatak, Teltet Nunatak and the Ketelersbreen Dry Valley. Only one site sampled by this study is included in the ASPA, namely the Teltet Nunatak, where only one lichen, *Lecidella siplei* (C.W.Dodge & G.E.Baker) May.Inoue, was recorded (Ertz et al. 2014).

In the harsh environment of this inland mountainous sites, the biological communities are limited to specific spots that combine favorable factors including the exposure to the North (sun), liquid water in summer from melting snow and/or humidity sources (dew), a stable substrate, and protection from the katabatic winds. These communities are mainly formed by microorganisms, mosses, lichens, microalgae, bacteria, fungi and tiny invertebrates. Therefore, the biodiversity surveys that were made in the ASPA sites are not based on classical inventories based on morphology. They are rather based on molecular taxonomy methods. The Small Subunit ribosomal RNA (SSU rRNA) gene sequence was used to identify the (micro)organisms. In summary, the eDNAs of the samples were extracted and a Polymerase Chain Reaction (PCR) was performed to amplify a segment of the SSU sequences of all organisms present in each sample, within the technical limits of the method. After this amplification, the sequences need to be individually characterized by sequencing. This step was previously performed by cloning, Denaturating Gradient Gel Electrophoresis (DGGE) and more recently by High-Throughput Sequencing. The latter technology is evolving very fast, with pyrosequencing (now stopped), Illumina, Nanopore, etc that allow to obtain very large datasets but also require quite complex bioinformatic analyses. In the publications referred to in this Information Paper, the treated sequences are clustered in groups of SSU rRNA sequences with more than 97% similarity, called Operational Taxonomic Units (OTU). A representative sequence for each OTU is used to identify it, but this identification can be more or less precise, as it depends on the similarity of the sequence with those in public databases. These databases do not cover all taxa with the same level of details, and become more complete with time.

***Presentation of the biodiversity surveys’ data***

Tables 1-5 in attachment are based on three different publications, namely:

* Tytgat et al. (2016): Bacterial biodiversity studied by MiSeq Illumina in 52 samples (see table 1).
* Savaglia et al. (in preparation): Bacterial and microeukaryotic biodiversity in 105 samples from 9 nunataks studied by MiSeq Illumina sequencing (see tables 2 and 3).
* Puschkareva et al. (2018): Cyanobacterial biodiversity of 8 samples of the biological crusts present in the control sites of OTC in Tanngarden (site A) and Pingvinane 4 (site C4) was studied by DGGE and pyrosequencing, whereas the control site for Teltet (site E) is only studied by DGGE (see tables 4 and 5).

These three publications concern the global biodiversity of the Western Sør Rondane Mountains. The data collected by these publications are not restricted to the seven sites of the proposed ASPA. For the purpose of this Information Paper, the data concerning the sites of the proposed ASPA were drawn out from these general data sets and presented in tables 1-5. The data of Tytgat et al. (2016) (see table 1) and Savaglia et al. (in preparation) (see tables 2 and 3) are organized to present the OTUs unique to each of the sites of the proposed ASPA, on the one hand, and the 50 most abundant OTUs in the general region, on the other hand. In order to distinguish both, a color code is used.

Statistical analyses by Tytgat et al (2016) showed that the factors structuring the bacterial biodiversity were mainly related to the bedrock type (mineralogy, weathering rates and substrate stability) and the presence of mosses or lichens. Indeed, “Acidobacteria (Chloracidobacteria) and Actinobacteria (Actinomycetales) dominated mineral soil samples situated on gneiss derived bedrock, while Proteobacteria (Sphingomonadaceae), Cyanobacteria, Armatimonadetes and candidate division FBP-dominated soil samples with a high total organic carbon content that were mainly situated on granite derived bedrock”. Savaglia et al. (in preparation) also conclude that diverse microbial communities are observed in inland Antarctic nunataks and valleys. Their structure can be globally explained by the environmental characteristics of the substrate types (including pH and total nitrogen).

Tables 1-5 demonstrate both similarities and differences in the microbial communities between sites. In terms of differences, the tables reflect the fact that certain OTUs were unique, found only in one site. As expected, Yûboku-dani valley (site F), which include the only lakes currently known in the area, has a very different biodiversity from the nunataks, highlighting the importance of its inclusion in the proposed ASPA.

Main findings

The tables attached to this Information Paper demonstrate the variability in the characteristics of each site of the proposed ASPA. Given this variability, different sites were selected with an aim to cover a large range of geological, environmental and microclimatic diversity, to ensure the best possible protection for the values described in the proposed Management Plan.

