Unravelling microalgal-bacterial interactions in aquatic ecosystems through 16S co-occurrence networks

Author list:

B.L.D. Uthpala Pushpakumara[*1] (Orcid ID: 0000-0002-0424-3697)

Kshitij Tandon[1](Orcid ID: 0000-0003-3022-0808)

Anusuya Willis[2](Orcid ID: 0000-0003-0829-7446)

Heroen Verbruggen[*1](Orcid ID: 0000-0002-6305-4749)

[1]School of BioSciences, University of Melbourne, Victoria, 3010, Australia

[2]Australian National Algae Culture Collection, CSIRO, Tasmania 7000, Australia

*Corresponding authors: e-mail: bpushpakumar@student.unimelb.edu.au, heroen@unimelb.edu.au

Keywords: 16S rRNA gene, metabarcoding, co-occurrence networks, microalgal-bacterial interactions

Unravelling microalgal-bacterial interactions in aquatic ecosystems through 16S co-occurrence networks

B.L.D.Uthpala Pushpakumara[*1], Kshitij Tandon[1], Anusuya Willis[2], Heroen Verbruggen[1]

[1]School of BioSciences, University of Melbourne, Victoria, 3010, Australia
[2]Australian National Algae Culture Collection, CSIRO, Tasmania 7000, Australia

*Corresponding author: e-mail: bpushpakumar@student.unimelb.edu.au

Abstract

Microalgae and bacteria have a wide spectrum of associations in aquatic environments. Since their interactions can directly influence global carbon and nutrient cycling, understanding these associations help us evaluate their influence on ecosystem productivity. Algal biodiversity is large, and bacterial associations have been characterised for a small fraction of them. While experiments based on algal-bacterial co-culturing are commonly used to infer interactions, deciphering all associations present in nature through such methods is impractical and approaches based on co-occurrence network analysis can help infer associations. In this study, we used microbial co-occurrence networks built from Earth microbiome project 16S metabarcoding data to detect microalgal-bacterial associations in aquatic environments. We analysed marine and freshwater environments to understand what groups of bacteria are tightly co-occurring with different algal

groups in both aquatic environments, to see patterns of interactions, and to evaluate the overall use of co-occurrence networks to infer meaningful algal-bacterial interactions. In line with expectations from co-culturing work, our results show that the phyla Proteobacteria and Bacteroidetes are the major bacterial associates of microalgae and the co-occurring bacteria may be specific to the algal host. From the independent analysis of environments, we also show that sample origin may be an important determinant of these interactions. By unravelling previously established microalgal-bacterial links as well as identifying a range of previously unknown interactions, we show that co-occurrence network analysis is a promising hypothesis-generating framework to study microalgal-bacterial interactions that can guide future research into the functional nature of interactions.

Introduction

Microalgae and bacteria are the most widespread and dominant planktonic organisms of the aquatic systems. Algae are primary producers and form the basis of aquatic food webs and bacteria govern the biogeochemical cycles at a global scale (Falkowski et al., 2008). A wide spectrum of associations has been discovered between these two major types of organisms, with many studies showing that bacteria can profoundly impact the growth and survival of the algae

(Gonzalez and Bashan, 2000; Kim et al., 2014). More importantly, their interactions can directly influence global carbon and nutrient cycling, as well as the energy flow in aquatic ecosystems. Understanding algal-bacterial associations is thus important to comprehend aquatic ecosystem productivity and the complex web of interactions associated with it.

Many studies have clarified the impact of bacteria on algal growth. Algae can cease to grow when associated bacteria are removed (Guillard and Keller, 1984; Bolch et al., 2017), their contribution to algal growth being similar in magnitude to light and temperature (Bolch et al., 2017). The widely known array of functions provided by bacteria that promote the growth and survival of algae includes the increased bioavailability of vitamins such as vitamin B12 (Croft et al., 2005; Kazamia et al., 2012; Xie et al., 2013) and metals such as iron (Keshtacher-Liebso et al., 1995; Butler, 1998; Amin et al., 2009,2012a,b; Baggesen, 2014), quorum sensing mediation (Johnson et al., 2016; Durham et al., 2017) and growth promoting hormones (Amin et al., 2015)

With the ubiquitous nature of microalgae and bacteria in different ecosystems of earth, we can assume that their interactions could be complex and might also be species specific. Addressing such complexity is challenging but once explored can provide important knowledge on different associations between microorganisms.

Moreover, the knowledge we have so far about specific microalgal-bacterial interactions represents only a small fraction of what potentially occurs in nature. Compiling knowledge about the microbiota of a wide range of microalgae through conventional methods, including culturing is labour intensive and therefore impractical. An alternative to the culturing is provided by environmental sequencing technologies, which can be combined with network analysis to evaluate interactions between microorganisms at larger scales by simplifying a complex system of associations (Lv et al., 2019). Such networks can be used as exploratory maps to showcase microbial co-occurrences providing an opportunity to explore a myriad of environments to study microalgal and bacterial interactions (Lima-Mendez et al., 2015; Ma et al., 2020)

The objective of this study was to detect (if any) co-occurrences between microalgae and bacteria using marker gene-based co-occurrence networks. We investigated whether this approach can help identify previously characterised links between bacteria and microalgae and uncover potentially novel microalgal-bacterial interactions. In doing so, we investigated the promise of this alternative approach to study the innumerable microalgal-bacterial interactions in nature, which may be difficult or impossible to study using conventional culture based methods. We also evaluated how the habitat or environment can potentially

influence the structure of microalgal-bacterial associations to understand if it is an important determinant of microalgal-bacterial interactions.

Materials and Methods

Data Acquisition

For the co-occurrence analysis between microalgae and bacteria, 12 studies (supplementary data: Table S1) linked to the Earth Microbiome Project (EMP) were selected (Thompson et al., 2017). Since metabarcoding data can be influenced by methodological variability, we restricted our analysis to data generated with the unified EMP workflow. The data analysed in this study have amplified the same 16S rRNA gene V4 hypervariable region using 515F- 'GTGCCAGCMGCCGCGGTAA' and 806R- 'GGACTACHVGGGTWTCTAAT' primer pairs (Caporaso et al., 2011; Caporaso et al., 2012) and sequenced on Illumina Hiseq2000.

Sequencing Data Workflow

Raw demultiplexed reads were downloaded from the European Nucleotide Archive. All the projects were analysed individually employing a single bioinformatic pipeline built on Qiime2 version 2019.10 (Bolyen et al., 2019). Primer sequences attached to all reads were trimmed using cutadapt (Martin,

2011). Sequence denoising, chimera checking and dereplication was performed in DADA2 (Callahan et al., 2016) to correct sequencing errors and remove low quality bases. Reads were truncated based on a median quality score of 30. The final outputs of DADA2, an abundance table of Amplicon Sequence Variants (ASVs) and fasta sequences of the ASVs were further processed as described below.

Taxonomy was assigned against Silva v132 (Quast et al., 2013) 16S sequences trained with a Naive Bayes classifier (Bokulich et al., 2018). Chloroplast sequences were filtered using the Silva taxonomy file by identifying sequences assigned as “chloroplast”. These chloroplast sequences were then classified again using a Qiime compatible version of PhytoRef (Decelle et al., 2015) database accessed at https://github.com/ndu-UCSD/Oceanic_database/tree/master/PhytoRef. The DADA2 abundance table was filtered to create a bacteria-only abundance table (by removing mitochondrial, Archaeal and chloroplast ASVs) and a chloroplast-only abundance table (by retaining only the ASV ids assigned as chloroplast). The bacteria-only table was then collapsed at the genus level to reduce weak links in downstream network building (Hemprich-Bennett et al., 2021) and was merged with the chloroplast-only table to create the final abundance table. ASVs identified as microalgae were not collapsed since the 16S marker is highly conserved in algae and ASVs likely correspond to species or higher-level

taxa (Decelle et al., 2015). This final abundance table was filtered to remove low prevalence organisms present in less than 10% of samples to prevent them from introducing artifacts in network inference (Berry and Widder, 2014).

Correlation analysis and network construction

We used a compositional data analysis tool, FastSpar (Watts et al., 2019), which is a rapid and parallelizable implementation of the SparCC algorithm (Friedmen and Alm, 2012) to compute correlations. FastSpar quantifies the correlation between all ASVs and assesses the statistical significance (p-values) of the inferred correlations using a bootstrap procedure. The correlation and p-value matrices created by FastSpar were used to create a network of significant correlations for each study separately. We created co-occurrence networks from the 12 EMP datasets using the igraph package (Csárdi and Nepusz, 2006) in R studio version 1.4.1106. Undirected weighted networks were created using statistically ($p<0.05$) significant correlations >0.5 or higher (0.5 for freshwater and 0.6 for marine datasets). Coefficient cut-off of 0.5 was selected for freshwater datasets as a value above that resulted in fewer algal nodes in networks compared to 0.5. The idea behind the coefficient cutoff selection was to preserve as many links as possible with microalgae in resulting networks while choosing a considerably higher

coefficient cut off to report stronger links. Networks were visualized in Cytoscape version 3.8 (Shannon et al., 2003).

Network Analysis and module detection

The Network Analyzer plugin (Assenov et al., 2008) in Cytoscape was used to compute global network properties of each network to get an overview of node specific and edge-specific attributes. Networks were checked for the scale free nature by identifying the presence of highly connected nodes coexisting with nodes with fewer links (Barabási, 2009), using the node attributes. In order to identify communities (Wang et al., 2017), networks were clustered using the Cytoscape plugin clusterMaker (Morris et al., 2011) using the MCL clustering algorithm (Van Dongen, 2000) with an inflation value of 2.0. Any module that had less than 4 nodes was not taken into consideration when reporting links between bacteria and microalgae. Microalgal nodes that directly form links with bacterial nodes were recorded and summarized in heatmaps using Pheatmap v1.0.12 (Kolde, 2012) in R.

Results and Discussion

Phyla Proteobacteria and Bacteroidetes are the major associates of microalgae in aquatic environments

Analysis of the modules derived from the co-occurrence networks identified (at class level) 40 algal nodes associated with at least one of 76 bacterial nodes in the marine environments and 134 algal nodes with at least one of 621 bacterial nodes in the freshwater environments (Figure: 1.1 and 1.2). All the networks created indicated scale free nature, a characteristic reported in real world networks (Albert et al., 1999; Eisenberg and Levanon, 2003). The summary of associations inferred from our network analysis (Figure: 2) show that phyla Proteobacteria and Bacteroidetes are the most recurring associates of microalgae. These clades are reported by other studies as major bacterial groups affiliated with microalgal microbiomes (Jones et al., 2007; Goecke et al., 2013; Krohn-Molt et al., 2013; Mendes et al., 2013; Knief, 2014; Knack et al., 2015; Ramanan et al., 2016). Apart from the major groups, this study also identifies links formed between microalgae and other bacterial phyla (Figure: 2) that had previously been identified with other techniques (Foster et al., 2011; Sanz et al., 2017; Pyle et al., 2020; Ferro et al., 2020).

When narrowing in on lower taxonomic levels, we identified known bacterial associates of microalgae such as Flavobacteria (Mann et al.,2013; Frias-Lopez et al., 2002; Barbeyron et al., 2001; Nedashkovskaya et al., 2003), Rhizobiales, (Rivas et al., 2010; Carney et al., 2014; Kim et al., 2014) Cytophagales (Coles, 1982; Fulbright et al., 2018) and Rhodobacterales (Zhou et al., 2018). Previously reported associations of microalgal genera with specific bacterial groups were also recovered in the analysis including those between the cosmopolitan Prymnesiophyceae genus *Phaeocystis* with the members of Bacteroidetes group (Figure: 3) and of the diatoms (Bacillariophyta) with the genus *Flavobacterium.* Members of Bacteroidetes group are reported to be present during *Phaeocysti*s blooms (Simon et al., 1999; Brussaard et al., 2005) and also involved in *Phaeocystis* mucopolysaccharide degradation (Janse et al., 2000). *Flavobacterium* is regarded as one of the major genera associated with diatom cultures (Grossart et al., 2005; Sapp et al., 2007a,b). These results show that the network analysis was robust and co-occurrence networks can help identify microbial associations in different environments.