***References:***

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3. Pushkareva, E., Pessi, I. S., Namsaraev, Z., Mano, M.-J., Elster, J., & Wilmotte, A. (2018). Cyanobacteria inhabiting biological soil crusts of a polar desert: Sør Rondane Mountains, Antarctica. Syst. Appl. Microbiol 41: 363-373.
4. Tytgat, B., Verleyen E., Sweetlove M., D'Hondt S., Clercx P., Van Ranst E., Peeters K., Roberts S.J., Namsaraev Z., Wilmotte A., Vyverman W. and Willems A. (2016). Bacterial community composition in relation to bedrock type and macrobiota in soils from the Sør Rondane Mountains, East Antarctica. FEMS Microbiol. Ecol. 92:fiw126
5. Savaglia, V., Lambrechts, S., Tytgat, B., Vanhellemont, Q., Elster, J., Willems, A., Wilmotte, A., Verleyen, E., Vyverman, W. (in preparation). Geology defines microbiome structure and composition in nunataks and valleys of the Sør Rondane Mountains, East Antarctica
6. **Table 1.** Bacterial OTUs based on 16S rRNA sequences (97 % 16S rRNA sequence similarity) in samples of Perlebandet North (site DN), Pingvinane 2 and 4 (subsites C2, C4) and Teltet (site E). Shades of green and blue indicate the OTUs present only in one of the 3 sites, whereas the yellow colour indicates OTUs that are among the 50 most abundant in the studied samples by Tytgat et al. (2016). See this study for experimental details.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| OTU | Phylum | Class | Order | Family | Genus | Species | Perlebandet | Pingvinane | Teltet |
|  |  |  |  |  |  |  |  |  |  |
| OTU\_52 | Proteobacteria | Alphaproteobacteria | Rhodospirillales | Acetobacteraceae | unclassified | unclassified | 77 | 0 | 0 |
| OTU\_276 | Chloroflexi | Ktedonobacteria | Thermogemmatisporales | Thermogemmatisporaceae | unclassified | unclassified | 42 | 0 | 0 |
| OTU\_138 | Proteobacteria | Alphaproteobacteria | Rhizobiales | unclassified | unclassified | unclassified | 27 | 0 | 0 |
| OTU\_237 | Armatimonadetes | Armatimonadia | FW68 | unclassified | unclassified | unclassified | 23 | 0 | 0 |
| OTU\_171 | Chloroflexi | Ktedonobacteria | unclassified | unclassified | unclassified | unclassified | 23 | 0 | 0 |
| OTU\_435 | Proteobacteria | Alphaproteobacteria | Rhodospirillales | Acetobacteraceae | unclassified | unclassified | 23 | 0 | 0 |
| OTU\_473 | Cyanobacteria | Oscillatoriophycideae | Chroococcales | Xenococcaceae | unclassified | unclassified | 20 | 0 | 0 |
| OTU\_329 | Cyanobacteria | unclassified | unclassified | unclassified | unclassified | unclassified | 18 | 0 | 0 |
| OTU\_396 | Proteobacteria | Alphaproteobacteria | Rhodobacterales | Rhodobacteraceae | Paracoccus | aminovorans | 18 | 0 | 0 |
| OTU\_545 | Chloroflexi | Anaerolineae | SBR1031 | A4b | unclassified | unclassified | 17 | 0 | 0 |
| OTU\_312 | Chloroflexi | Ktedonobacteria | Thermogemmatisporales | Thermogemmatisporaceae | unclassified | unclassified | 16 | 0 | 0 |
| OTU\_361 | Chloroflexi | Ktedonobacteria | Thermogemmatisporales | Thermogemmatisporaceae | unclassified | unclassified | 15 | 0 | 0 |
| OTU\_448 | Cyanobacteria | Oscillatoriophycideae | unclassified | unclassified | unclassified | unclassified | 14 | 0 | 0 |
| OTU\_484 | Actinobacteria | Actinobacteria | Actinomycetales | unclassified | unclassified | unclassified | 13 | 0 | 0 |
| OTU\_283 | Armatimonadetes | Armatimonadia | Armatimonadales | Armatimonadaceae | unclassified | unclassified | 13 | 0 | 0 |
| OTU\_790 | Fusobacteria | Fusobacteriia | Fusobacteriales | Fusobacteriaceae | Fusobacterium | unclassified | 12 | 0 | 0 |
| OTU\_121 | Armatimonadetes | Armatimonadia | Armatimonadales | Armatimonadaceae | unclassified | unclassified | 0 | 54 | 0 |
| OTU\_148 | Armatimonadetes | Chthonomonadetes | Chthonomonadales | Chthonomonadaceae | unclassified | unclassified | 0 | 31 | 0 |
| OTU\_202 | Armatimonadetes | Armatimonadia | Armatimonadales | Armatimonadaceae | unclassified | unclassified | 0 | 22 | 0 |
| OTU\_626 | Cyanobacteria | Nostocophycideae | Stigonematales | Rivulariaceae | Calothrix | unclassified | 0 | 20 | 0 |
| OTU\_232 | Armatimonadetes | Armatimonadia | Armatimonadales | Armatimonadaceae | unclassified | unclassified | 0 | 16 | 0 |
| OTU\_3088 | Proteobacteria | Alphaproteobacteria | Sphingomonadales | Sphingomonadaceae | unclassified | unclassified | 0 | 16 | 0 |
| OTU\_357 | Armatimonadetes | Armatimonadia | Armatimonadales | Armatimonadaceae | unclassified | unclassified | 0 | 15 | 0 |
| OTU\_369 | Chloroflexi | C0119 | unclassified | unclassified | unclassified | unclassified | 0 | 14 | 0 |
| OTU\_415 | Armatimonadetes | Armatimonadia | Armatimonadales | Armatimonadaceae | unclassified | unclassified | 0 | 13 | 0 |
| OTU\_331 | Proteobacteria | Alphaproteobacteria | Sphingomonadales | Sphingomonadaceae | Zymomonas | unclassified | 0 | 12 | 0 |
| OTU\_677 | Armatimonadetes | Armatimonadia | Armatimonadales | Armatimonadaceae | unclassified | unclassified | 0 | 11 | 0 |
| OTU\_275 | Proteobacteria | Alphaproteobacteria | Rhodobacterales | Rhodobacteraceae | Jannaschia | unclassified | 0 | 0 | 16 |
| OTU\_184 | Actinobacteria | Actinobacteria | Actinomycetales | Sporichthyaceae | unclassified | unclassified | 0 | 0 | 12 |
| OTU\_3797 | Cyanobacteria | Oscillatoriophycideae | unclassified | unclassified | unclassified | unclassified | 234 | 8 | 0 |
| OTU\_9 | Cyanobacteria | Synechococcophycideae | Pseudanabaenales | Pseudanabaenaceae | Pseudanabaena | unclassified | 0 | 0 | 306 |
| OTU\_2003 | Proteobacteria | Alphaproteobacteria | Sphingomonadales | Sphingomonadaceae | unclassified | unclassified | 14 | 5 | 0 |
| OTU\_32 | Proteobacteria | Alphaproteobacteria | Sphingomonadales | Sphingomonadaceae | Sphingomonas | wittichii | 12 | 2 | 0 |
| OTU\_1297 | Cyanobacteria | Oscillatoriophycideae | Oscillatoriales | Phormidiaceae | Phormidium | unclassified | 149 | 0 | 115 |
| OTU\_606 | Proteobacteria | Alphaproteobacteria | Sphingomonadales | Sphingomonadaceae | unclassified | unclassified | 28 | 9 | 0 |
| OTU\_11 | Cyanobacteria | Nostocophycideae | Nostocales | Nostocaceae | Nostoc | unclassified | 0 | 19 | 2 |
| OTU\_10 | Actinobacteria | Actinobacteria | Actinomycetales | unclassified | unclassified | unclassified | 9 | 0 | 0 |
| OTU\_7 | Cyanobacteria | Nostocophycideae | Nostocales | Nostocaceae | Toxopsis | unclassified | 23 | 10 | 9 |
| OTU\_193 | Actinobacteria | Actinobacteria | Actinomycetales | Sporichthyaceae | unclassified | unclassified | 0 | 0 | 23 |
| OTU\_16 | FBP | unclassified | unclassified | unclassified | unclassified | unclassified | 0 | 43 | 3 |
| OTU\_103 | Cyanobacteria | Oscillatoriophycideae | unclassified | unclassified | unclassified | unclassified | 0 | 97 | 18 |
| OTU\_28 | Actinobacteria | Actinobacteria | Actinomycetales | unclassified | unclassified | unclassified | 0 | 3 | 41 |
| OTU\_53 | Acidobacteria | Chloracidobacteria | RB41 | Ellin6075 | unclassified | unclassified | 11 | 41 | 1 |
| OTU\_45 | Cyanobacteria | Synechococcophycideae | Synechococcales | Chamaesiphonaceae | unclassified | unclassified | 4 | 0 | 67 |
| OTU\_2364 | Proteobacteria | Alphaproteobacteria | Sphingomonadales | Sphingomonadaceae | unclassified | unclassified | 1 | 57 | 2 |
| OTU\_43 | Actinobacteria | Acidimicrobiia | Acidimicrobiales | unclassified | unclassified | unclassified | 0 | 0 | 15 |
| OTU\_81 | Actinobacteria | Actinobacteria | Actinomycetales | unclassified | unclassified | unclassified | 0 | 0 | 57 |
| OTU\_14 | Proteobacteria | Alphaproteobacteria | Sphingomonadales | Sphingomonadaceae | unclassified | unclassified | 33 | 27 | 7 |
| OTU\_2 | Cyanobacteria | Oscillatoriophycideae | Oscillatoriales | Phormidiaceae | Phormidium | unclassified | 85 | 4 | 27 |
| OTU\_35 | Cyanobacteria | unclassified | unclassified | unclassified | unclassified | unclassified | 0 | 104 | 3 |
| OTU\_69 | Actinobacteria | Actinobacteria | Actinomycetales | unclassified | unclassified | unclassified | 0 | 2 | 8 |
| OTU\_62 | Proteobacteria | Alphaproteobacteria | Rhodospirillales | Acetobacteraceae | unclassified | unclassified | 1 | 5 | 0 |
| OTU\_1457 | FBP | unclassified | unclassified | unclassified | unclassified | unclassified | 3 | 98 | 0 |
| OTU\_474 | Acidobacteria | Chloracidobacteria | RB41 | Ellin6075 | unclassified | unclassified | 5 | 0 | 16 |
| OTU\_531 | Actinobacteria | Actinobacteria | Actinomycetales | unclassified | unclassified | unclassified | 0 | 3 | 6 |
| OTU\_140 | Proteobacteria | Alphaproteobacteria | Rhodobacterales | Rhodobacteraceae | Rubellimicrobium | unclassified | 0 | 94 | 60 |
| OTU\_152 | Proteobacteria | Alphaproteobacteria | Rhizobiales | Beijerinckiaceae | unclassified | unclassified | 0 | 5 | 10 |
| OTU\_31 | Cyanobacteria | Oscillatoriophycideae | Oscillatoriales | Phormidiaceae | Phormidium | unclassified | 31 | 116 | 123 |
| OTU\_27 | Acidobacteria | Chloracidobacteria | RB41 | Ellin6075 | unclassified | unclassified | 7 | 3 | 7 |
| OTU\_36 | Cyanobacteria | Synechococcophycideae | Pseudanabaenales | Pseudanabaenaceae | Leptolyngbya | unclassified | 28 | 58 | 4 |
| OTU\_3 | Acidobacteria | Chloracidobacteria | RB41 | Ellin6075 | unclassified | unclassified | 41 | 224 | 65 |
| OTU\_129 | Acidobacteria | Chloracidobacteria | RB41 | Ellin6075 | unclassified | unclassified | 196 | 248 | 177 |
| OTU\_8 | Acidobacteria | Chloracidobacteria | RB41 | Ellin6075 | unclassified | unclassified | 24 | 247 | 63 |
| OTU\_17 | Acidobacteria | Chloracidobacteria | RB41 | Ellin6075 | unclassified | unclassified | 11 | 45 | 73 |
| OTU\_812 | Proteobacteria | Alphaproteobacteria | Sphingomonadales | Sphingomonadaceae | unclassified | unclassified | 96 | 477 | 65 |
| OTU\_12 | Acidobacteria | Chloracidobacteria | RB41 | Ellin6075 | unclassified | unclassified | 51 | 126 | 9 |
| OTU\_323 | Acidobacteria | Chloracidobacteria | RB41 | Ellin6075 | unclassified | unclassified | 45 | 84 | 67 |
| OTU\_34 | Acidobacteria | Chloracidobacteria | RB41 | Ellin6075 | unclassified | unclassified | 2 | 30 | 15 |
| OTU\_38 | Actinobacteria | Actinobacteria | Actinomycetales | Nocardioidaceae | Aeromicrobium | unclassified | 2 | 4 | 29 |
| OTU\_1966 | Acidobacteria | Chloracidobacteria | RB41 | Ellin6075 | unclassified | unclassified | 1 | 4 | 4 |
| OTU\_6 | Cyanobacteria | Oscillatoriophycideae | Chroococcales | Xenococcaceae | unclassified | unclassified | 40 | 50 | 339 |
| OTU\_2514 | Acidobacteria | Chloracidobacteria | RB41 | Ellin6075 | unclassified | unclassified | 7 | 3 | 8 |
| OTU\_2270 | Proteobacteria | Alphaproteobacteria | Sphingomonadales | Sphingomonadaceae | unclassified | unclassified | 15 | 58 | 18 |
| OTU\_56 | Proteobacteria | Alphaproteobacteria | Rhizobiales | Bradyrhizobiaceae | unclassified | unclassified | 6 | 4 | 12 |