Novel and emerging microalgal-bacterial interaction that can guide functional studies

Our co-occurrence networks identified potential interactions that had not yet been observed or described well in the literature. We observed frequent co-occurrences of Bacillariophyta with OM190 (SILVA taxonomy), an uncultured clade of Planctomycetes. This Planctomycetes clade was also found to be forming direct links with other microalgal groups (e.g.- Pyrenomonadales and Chaetocerotales) (Figure: 4). OM190 is found in different environments such as soil and seawater and shows deep branching within the Planctomycetes group. Since this lineage is yet uncultured, information on its metabolism is scarce. A metagenome-assembled-genome for OM190 has been reported by Ludington et al (2017) showcasing a rich diversity of secondary metabolites. Members of this clade have also been reported as associates of macroalgae, such as red (Longford et al., 2007; Bondoso et al., 2013) and brown algae (Bengtsson and Ovreas, 2010; Bengtsson et al., 2010). However, with no cultured isolates present, depicting functional roles with higher confidence is not possible.

While successful associations are known between macroalgae and Planctomycetes, (Longford et al., 2007; Bengtsson et al., 2010; Lage and Bondoso, 2011) interactions with microalgae are largely unknown. Analysis of networks derived

from Tara oceans data by Vincent and Bowler (2020) shows that diatoms do not significantly co-occur with any specific bacterial nutritional groups, although diatom specific patterns are exhibited. However, a study by Morris et al (2006) showed members of the Planctomycetes group as the dominant lineages associated with diatom bloom samples. This evidence together with our observations suggest that exploring OM190-diatom interactions may help unravel unknown links between the two groups.

Among the diverse proteobacterial interactions, uncultured Deltaproteobacteria order NB1-j and the recently classified Gammaproteobacterial order Cellvibrionales (Spring et al., 2015) showed notable co-occurrences with microalgae. NB1-j was identified as one of the most frequently co-occurring Proteobacterial groups (Figure: 5). There's little information on functions of NB1-j in marine ecosystems and it is believed to be involved in hydrocarbon degradation (Coelho et al., 2016). It has also been suggested through a predictive metagenomic approach based on sponge samples originating from reef sites in West Java (Indonesia) that the order NB1-j may be involved in nitrogen metabolism (de Voogd et al., 2015). In their study, de Voogd et al (2015) found that the predictive gene count corresponding to N-cycling genes such as those encoding nitric oxide reductase (*norB)*, nitrogenase (*nifD*) and hydroxylamine reductase were elevated in

the studied samples due to order NB1-j. A study by Vigneron et al (2018) on cyanobacterial mats reports this order as a part of the mat microbiome. With the available information, it can be hypothesized that the interactions with microalgae may most likely be due to the ability of the members of NB1-j to cycle nitrogen in the environment. However, which reaction is carried out by the NB1-j associated with microalgae cannot be confirmed as predicted genes represent different reactions of N-cycle such as nitrogen fixation (*nifD*), denitrification (*norB*) and ammonium oxidation.

In a recent study, it was found that Cellvibrionales can benefit from organic carbon producing microalgae such as Mychonastes (Sorenson et al., 2021). Our analysis shows frequent co-occurrences of Cellvibrionales with a range of microalgae taxa (Prasinophyceae, Prymnesiophyceae, Bacillariophyta, Cryptophyceae, Dictyochophyceae, Pelagophyceae, Trebouxiophyceae and Embryophyceae) (Figures: 1.1 and 1.2). The Cellvibrionales bacteria discovered in this study are taxonomically identified at the family level as Halieaceae and Porticoccaceae and are considered oligotrophs. Both these families include some strains capable of photoheterotrophic growth using light harvesting pigments such as proteorhodopsin (Spring et al., 2015). As photoheterotrophs, these bacteria use

light to generate energy and use organic carbon compounds from the environment to satisfy their carbon needs.

Work by Bryson et al (2017) on resource partitioning in the coastal microbial communities show that members of this group assimilate specific organic carbon sources such as starch and glucose. This implies that the associations with microalgal groups benefit the bacteria by providing its specific organic carbon requirements to support the photoheterotrophic growth. Associations with a range of microalgae, as inferred from our network analysis, may be showcasing the ability of this bacterial group to interact with different microalgal groups to acquire these carbohydrate needs. To shed light on potential associations driven by other factors, it would be interesting to investigate if there are additional benefits to the microalgae other than provision of inorganic carbon. It is also interesting to investigate if there's competition for light by the microalga and its associated photoheterotrophic bacteria.

Consistent associations were observed between the members of Verrucomicrobia (Opitutales, Verrucomicrobiales, Chthoniobacterales, Pedosphaerales) and microalgae including diatoms, haptophytes and green algae. Though widely distributed, there's little functional information on the role of Verrucomicrobia in

the aquatic ecosystem (Bohórquez et al., 2017). Some members of this group can consume algal extracellular polymeric substances and carry out the hydrolysis of various polysaccharides (Martinez-Garcia et al., 2012; Cardman et al., 2014; Landa et al., 2014; Orsi et al., 2016), but work focusing on the underlying benefits of these interactions and specific associations between members of the Verrucomicrobia and particular algal groups is lacking. Among the genus-specific associations revealed in our network analysis is that of the Verrucomicrobial genus *Lentimonas* and microalgal genera *Pyramimonas* (class_Prasinophyceae), *Phaeocystis*, *Tisochrysis*, *Haptolina*, and *Chrysochromulina* (class_Prymnesiophyceae). A recent study by Sichert et al (2020) showed hundreds of *Lentimonas* enzymes able to digest brown algal fucoidan. Although fucose-containing sulphated polysaccharides (FCSP) were regarded as a macroalgal polysaccharide, Vidal-Melgosa et al (2021) shows that diatoms can produce them too. Observations from our work suggest that there may be other microalgae capable of producing FCSP or on the other hand, members of *Lentimonas* may have a broader palate than just FCSP.

Sample origin is an important determinant of algal-bacterial interactions

From the independent analysis of projects, we found that, except for a few, there was no recurrence of bacterial genera across environments. Although similar bacterial groups were identified in different projects at a higher taxonomic level and they formed links with similar groups of microalgae (eg: Flavobacteriales with diatoms in ERP020022, ERP016541, ERP016287) their lower taxonomic affiliations were different. Moreover, most bacterial nodes could not be identified at a lower taxonomic level (family and genus) or were identified as uncultured bacteria based on sequence similarity. This indicates species specificity of microalgal-bacterial associations and provides further evidence that the microalgae form an environment with strong potential for bacterial species discovery (Goecke et al., 2013). These results may also be suggesting that the sample origin may also have an impact on the algal-bacterial associations. Interestingly, a recent study (Martin et al., 2021) has provided evidence for biogeographic differentiation of algal microbiomes, showing ecological boundaries driven by differences in environmental conditions altering the spatial scaling of the algal microbiomes.

To understand if there is any factor driving general patterns of interactions, some insights may be gleaned from known functions of the bacteria involved. We found

that the general patterns of interactions are seen at a functional level. That is microalgae tend to co-occur with bacterial groups that can carry out specific metabolic functions (E.g.- co-occurrences with algal polysaccharide degraders, Vitamin B12 synthesizers etc) and these groups of bacteria may be taxonomically different in different environments. For example, most of the microalgal nodes co-occur with bacteria that are capable of polysaccharide degradation (e.g.- cooccurrences with members of Bacteroidetes (Janse et al., 2000) and Verrucomicrobia (Martinez-Garcia et al., 2012)). Another example from our analysis is the co-occurrences of some microalgal groups with bacteria regarded as vitamin B12 synthesizers (e.g.- co-occurrences with Rhizobiales (Newton et al., 2010), Rhodobacterales (Sañudo-Wilhelmy et al., 2014) and SAR116 (Durham et al., 2015)). These results imply that the microalgal-bacterial communities may be functionally driven and constitute environmental specific bacteria and microalgae as its components.

Conclusion

Single marker gene-based co-occurrence network analysis is a convenient addition to the toolkit for deriving interactions between microalgae and bacteria. It stands as a hypothesis-generating framework on microalgal-bacterial associations at a global scale which would be impractical to be studied using experimental approaches.

Our study identified a range of interactions between microalgae and bacteria and shows that members of the Phyla Proteobacteria and Bacteroidetes are the most recurring bacterial associates of microalgae. This study also sheds light on novel and uncharacterized microalgal-bacterial interactions that can help constrain the work of experimentalists by guiding more focused research. We also show that "sample origin" may be an important determinant of microalgal-bacterial interactions, a microalgal-bacterial community constitutes specific bacterial associates and the general patterns of interactions in the community can be seen at a functional level.

Acknowledgments

We acknowledge the funding from the Melbourne Research Scholarship and the ResearchPlus Postgraduate Top-Up Scholarship Grants Program and National Research Collections Australia, CSIRO.

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Author contribution

UP, HV and AW formulated the project. UP analyzed the data and wrote the manuscript with inputs from all the authors. HV, AW and KT contributed ideas and helped with analysis. All authors read and approved the final version of the manuscript.

Conflict of interest

On behalf of all authors, the corresponding author states that there is no conflict of interest

Figure legends

Figure 1.1: Summarised interactions in marine environments

Heatmap of co-occurring microalgae (columns) and bacteria (rows) in marine environments. "Taxonomy" represents the taxonomic affiliations of microalgal nodes at class level. "Taxonomy2" represents the taxonomic affiliations of bacteria (p_, c_, o_, f_ and g_ represent phylum, class, order, family and genus, respectively). "Project" represents the ebi_accessions of EMP projects and indicate which project the microalgal and bacterial nodes were recovered from.

Figure 1.2: Summarised interactions in freshwater environments

Heatmap of co-occurring microalgae (columns) and bacteria (rows) in freshwater environments. "Taxonomy" represents the taxonomic affiliations of microalgal nodes at class level. "Taxonomy2" represents the taxonomic affiliations of bacteria (p_, c_, o_, f_ and g_ represent phylum, class, order, family and genus, respectively). "Project" represents the ebi_accessions of EMP projects and indicate which project the microalgal and bacterial nodes were recovered from.

Figure 2: Major bacterial Phyla associated with microalgae in [A] freshwater and [B] marine environments

Bars represent the number of bacterial nodes affiliated with each phylum. The total number of bacterial nodes identified to be co-occurring with microalgae in marine environments were 76 and freshwater environments were 621.

Figure 3: Microalgal-bacterial community showcasing interactions formed by the genus *Phaeocystis*.

The first neighbours of the microalga *(Phaeocytis)* representing the directly interacting nodes are shown. Edge width is mapped to correlation coefficient (edge weight). Members of the Bacteroidetes marked with *. Nodes labeled at the order level (If unclassified at the order level, higher taxonomic affiliations are provided)

Figure 4: Planctomycetes class OM190 interacting with microalgal taxa in a marine (A) and freshwater (B) environment.