1. **Table 2**. Bacterial OTUs based on 16S rRNA sequences (97 % 16S rRNA sequence similarity) in samples of Pingvinane 3 (subsite C3), Perlebandet North (site DN) and South (site DS), Petrellnuten (site B) and Yûboku-dani valley (site F). Shades of red, orange, purple and blue indicate the OTUs present only in one of these six sites, whereas the yellow colour indicates OTUs that are among the 50 most abundant ones in the 105 studied samples from 9 sites by Savaglia et al. (in preparation). Three of these sites were not included in the sites of the proposed ASPA, but contributed to the calculation of the 50 most abundant OTUs and the determination of unique OTUs: Austkampane; Dry Valley and Utsteinen ridge.
2. Material and methods
3. Sequences were analyzed by a methodology based on Operational Taxonomic Units (OTUs), using a well-established in-house pipeline. Paired-end merging was performed using PEAR. The minimum length was set to 300 bp, and the maximum length to 550 bp with a minimum overlap of 10 bp. Further, sequence quality filtering and processing were done using USEARCH, with a minimal Phred score set to Q20 and a maximum expected error of 2. De novo chimera filtering was done with UCHIME. Sequences were clustered in Operational Taxonomic Units (OTUs) with a default similarity cut-off of 97% using UPARSE. Curated reference taxonomic databases SILVA v138.1 and PR2 version 4.14.0 were used with the naïve Bayesian classifier implemented in Mothur to infer taxonomic identification of the resulting OTUs for 16S and 18S, respectively.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| OTU | Pingvinane North (or III) | Pingvinane South | Perlebandet North | Perlebandet South | Petrellnuten | Yûboku-dani Valley | Phylum | Order | Family | Genus |
| OTU\_294 | 104 | 0 | 0 | 0 | 0 | 0 | Cyanobacteria | Oxyphotobacteria | Unknown\_Family | CENA359 |
| OTU\_335 | 66 | 0 | 0 | 0 | 0 | 0 | Chloroflexi | Chloroflexales | Chloroflexaceae | Chloroflexaceae |
| OTU\_23087 | 35 | 0 | 0 | 0 | 0 | 0 | Cyanobacteria | Nostocales | Nostocaceae | Nostocaceae |
| OTU\_1099 | 33 | 0 | 0 | 0 | 0 | 0 | Cyanobacteria | Oxyphotobacteria | Oxyphotobacteria | Oxyphotobacteria |
| OTU\_22434 | 31 | 0 | 0 | 0 | 0 | 0 | Actinobacteria | Solirubrobacterales | Solirubrobacteraceae | Solirubrobacteraceae |
| OTU\_25742 | 25 | 0 | 0 | 0 | 0 | 0 | Cyanobacteria | Leptolyngbyales | Leptolyngbyaceae | Leptolyngbya\_FYG |
| OTU\_772 | 21 | 0 | 0 | 0 | 0 | 0 | Armatimonadetes | Armatimonadales | Armatimonadales | Armatimonadales |
| OTU\_897 | 17 | 0 | 0 | 0 | 0 | 0 | Bacteroidetes | Cytophagales | Hymenobacteraceae | Hymenobacter |
| OTU\_1132 | 16 | 0 | 0 | 0 | 0 | 0 | Proteobacteria | Acetobacterales | Acetobacteraceae | Acetobacteraceae |
| OTU\_815 | 14 | 0 | 0 | 0 | 0 | 0 | Patescibacteria | Saccharimonadales | Saccharimonadales\_fa | Saccharimonadales\_ge |
| OTU\_2741 | 12 | 0 | 0 | 0 | 0 | 0 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_1516 | 11 | 0 | 0 | 0 | 0 | 0 | Actinobacteria | Micromonosporales | Micromonosporaceae | Micromonosporaceae |
| OTU\_19083 | 11 | 0 | 0 | 0 | 0 | 0 | Proteobacteria | Sphingomonadales | Sphingomonadaceae | Sphingomonadaceae |
| OTU\_1829 | 10 | 0 | 0 | 0 | 0 | 0 | FBP | FBP\_or | FBP\_fa | FBP\_ge |
| OTU\_3244 | 10 | 0 | 0 | 0 | 0 | 0 | Actinobacteria | Actinobacteria | Actinobacteria | Actinobacteria |
| OTU\_3702 | 10 | 0 | 0 | 0 | 0 | 0 | Proteobacteria | Betaproteobacteriales | Burkholderiaceae | Rhizobacter |
| OTU\_10713 | 10 | 0 | 0 | 0 | 0 | 0 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_24342 | 10 | 0 | 0 | 0 | 0 | 0 | Proteobacteria | Sphingomonadales | Sphingomonadaceae | Sphingomonadaceae |
| OTU\_6899 | 0 | 111 | 0 | 0 | 0 | 0 | Cyanobacteria | Nostocales | Phormidiaceae | Tychonema\_CCAP\_1459-11B |
| OTU\_2521 | 0 | 83 | 0 | 0 | 0 | 0 | Cyanobacteria | Oxyphotobacteria | Oxyphotobacteria | Oxyphotobacteria |
| OTU\_2834 | 0 | 31 | 0 | 0 | 0 | 0 | Bacteroidetes | Chitinophagales | Chitinophagaceae | Flavisolibacter |
| OTU\_5886 | 0 | 18 | 0 | 0 | 0 | 0 | Bacteroidetes | Chitinophagales | Chitinophagaceae | Segetibacter |
| OTU\_433 | 0 | 14 | 0 | 0 | 0 | 0 | Proteobacteria | Rickettsiales | Rickettsiales | Rickettsiales |
| OTU\_2308 | 0 | 14 | 0 | 0 | 0 | 0 | Actinobacteria | Micrococcales | Micrococcaceae | Arthrobacter |
| OTU\_1378 | 0 | 12 | 0 | 0 | 0 | 0 | Proteobacteria | Betaproteobacteriales | Burkholderiaceae | Burkholderiaceae |
| OTU\_1604 | 0 | 12 | 0 | 0 | 0 | 0 | Bacteroidetes | Cytophagales | Cytophagales | Cytophagales |
| OTU\_70 | 0 | 0 | 156 | 0 | 0 | 0 | Deinococcus-Thermus | Deinococcales | Trueperaceae | Truepera |
| OTU\_1002 | 0 | 0 | 136 | 0 | 0 | 0 | Actinobacteria | Euzebyales | Euzebyaceae | uncultured |
| OTU\_9791 | 0 | 0 | 130 | 0 | 0 | 0 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_5988 | 0 | 0 | 127 | 0 | 0 | 0 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatella |
| OTU\_24561 | 0 | 0 | 100 | 0 | 0 | 0 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_904 | 0 | 0 | 90 | 0 | 0 | 0 | Deinococcus-Thermus | Deinococcales | Trueperaceae | Truepera |
| OTU\_4242 | 0 | 0 | 90 | 0 | 0 | 0 | Cyanobacteria | Oxyphotobacteria | Oxyphotobacteria | Oxyphotobacteria |
| OTU\_2923 | 0 | 0 | 88 | 0 | 0 | 0 | Deinococcus-Thermus | Deinococcales | Trueperaceae | Truepera |
| OTU\_19472 | 0 | 0 | 86 | 0 | 0 | 0 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_1905 | 0 | 0 | 85 | 0 | 0 | 0 | Cyanobacteria | Nostocales | Nostocales | Nostocales |
| OTU\_429 | 0 | 0 | 83 | 0 | 0 | 0 | Chloroflexi | Thermomicrobiales | AKYG1722 | AKYG1722\_ge |
| OTU\_623 | 0 | 0 | 72 | 0 | 0 | 0 | Bacteroidetes | Cytophagales | Hymenobacteraceae | Hymenobacter |
| OTU\_390 | 0 | 0 | 71 | 0 | 0 | 0 | Bacteroidetes | Cytophagales | MWH-CFBk5 | MWH-CFBk5\_ge |
| OTU\_359 | 0 | 0 | 64 | 0 | 0 | 0 | Bacteroidetes | Cytophagales | Cytophagales | Cytophagales |
| OTU\_3247 | 0 | 0 | 53 | 0 | 0 | 0 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_1390 | 0 | 0 | 52 | 0 | 0 | 0 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_321 | 0 | 0 | 50 | 0 | 0 | 0 | Bacteroidetes | Cytophagales | Cytophagales | Cytophagales |
| OTU\_1743 | 0 | 0 | 50 | 0 | 0 | 0 | Cyanobacteria | Oxyphotobacteria | Oxyphotobacteria | Oxyphotobacteria |
| OTU\_9411 | 0 | 0 | 48 | 0 | 0 | 0 | Cyanobacteria | Nostocales | Nostocales | Nostocales |
| OTU\_483 | 0 | 0 | 47 | 0 | 0 | 0 | Bacteroidetes | Cytophagales | Spirosomaceae | Spirosoma |
| OTU\_7966 | 0 | 0 | 47 | 0 | 0 | 0 | Cyanobacteria | Nostocales | Nostocales | Nostocales |
| OTU\_976 | 0 | 0 | 44 | 0 | 0 | 0 | Deinococcus-Thermus | Deinococcales | Trueperaceae | Truepera |
| OTU\_11889 | 0 | 0 | 44 | 0 | 0 | 0 | Cyanobacteria | Oxyphotobacteria | Oxyphotobacteria | Oxyphotobacteria |
| OTU\_866 | 0 | 0 | 43 | 0 | 0 | 0 | Bacteroidetes | Cytophagales | Cytophagales | Cytophagales |
| OTU\_25804 | 0 | 0 | 43 | 0 | 0 | 0 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_1963 | 0 | 0 | 38 | 0 | 0 | 0 | Bacteroidetes | Cytophagales | Hymenobacteraceae | Hymenobacter |
| OTU\_1650 | 0 | 0 | 37 | 0 | 0 | 0 | Chloroflexi | Kallotenuales | AKIW781 | AKIW781\_ge |
| OTU\_15877 | 0 | 0 | 36 | 0 | 0 | 0 | Armatimonadetes | Armatimonadales | Armatimonadales\_fa | Armatimonadales\_ge |
| OTU\_369 | 0 | 0 | 35 | 0 | 0 | 0 | Bacteroidetes | Cytophagales | Hymenobacteraceae | Hymenobacter |
| OTU\_13360 | 0 | 0 | 32 | 0 | 0 | 0 | Actinobacteria | Euzebyales | Euzebyaceae | Euzebyaceae |
| OTU\_710 | 0 | 0 | 30 | 0 | 0 | 0 | Proteobacteria | Rhodobacterales | Rhodobacteraceae | Rhodobacteraceae |
| OTU\_1294 | 0 | 0 | 28 | 0 | 0 | 0 | Proteobacteria | Rhodobacterales | Rhodobacteraceae | Rubellimicrobium |
| OTU\_3739 | 0 | 0 | 28 | 0 | 0 | 0 | Actinobacteria | Propionibacteriales | Propionibacteriaceae | Friedmanniella |
| OTU\_1524 | 0 | 0 | 27 | 0 | 0 | 0 | Chloroflexi | Thermomicrobiales | JG30-KF-CM45 | JG30-KF-CM45\_ge |
| OTU\_2307 | 0 | 0 | 26 | 0 | 0 | 0 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_15815 | 0 | 0 | 26 | 0 | 0 | 0 | Cyanobacteria | Nostocales | Nostocales | Nostocales |
| OTU\_1305 | 0 | 0 | 23 | 0 | 0 | 0 | Acidobacteria | Blastocatellales | Blastocatellaceae | uncultured |
| OTU\_5336 | 0 | 0 | 22 | 0 | 0 | 0 | Bacteroidetes | Cytophagales | Cytophagales | Cytophagales |
| OTU\_2351 | 0 | 0 | 20 | 0 | 0 | 0 | Bacteroidetes | Cytophagales | Spirosomaceae | Spirosoma |
| OTU\_619 | 0 | 0 | 19 | 0 | 0 | 0 | Acidobacteria | Acidobacteriales | Acidobacteriaceae\_(Subgroup\_1) | Bryocella |
| OTU\_1557 | 0 | 0 | 19 | 0 | 0 | 0 | Actinobacteria | Solirubrobacterales | 67-14 | 67-14\_ge |
| OTU\_9403 | 0 | 0 | 19 | 0 | 0 | 0 | Cyanobacteria | Nostocales | Nostocales | Nostocales |
| OTU\_17110 | 0 | 0 | 19 | 0 | 0 | 0 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_24750 | 0 | 0 | 19 | 0 | 0 | 0 | Cyanobacteria | Nostocales | Nostocales | Nostocales |
| OTU\_1079 | 0 | 0 | 18 | 0 | 0 | 0 | Bacteroidetes | Cytophagales | Spirosomaceae | Spirosoma |
| OTU\_1126 | 0 | 0 | 18 | 0 | 0 | 0 | Actinobacteria | Frankiales | Frankiales | Frankiales |
| OTU\_1761 | 0 | 0 | 18 | 0 | 0 | 0 | Planctomycetes | Tepidisphaerales | WD2101\_soil\_group | WD2101\_soil\_group\_ge |
| OTU\_2652 | 0 | 0 | 18 | 0 | 0 | 0 | Bacteroidetes | Cytophagales | Spirosomaceae | Spirosoma |
| OTU\_2747 | 0 | 0 | 18 | 0 | 0 | 0 | Actinobacteria | Propionibacteriales | Propionibacteriaceae | Microlunatus |
| OTU\_3263 | 0 | 0 | 18 | 0 | 0 | 0 | Bacteroidetes | Cytophagales | Hymenobacteraceae | Hymenobacter |
| OTU\_1639 | 0 | 0 | 17 | 0 | 0 | 0 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_2115 | 0 | 0 | 17 | 0 | 0 | 0 | Planctomycetes | Tepidisphaerales | WD2101\_soil\_group | WD2101\_soil\_group\_ge |
| OTU\_6578 | 0 | 0 | 17 | 0 | 0 | 0 | Cyanobacteria | Nostocales | Nostocales | Nostocales |
| OTU\_9831 | 0 | 0 | 17 | 0 | 0 | 0 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatellaceae |
| OTU\_1711 | 0 | 0 | 16 | 0 | 0 | 0 | Chloroflexi | Thermomicrobiales | AKYG1722 | AKYG1722\_ge |
| OTU\_1903 | 0 | 0 | 15 | 0 | 0 | 0 | Acidobacteria | Solibacterales | Solibacteraceae | Solibacteraceae\_(Subgroup\_3) |
| OTU\_2007 | 0 | 0 | 15 | 0 | 0 | 0 | Acidobacteria | Blastocatellia\_ | Blastocatellia\_ | Blastocatellia\_ |
| OTU\_4051 | 0 | 0 | 15 | 0 | 0 | 0 | Cyanobacteria | Nostocales | Chroococcidiopsaceae | Chroococcidiopsaceae |
| OTU\_24189 | 0 | 0 | 15 | 0 | 0 | 0 | Cyanobacteria | Nostocales | Nostocales | Nostocales |
| OTU\_25614 | 0 | 0 | 15 | 0 | 0 | 0 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatellaceae |
| OTU\_25783 | 0 | 0 | 15 | 0 | 0 | 0 | Cyanobacteria | Oxyphotobacteria | Oxyphotobacteria | Oxyphotobacteria |
| OTU\_917 | 0 | 0 | 14 | 0 | 0 | 0 | Proteobacteria | Acetobacterales | Acetobacteraceae | Acidisphaera |
| OTU\_1542 | 0 | 0 | 14 | 0 | 0 | 0 | Acidobacteria | Acidobacteriales | Acidobacteriaceae | Granulicella |
| OTU\_5880 | 0 | 0 | 14 | 0 | 0 | 0 | Actinobacteria | Euzebyales | Euzebyaceae | Euzebyaceae |
| OTU\_13737 | 0 | 0 | 14 | 0 | 0 | 0 | Cyanobacteria | Oxyphotobacteria | Oxyphotobacteria | Oxyphotobacteria |
| OTU\_230 | 0 | 0 | 13 | 0 | 0 | 0 | Bacteroidetes | Cytophagales | Hymenobacteraceae | Pontibacter |
| OTU\_4692 | 0 | 0 | 13 | 0 | 0 | 0 | Cyanobacteria | Nostocales | Nostocales | Nostocales |
| OTU\_6625 | 0 | 0 | 13 | 0 | 0 | 0 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatellaceae |
| OTU\_15417 | 0 | 0 | 13 | 0 | 0 | 0 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_17673 | 0 | 0 | 13 | 0 | 0 | 0 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatellaceae |
| OTU\_21716 | 0 | 0 | 13 | 0 | 0 | 0 | Cyanobacteria | Nostocales | Nostocales | Nostocales |
| OTU\_479 | 0 | 0 | 12 | 0 | 0 | 0 | Armatimonadetes | Armatimonadales | Armatimonadales\_fa | Armatimonadales\_ge |
| OTU\_7290 | 0 | 0 | 12 | 0 | 0 | 0 | Proteobacteria | Caulobacterales | Caulobacteraceae | uncultured |
| OTU\_11931 | 0 | 0 | 12 | 0 | 0 | 0 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_22278 | 0 | 0 | 12 | 0 | 0 | 0 | Deinococcus-Thermus | Deinococcales | Deinococcales | Deinococcales |
| OTU\_913 | 0 | 0 | 11 | 0 | 0 | 0 | Actinobacteria | Micrococcales | Intrasporangiaceae | Ornithinimicrobium |
| OTU\_2210 | 0 | 0 | 11 | 0 | 0 | 0 | Cyanobacteria | Nostocales | Nostocales | Nostocales |
| OTU\_3382 | 0 | 0 | 11 | 0 | 0 | 0 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_4042 | 0 | 0 | 11 | 0 | 0 | 0 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_7502 | 0 | 0 | 11 | 0 | 0 | 0 | Acidobacteria | Acidobacteriales | Acidobacteriaceae | Acidobacteriaceae\_(Subgroup\_1) |
| OTU\_13033 | 0 | 0 | 11 | 0 | 0 | 0 | Cyanobacteria | Nostocales | Nostocales | Nostocales |
| OTU\_17651 | 0 | 0 | 11 | 0 | 0 | 0 | Cyanobacteria | Nostocales | Chroococcidiopsaceae | uncultured |
| OTU\_19143 | 0 | 0 | 11 | 0 | 0 | 0 | Planctomycetes | Tepidisphaerales | WD2101\_soil\_group | WD2101\_soil\_group\_ge |
| OTU\_1509 | 0 | 0 | 10 | 0 | 0 | 0 | Actinobacteria | Euzebyales | Euzebyaceae | uncultured |
| OTU\_2595 | 0 | 0 | 10 | 0 | 0 | 0 | Bacteroidetes | Cytophagales | Hymenobacteraceae | Hymenobacter |
| OTU\_2596 | 0 | 0 | 10 | 0 | 0 | 0 | Planctomycetes | Tepidisphaerales | WD2101\_soil\_group | WD2101\_soil\_group\_ge |
| OTU\_3294 | 0 | 0 | 10 | 0 | 0 | 0 | Cyanobacteria | Nostocales | Nostocales | Nostocales |
| OTU\_4609 | 0 | 0 | 10 | 0 | 0 | 0 | Cyanobacteria | Nostocales | Nostocales | Nostocales |
| OTU\_4798 | 0 | 0 | 10 | 0 | 0 | 0 | Chloroflexi | Caldilineales | Caldilineaceae | uncultured |
| OTU\_5778 | 0 | 0 | 10 | 0 | 0 | 0 | Cyanobacteria | Nostocales | Chroococcidiopsaceae | uncultured |
| OTU\_7045 | 0 | 0 | 10 | 0 | 0 | 0 | Bacteroidetes | Chitinophagales | Chitinophagaceae | Segetibacter |
| OTU\_394 | 0 | 0 | 0 | 170 | 0 | 0 | Proteobacteria | Rhizobiales | Rhizobiales | Rhizobiales |
| OTU\_23440 | 0 | 0 | 0 | 58 | 0 | 0 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_1625 | 0 | 0 | 0 | 35 | 0 | 0 | Bacteroidetes | Cytophagales | Spirosomaceae | Spirosoma |
| OTU\_4605 | 0 | 0 | 0 | 35 | 0 | 0 | Cyanobacteria | Nostocales | Nostocales | Nostocales |
| OTU\_1731 | 0 | 0 | 0 | 32 | 0 | 0 | Cyanobacteria | Nostocales | Nostocales | Nostocales |
| OTU\_887 | 0 | 0 | 0 | 24 | 0 | 0 | Cyanobacteria | Nostocales | Nostocales | Nostocales |
| OTU\_23527 | 0 | 0 | 0 | 19 | 0 | 0 | Chloroflexi | Ktedonobacterales | Ktedonobacteraceae | Ktedonobacteraceae |
| OTU\_21267 | 0 | 0 | 0 | 17 | 0 | 0 | Cyanobacteria | Nostocales | Chroococcidiopsaceae | Chlorogloea\_SAG\_10.99 |
| OTU\_2143 | 0 | 0 | 0 | 16 | 0 | 0 | Cyanobacteria | Nostocales | Nostocales | Nostocales |
| OTU\_1720 | 0 | 0 | 0 | 11 | 0 | 0 | FBP | FBP\_or | FBP\_fa | FBP\_ge |
| OTU\_4474 | 0 | 0 | 0 | 10 | 0 | 0 | Cyanobacteria | Nostocales | Chroococcidiopsaceae | Chlorogloea\_SAG\_10.99 |
| OTU\_8032 | 0 | 0 | 0 | 10 | 0 | 0 | Cyanobacteria | Nostocales | Chroococcidiopsaceae | Chlorogloea\_SAG\_10.99 |
| OTU\_25101 | 0 | 0 | 0 | 0 | 26 | 0 | Cyanobacteria | Nostocales | Chroococcidiopsaceae | Crinalium\_SAG\_22.89 |
| OTU\_215 | 0 | 0 | 0 | 0 | 0 | 818 | Actinobacteria | Micrococcales | Micrococcaceae | Arthrobacter |
| OTU\_583 | 0 | 0 | 0 | 0 | 0 | 537 | Firmicutes | Bacillales | Planococcaceae | Planococcus |
| OTU\_62 | 0 | 0 | 0 | 0 | 0 | 467 | Bacteroidetes | Sphingobacteriales | Sphingobacteriaceae | Sphingobacteriaceae |
| OTU\_110 | 0 | 0 | 0 | 0 | 0 | 289 | Bacteroidetes | Flavobacteriales | Flavobacteriaceae | Flavobacterium |
| OTU\_492 | 0 | 0 | 0 | 0 | 0 | 182 | Proteobacteria | Sphingomonadales | Sphingomonadaceae | Sphingomonadaceae |
| OTU\_377 | 0 | 0 | 0 | 0 | 0 | 165 | Proteobacteria | Betaproteobacteriales | Burkholderiaceae | Burkholderiaceae |
| OTU\_481 | 0 | 0 | 0 | 0 | 0 | 155 | Bacteroidetes | Cytophagales | Cyclobacteriaceae | Algoriphagus |
| OTU\_35 | 0 | 0 | 0 | 0 | 0 | 143 | Chloroflexi | Chloroflexales | Chloroflexaceae | Candidatus\_Chloroploca |
| OTU\_127 | 0 | 0 | 0 | 0 | 0 | 142 | Cyanobacteria | Oxyphotobacteria | Unknown\_Family | Leptolyngbya\_ANT.L67.1 |
| OTU\_2296 | 0 | 0 | 0 | 0 | 0 | 138 | Actinobacteria | Micrococcales | Micrococcaceae | Arthrobacter |
| OTU\_532 | 0 | 0 | 0 | 0 | 0 | 125 | Actinobacteria | Micrococcales | Micrococcaceae | Arthrobacter |
| OTU\_2507 | 0 | 0 | 0 | 0 | 0 | 116 | Actinobacteria | Acidimicrobiia | Acidimicrobiia | Acidimicrobiia |
| OTU\_135 | 0 | 0 | 0 | 0 | 0 | 114 | Proteobacteria | Acetobacterales | Acetobacteraceae | Acetobacteraceae |
| OTU\_118 | 0 | 0 | 0 | 0 | 0 | 79 | Chloroflexi | SBR1031 | A4b | A4b\_ge |
| OTU\_256 | 0 | 0 | 0 | 0 | 0 | 76 | Bacteroidetes | Cytophagales | Spirosomaceae | Spirosoma |
| OTU\_7043 | 0 | 0 | 0 | 0 | 0 | 74 | Cyanobacteria | Oxyphotobacteria | Oxyphotobacteria | Oxyphotobacteria |
| OTU\_3484 | 0 | 0 | 0 | 0 | 0 | 68 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatellaceae |
| OTU\_245 | 0 | 0 | 0 | 0 | 0 | 64 | Bacteroidetes | Cytophagales | Cytophagales | Cytophagales |
| OTU\_6014 | 0 | 0 | 0 | 0 | 0 | 62 | Cyanobacteria | Leptolyngbyales | Leptolyngbyaceae | Leptolyngbyaceae |
| OTU\_405 | 0 | 0 | 0 | 0 | 0 | 61 | Actinobacteria | Micrococcales | Micrococcaceae | Pseudarthrobacter |
| OTU\_259 | 0 | 0 | 0 | 0 | 0 | 59 | Proteobacteria | Sphingomonadales | Sphingomonadaceae | Sphingomonadaceae |
| OTU\_430 | 0 | 0 | 0 | 0 | 0 | 57 | Chloroflexi | Caldilineales | Caldilineaceae | uncultured |
| OTU\_368 | 0 | 0 | 0 | 0 | 0 | 55 | Actinobacteria | Frankiales | uncultured | uncultured\_ge |
| OTU\_261 | 0 | 0 | 0 | 0 | 0 | 53 | Bacteroidetes | Cytophagales | Hymenobacteraceae | Hymenobacter |
| OTU\_1056 | 0 | 0 | 0 | 0 | 0 | 52 | Actinobacteria | Microtrichales | Iamiaceae | Iamia |
| OTU\_198 | 0 | 0 | 0 | 0 | 0 | 49 | Proteobacteria | Sphingomonadales | Sphingomonadaceae | Sphingomonadaceae |
| OTU\_550 | 0 | 0 | 0 | 0 | 0 | 45 | Cyanobacteria | Oxyphotobacteria | Oxyphotobacteria | Oxyphotobacteria |
| OTU\_210 | 0 | 0 | 0 | 0 | 0 | 44 | Gemmatimonadetes | Gemmatimonadales | Gemmatimonadaceae | Gemmatimonas |
| OTU\_864 | 0 | 0 | 0 | 0 | 0 | 43 | Proteobacteria | Xanthomonadales | Xanthomonadaceae | Pseudoxanthomonas |
| OTU\_466 | 0 | 0 | 0 | 0 | 0 | 39 | Acidobacteria | Solibacterales | Solibacteraceae | Paludibaculum |
| OTU\_340 | 0 | 0 | 0 | 0 | 0 | 37 | Proteobacteria | Acetobacterales | Acetobacteraceae | Roseomonas |
| OTU\_541 | 0 | 0 | 0 | 0 | 0 | 36 | Proteobacteria | Sphingomonadales | Sphingomonadaceae | Sphingomonadaceae |
| OTU\_1536 | 0 | 0 | 0 | 0 | 0 | 36 | Proteobacteria | Rhodobacterales | Rhodobacteraceae | Rhodobacteraceae |
| OTU\_441 | 0 | 0 | 0 | 0 | 0 | 35 | Actinobacteria | Propionibacteriales | Nocardioidaceae | Nocardioides |
| OTU\_498 | 0 | 0 | 0 | 0 | 0 | 34 | Bacteroidetes | Cytophagales | Spirosomaceae | Spirosomaceae |
| OTU\_4015 | 0 | 0 | 0 | 0 | 0 | 33 | Chloroflexi | Kallotenuales | AKIW781 | AKIW781\_ge |
| OTU\_3001 | 0 | 0 | 0 | 0 | 0 | 31 | Actinobacteria | Solirubrobacterales | Solirubrobacteraceae | Solirubrobacteraceae |
| OTU\_3005 | 0 | 0 | 0 | 0 | 0 | 30 | Cyanobacteria | Oxyphotobacteria | Unknown\_Family | Unknown\_Family |
| OTU\_24853 | 0 | 0 | 0 | 0 | 0 | 28 | Cyanobacteria | Oxyphotobacteria | Unknown\_Family | Unknown\_Family |
| OTU\_592 | 0 | 0 | 0 | 0 | 0 | 25 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_6026 | 0 | 0 | 0 | 0 | 0 | 25 | Actinobacteria | Propionibacteriales | Nocardioidaceae | Marmoricola |
| OTU\_191 | 0 | 0 | 0 | 0 | 0 | 24 | Planctomycetes | Tepidisphaerales | Tepidisphaeraceae | Tepidisphaeraceae\_ge |
| OTU\_1382 | 0 | 0 | 0 | 0 | 0 | 24 | Proteobacteria | Rhodobacterales | Rhodobacteraceae | Rhodobacteraceae |
| OTU\_25453 | 0 | 0 | 0 | 0 | 0 | 24 | Actinobacteria | Microtrichales | Microtrichales | Microtrichales |