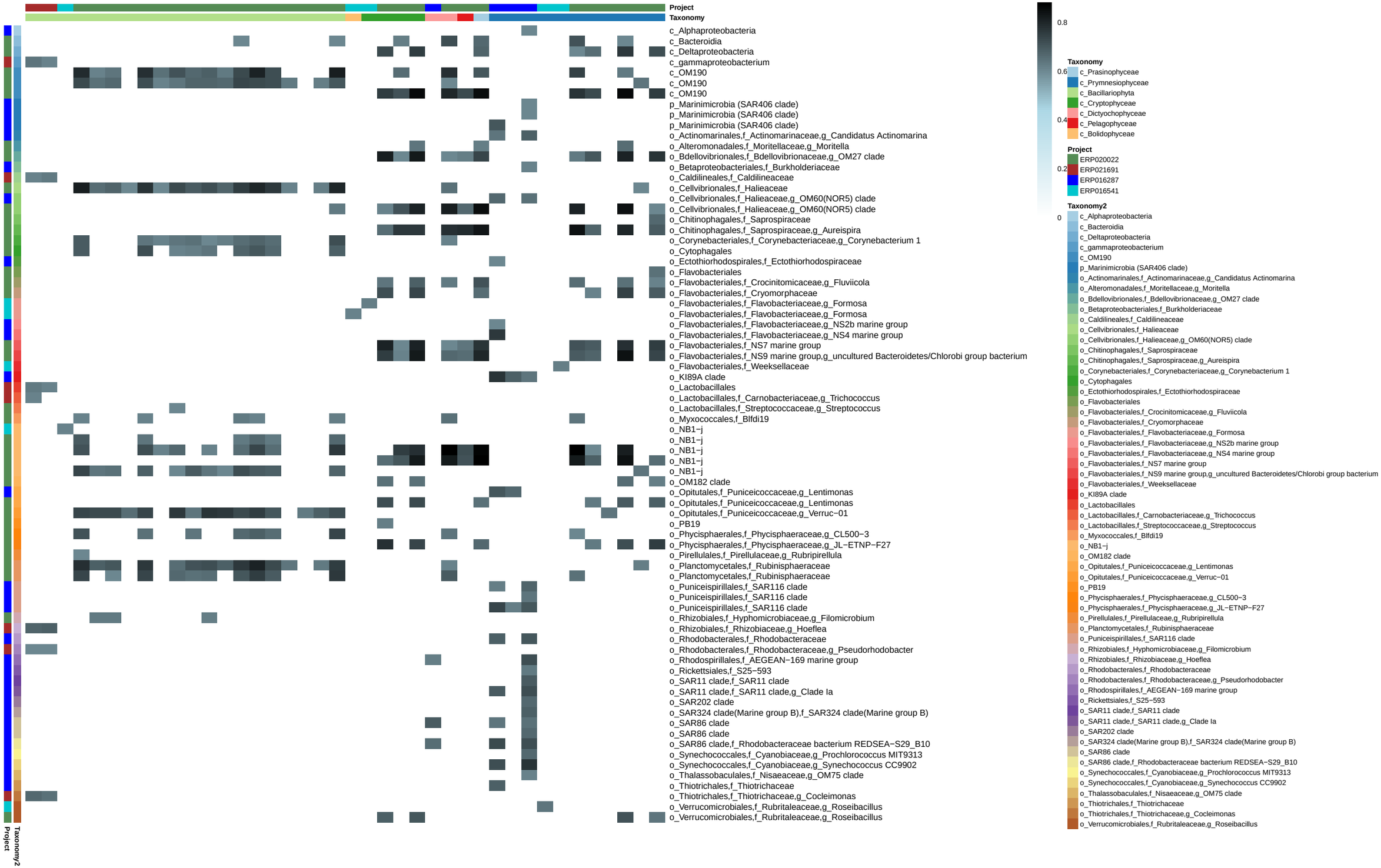
Networks (A, B) created from a microalgal-bacterial module by selecting the first neighbours of the OM190 to showcase the complex interactions with the neighbouring microalgal taxa. The edge width is continuously mapped to edge weight. Marine and Freshwater environments represent EMP project ERP020022 and ERP016492, respectively. Nodes labeled at order level (If unclassified at the order level, higher taxonomic affiliations are provided).

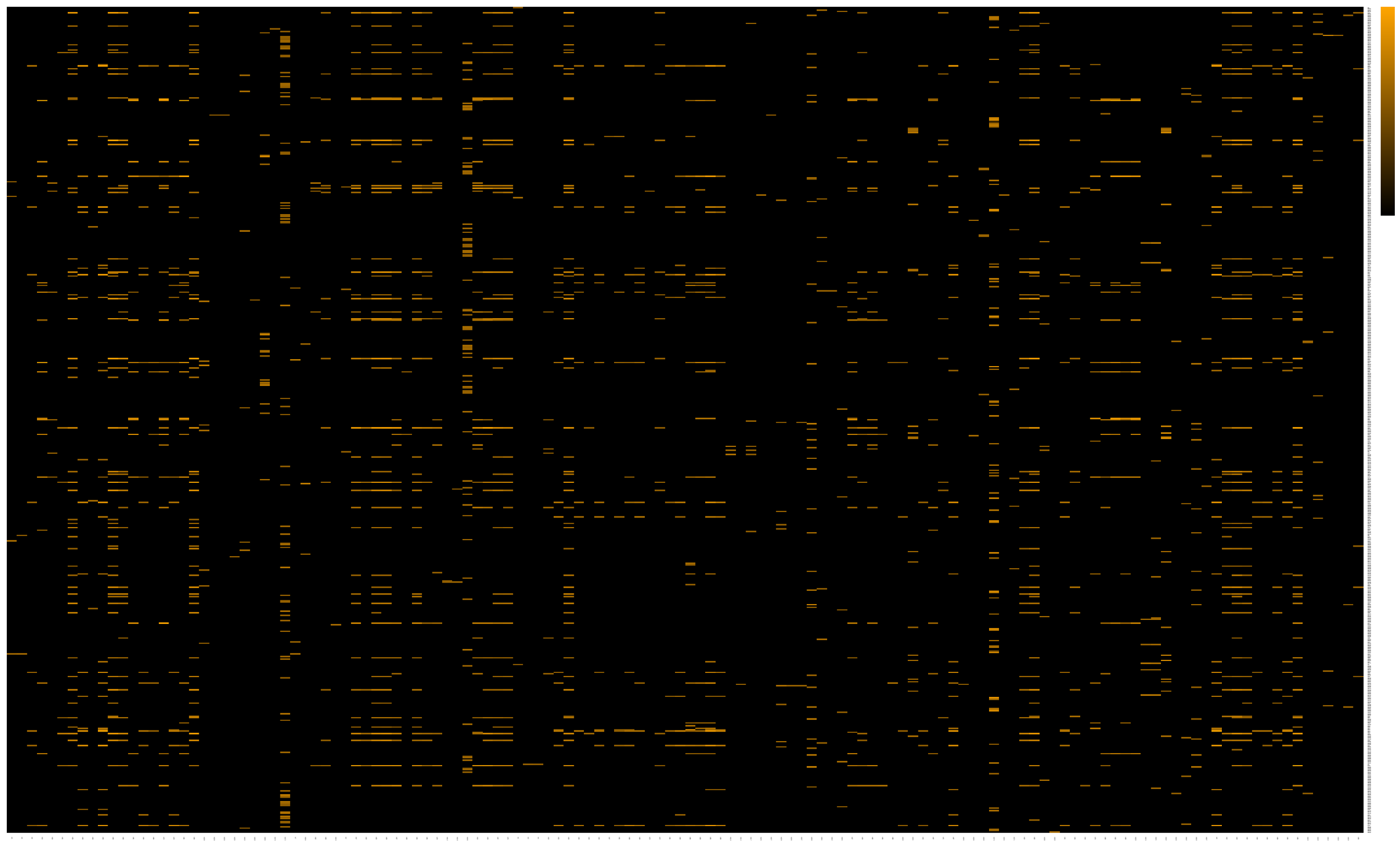
Figure 5: Interactions of the Deltaproteobacterial order NB1-j with microalgae in marine environments.

Microalgal taxa co-occurring with Deltaproteobacterial order NB1-j in two marine environments (A-Project ERP020022 and B-Project ERP016541) are shown. **A)** is created by selecting the first neighbours of NB1-j and **B)** represents a microalgal-bacterial module where NB1-j forms a direct link only with Bacillariophyta. Both the networks of NB1-j comprise similar microalgal taxa; Bacillariophyta, Pyrenomonadales (c_Cryptophyceae), Prymnesiales (c_Prymnesiophyceae) and Isochrysidales(c_Prymnesiophyceae) showing similar community structure. Nodes labeled at the order level (If unclassified at the order level, higher taxonomic affiliations are provided). The edge width is continuously mapped to edge weight.

Supplementary data:

Table S1: Information on selected EMP studies


Project
Taxonomy
c_Alphaproteobacteria
c_Bacteroidia
c_Deltaproteobacteria
c_gammaproteobacterium
c_OM190
c_OM190
c_OM190
p_Marinimicrobia (SAR406 clade)
p_Marinimicrobia (SAR406 clade)
p_Marinimicrobia (SAR406 clade)
o_Actinomarinales,f_Actinomarinaceae,g_Candidatus Actinomarina
o_Alteromonadales,f_Moritellaceae,g_Moritella
o_Bdellovibrionales,f_Bdellovibrionaceae,g_OM27 clade
o_Betaproteobacteriales,f_Burkholderiaceae
o_Caldilineales,f_Caldilineaceae
o_Cellvibrionales,f_Halieaceae
o_Cellvibrionales,f_Halieaceae,g_OM60(NOR5) clade
o_Cellvibrionales,f_Halieaceae,g_OM60(NOR5) clade
o_Chitinophagales,f_Saprospiraceae
o_Chitinophagales,f_Saprospiraceae,g_Aureispira
o_Corynebacteriales,f_Corynebacteriaceae,g_Corynebacterium 1
o_Cytophagales
o_Ectothiorhodospirales,f_Ectothiorhodospiraceae
o_Flavobacteriales
o_Flavobacteriales,f_Crocinitomicaceae,g_Fluviicola
o_Flavobacteriales,f_Cryomorphaceae
o_Flavobacteriales,f_Flavobacteriaceae,g_Formosa
o_Flavobacteriales,f_Flavobacteriaceae,g_Formosa
o_Flavobacteriales,f_Flavobacteriaceae,g_NS2b marine group
o_Flavobacteriales,f_Flavobacteriaceae,g_NS4 marine group
o_Flavobacteriales,f_NS7 marine group
o_Flavobacteriales,f_NS9 marine group,g_uncultured Bacteroidetes/Chlorobi group bacterium
o_Flavobacteriales,f_Weeksellaceae
o_KI89A clade
o_Lactobacillales
o_Lactobacillales,f_Carnobacteriaceae,g_Trichococcus
o_Lactobacillales,f_Streptococcaceae,g_Streptococcus
o_Myxococcales,f_Blfdi19
o_NB1−j
o_NB1−j
o_NB1−j
o_NB1−j
o_NB1−j
o_OM182 clade
o_Opitutales,f_Puniceicoccaceae,g_Lentimonas
o_Opitutales,f_Puniceicoccaceae,g_Lentimonas
o_Opitutales,f_Puniceicoccaceae,g_Verruc−01
o_PB19
o_Phycisphaerales,f_Phycisphaeraceae,g_CL500−3
o_Phycisphaerales,f_Phycisphaeraceae,g_JL−ETNP−F27
o_Pirellulales,f_Pirellulaceae,g_Rubripirellula
o_Planctomycetales,f_Rubinisphaeraceae
o_Planctomycetales,f_Rubinisphaeraceae
o_Puniceispirillales,f_SAR116 clade
o_Puniceispirillales,f_SAR116 clade
o_Puniceispirillales,f_SAR116 clade
o_Rhizobiales,f_Hyphomicrobiaceae,g_Filomicrobium
o_Rhizobiales,f_Rhizobiaceae,g_Hoeflea
o_Rhodobacterales,f_Rhodobacteraceae
o_Rhodobacterales,f_Rhodobacteraceae,g_Pseudorhodobacter
o_Rhodospirillales,f_AEGEAN−169 marine group
o_Rickettsiales,f_S25−593
o_SAR11 clade,f_SAR11 clade
o_SAR11 clade,f_SAR11 clade,g_Clade Ia
o_SAR202 clade
o_SAR324 clade(Marine group B),f_SAR324 clade(Marine group B)
o_SAR86 clade
o_SAR86 clade
o_SAR86 clade,f_Rhodobacteraceae bacterium REDSEA−S29_B10
o_Synechococcales,f_Cyanobiaceae,g_Prochlorococcus MIT9313
o_Synechococcales,f_Cyanobiaceae,g_Synechococcus CC9902
o_Thalassobaculales,f_Nisaeaceae,g_OM75 clade
o_Thiotrichales,f_Thiotrichaceae
o_Thiotrichales,f_Thiotrichaceae,g_Cocleimonas
o_Verrucomicrobiales,f_Rubritaleaceae,g_Roseibacillus
o_Verrucomicrobiales,f_Rubritaleaceae,g_Roseibacillus
Project
Taxonomy2
0.8
0.6
0.4
0.2
0
Taxonomy
c_Prasinophyceae
c_Prymnesiophyceae
c_Bacillariophyta
c_Cryptophyceae
c_Dictyochophyceae
c_Pelagophyceae
c_Bolidophyceae
Project
ERP020022
ERP021691
ERP016287
ERP016541
Taxonomy2
c_Alphaproteobacteria
c_Bacteroidia
c_Deltaproteobacteria
c_gammaproteobacterium
c_OM190
p_Marinimicrobia (SAR406 clade)
o_Actinomarinales,f_Actinomarinaceae,g_Candidatus Actinomarina
o_Alteromonadales,f_Moritellaceae,g_Moritella
o_Bdellovibrionales,f_Bdellovibrionaceae,g_OM27 clade
o_Betaproteobacteriales,f_Burkholderiaceae
o_Caldilineales,f_Caldilineaceae
o_Cellvibrionales,f_Halieaceae
o_Cellvibrionales,f_Halieaceae,g_OM60(NOR5) clade
o_Chitinophagales,f_Saprospiraceae
o_Chitinophagales,f_Saprospiraceae,g_Aureispira
o_Corynebacteriales,f_Corynebacteriaceae,g_Corynebacterium 1
o_Cytophagales
o_Ectothiorhodospirales,f_Ectothiorhodospiraceae
o_Flavobacteriales
o_Flavobacteriales,f_Crocinitomicaceae,g_Fluviicola
o_Flavobacteriales,f_Cryomorphaceae
o_Flavobacteriales,f_Flavobacteriaceae,g_Formosa
o_Flavobacteriales,f_Flavobacteriaceae,g_NS2b marine group
o_Flavobacteriales,f_Flavobacteriaceae,g_NS4 marine group
o_Flavobacteriales,f_NS7 marine group
o_Flavobacteriales,f_NS9 marine group,g_uncultured Bacteroidetes/Chlorobi group bacterium
o_Flavobacteriales,f_Weeksellaceae
o_KI89A clade
o_Lactobacillales
o_Lactobacillales,f_Carnobacteriaceae,g_Trichococcus
o_Lactobacillales,f_Streptococcaceae,g_Streptococcus
o_Myxococcales,f_Blfdi19
o_NB1−j
o_OM182 clade
o_Opitutales,f_Puniceicoccaceae,g_Lentimonas
o_Opitutales,f_Puniceicoccaceae,g_Verruc−01
o_PB19
o_Phycisphaerales,f_Phycisphaeraceae,g_CL500−3
o_Phycisphaerales,f_Phycisphaeraceae,g_JL−ETNP−F27
o_Pirellulales,f_Pirellulaceae,g_Rubripirellula
o_Planctomycetales,f_Rubinisphaeraceae
o_Puniceispirillales,f_SAR116 clade
o_Rhizobiales,f_Hyphomicrobiaceae,g_Filomicrobium
o_Rhizobiales,f_Rhizobiaceae,g_Hoeflea
o_Rhodobacterales,f_Rhodobacteraceae
o_Rhodobacterales,f_Rhodobacteraceae,g_Pseudorhodobacter
o_Rhodospirillales,f_AEGEAN−169 marine group
o_Rickettsiales,f_S25−593
o_SAR11 clade,f_SAR11 clade
o_SAR11 clade,f_SAR11 clade,g_Clade Ia
o_SAR202 clade
o_SAR324 clade(Marine group B),f_SAR324 clade(Marine group B)
o_SAR86 clade
o_SAR86 clade,f_Rhodobacteraceae bacterium REDSEA−S29_B10
o_Synechococcales,f_Cyanobiaceae,g_Prochlorococcus MIT9313
o_Synechococcales,f_Cyanobiaceae,g_Synechococcus CC9902
o_Thalassobaculales,f_Nisaeaceae,g_OM75 clade
o_Thiotrichales,f_Thiotrichaceae
o_Thiotrichales,f_Thiotrichaceae,g_Cocleimonas
o_Verrucomicrobiales,f_Rubritaleaceae,g_Roseibacillus



Algal_log	Taxonomy	Project (ebi_accession)	Algal_log	Taxonomy	Project (ebi_accession)
A5	c_Bacillariophyta	ERP016468	A164	c_Charophyceae	ERP016880
A6	c_Bacillariophyta	ERP016468	A52	c_Chlorodendrophyceae	ERP016492
A8	c_Bacillariophyta	ERP016492	A63	c_Chlorophyceae	ERP016492
A14	c_Bacillariophyta	ERP016492	A116	c_Chlorophyceae	ERP020508
A18	c_Bacillariophyta	ERP016492	A2	c_Chrysophyceae	ERP016854
A31	c_Bacillariophyta	ERP016492	A17	c_Chrysophyceae	ERP016492
A35	c_Bacillariophyta	ERP016492	A24	c_Chrysophyceae	ERP016492
A48	c_Bacillariophyta	ERP016492	A25	c_Chrysophyceae	ERP016492
A49	c_Bacillariophyta	ERP016492	A29	c_Chrysophyceae	ERP016492
A50	c_Bacillariophyta	ERP016492	A37	c_Chrysophyceae	ERP016492
A59	c_Bacillariophyta	ERP016492	A38	c_Chrysophyceae	ERP016492
A60	c_Bacillariophyta	ERP016492	A54	c_Chrysophyceae	ERP016492
A61	c_Bacillariophyta	ERP016492	A55	c_Chrysophyceae	ERP016492
A64	c_Bacillariophyta	ERP016492	A79	c_Chrysophyceae	ERP016492
A66	c_Bacillariophyta	ERP016492	A112	c_Chrysophyceae	ERP020508
A73	c_Bacillariophyta	ERP016492	A118	c_Chrysophyceae	ERP020508
A78	c_Bacillariophyta	ERP016492	A146	c_Chrysophyceae	ERP020021
A91	c_Bacillariophyta	ERP016492	A13	c_Chrysophyceae-Synurophyceae	ERP016492
A94	c_Bacillariophyta	ERP016492	A33	c_Chrysophyceae-Synurophyceae	ERP016492
A109	c_Bacillariophyta	ERP020508	A57	c_Chrysophyceae-Synurophyceae	ERP016492
A128	c_Bacillariophyta	ERP016591	A75	c_Chrysophyceae-Synurophyceae	ERP016492
A130	c_Bacillariophyta	ERP016591	A1	c_Cryptophyceae	ERP016854
A135	c_Bacillariophyta	ERP016591	A3	c_Cryptophyceae	ERP016854
A143	c_Bacillariophyta	ERP020021	A4	c_Cryptophyceae	ERP016854
A159	c_Bacillariophyta	ERP022245	A10	c_Cryptophyceae	ERP016492
A166	c_Bacillariophyta	ERP016880	A15	c_Cryptophyceae	ERP016492
A170	c_Bacillariophyta	ERP016880	A20	c_Cryptophyceae	ERP016492
A172	c_Bacillariophyta	ERP016880	A26	c_Cryptophyceae	ERP016492
A7	c_Bacillariophyta	ERP016468	A30	c_Cryptophyceae	ERP016492
			A34	c_Cryptophyceae	ERP016492

A47	c_Cryptophyceae	ERP016492	A171	c_Euglenozoa	ERP016880
A51	c_Cryptophyceae	ERP016492	A22	c_Eustigmatophyceae	ERP016492
A68	c_Cryptophyceae	ERP016492	A62	c_Eustigmatophyceae	ERP016492
A69	c_Cryptophyceae	ERP016492	A108	c_Eustigmatophyceae	ERP020508
A70	c_Cryptophyceae	ERP016492	A169	c_Eustigmatophyceae	ERP016880
A72	c_Cryptophyceae	ERP016492	A41	c_Pavlovophyceae	ERP016492
A81	c_Cryptophyceae	ERP016492	A45	c_Phaeophyceae	ERP016492
A83	c_Cryptophyceae	ERP016492	A43	c_Prymnesiophyceae	ERP016492
A86	c_Cryptophyceae	ERP016492	A76	c_Prymnesiophyceae	ERP016492
A90	c_Cryptophyceae	ERP016492	A89	c_Prymnesiophyceae	ERP016492
A95	c_Cryptophyceae	ERP016492	A92	c_Prymnesiophyceae	ERP016492
A98	c_Cryptophyceae	ERP016492	A99	c_Prymnesiophyceae	ERP016492
A110	c_Cryptophyceae	ERP020508	A103	c_Prymnesiophyceae	ERP016492
A114	c_Cryptophyceae	ERP020508	A115	c_Prymnesiophyceae	ERP020508
A117	c_Cryptophyceae	ERP020508	A121	c_Prymnesiophyceae	ERP020508
A126	c_Cryptophyceae	ERP016591	A132	c_Prymnesiophyceae	ERP016591
A127	c_Cryptophyceae	ERP016591	A133	c_Prymnesiophyceae	ERP016591
A129	c_Cryptophyceae	ERP016591	A142	c_Prymnesiophyceae	ERP020021
A136	c_Cryptophyceae	ERP016591	A163	c_Prymnesiophyceae	ERP022245
A137	c_Cryptophyceae	ERP016591	A167	c_Prymnesiophyceae	ERP016880
A158	c_Cryptophyceae	ERP022245	A9	c_Trebouxiophyceae	ERP016492
A161	c_Cryptophyceae	ERP022245	A12	c_Trebouxiophyceae	ERP016492
A162	c_Cryptophyceae	ERP022245	A23	c_Trebouxiophyceae	ERP016492
A165	c_Cryptophyceae	ERP016880	A32	c_Trebouxiophyceae	ERP016492
A27	c_Dictyochophyceae	ERP016492	A40	c_Trebouxiophyceae	ERP016492
A39	c_Dictyochophyceae	ERP016492	A46	c_Trebouxiophyceae	ERP016492
A82	c_Dictyochophyceae	ERP016492	A58	c_Trebouxiophyceae	ERP016492
A84	c_Dictyochophyceae	ERP016492	A65	c_Trebouxiophyceae	ERP016492
A88	c_Dictyochophyceae	ERP016492	A85	c_Trebouxiophyceae	ERP016492
A100	c_Dictyochophyceae	ERP016492	A123	c_Trebouxiophyceae	ERP016591
A131	c_Dictyochophyceae	ERP016591	A149	c_Trebouxiophyceae	ERP020021
A44	c_Embryophyceae	ERP016492	A153	c_Trebouxiophyceae	ERP020021
A67	c_Embryophyceae	ERP016492	A156	c_Trebouxiophyceae	ERP020021
A71	c_Embryophyceae	ERP016492	A160	c_Trebouxiophyceae	ERP022245
A97	c_Embryophyceae	ERP016492	A56	c_Zygnemophyceae	ERP016492
A104	c_Embryophyceae	ERP020508			
A106	c_Embryophyceae	ERP020508			
A168	c_Embryophyceae	ERP016880			
A173	c_Embryophyceae	ERP016880			
A134	c_Euglenozoa	ERP016591			