| OTU\_426 | 0 | 0 | 0 | 0 | 0 | 23 | Cyanobacteria | Oxyphotobacteria | Oxyphotobacteria | Oxyphotobacteria |
| OTU\_666 | 0 | 0 | 0 | 0 | 0 | 22 | Planctomycetes | Tepidisphaerales | WD2101\_soil\_group | WD2101\_soil\_group\_ge |
| OTU\_697 | 0 | 0 | 0 | 0 | 0 | 22 | Proteobacteria | Betaproteobacteriales | Burkholderiaceae | Burkholderiaceae |
| OTU\_819 | 0 | 0 | 0 | 0 | 0 | 22 | Gemmatimonadetes | Gemmatimonadales | Gemmatimonadaceae | Gemmatimonadaceae |
| OTU\_6761 | 0 | 0 | 0 | 0 | 0 | 21 | Actinobacteria | Propionibacteriales | Nocardioidaceae | Nocardioides |
| OTU\_452 | 0 | 0 | 0 | 0 | 0 | 20 | Actinobacteria | IMCC26256 | IMCC26256\_fa | IMCC26256\_ge |
| OTU\_582 | 0 | 0 | 0 | 0 | 0 | 20 | Actinobacteria | Microtrichales | Ilumatobacteraceae | Ilumatobacter |
| OTU\_737 | 0 | 0 | 0 | 0 | 0 | 20 | Bacteroidetes | Cytophagales | Microscillaceae | uncultured |
| OTU\_982 | 0 | 0 | 0 | 0 | 0 | 19 | Actinobacteria | Propionibacteriales | Nocardioidaceae | Nocardioides |
| OTU\_930 | 0 | 0 | 0 | 0 | 0 | 18 | Actinobacteria | Micrococcales | Microbacteriaceae | Marisediminicola |
| OTU\_571 | 0 | 0 | 0 | 0 | 0 | 17 | Proteobacteria | Rhodobacterales | Rhodobacteraceae | Rhodobacteraceae |
| OTU\_659 | 0 | 0 | 0 | 0 | 0 | 17 | Chloroflexi | SBR1031 | A4b | A4b\_ge |
| OTU\_785 | 0 | 0 | 0 | 0 | 0 | 17 | Chloroflexi | Thermomicrobiales | JG30-KF-CM45 | JG30-KF-CM45\_ge |
| OTU\_1029 | 0 | 0 | 0 | 0 | 0 | 17 | Proteobacteria | Acetobacterales | Acetobacteraceae | Roseococcus |
| OTU\_1058 | 0 | 0 | 0 | 0 | 0 | 17 | Chloroflexi | SBR1031 | A4b | A4b\_ge |
| OTU\_1183 | 0 | 0 | 0 | 0 | 0 | 17 | Proteobacteria | Sphingomonadales | Sphingomonadaceae | Sphingomonadaceae |
| OTU\_22136 | 0 | 0 | 0 | 0 | 0 | 17 | Cyanobacteria | Oxyphotobacteria | Oxyphotobacteria | Oxyphotobacteria |
| OTU\_769 | 0 | 0 | 0 | 0 | 0 | 15 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_1153 | 0 | 0 | 0 | 0 | 0 | 15 | Actinobacteria | Microtrichales | Ilumatobacteraceae | Ilumatobacter |
| OTU\_1760 | 0 | 0 | 0 | 0 | 0 | 15 | Actinobacteria | Micrococcales | Cellulomonadaceae | Actinotalea |
| OTU\_3497 | 0 | 0 | 0 | 0 | 0 | 15 | Bacteroidetes | Chitinophagales | Chitinophagaceae | Flavisolibacter |
| OTU\_22594 | 0 | 0 | 0 | 0 | 0 | 15 | Bacteroidetes | Flavobacteriales | Flavobacteriaceae | Flavobacteriaceae |
| OTU\_228 | 0 | 0 | 0 | 0 | 0 | 14 | Bacteroidetes | Cytophagales | Spirosomaceae | Spirosomaceae\_ge |
| OTU\_488 | 0 | 0 | 0 | 0 | 0 | 14 | Proteobacteria | Betaproteobacteriales | Burkholderiaceae | Burkholderiaceae |
| OTU\_1767 | 0 | 0 | 0 | 0 | 0 | 14 | Proteobacteria | Rhodobacterales | Rhodobacteraceae | Jannaschia |
| OTU\_706 | 0 | 0 | 0 | 0 | 0 | 13 | Proteobacteria | Rhodobacterales | Rhodobacteraceae | Cereibacter |
| OTU\_1712 | 0 | 0 | 0 | 0 | 0 | 13 | Proteobacteria | Betaproteobacteriales | Burkholderiaceae | Caenimonas |
| OTU\_2824 | 0 | 0 | 0 | 0 | 0 | 13 | Proteobacteria | Xanthomonadales | Xanthomonadaceae | Xanthomonadaceae |
| OTU\_3095 | 0 | 0 | 0 | 0 | 0 | 13 | Actinobacteria | Thermoleophilia | Thermoleophilia | Thermoleophilia |
| OTU\_3423 | 0 | 0 | 0 | 0 | 0 | 13 | Cyanobacteria | Oxyphotobacteria | Oxyphotobacteria | Oxyphotobacteria |
| OTU\_24928 | 0 | 0 | 0 | 0 | 0 | 13 | Chloroflexi | Thermomicrobiales | AKYG1722 | AKYG1722\_ge |
| OTU\_1613 | 0 | 0 | 0 | 0 | 0 | 12 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_1994 | 0 | 0 | 0 | 0 | 0 | 12 | Cyanobacteria | Pseudanabaenales | Pseudanabaenaceae | uncultured |
| OTU\_7216 | 0 | 0 | 0 | 0 | 0 | 12 | Proteobacteria | Xanthomonadales | Rhodanobacteraceae | uncultured |
| OTU\_821 | 0 | 0 | 0 | 0 | 0 | 11 | Actinobacteria | Actinobacteria | Actinobacteria | Actinobacteria |
| OTU\_832 | 0 | 0 | 0 | 0 | 0 | 11 | Patescibacteria | Saccharimonadales | Saccharimonadales\_fa | Saccharimonadales\_ge |
| OTU\_892 | 0 | 0 | 0 | 0 | 0 | 11 | Chloroflexi | Thermomicrobiales | AKYG1722 | AKYG1722\_ge |
| OTU\_978 | 0 | 0 | 0 | 0 | 0 | 11 | Actinobacteria | Solirubrobacterales | Solirubrobacteraceae | Solirubrobacter |
| OTU\_1792 | 0 | 0 | 0 | 0 | 0 | 11 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_188 | 0 | 0 | 0 | 0 | 0 | 10 | Planctomycetes | Tepidisphaerales | WD2101\_soil\_group | WD2101\_soil\_group\_ge |
| OTU\_437 | 0 | 0 | 0 | 0 | 0 | 10 | Actinobacteria | Propionibacteriales | Nocardioidaceae | Nocardioides |
| OTU\_1277 | 0 | 0 | 0 | 0 | 0 | 10 | Planctomycetes | Gemmatales | Gemmataceae | uncultured |
| OTU\_1904 | 0 | 0 | 0 | 0 | 0 | 10 | Proteobacteria | Acetobacterales | Acetobacteraceae | Roseococcus |
| OTU\_1 | 7 | 0 | 1728 | 1 | 6 | 14 | Actinobacteria | Pseudonocardiales | Pseudonocardiaceae | Crossiella |
| OTU\_2 | 2543 | 1516 | 3385 | 1330 | 1075 | 7 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatella |
| OTU\_5 | 9048 | 7870 | 7 | 7 | 2971 | 0 | Cyanobacteria | Nostocales | Nostocaceae | Nostoc\_PCC-73102 |
| OTU\_6 | 0 | 0 | 1 | 2 | 0 | 1771 | Cyanobacteria | Oxyphotobacteria | Unknown\_Family | Unknown\_Family |
| OTU\_7 | 626 | 90 | 22022 | 401 | 21 | 1 | Cyanobacteria | Nostocales | Chroococcidiopsaceae | Aliterella\_CENA595 |
| OTU\_9 | 236 | 2 | 4 | 0 | 0 | 1553 | Cyanobacteria | Oxyphotobacteria | Unknown\_Family | Phormidium\_CYN64 |
| OTU\_10 | 154 | 1110 | 2763 | 262 | 208 | 102 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatella |
| OTU\_11 | 53 | 259 | 3253 | 537 | 12 | 90 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatella |
| OTU\_12 | 1623 | 860 | 8525 | 1972 | 1893 | 165 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatella |
| OTU\_13 | 0 | 0 | 971 | 0 | 1 | 54 | Actinobacteria | Solirubrobacterales | Solirubrobacterales | Solirubrobacterales |
| OTU\_14 | 53 | 144 | 4663 | 50 | 97 | 425 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatella |
| OTU\_17 | 1793 | 0 | 107 | 0 | 451 | 0 | Actinobacteria | Solirubrobacterales | Solirubrobacteraceae | uncultured |
| OTU\_18 | 96 | 520 | 4893 | 44 | 8 | 23 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatella |
| OTU\_19 | 594 | 0 | 0 | 0 | 0 | 0 | Actinobacteria | Actinobacteria | Actinobacteria | Actinobacteria |
| OTU\_22 | 1455 | 3774 | 171 | 0 | 1 | 1 | Cyanobacteria | Nostocales | Phormidiaceae | Tychonema\_CCAP\_1459-11B |
| OTU\_24 | 36 | 523 | 334 | 7 | 3 | 0 | Bacteria | Bacteria | Bacteria | Bacteria |
| OTU\_27 | 4643 | 0 | 40 | 8 | 0 | 0 | Cyanobacteria | Nostocales | Nostocaceae | Nostocaceae |
| OTU\_29 | 3 | 0 | 3031 | 1717 | 0 | 2 | Cyanobacteria | Nostocales | Chroococcidiopsaceae | Chlorogloea\_SAG\_10.99 |
| OTU\_31 | 3 | 1 | 96 | 4 | 0 | 798 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatella |
| OTU\_34 | 1 | 49 | 1926 | 135 | 0 | 0 | Deinococcus-Thermus | Deinococcales | Trueperaceae | Truepera |
| OTU\_36 | 16 | 1 | 63 | 0 | 0 | 0 | Actinobacteria | Actinobacteria | Actinobacteria | Actinobacteria |
| OTU\_43 | 0 | 0 | 717 | 151 | 0 | 0 | Acidobacteria | Acidobacteriales | Acidobacteriaceae\_(Subgroup\_1) | Acidobacteriaceae\_(Subgroup\_1) |
| OTU\_45 | 0 | 0 | 2047 | 14 | 0 | 0 | Bacteroidetes | Cytophagales | Spirosomaceae | Spirosoma |
| OTU\_46 | 16 | 0 | 9 | 0 | 614 | 3 | Cyanobacteria | Nostocales | Chroococcidiopsaceae | Crinalium\_SAG\_22.89 |
| OTU\_59 | 1 | 68 | 8868 | 1078 | 22 | 0 | Bacteroidetes | Cytophagales | Spirosomaceae | Spirosoma |
| OTU\_64 | 52 | 13 | 216 | 7 | 3 | 39 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatella |
| OTU\_71 | 148 | 1524 | 230 | 0 | 2 | 12 | Cyanobacteria | Nostocales | Phormidiaceae | Tychonema\_CCAP\_1459-11B |
| OTU\_73 | 313 | 8 | 268 | 21 | 9 | 0 | Acidobacteria | Blastocatellales | Blastocatellaceae | uncultured |
| OTU\_75 | 1 | 0 | 0 | 0 | 0 | 0 | Chloroflexi | Chloroflexales | Chloroflexaceae | Chloroflexaceae |
| OTU\_78 | 1092 | 1 | 6 | 1 | 0 | 0 | Cyanobacteria | Nostocales | Nostocaceae | Scytonema\_UTEX\_2349 |
| OTU\_111 | 24 | 0 | 1 | 0 | 0 | 0 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatella |
| OTU\_114 | 4 | 1323 | 1 | 0 | 7 | 1 | Cyanobacteria | Oxyphotobacteria | Oxyphotobacteria | Oxyphotobacteria |
| OTU\_120 | 0 | 0 | 1221 | 15 | 0 | 0 | Actinobacteria | Euzebyales | Euzebyaceae | uncultured |
| OTU\_125 | 3 | 1 | 166 | 5 | 0 | 4 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatella |
| OTU\_133 | 177 | 49 | 298 | 85 | 9 | 0 | FBP | FBP\_or | FBP\_fa | FBP\_ge |
| OTU\_148 | 88 | 16 | 217 | 27 | 2 | 0 | Proteobacteria | Acetobacterales | Acetobacteraceae | Acidiphilium |
| OTU\_178 | 0 | 1 | 1489 | 507 | 0 | 0 | Cyanobacteria | Nostocales | Chroococcidiopsaceae | uncultured |
| OTU\_215 | 0 | 0 | 0 | 0 | 0 | 826 | Actinobacteria | Micrococcales | Micrococcaceae | Arthrobacter |
| OTU\_251 | 0 | 0 | 0 | 0 | 0 | 752 | Proteobacteria | Betaproteobacteriales | Burkholderiaceae | Polaromonas |
| OTU\_315 | 0 | 1 | 0 | 0 | 0 | 906 | Actinobacteria | Micrococcales | Micrococcaceae | Arthrobacter |
| OTU\_388 | 0 | 0 | 0 | 0 | 0 | 1025 | Actinobacteria | Acidimicrobiia | Acidimicrobiia | Acidimicrobiia |
| OTU\_439 | 177 | 1 | 362 | 290 | 54 | 0 | Cyanobacteria | Nostocales | Chroococcidiopsaceae | Chlorogloea\_SAG\_10.99 |
| OTU\_490 | 266 | 72 | 216 | 16 | 51 | 0 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatella |
| OTU\_565 | 142 | 1 | 421 | 15 | 0 | 0 | Cyanobacteria | Nostocales | Chroococcidiopsaceae | Chroococcidiopsaceae |
| OTU\_613 | 81 | 355 | 88 | 39 | 1 | 1 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatella |
| OTU\_681 | 117 | 79 | 4347 | 91 | 107 | 346 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatella |
| OTU\_739 | 3 | 0 | 5 | 0 | 0 | 0 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatella |
| OTU\_1688 | 802 | 81 | 6 | 0 | 3 | 0 | Cyanobacteria | Oxyphotobacteria | Oxyphotobacteria | Oxyphotobacteria |
| OTU\_2194 | 0 | 0 | 544 | 78 | 0 | 0 | Cyanobacteria | Nostocales | Chroococcidiopsaceae | Chroococcidiopsaceae |
| OTU\_2439 | 6 | 336 | 98 | 33 | 2 | 0 | Acidobacteria | Blastocatellales | Blastocatellaceae | Blastocatella |