Bacteria_log	Taxonomy2	Project
B1	c_Acidimicrobiia	ERP016854
B2	o_Rhodospirillales,f_Magnetospirillaceae,g_Telmatospirillum	ERP016854
B3	o_Betaproteobacteriales,f_Ferrovaceae,g_Ferrovum	ERP016854
B4	o_Frankiales,f_Sporichthyaceae,g_hgcI clade	ERP016854
B5	o_Chitinophagales,f_Chitinophagaceae,g_Parasediminibacterium	ERP016854
B6	o_Betaproteobacteriales,f_Burkholderiaceae,g_Limnohabitans	ERP016854
B7	o_Synechococcales,f_Cyanobiaceae,g_Cyanobium PCC-6307	ERP016854
B8	o_Microtrichales,f_Ilumatobacteraceae,g_Ilumatobacter	ERP016468
B9	o_Chitinophagales,f_Chitinophagaceae,g_Lacibacter	ERP016468
B10	o_Cytophagales,f_Amoebophilaceae,g_Candidatus Amoebophilus	ERP016468
B11	o_Rhizobiales,f_Rhizobiaceae	ERP016468
B12	o_Rhodobacterales,f_Rhodobacteraceae	ERP016468
B13	o_Myxococcales,f_Archangiaceae,g_Anaeromyxobacter	ERP016468
B14	o_Betaproteobacteriales,f_Burkholderiaceae	ERP016468
B15	o_Betaproteobacteriales,f_Chitinimonadaceae,g_Chitinimonas	ERP016468
B17	o_Holophagales,f_Holophagaceae	ERP016492
B18	p_Acidobacteria,c_Subgroup 6	ERP016492
B19	c_Acidimicrobiia,o_IMCC26256	ERP016492
B20	o_Microtrichales,f_Iamiaceae,g_Iamia	ERP016492
B21	o_Microtrichales,f_Ilumatobacteraceae,g_CL500-29 marine group	ERP016492
B22	o_Microtrichales,f_Microtrichaceae,g_IMCC26207	ERP016492
B23	o_Microtrichales	ERP016492
B24	o_Corynebacteriales,f_Mycobacteriaceae,g_Mycobacterium	ERP016492
B25	o_Frankiales,f_Sporichthyaceae	ERP016492
B26	o_Frankiales,f_Sporichthyaceae,g_Candidatus Planktophila	ERP016492
B27	o_Frankiales,f_Sporichthyaceae,g_hgcI clade	ERP016492
B28	o_Micrococcales,f_Microbacteriaceae,g_Candidatus Limnoluna	ERP016492
B29	o_Micrococcales,f_Microbacteriaceae,g_MWH-Ta3	ERP016492
B30	c_Actinobacteria,o_PeM15	ERP016492
B31	p_Actinobacteria,c_MB-A2-108	ERP016492
B32	o_Gaiellales	ERP016492
B33	o_Solirubrobacterales,f_Solirubrobacteraceae	ERP016492
B35	o_Armatimonadales,f_Armatimonadaceae,g_Armatimonas	ERP016492
B36	o_Bacteroidales	ERP016492
B37	o_Chitinophagales	ERP016492
B38	o_Chitinophagales,f_Chitinophagaceae,g_Dinghuibacter	ERP016492
B39	o_Chitinophagales,f_Chitinophagaceae,g_Ferruginibacter	ERP016492
B40	o_Chitinophagales,f_Chitinophagaceae,g_Sediminibacterium	ERP016492
B41	o_Chitinophagales,f_Saprospiraceae,g_Aureispira	ERP016492
B42	o_Chitinophagales,f_Saprospiraceae,g_Candidatus Aquirestis	ERP016492
B43	o_Chitinophagales,f_Saprospiraceae	ERP016492

B44	o_Chitinophagales	ERP016492
B45	o_Chitinophagales	ERP016492
B46	o_Chitinophagales	ERP016492
B47	o_Cytophagales,f_Cyclobacteriaceae,g_Algoriphagus	ERP016492
B48	o_Cytophagales,f_Microscillaceae	ERP016492
B49	o_Cytophagales,f_Microscillaceae,g_OLB12	ERP016492
B50	o_Cytophagales,f_Spirosomaceae,g_Pseudarcicella	ERP016492
B51	o_Flavobacteriales,f_Crocinitomicaceae	ERP016492
B52	o_Flavobacteriales,f_Crocinitomicaceae,g_Fluviicola	ERP016492
B53	o_Flavobacteriales,f_Cryomorphaceae	ERP016492
B54	o_Flavobacteriales,f_Flavobacteriaceae,g_Flavobacterium	ERP016492
B55	o_Flavobacteriales,f_NS9 marine group	ERP016492
B56	o_Sphingobacteriales,f_env.OPS 17	ERP016492
B57	o_Sphingobacteriales,f_env.OPS 17	ERP016492
B58	o_Sphingobacteriales,f_KD3-93	ERP016492
B59	o_Sphingobacteriales,f_LiUU-11-161	ERP016492
B60	o_Sphingobacteriales,f_LiUU-11-161	ERP016492
B61	o_Sphingobacteriales,f_NS11-12 marine group	ERP016492
B62	o_Sphingobacteriales,f_NS11-12 marine group	ERP016492
B63	o_Sphingobacteriales,f_NS11-12 marine group	ERP016492
B64	o_Sphingobacteriales,f_NS11-12 marine group	ERP016492
B65	o_Sphingobacteriales,f_NS11-12 marine group	ERP016492
B66	o_Sphingobacteriales,f_Sphingobacteriaceae	ERP016492
B67	o_Sphingobacteriales,f_Sphingobacteriaceae,g_Pedobacter	ERP016492
B68	c_Ignavibacteria,o_OPB56	ERP016492
B69	c_Ignavibacteria,o_OPB56	ERP016492
B71	o_Anaerolineales,f_Anaerolineaceae	ERP016492
B72	o_Caldilineales,f_Caldilineaceae	ERP016492
B73	o_Chloroflexales,f_Roseiflexaceae	ERP016492
B74	p_Chloroflexi,c_KD4-96	ERP016492
B75	p_Chloroflexi,c_SL56 marine group	ERP016492
B76	o_Leptolyngbyales,f_Leptolyngbyaceae	ERP016492
B77	o_Pseudanabaenales,f_Pseudanabaenaceae,g_Pseudanabaena PCC-7429	ERP016492
B78	o_Synechococcales,f_Cyanobiaceae,g_Cyanobium PCC-6307	ERP016492
B79	o_Gemmatimonadales,f_Gemmatimonadaceae,g_Gemmatimonas	ERP016492
B80	o_Gemmatimonadales,f_Gemmatimonadaceae	ERP016492
B81	c_Kiritimatiellae,o_WCHB1-41	ERP016492
B82	o_Saccharimonadales candidate division WS5 bacterium	ERP016492
B83	c_OM190	ERP016492
B84	o_Phycisphaerales,f_Phycisphaeraceae,g_CL500-3	ERP016492
B85	o_Gemmatales,f_Gemmataceae,g_Gemmata	ERP016492

B86	o_Isosphaerales,f_Isosphaeraceae	ERP016492
B87	o_Pirellulales,f_Pirellulaceae,g_Pirellula	ERP016492
B88	o_Planctomycetales	ERP016492
B90	o_Acetobacterales,f_Acetobacteraceae	ERP016492
B91	o_Acetobacterales,f_Acetobacterales Incertae Sedis	ERP016492
B92	o_Caulobacterales,f_Caulobacteraceae	ERP016492
B93	o_Caulobacterales,f_Hyphomonadaceae,g_SWB02	ERP016492
B94	o_Paracaedibacterales,f_Paracaedibacteraceae	ERP016492
B95	o_Rhizobiales,f_Beijerinckiaceae,g_Methylorosula	ERP016492
B96	o_Rhodobacterales,f_Rhodobacteraceae,g_Rhodobacter	ERP016492
B97	o_Rhodospirillales	ERP016492
B98	o_Rickettsiales,f_Rickettsiaceae,g_Candidatus Arcanobacter	ERP016492
B99	o_Rickettsiales,f_Rickettsiaceae,g_Candidatus Megaira	ERP016492
B100	o_SAR11 clade,f_Clade III	ERP016492
B101	o_Sneathiellales,f_Sneathiellaceae,g_Taonella	ERP016492
B102	o_Sphingomonadales,f_Sphingomonadaceae,g_Sphingorhabdus	ERP016492
B103	o_Sphingomonadales,f_Sphingomonadaceae	ERP016492
B104	o_Bdellovibrionales,f_Bacteriovoracaceae,g_Peredibacter	ERP016492
B105	o_Desulfarculales,f_Desulfarculaceae	ERP016492
B106	o_Myxococcales,f_Blfdi19	ERP016492
B107	o_Myxococcales,f_mle1-27	ERP016492
B108	o_Oligoflexales,f_Oligoflexaceae	ERP016492
B109	o_SAR324 clade(Marine group B)	ERP016492
B110	c_Gammaproteobacteria	ERP016492
B111	o_Betaproteobacteriales,f_Burkholderiaceae	ERP016492
B112	o_Betaproteobacteriales,f_Burkholderiaceae,g_GKS98 freshwater group	ERP016492
B113	o_Betaproteobacteriales,f_Burkholderiaceae,g_Limnohabitans	ERP016492
B114	o_Betaproteobacteriales,f_Burkholderiaceae,g_Polaromonas	ERP016492
B115	o_Betaproteobacteriales,f_Burkholderiaceae,g_Polynucleobacter	ERP016492
B116	o_Betaproteobacteriales,f_Burkholderiaceae,g_Rhodoferax	ERP016492
B117	o_Betaproteobacteriales,f_Nitrosomonadaceae,g_966-1	ERP016492
B118	o_Betaproteobacteriales,f_Nitrosomonadaceae,g_Nitrosomonas	ERP016492
B119	o_Betaproteobacteriales,f_TRA3-20	ERP016492
B120	c_Gammaproteobacteria,o_CCM19a	ERP016492
B121	o_Cellvibrionales,f_Halieaceae,g_OM60(NOR5) clade	ERP016492
B122	o_Gammaproteobacteria Incertae Sedis	ERP016492
B123	c_Gammaproteobacteria,o_JG36-TzT-191	ERP016492
B124	o_Legionellales,f_Legionellaceae,g_Legionella	ERP016492
B125	o_Oceanospirillales,f_Pseudohongiellaceae,g_Blyi10	ERP016492
B126	o_Oceanospirillales,f_Pseudohongiellaceae,g_Pseudohongiella	ERP016492
B127	c_Verrucomicrobiae	ERP016492

B128	o_Arctic97B-4 marine group,f_marine metagenome,g_marine metagenome	ERP016492
B129	o_Chthoniobacterales,f_Chthoniobacteraceae,g_LD29	ERP016492
B130	o_Chthoniobacterales,f_Terrimicrobiaceae,g_Terrimicrobium	ERP016492
B131	o_Methylacidiphilales,f_Methylacidiphilaceae	ERP016492
B132	o_Opitutales,f_Opitutaceae	ERP016492
B133	o_Opitutales,f_Opitutaceae,g_Lacunisphaera	ERP016492
B134	o_Opitutales,f_Opitutaceae	ERP016492
B135	o_Pedosphaerales,f_Pedosphaeraceae	ERP016492
B136	o_Pedosphaerales,f_Pedosphaeraceae,g_bacterium SH3-11	ERP016492
B137	o_Pedosphaerales,f_Pedosphaeraceae	ERP016492
B138	c_Verrucomicrobiae	ERP016492
B139	c_Verrucomicrobiae	ERP016492
B140	o_Verrucomicrobiales,f_Rubritaleaceae,g_Luteolibacter	ERP016492
B141	o_Verrucomicrobiales,f_Verrucomicrobiaceae	ERP016492
B142	o_Microtrichales,f_Ilumatobacteraceae,g_CL500-29 marine group	ERP020508
B143	o_Microtrichales,f_Microtrichaceae,g_Sva0996 marine group	ERP020508
B144	o_Frankiales,f_Sporichthyaceae	ERP020508
B145	o_Frankiales,f_Sporichthyaceae,g_Candidatus Planktophila	ERP020508
B146	o_Frankiales,f_Sporichthyaceae,g_hgcI clade	ERP020508
B147	c_Actinobacteria,o_PeM15	ERP020508
B148	o_Chitinophagales,f_Saprospiraceae,g_Lewinella	ERP020508
B149	o_Chitinophagales,f_Saprospiraceae	ERP020508
B150	o_Cytophagales,f_Cyclobacteriaceae	ERP020508
B151	o_Cytophagales,f_Cyclobacteriaceae,g_Marivirga	ERP020508
B152	o_Flavobacteriales,f_Crocinitomicaceae,g_Fluviicola	ERP020508
B153	o_Flavobacteriales,f_Cryomorphaceae	ERP020508
B154	o_Flavobacteriales,f_Cryomorphaceae,g_Cryomorpha	ERP020508
B155	o_Flavobacteriales,f_Flavobacteriaceae,g_Flavobacterium	ERP020508
B156	o_Sphingobacteriales,f_NS11-12 marine group	ERP020508
B157	o_Oxyphotobacteria Incertae Sedis	ERP020508
B158	o_Oxyphotobacteria Incertae Sedis	ERP020508
B159	o_Pseudanabaenales,f_Pseudanabaenaceae,g_Pseudanabaena PCC-7429	ERP020508
B160	o_Candidatus Kaiserbacteria	ERP020508
B161	o_Candidatus Kaiserbacteria	ERP020508
B162	o_Isosphaerales,f_Isosphaeraceae	ERP020508
B163	o_Planctomycetales,f_Rubinisphaeraceae,g_Fuerstia	ERP020508
B164	o_Planctomycetales,f_Rubinisphaeraceae,g_Rubinisphaera	ERP020508
B165	o_Planctomycetales,f_Rubinisphaeraceae	ERP020508
B166	o_Caulobacterales,f_Hyphomonadaceae	ERP020508
B167	o_Parvibaculales	ERP020508

B168	o_Rhizobiales,f_Beijerinckiaceae,g_Bosea	ERP020508
B169	o_Rhizobiales,f_Rhizobiaceae,g_Ahrensia	ERP020508
B170	o_Rhizobiales,f_Rhizobiales Incertae Sedis,g_Anderseniella	ERP020508
B171	o_Rhodospirillales,f_Magnetospiraceae,g_Magnetospira	ERP020508
B172	o_Rickettsiales,f_Rickettsiaceae	ERP020508
B173	o_SAR11 clade,f_Clade III	ERP020508
B174	o_Sneathiellales,f_Sneathiellaceae,g_Sneathiella	ERP020508
B175	o_Sphingomonadales,f_Sphingomonadaceae,g_Porphyrobacter	ERP020508
B176	o_Bradymonadales	ERP020508
B177	o_Gammaproteobacteria Incertae Sedis	ERP020508
B178	o_OM182 clade	ERP020508
B179	o_Xanthomonadales,f_Rhodanobacteraceae,g_Dokdonella	ERP020508
B180	o_Chthoniobacterales,f_Xiphinematobacteraceae,g_Candidatus Xiphinematobacter	ERP020508
B181	o_Opitutales,f_Puniceicoccaceae	ERP020508
B182	o_Verrucomicrobiales,f_DEV007	ERP020508
B183	o_Verrucomicrobiales,f_Rubritaleaceae,g_Roseibacillus	ERP020508
B186	o_Microtrichales	ERP016591
B187	o_Microtrichales,f_Ilumatobacteraceae	ERP016591
B188	o_Solirubrobacterales,f_Solirubrobacteraceae	ERP016591
B189	o_Flavobacteriales,f_Crocinitomicaceae,g_Fluviicola	ERP016591
B190	o_Flavobacteriales,f_Cryomorphaceae	ERP016591
B191	o_Flavobacteriales,f_Flavobacteriaceae,g_NS3a marine group	ERP016591
B192	o_Flavobacteriales,f_Flavobacteriaceae,g_Ulvibacter	ERP016591
B193	o_Flavobacteriales,f_Flavobacteriaceae	ERP016591
B194	o_Sphingobacteriales,f_NS11-12 marine group	ERP016591
B195	o_Sphingobacteriales,f_Sphingobacteriaceae	ERP016591
B196	o_Sphingobacteriales,f_Sphingobacteriaceae,g_Solitalea	ERP016591
B197	c_Oxyphotobacteria	ERP016591
B198	o_Nostocales,f_Nostocaceae,g_Dolichospermum NIES41	ERP016591
B199	o_Clostridiales,f_Peptostreptococcaceae,g_Clostridioides	ERP016591
B200	o_Clostridiales,f_Peptostreptococcaceae,g_Paeniclostridium	ERP016591
B201	o_Erysipelotrichales,f_Erysipelotrichaceae,g_Turicibacter	ERP016591
B202	o_Acetobacterales,f_Acetobacterales Incertae Sedis	ERP016591
B203	o_Puniceispirillales,f_SAR116 clade	ERP016591
B204	o_Rhodobacterales,f_Rhodobacteraceae,g_Amylibacter	ERP016591
B205	o_Rhodobacterales,f_Rhodobacteraceae,g_Sulfitobacter	ERP016591
B206	o_SAR11 clade,f_Clade I,g_Clade Ia	ERP016591
B207	o_SAR11 clade,f_Clade III	ERP016591
B208	o_SAR11 clade,f_Clade III	ERP016591
B209	o_Alteromonadales,f_Alteromonadaceae	ERP016591
B210	o_Alteromonadales,f_Alteromonadaceae,g_Paraglaciecola	ERP016591

B211	o_Alteromonadales,f_Colwelliaceae,g_Colwellia	ERP016591
B212	o_Alteromonadales,f_Pseudoalteromonadaceae,g_Pseudoalteromonas	ERP016591
B213	o_Betaproteobacteriales,f_Chitinibacteraceae,g_Iodobacter	ERP016591
B214	o_Betaproteobacteriales,f_Methylophilaceae	ERP016591
B215	o_Betaproteobacteriales,f_Methylophilaceae,g_OM43 clade	ERP016591
B216	o_Betaproteobacteriales,f_Rhodocyclaceae,g_Sulfuritalea	ERP016591
B217	o_Cellvibrionales,f_Porticoccaceae,g_Porticoccus	ERP016591
B218	o_Cellvibrionales,f_Porticoccaceae,g_SAR92 clade	ERP016591
B219	o_Methylococcales,f_Methylomonaceae	ERP016591
B220	o_Nitrosococcales,f_Methylophagaceae	ERP016591
B221	o_Oceanospirillales,f_Nitrincolaceae	ERP016591
B222	o_SAR86 clade	ERP016591
B223	o_Xanthomonadales,f_Rhodanobacteraceae,g_Dokdonella	ERP016591
B224	o_Acidobacteriales	ERP020021
B225	o_Acidobacteriales,f_Acidobacteriaceae (Subgroup 1)	ERP020021
B226	c_Acidobacteriia,o_Subgroup 2	ERP020021
B227	c_Acidobacteriia,o_Subgroup 2	ERP020021
B228	o_Aminicenantales	ERP020021
B229	c_Blastocatellia (Subgroup 4)	ERP020021
B230	c_Blastocatellia (Subgroup 4)	ERP020021
B231	p_Acidobacteria,c_Subgroup 15	ERP020021
B232	p_Acidobacteria,c_Subgroup 17	ERP020021
B233	c_Acidimicrobiia,o_IMCC26256	ERP020021
B234	o_Micrococcales,f_Microbacteriaceae,g_Microbacterium	ERP020021
B235	c_Actinobacteria,o_PeM15	ERP020021
B236	o_Propionibacteriales,f_Nocardioidaceae,g_Nocardioides	ERP020021
B237	o_Solirubrobacterales	ERP020021
B238	o_Solirubrobacterales,f_Solirubrobacteraceae	ERP020021
B239	o_Solirubrobacterales,f_Solirubrobacteraceae	ERP020021
B241	o_Fimbriimonadales,f_Fimbriimonadaceae	ERP020021
B242	o_Bacteroidales	ERP020021
B243	o_Bacteroidales,f_Bacteroidetes BD2-2	ERP020021
B244	o_Bacteroidales,f_Bacteroidetes vadinHA17	ERP020021
B245	o_Bacteroidales,f_Prolixibacteraceae	ERP020021
B246	o_Bacteroidales,f_Rikenellaceae,g_Blvii28 wastewater-sludge group	ERP020021
B247	o_Bacteroidetes VC2.1 Bac22	ERP020021
B248	o_Chitinophagales,f_Chitinophagaceae,g_Taibaiella	ERP020021
B249	o_Chitinophagales,f_Chitinophagaceae	ERP020021
B250	o_Flavobacteriales,f_Cryomorphaceae,g_Cryomorpha	ERP020021
B251	o_Flavobacteriales,f_Weeksellaceae,g_Chryseobacterium	ERP020021
B252	o_Sphingobacteriales,f_AKYH767	ERP020021
B253	o_Sphingobacteriales,f_KD3-93	ERP020021

B254	o_Sphingobacteriales,f_Lentimicrobiaceae	ERP020021
B255	o_Sphingobacteriales,f_NS11-12 marine group	ERP020021
B256	o_Chlorobiales,f_Chloroherpetonaceae,g_GBChlB	ERP020021
B257	o_Ignavibacteriales,f_PHOS-HE36	ERP020021
B258	o_Kryptoniales,f_MSB-3C8	ERP020021
B259	o_Caldisericales,f_WCHB1-02	ERP020021
B260	o_Calditrichales,f_Calditrichaceae,g_JdFR-76	ERP020021
B261	o_Chlamydiales,f_Criblamydiaceae	ERP020021
B262	o_Chlamydiales,f_cvE6	ERP020021
B263	o_Anaerolineales,f_Anaerolineaceae,g_Anaerolinea	ERP020021
B264	o_Anaerolineales,f_Anaerolineaceae,g_Leptolinea	ERP020021
B265	o_SBR1031	ERP020021
B266	o_SBR1031,f_A4b	ERP020021
B267	o_Chloroflexales,f_Chloroflexaceae,g_Candidatus Chlorothrix	ERP020021
B268	o_Chloroflexales,f_Roseiflexaceae	ERP020021
B269	o_Thermomicrobiales,f_JG30-KF-CM45	ERP020021
B270	o_SAR202 clade	ERP020021
B271	o_Ktedonobacterales,f_Ktedonobacteraceae	ERP020021
B272	p_Chloroflexi,c_P2-11E	ERP020021
B273	o_Caenarcaniphilales	ERP020021
B274	o_Gastranaerophilales	ERP020021
B275	o_Nostocales,f_Nostocaceae	ERP020021
B276	o_Nostocales,f_Phormidiaceae	ERP020021
B277	o_Nostocales,f_Phormidiaceae,g_Planktothrix NIVA-CYA 15	ERP020021
B278	o_Oxyphotobacteria Incertae Sedis	ERP020021
B279	o_Dadabacteriales	ERP020021
B280	o_Dadabacteriales	ERP020021
B281	o_Babeliales,f_Babeliaceae	ERP020021
B282	o_Babeliales,f_UBA12409	ERP020021
B283	o_Babeliales,f_UBA12409	ERP020021
B284	o_Babeliales	ERP020021
B285	o_Babeliales	ERP020021
B286	p_Elusimicrobia,c_Lineage IIa	ERP020021
B287	o_Entotheonellales,f_Entotheonellaceae	ERP020021
B288	o_Campylobacterales,f_Helicobacteraceae	ERP020021
B289	o_Campylobacterales,f_Sulfurospirillaceae,g_Sulfurospirillum	ERP020021
B290	o_Fibrobacterales	ERP020021
B291	o_Bacillales,f_Planococcaceae	ERP020021
B292	o_Bacillales,f_Staphylococcaceae,g_Staphylococcus	ERP020021
B293	o_Lactobacillales,f_Streptococcaceae,g_Streptococcus	ERP020021
B294	o_Clostridiales	ERP020021
B295	o_Clostridiales,f_Christensenellaceae	ERP020021