1. **Table 3**. Eukaryotic OTUs based on 16S rRNA sequences (97 % 16S rRNA sequence similarity) in samples of Pingvinane 3 (subsite C3), Perlebandet North (site DN) and South (site DS), Petrellnuten (site B) and Yûboku-dani valley (site F). Shades of red, orange and blue indicate the OTUs present only in one of these six sites, whereas the yellow colour indicates OTUs that are among the 50 most abundant ones in the 105 studied samples from 9 sites by Savaglia et al. (in preparation). Three of these sites were not included in the sites of the proposed ASPA but contributed to the calculation of the 50 most abundant OTUs and the determination of unique OTUs: Austkampane; Dry Valley and Utsteinen ridge.
2. Material and methods
3. Sequences were analyzed by a methodology based on Operational Taxonomic Units (OTUs), using a well-established in-house pipeline. Paired-end merging was performed using PEAR. The minimum length was set to 300 bp, and the maximum length to 550 bp with a minimum overlap of 10 bp. Further, sequence quality filtering and processing were done using USEARCH, with a minimal Phred score set to Q20 and a maximum expected error of 2. De novo chimera filtering was done with UCHIME. Sequences were clustered in Operational Taxonomic Units (OTUs) with a default similarity cut-off of 97% using UPARSE. Curated reference taxonomic databases SILVA v138.1 and PR2 version 4.14.0 were used with the naïve Bayesian classifier implemented in Mothur to infer taxonomic identification of the resulting OTUs for 16S and 18S, respectively.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| OTU | Pingvin-ane North (or III) | Pingvin-ane South | Perleban-det North | Perleban-det South | Petrell-nuten | Yûboku-dani Valley | Phylum | Order | Family | Genus |
| OTU\_425 | 11 | 0 | 0 | 0 | 0 | 0 | Fungi | Pezizomycotina | Pezizomycotina | Pezizomycotina |
| OTU\_155 | 0 | 38 | 0 | 0 | 0 | 0 | Ciliophora | Cyrtophoria\_\_4 | Chilodonellidae | Chilodonellidae |
| OTU\_220 | 0 | 0 | 74 | 0 | 0 | 0 | Cercozoa | Glissomonadida | Bodomorphidae | Bodomorpha |
| OTU\_223 | 0 | 0 | 70 | 0 | 0 | 0 | Ciliophora | Colpodea | Colpodida | Colpodida |
| OTU\_457 | 0 | 0 | 60 | 0 | 0 | 0 | Cercozoa | Glissomonadida | Sandonidae | Sandonidae |
| OTU\_123 | 0 | 0 | 51 | 0 | 0 | 0 | Chlorophyta | Pyramimonadales | Pyramimonadales | Pyramimonadales |
| OTU\_105 | 0 | 0 | 49 | 0 | 0 | 0 | Ochrophyta | Bacillariophyta | Polar-centric-Mediophyceae | Chaetoceros |
| OTU\_132 | 0 | 0 | 41 | 0 | 0 | 0 | Archaeplastida | Archaeplastida | Archaeplastida | Archaeplastida |
| OTU\_241 | 0 | 0 | 35 | 0 | 0 | 0 | Cercozoa | Glissomonadida | Sandonidae | Sandonidae |
| OTU\_183 | 0 | 0 | 34 | 0 | 0 | 0 | Chlorophyta | Chlorophyta | Chlorophyta | Chlorophyta |
| OTU\_145 | 0 | 0 | 34 | 0 | 0 | 0 | Ochrophyta | Bacillariophyta | Polar-centric-Mediophyceae | Chaetoceros |
| OTU\_247 | 0 | 0 | 32 | 0 | 0 | 0 | Eukaryota | Eukaryota | Eukaryota | Eukaryota |
| OTU\_120 | 0 | 0 | 32 | 0 | 0 | 0 | Fungi | Chytridiomycotina | Chytridiomycetes | Chytridiomycetes |
| OTU\_64 | 0 | 0 | 31 | 0 | 0 | 0 | Cercozoa | Glissomonadida | Allapsidae | Allapsidae |
| OTU\_96 | 0 | 0 | 31 | 0 | 0 | 0 | Cercozoa | Glissomonadida | Allapsidae | Allapsidae |
| OTU\_196 | 0 | 0 | 28 | 0 | 0 | 0 | Ciliophora | Tintinnida | Tintinnida | Tintinnida |
| OTU\_101 | 0 | 0 | 27 | 0 | 0 | 0 | Ciliophora | Colpodea | Colpodida | Colpodida |
| OTU\_261 | 0 | 0 | 26 | 0 | 0 | 0 | Ochrophyta | Xanthophyceae | Xanthophyceae | Xanthonema |
| OTU\_459 | 0 | 0 | 24 | 0 | 0 | 0 | Apicomplexa | Eugregarinorida | Gregarinidae | Leidyana1 |
| OTU\_254 | 0 | 0 | 24 | 0 | 0 | 0 | Lobosa | Arcellinida | Arcellinida-A3 | Spumochlamys |
| OTU\_248 | 0 | 0 | 22 | 0 | 0 | 0 | Cercozoa | Filosa-Sarcomonadea | Filosa-Sarcomonadea | Filosa-Sarcomonadea |
| OTU\_253 | 0 | 0 | 18 | 0 | 0 | 0 | Fungi | Chytridiomycotina | Chytridiomycetes | Chytridiomycetes |
| OTU\_523 | 0 | 0 | 18 | 0 | 0 | 0 | Cercozoa | Cercozoa | Cercozoa | Cercozoa |
| OTU\_222 | 0 | 0 | 17 | 0 | 0 | 0 | Cercozoa | Filosa-Imbricatea | Novel-clade-2 | Novel-clade-2 |
| OTU\_100 | 0 | 0 | 17 | 0 | 0 | 0 | Cercozoa | Cercozoa | Cercozoa | Cercozoa |
| OTU\_692 | 0 | 0 | 16 | 0 | 0 | 0 | Metazoa | Metazoa | Metazoa | Metazoa |
| OTU\_617 | 0 | 0 | 16 | 0 | 0 | 0 | Cercozoa | Cryomonadida | Rhogostoma-lineage | Rhogostoma-lineage |
| OTU\_577 | 0 | 0 | 12 | 0 | 0 | 0 | Eukaryota | Eukaryota | Eukaryota | Eukaryota |
| OTU\_677 | 0 | 0 | 12 | 0 | 0 | 0 | Cercozoa | Cryomonadida | Rhogostoma-lineage | Rhogostoma-lineage |
| OTU\_605 | 0 | 0 | 11 | 0 | 0 | 0 | Cercozoa | Cryomonadida | Cryomonadida | Cryomonadida |
| OTU\_243 | 0 | 0 | 10 | 0 | 0 | 0 | Ciliophora | Haptoria\_\_5 | Pleurostomatida | Pleurostomatida |
| OTU\_43 | 0 | 0 | 0 | 0 | 0 | 488 | Ciliophora | Karyorelictea | Trachelocercidae | Trachelocercidae |
| OTU\_42 | 0 | 0 | 0 | 0 | 0 | 345 | Streptophyta | Embryophyceae | Embryophyceae | Allium |
| OTU\_24 | 0 | 0 | 0 | 0 | 0 | 323 | Ciliophora | Cyrtophoria\_\_4 | Chilodonellidae | Chilodonellidae |
| OTU\_37 | 0 | 0 | 0 | 0 | 0 | 219 | Conosa | Variosea | Acramoebidae | Acramoebidae |
| OTU\_47 | 0 | 0 | 0 | 0 | 0 | 158 | Centroheliozoa | Centroheliozoa | Centroheliozoa | Centroheliozoa |
| OTU\_45 | 0 | 0 | 0 | 0 | 0 | 113 | Ciliophora | Suctoria | Evaginogenida | Evaginogenida |
| OTU\_25 | 0 | 0 | 0 | 0 | 0 | 111 | Eukaryota | Eukaryota | Eukaryota | Eukaryota |
| OTU\_119 | 0 | 0 | 0 | 0 | 0 | 103 | Cercozoa | Cercozoa | Cercozoa | Cercozoa |
| OTU\_131 | 0 | 0 | 0 | 0 | 0 | 59 | Cercozoa | Filosa-Sarcomonadea | Filosa-Sarcomonadea | Filosa-Sarcomonadea |
| OTU\_49 | 0 | 0 | 0 | 0 | 0 | 41 | Ciliophora | Hypotrichia | Oxytrichidae | Oxytricha |
| OTU\_122 | 0 | 0 | 0 | 0 | 0 | 38 | Conosa | Variosea | Acramoebidae | Acramoebidae |
| OTU\_31 | 0 | 0 | 0 | 0 | 0 | 20 | Ciliophora | Nassophorea | Nassulida | Nassulida |
| OTU\_39 | 0 | 0 | 0 | 0 | 0 | 18 | Conosa | Variosea | Variosea | VarioseaX |
| OTU\_258 | 0 | 0 | 0 | 0 | 0 | 18 | Cercozoa | Cercozoa | Cercozoa | Cercozoa |
| OTU\_75 | 0 | 0 | 0 | 0 | 0 | 12 | Eukaryota | Eukaryota | Eukaryota | Eukaryota |
| OTU\_289 | 0 | 0 | 0 | 0 | 0 | 11 | Opalozoa | Pseudodendromo-nadales | Pseudodendromo-nadales | Pseudodendromo-nadales |
| OTU\_43 | 0 | 0 | 0 | 0 | 0 | 488 | Ciliophora | Karyorelictea | Trachelocercidae | Trachelocercidae |
| OTU\_11 | 6501 | 0 | 1 | 0 | 0 | 0 | Ciliophora | Nassophorea | Nassulida | Nassulida |
| OTU\_6 | 374 | 2075 | 3280 | 134 | 432 | 1 | Ciliophora | Cyrtophoria\_\_4 | Chilodonellidae | Chilodonellidae |
| OTU\_16 | 36 | 96 | 261 | 52 | 3 | 0 | Ciliophora | Hypotrichia | Oxytrichidae | Oxytrichidae |
| OTU\_18 | 1 | 16 | 52 | 0 | 3521 | 213 | Chlorophyta | Chlamydomonada-les | Chlamydomona-dales | Chlamydomona-dales |
| OTU\_58 | 62 | 143 | 829 | 113 | 35 | 196 | Chlorophyta | Chlamydomonadales | Chlamydomonadales | Gloeocystis |
| OTU\_41 | 0 | 0 | 0 | 0 | 0 | 628 | Chlorophyta | Chlamydomonadales | Chlamydomonadales | Chlamydomonadales |
| OTU\_9 | 1 | 0 | 0 | 0 | 0 | 1282 | Chlorophyta | Chlorellales | Chlorellales | Oocystis |
| OTU\_250 | 1756 | 1744 | 9800 | 889 | 1933 | 47 | Chlorophyta | Microthamniales | Microthamniales | Trebouxia |
| OTU\_558 | 96 | 120 | 441 | 48 | 81 | 5 | Chlorophyta | Microthamniales | Microthamniales | Trebouxia |
| OTU\_1 | 12728 | 10796 | 65188 | 6653 | 10144 | 2854 | Chlorophyta | Microthamniales | Microthamniales | Trebouxia |
| OTU\_2 | 4796 | 3931 | 4813 | 288 | 675 | 217 | Chlorophyta | Prasiolales | Prasiolales | Desmococcus |
| OTU\_535 | 254 | 743 | 1488 | 308 | 91 | 30 | Chlorophyta | Prasiolales | Prasiolales | Prasiolales |
| OTU\_764 | 502 | 410 | 415 | 30 | 86 | 14 | Chlorophyta | Prasiolales | Prasiolales | Desmococcus |
| OTU\_30 | 467 | 312 | 1416 | 662 | 159 | 48 | Chlorophyta | Prasiolales | Prasiolales | Prasiolales |
| OTU\_10 | 778 | 11 | 1811 | 55 | 1 | 311 | Chlorophyta | Watanabea-Clade | Watanabea-Clade | Chloroidium |
| OTU\_66 | 360 | 243 | 115 | 7 | 35 | 3 | Chlorophyta | Prasiolales | Prasiolales | Prasiolales |
| OTU\_401 | 129 | 162 | 243 | 46 | 70 | 8 | Chlorophyta | Prasiolales | Prasiolales | Prasiolales |
| OTU\_20 | 64 | 153 | 1114 | 88 | 55 | 440 | Chlorophyta | Microthamniales | Microthamniales | Microthamniales |
| OTU\_200 | 210 | 254 | 488 | 119 | 56 | 6 | Chlorophyta | Watanabea-Clade | Watanabea-Clade | Diplosphaera |
| OTU\_48 | 3 | 2 | 306 | 79 | 1 | 0 | Eukaryota | Eukaryota | Eukaryota | Eukaryota |
| OTU\_29 | 0 | 196 | 1 | 0 | 608 | 0 | Metazoa | Hexapoda | Collembola | Collembola |
| OTU\_15 | 249 | 148 | 1889 | 763 | 120 | 197 | Metazoa | Rotifera | Rotifera | Rotifera |
| OTU\_205 | 248 | 41 | 555 | 168 | 53 | 229 | Metazoa | Rotifera | Rotifera | Rotifera |
| OTU\_269 | 13 | 71 | 243 | 8 | 7 | 4 | Metazoa | Rotifera | Rotifera | Rotifera |
| OTU\_3 | 4359 | 709 | 13075 | 3478 | 1166 | 5470 | Metazoa | Rotifera | Rotifera | Rotifera |
| OTU\_32 | 1268 | 306 | 4298 | 360 | 254 | 2257 | Metazoa | Rotifera | Rotifera | Rotifera |
| OTU\_494 | 5 | 5 | 340 | 12 | 11 | 206 | Metazoa | Rotifera | Rotifera | Rotifera |
| OTU\_683 | 42 | 9 | 453 | 105 | 47 | 200 | Metazoa | Rotifera | Rotifera | Rotifera |
| OTU\_8 | 3 | 39 | 14 | 815 | 1 | 40 | Metazoa | Tardigrada | Tardigrada | Acutuncus |
| OTU\_4 | 3269 | 319 | 15642 | 0 | 1 | 267 | Metazoa | Tardigrada | Tardigrada | Diphascon |
| OTU\_301 | 1127 | 101 | 409 | 0 | 1 | 96 | Metazoa | Tardigrada | Tardigrada | Diphascon |
| OTU\_35 | 3 | 125 | 22 | 1416 | 6 | 10 | Metazoa | Tardigrada | Tardigrada | Hebesuncus |
| OTU\_22 | 469 | 469 | 731 | 0 | 0 | 0 | Metazoa | Tardigrada | Tardigrada | Macrobiotus |
| OTU\_33 | 13 | 0 | 822 | 0 | 96 | 4 | Opisthokonta | Opisthokonta | Opisthokonta | Opisthokonta |
| OTU\_5 | 83 | 0 | 4510 | 27 | 1178 | 17 | Metazoa | Metazoa | Metazoa | Metazoa |
| OTU\_65 | 0 | 0 | 255 | 3 | 0 | 218 | Opisthokonta | Opisthokonta | Opisthokonta | Opisthokonta |
| OTU\_26 | 1 | 3 | 757 | 7 | 0 | 3 | Cercozoa | Cercomonadida | Cercomonadidae | Cercomonas |
| OTU\_36 | 21 | 0 | 2386 | 65 | 68 | 4 | Cercozoa | Glissomonadida | Sandonidae | Sandona |
| OTU\_14 | 48 | 0 | 1241 | 16 | 647 | 11 | Cercozoa | Glissomonadida | Sandonidae | Sandonidae |
| OTU\_194 | 4 | 0 | 543 | 0 | 473 | 1 | Cercozoa | Glissomonadida | Sandonidae | Sandonidae |
| OTU\_276 | 2 | 0 | 386 | 8 | 0 | 0 | Cercozoa | Glissomonadida | Sandonidae | Sandonidae |
| OTU\_62 | 1 | 0 | 1508 | 6 | 1 | 2 | Cercozoa | Glissomonadida | Sandonidae | Sandonidae |
| OTU\_19 | 3 | 0 | 557 | 0 | 596 | 5 | Cercozoa | Glissomonadida | Sandonidae | Sandonidae |
| OTU\_335 | 2 | 0 | 342 | 0 | 427 | 1 | Cercozoa | Glissomonadida | Sandonidae | Sandonidae |
| OTU\_17 | 262 | 2 | 634 | 576 | 19 | 1 | Cercozoa | Cryomonadida | Rhogostoma-lineage | Rhogostoma-lineage |
| OTU\_12 | 104 | 0 | 5909 | 128 | 1 | 9 | Cercozoa | Cryomonadida | Rhogostoma-lineage | Rhogostoma-lineage |
| OTU\_178 | 57 | 0 | 1413 | 90 | 3 | 8 | Cercozoa | Cryomonadida | Rhogostoma-lineage | Rhogostoma-lineage |
| OTU\_134 | 8 | 0 | 876 | 1 | 0 | 5 | Cercozoa | Cryomonadida | Rhogostoma-lineage | Rhogostoma-lineage |
| OTU\_21 | 0 | 0 | 206 | 7 | 0 | 59 | Cercozoa | Cercozoa | Cercozoa | Cercozoa |