B296	o_Clostridiales,f_Christensenellaceae	ERP020021
B297	o_Clostridiales,f_Clostridiaceae 1,g_Clostridium sensu stricto 10	ERP020021
B298	o_Clostridiales,f_Clostridiaceae 1,g_Clostridium sensu stricto 13	ERP020021
B299	o_Clostridiales,f_Eubacteriaceae,g_Acetobacterium	ERP020021
B300	o_Clostridiales,f_Family XIII	ERP020021
B301	o_Clostridiales,f_Peptococcaceae	ERP020021
B302	o_Clostridiales,f_Ruminococcaceae,g_[Eubacterium] coprostanoligenes group	ERP020021
B303	o_Clostridiales,f_Ruminococcaceae,g_Ruminiclostridium	ERP020021
B304	o_Clostridiales,f_Ruminococcaceae,g_Ruminiclostridium 1	ERP020021
B305	o_Clostridiales,f_Ruminococcaceae,g_Ruminococcaceae UCG-014	ERP020021
B306	o_Fusobacteriales,f_Fusobacteriaceae	ERP020021
B307	c_Kiritimatiellae,o_WCHB1-41	ERP020021
B309	o_Candidatus Falkowbacteria	ERP020021
B310	o_Candidatus Kerfeldbacteria	ERP020021
B311	o_Candidatus Kerfeldbacteria	ERP020021
B312	o_Candidatus Kuenenbacteria	ERP020021
B313	o_Absconditabacteriales (SR1)	ERP020021
B314	o_Absconditabacteriales (SR1)	ERP020021
B315	o_Absconditabacteriales (SR1)	ERP020021
B316	o_Absconditabacteriales (SR1)	ERP020021
B317	o_Candidatus Peregrinibacteria	ERP020021
B318	c_Gracilibacteria	ERP020021
B319	c_Gracilibacteria	ERP020021
B320	c_Microgenomatia	ERP020021
B321	o_Candidatus Collierbacteria	ERP020021
B322	o_Candidatus Pacebacteria	ERP020021
B323	o_Candidatus Pacebacteria	ERP020021
B324	o_Candidatus Shapirobacteria	ERP020021
B325	o_Candidatus Shapirobacteria	ERP020021
B326	o_Candidatus Moranbacteria	ERP020021
B327	o_Candidatus Moranbacteria	ERP020021
B328	o_Candidatus Vogelbacteria	ERP020021
B329	c_Parcubacteria	ERP020021
B330	c_Parcubacteria	ERP020021
B331	c_OM190	ERP020021
B332	c_Phycisphaerae,o_CCM11a	ERP020021
B333	c_Phycisphaerae,o_CCM11a	ERP020021
B334	o_Phycisphaerales,f_AKAU3564 sediment group	ERP020021
B335	o_Phycisphaerales,f_Phycisphaeraceae,g_I-8	ERP020021
B336	c_Phycisphaerae,o_S-70	ERP020021
B337	o_Tepidisphaerales,f_CPla-3 termite group	ERP020021

B338	c_Pla3 lineage	ERP020021
B339	o_Isosphaerales,f_Isosphaeraceae,g_Isosphaera	ERP020021
B340	o_Acetobacterales,f_Acetobacteraceae,g_Roseomonas	ERP020021
B341	o_Caulobacterales,f_Caulobacteraceae	ERP020021
B342	o_Micavibrionales	ERP020021
B343	o_Rhizobiales,f_Amb-16S-1323	ERP020021
B344	o_Rhizobiales,f_Beijerinckiaceae	ERP020021
B345	o_Rhizobiales,f_Beijerinckiaceae,g_Bosea	ERP020021
B346	o_Rhizobiales,f_Xanthobacteraceae,g_Blastochloris	ERP020021
B347	o_Rhizobiales,f_Xanthobacteraceae	ERP020021
B348	o_Rhodospirillales,f_Rhodopirillaceae,g_Defluviicoccus	ERP020021
B349	o_Rickettsiales	ERP020021
B350	o_Rickettsiales,f_Midichloriaceae,g_MD3-55	ERP020021
B351	o_Rickettsiales,f_Rickettsiaceae	ERP020021
B352	o_SAR11 clade,f_Clade I,g_Clade Ia	ERP020021
B353	o_Thalassobaculales	ERP020021
B354	o_Tistrellales,f_Geminicoccaceae,g_Candidatus Alysiosphaera	ERP020021
B355	o_Bdellovibrionales,f_Bacteriovoracaceae,g_Halobacteriovorax	ERP020021
B356	o_Deltaproteobacteria Incertae Sedis,f_Syntrophorhabdaceae,g_Syntrophorhabdus	ERP020021
B357	o_Desulfarculales,f_Desulfarculaceae,g_Desulfatiglans	ERP020021
B358	o_Desulfobacterales,f_Desulfobacteraceae,g_Desulfatirhabdium	ERP020021
B359	o_Desulfobacterales,f_Desulfobacteraceae,g_Sva0081 sediment group	ERP020021
B360	o_Desulfobacterales,f_Desulfobulbaceae	ERP020021
B361	o_Desulfovibrionales,f_Desulfomicrobiaceae,g_Desulfomicrobium	ERP020021
B362	o_Desulfovibrionales,f_Desulfovibrionaceae	ERP020021
B363	o_Desulfovibrionales,f_Desulfovibrionaceae,g_Desulfovibrio	ERP020021
B364	o_Desulfuromonadales,f_Geobacteraceae,g_Geobacter	ERP020021
B365	o_Myxococcales,f_bacteriap25	ERP020021
B366	o_Myxococcales,f_Sandaracinaceae	ERP020021
B367	c_Deltaproteobacteria,o_PB19	ERP020021
B368	o_Syntrophobacterales,f_Syntrophaceae,g_Smithella	ERP020021
B369	o_Syntrophobacterales,f_Syntrophaceae,g_Syntrophus	ERP020021
B370	o_Syntrophobacterales,f_Syntrophobacteraceae	ERP020021
B371	o_Betaproteobacteriales,f_Chitinibacteraceae,g_Deefgea	ERP020021
B372	c_Gammaproteobacteria,o_CHAB-XI-27	ERP020021
B373	o_Competibacterales,f_Competibacteraceae	ERP020021
B374	o_Competibacterales,f_Competibacteraceae,g_Candidatus Competibacter	ERP020021
B375	o_Competibacterales,f_Competibacteraceae,g_Candidatus Contendobacter	ERP020021
B376	o_Diplorickettsiales,f_Diplorickettsiaceae	ERP020021

B377	o_Diplorickettsiales,f_Diplorickettsiaceae,g_Aquicella	ERP020021
B378	o_Gammaproteobacteria Incertae Sedis	ERP020021
B379	o_Gammaproteobacteria Incertae Sedis	ERP020021
B380	o_Halothiobacillales,f_Halothiobacillaceae	ERP020021
B381	o_Orbales,f_Orbaceae	ERP020021
B382	o_Pseudomonadales	ERP020021
B383	c_Gammaproteobacteria,o_R7C24	ERP020021
B384	c_Gammaproteobacteria,o_WD260 bacterium	ERP020021
B385	o_Methylomirabilales,f_Methylomirabilaceae	ERP020021
B386	o_Methylomirabilales,f_Methylomirabilaceae,g_Candidatus Methylomirabilis	ERP020021
B387	o_Leptospirales,f_Leptospiraceae	ERP020021
B388	o_Leptospirales,f_Leptospiraceae,g_RBG-16-49-21	ERP020021
B389	o_Spirochaetales,f_Spirochaetaceae,g_M2PT2-76 termite group	ERP020021
B390	o_Spirochaetales,f_Spirochaetaceae,g_Spirochaeta 2	ERP020021
B391	o_Spirochaetales,f_Spirochaetaceae,g_Treponema	ERP020021
B392	o_Spirochaetales,f_Spirochaetaceae	ERP020021
B393	o_Mollicutes RF39	ERP020021
B394	o_Chthoniobacterales,f_Terrimicrobiaceae,g_Terrimicrobium	ERP020021
B395	o_Chthoniobacterales	ERP020021
B396	c_Verrucomicrobiae,o_LD1-PB3	ERP020021
B397	o_Opitutales,f_Puniceicoccaceae,g_Verruc-01	ERP020021
B398	o_Verrucomicrobiales	ERP020021
B399	o_Verrucomicrobiales,f_DEV007	ERP020021
B400	o_Verrucomicrobiales,f_Rubritaleaceae	ERP020021
B404	c_Acidimicrobiia,o_IMCC26256 actinobacterium	ERP022245
B405	o_Microtrichales,f_Ilumatobacteraceae,g_CL500-29 marine group	ERP022245
B406	c_Acidimicrobiia	ERP022245
B407	c_Acidimicrobiia	ERP022245
B408	o_Frankiales,f_Sporichthyaceae	ERP022245
B409	o_Gaiellales	ERP022245
B410	o_Solirubrobacterales,f_Solirubrobacteraceae	ERP022245
B411	o_Chitinophagales,f_Chitinophagaceae,g_Dinghuibacter	ERP022245
B412	o_Chitinophagales,f_Chitinophagaceae,g_Parasediminibacterium	ERP022245
B413	o_Chitinophagales,f_Saprospiraceae,g_Candidatus Aquirestis	ERP022245
B414	o_Cytophagales,f_Cyclobacteriaceae,g_Algoriphagus	ERP022245
B415	o_Flavobacteriales,f_Crocinitomicaceae,g_Fluviicola	ERP022245
B416	o_Flavobacteriales,f_Cryomorphaceae	ERP022245
B417	o_Flavobacteriales,f_NS9 marine group	ERP022245
B418	o_Sphingobacteriales,f_env.OPS 17	ERP022245
B419	o_Sphingobacteriales,f_NS11-12 marine group	ERP022245
B420	o_Sphingobacteriales,f_Sphingobacteriaceae,g_Mucilaginibacter	ERP022245

B421	o_Sphingobacteriales,f_Sphingobacteriaceae,g_Solitalea	ERP022245
B422	c_Ignavibacteria,o_OPB56	ERP022245
B423	c_SL56 marine group	ERP022245
B424	o_Synechococcales,f_Cyanobiaceae,g_Cyanobium PCC-6307	ERP022245
B425	o_Campylobacterales,f_Thiovulaceae,g_Sulfurimonas	ERP022245
B426	o_Phycisphaerales,f_Phycisphaeraceae,g_CL500-3	ERP022245
B427	o_Gemmatales,f_Gemmataceae	ERP022245
B428	o_Pirellulales,f_Pirellulaceae	ERP022245
B429	o_Caulobacterales,f_Caulobacteraceae	ERP022245
B430	o_Rhizobiales,f_Beijerinckiaceae,g_Roseiarcus	ERP022245
B431	o_Rickettsiales,f_Rickettsiaceae,g_Candidatus Megaira	ERP022245
B432	o_SAR11 clade,f_Clade III	ERP022245
B433	o_Sphingomonadales,f_Sphingomonadaceae,g_Sphingorhabdus	ERP022245
B434	o_Bdellovibrionales,f_Bacteriovoracaceae,g_Peredibacter	ERP022245
B435	o_Bdellovibrionales,f_Bdellovibrionaceae,g_OM27 clade	ERP022245
B436	o_Betaproteobacteriales,f_Methylophilaceae	ERP022245
B437	o_Betaproteobacteriales,f_Methylophilaceae,g_Candidatus Methylopumilus	ERP022245
B438	c_Gammaproteobacteria,o_JG36-TzT-191	ERP022245
B439	o_Chthoniobacterales,f_Terrimicrobiaceae,g_Terrimicrobium	ERP022245
B440	o_Methylacidiphilales,f_Methylacidiphilaceae	ERP022245
B441	o_Opitutales,f_Opitutaceae	ERP022245
B442	o_Pedosphaerales,f_Pedosphaeraceae	ERP022245
B443	o_Pedosphaerales,f_Pedosphaeraceae	ERP022245
B444	c_Verrucomicrobiae	ERP022245
B445	o_Verrucomicrobiales,f_Rubritaleaceae,g_Luteolibacter	ERP022245
B446	o_Acidobacteriales	ERP016880
B447	o_Acidobacteriales,f_Acidobacteriaceae (Subgroup 1)	ERP016880
B448	o_Acidobacteriales,f_Acidobacteriaceae (Subgroup 1),g_Granulicella	ERP016880
B449	o_Acidobacteriales,f_Koribacteraceae,g_Candidatus Koribacter	ERP016880
B450	o_Acidobacteriales	ERP016880
B451	o_Acidobacteriales	ERP016880
B452	o_Solibacterales,f_Solibacteraceae (Subgroup 3),g_Bryobacter	ERP016880
B453	o_Solibacterales,f_Solibacteraceae (Subgroup 3),g_Candidatus Solibacter	ERP016880
B454	c_Acidobacteriia,o_Subgroup 2	ERP016880
B455	c_Acidobacteriia,o_Subgroup 2	ERP016880
B456	c_Acidobacteriia,o_Subgroup 2	ERP016880
B457	p_Acidobacteria,c_AT-s3-28	ERP016880
B458	c_Blastocatellia (Subgroup 4)	ERP016880
B459	o_Blastocatellales,f_Blastocatellaceae	ERP016880
B460	c_Blastocatellia (Subgroup 4)	ERP016880