1. **Table 4**. Cyanobacterial OTUs based on 16S rRNA sequences (97 % 16S rRNA sequence similarity) in samples of Pingvinane 4 (subsite C4), Tanngarden (site A) and Teltet (site E) obtained by DGGE.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **OTU** | **Representative sequence** | **Accession number** | **Number of sequences** | | | **Best SeqMatch isolate hit (ID %)** | **Best SeqMatch uncultured hit (ID %)** |
| **Pingvinane 4 (C4)** | **Tanngarden (A)** | **Teltet (E)** |  |  |
| DGGE\_OTU 1 | 10TN45a01C | MF468232 | 0 | 0 | 7 | *Hormoscilla pringsheimii* SAG 1407-1; KC572078 (98.6%) | uncultured bacterium; SPIT\_D12; GQ306044 (99.3%) |
| DGGE\_OTU 2 | 10PI43b03C | MF468229 | 2 | 0 | 0 | *Phormidesmis priestleyi* ANT.L52.4;AY493578(98.2%) | uncultured cyanobacterium; H-C07; DQ181722 (99.1%) |
| DGGE\_OTU 3 | 10PI43a01S | MF468230 | 10 | 0 | 2 | *Microcoleus antarcticus* UTCC 474; AF218373 (100%) | uncultured cyanobacterium; 89-23; JN814349 (100%) |
| DGGE\_OTU 4 | 10TA32a01C | MF468234 | 1 | 2 | 0 | *Leptolyngbya* sp. ANT.L52.1; AY493584 (97.2%) | uncultured Oscillatoriales cyanobacterium; H\_21; FJ490341 (98.9%) |
| DGGE\_OTU 5 | 10TN47b04C | MF468226 | 0 | 0 | 1 | *Hormoscilla pringsheimii* SAG 1407-1; KC572078(92.7%) | uncultured bacterium; Bact\_SIP\_153; JX204373 (93.3%) |
| DGGE\_OTU 6 | 10PI43a01C | MF468233 | 1 | 0 | 1 | *cyanobacterium OU\_20; GQ162224* (95.8%) | uncultured Nostocales cyanobacterium; C\_4; FJ490241 (99.4%) |
| DGGE\_OTU 7 | 10PI42a01C | MF468231 | 3 | 0 | 0 | *Phormidium pseudopriestleyi* ANT.LACV5.3; AY493600 (99.7%) | uncultured Antarctic cyanobacterium; SalP10; AY541536 (99.7%) |
| DGGE\_OTU 8 | 10TN46b03S | MF468222 | 0 | 4 | 5 | Nostoc sp. ANT.LG2.6; AY493595 (99.1%) | uncultured bacterium; abscm03.1.110; JX255112 (99.1%) |
| DGGE\_OTU 9 | 10TA39a02C | MF468223 | 0 | 4 | 0 | *Nostoc sp. PCC 9305; AY742453* (99.4%) | uncultured Nostoc sp.; MVMG1; EU359045 (99.4%) |
| DGGE\_OTU 10 | 10TA40a04S | MF468224 | 0 | 1 | 0 | *Nostoc* sp. CCAP 1453/31; HE974996 (98.3%) | uncultured Nostoc sp.; B9\_47; AM940880 (98.3%) |
| DGGE\_OTU 11 | 10TN47a04C | MF468225 | 0 | 1 | 3 | *Nostoc* sp. 9.4.22; AY328896 (98.8%) | uncultured cyanobacterium; B6\_63; AM940825 (98.8%) |
| DGGE\_OTU 12 | 10PI44b03C | MF468235 | 1 | 0 | 0 | *Leptolyngbya* sp. Greenland\_7; DQ431002 (93.1%) | uncultured cyanobacterium; BksYy25500; KC463305 (97.0%) |
| DGGE\_OTU 13 | 10PI44b04C | MF468237 | 8 | 0 | 2 | *Phormidium* sp. CYN64; JQ687330 (97.2%) | uncultured Antarctic cyanobacterium; Fr396; AY151763 (97.5%) |
| DGGE\_OTU 14 | 10PI44b01C | MF468236 | 1 | 0 | 0 | *Phormidium* sp. CYN64; JQ687330 (97.5%) | uncultured Antarctic cyanobacterium; Fr396; AY151763 (97.5%) |
| DGGE\_OTU 15 | 10PI44b03C | MF468228 | 2 | 0 | 0 | *Phormidesmis priestleyi* ANT.L66.1; AY493581 (99.0%) | uncultured *Phormidium* sp.; 5f-12; JF832301 (100.0%) |
| DGGE\_OTU 16 | 10PI43b04S | MF468227 | 2 | 1 | 0 | *Cyanothece aeruginosa;NIVA-CYA 258/2; Z82775(93.7%)* | uncultured bacterium; PB17018-1\_F01; JX172409 (95.4%) |

1. **Table 5**. Cyanobacterial OTUs based on 16S rRNA sequences (97 % 16S rRNA sequence similarity) in samples of Pingvinane 4 (site C4), and Tanngarden (site A) obtained by pyrosequencing.
2. The number of sequences and relative abundances were calculated after rarefying datasets to 459 sequences per sample.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **OTU** | **Accession number** | **Relative abundance, %** | | **Best SeqMatch isolate hit (ID %)** | **Best SeqMatch uncultured hit (ID %)** |
| **Pingvinane 4 (C4)** | **Tanngarden (A)** |  |  |
| OTU 1 | MF468238 | 15.98 | 55.70 | *Leptolyngbya* sp. ANT.RI8.1; AY493619 (97.4%) | uncultured Oscillatoriales cyanobacterium; H\_21; FJ490341 (99.2%) |
| OTU 2 | MF468252 | 42.85 | 22.73 | *Phormidium autumnale* CCALA 697; AM778710 (100.0%) | uncultured cyanobacterium; 89-23; JN814349 (100.0%) |
| OTU 3 | MF468259 | 23.97 | 0.00 | *Leptolyngbya compacta* GSE-PSE28-08A; HQ132933(99.2%) | uncultured cyanobacterium; LVG1348; KC936989 (98.9%) |
| OTU 4 | MF468244 | 7.12 | 13.22 | *Nostoc indistinguendum* CM1-VF10; AY577538(100.0%) | uncultured bacterium; bscm1.1.294; JX255063 (100.0%) |
| OTU 7 | MF468239 | 0.00 | 7.92 | *Leptolyngbya* cf. *foveolarum* TM2ULC129; EU852496(99.7%) | uncultured cyanobacterium; GL2-21; EF215735 (98.6%) |
| OTU 8 | MF468254 | 2.76 | 0.00 | *Phormidesmis priestleyi* ANT.LMA.2; AY493613 (98.9%) | uncultured cyanobacterium; B9\_81; AM940913 (100.0%) |
| OTU 9 | MF468245 | 3.20 | 0.00 | *Godleya alpina* LCR-CYTOL; HQ012539(100.0%) | uncultured cyanobacterium; S282; JQ776464 (100.0%) |
| OTU 13 | MF468255 | 0.15 | 0.00 | *Leptolyngbya frigida* ANT.LJA.1; AY493614 (100.0%) | cyanobacterium enrichment culture clone 4\_4\_4.3.1\_F08-T7; JQ310380 (99.7%) |
| OTU 14 | MF468240 | 2.03 | 0.00 | *Cyanothece aeruginosa* NIVA-CYA 258/2; Z82775 (99.7%) | uncultured bacterium; PB17018-1\_A08; JX172360 (95.3%) |
| OTU 15 | MF468261 | 0.36 | 0.07 | *Leptolyngbya* sp. Greenland\_6; DQ431001 (92.3%) | uncultured cyanobacterium; CW1\_P2\_3B; KC110372 (97.0%) |
| OTU 17 | MF468242 | 0.22 | 0.29 | cyanobacterium cCLB-9; HQ230230 (100.0%) | Uncultured cyanobacterium; MB5-20; HM104593 (100.0%) |
| OTU 19 | MF468251 | 1.09 | 0.00 | *Hormoscilla pringsheimii* SAG 1407-1; KJ140096 (98.1%) | uncultured bacterium; SPIT\_D12; GQ306044 (99.6%) |
| OTU 21 | MF468241 | 0.22 | 0.00 | *Cyanothece aeruginosa* NIVA-CYA 258/2; Z82775(95.6%) | uncultured bacterium; PB17018-1\_D07; JX172394 (100.0%) |
| OTU 31 | MF468243 | 0.07 | 0.07 | cyanobacterium cCLB-12; HQ230231(98.4%) | uncultured cyanobacterium; CNY\_02997; JQ402596 (98.9%) |