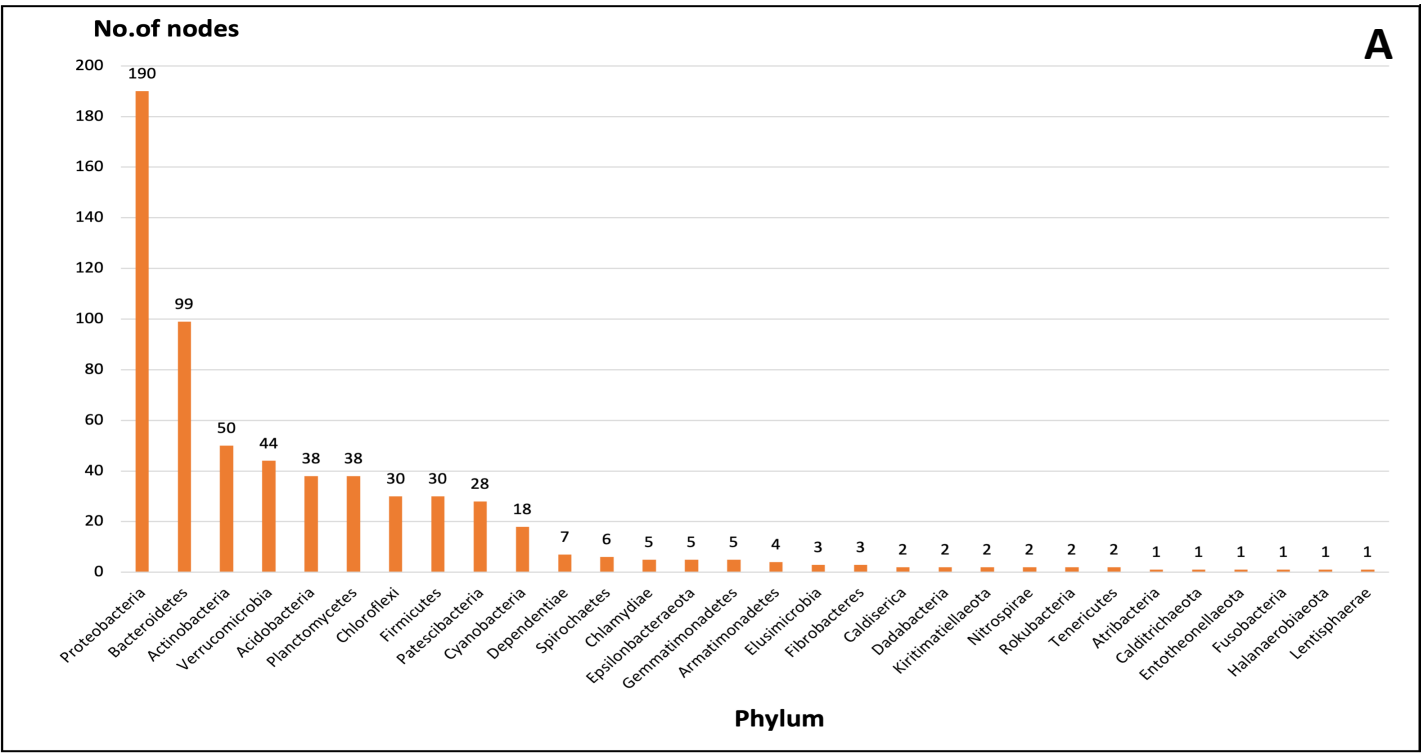
B461	o_Pyrinomonadales,f_Pyrinomonadaceae,g_RB41	ERP016880
B462	o_Holophagales,f_Holophagaceae	ERP016880
B463	p_Acidobacteria,c_Subgroup 11	ERP016880
B464	p_Acidobacteria,c_Subgroup 17	ERP016880
B465	p_Acidobacteria,c_Subgroup 20	ERP016880
B466	p_Acidobacteria,c_Subgroup 22	ERP016880
B467	p_Acidobacteria,c_Subgroup 22	ERP016880
B468	p_Acidobacteria,c_Subgroup 22	ERP016880
B469	p_Acidobacteria,c_Subgroup 5	ERP016880
B470	p_Acidobacteria,c_Subgroup 6	ERP016880
B471	p_Acidobacteria,c_Subgroup 6	ERP016880
B472	p_Acidobacteria,c_Subgroup 6	ERP016880
B473	o_Microtrichales	ERP016880
B474	o_Microtrichales,f_Ilumatobacteraceae,g_CL500-29 marine group	ERP016880
B475	c_Acidimicrobiia	ERP016880
B476	o_Actinomycetales,f_Actinomycetaceae,g_Actinomyces	ERP016880
B477	o_Frankiales,f_Acidothermaceae,g_Acidothermus	ERP016880
B478	o_Micrococcales,f_Micrococcaceae,g_Kocuria	ERP016880
B479	p_Actinobacteria,c_MB-A2-108	ERP016880
B480	o_Solirubrobacterales,f_Solirubrobacteraceae,g_Conexibacter	ERP016880
B481	o_Solirubrobacterales,f_Solirubrobacteraceae	ERP016880
B482	o_Armatimonadales	ERP016880
B483	o_Fimbriimonadales,f_Fimbriimonadaceae	ERP016880
B484	o_Caldatribacteriales,f_Caldatribacteriaceae,g_Candidatus Caldatribacterium	ERP016880
B485	o_Bacteroidales	ERP016880
B486	o_Bacteroidales,f_Marinilabiliaceae,g_Mangroviflexus	ERP016880
B487	o_Bacteroidales,f_Paludibacteraceae,g_Paludibacter	ERP016880
B488	o_Chitinophagales,f_37-13	ERP016880
B489	o_Chitinophagales,f_Chitinophagaceae	ERP016880
B490	o_Chitinophagales,f_Chitinophagaceae,g_Flavitalea	ERP016880
B491	o_Chitinophagales,f_Chitinophagaceae	ERP016880
B492	o_Cytophagales,f_Microscillaceae	ERP016880
B493	o_Cytophagales,f_Microscillaceae,g_Ohtaekwangia	ERP016880
B494	o_Sphingobacteriales	ERP016880
B495	o_Sphingobacteriales,f_AKYH767	ERP016880
B496	o_Sphingobacteriales,f_KD3-93	ERP016880
B497	o_Sphingobacteriales	ERP016880
B498	o_Sphingobacteriales,f_Sphingobacteriaceae,g_Mucilaginibacter	ERP016880
B499	o_Ignavibacteriales,f_BSN166	ERP016880
B500	o_Kryptoniales,f_BSV26	ERP016880
B501	o_Caldisericales,f_WCHB1-02	ERP016880

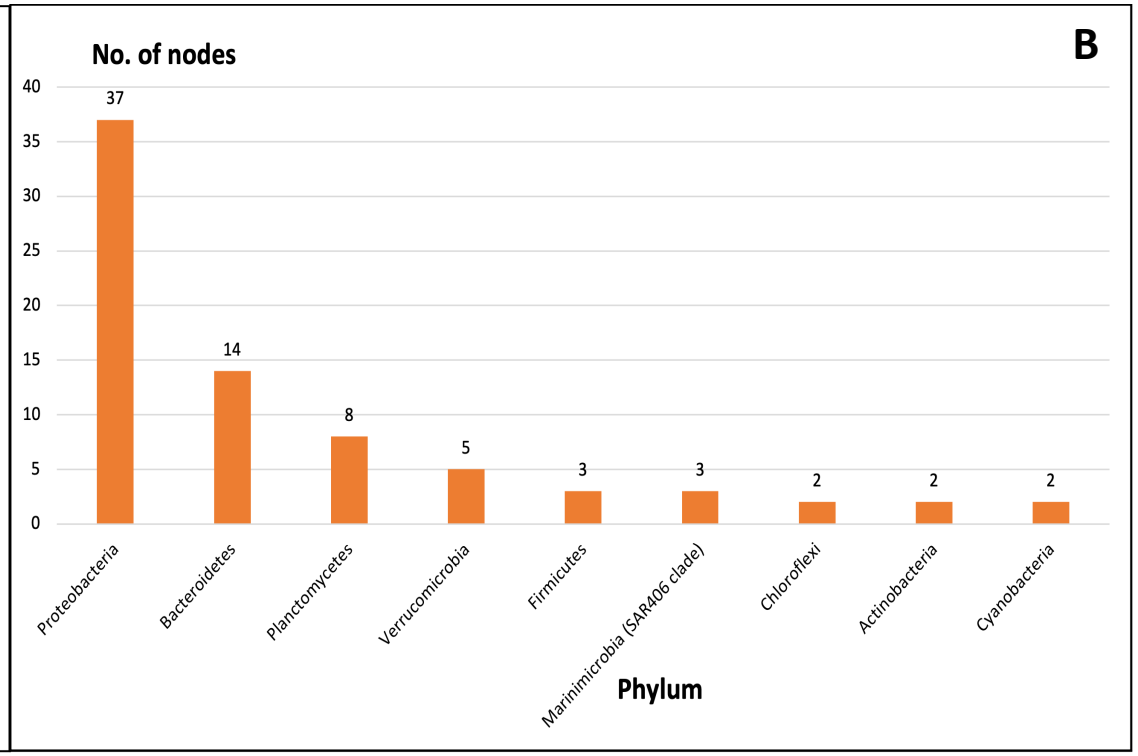
B502	o_Chlamydiales,f_cvE6	ERP016880
B503	o_Chlamydiales,f_Parachlamydiaceae	ERP016880
B504	o_Chlamydiales,f_Simkaniaceae	ERP016880
B505	o_Anaerolineales,f_Anaerolineaceae	ERP016880
B506	o_Ardenticatenales	ERP016880
B507	c_Anaerolineae,o_RBG-13-54-9	ERP016880
B508	c_Anaerolineae,o_RBG-13-54-9	ERP016880
B509	c_Anaerolineae,o_SBR1031	ERP016880
B510	c_Dehalococcoidia,o_S085	ERP016880
B511	c_Dehalococcoidia,o_S085	ERP016880
B512	c_Dehalococcoidia,o_S085	ERP016880
B513	p_Chloroflexi,c_JG30-KF-CM66	ERP016880
B514	p_Chloroflexi,c_JG30-KF-CM66	ERP016880
B515	o_Ktedonobacterales,f_Ktedonobacteraceae,g_HSB OF53-F07	ERP016880
B516	p_Chloroflexi,c_OLB14	ERP016880
B517	p_Chloroflexi,c_OLB14	ERP016880
B518	p_Chloroflexi,c_TK10	ERP016880
B519	o_Nostocales,f_Microcystaceae,g_SU2 symbiont group	ERP016880
B520	o_Nostocales,f_Nostocaceae,g_Nostoc PCC-73102	ERP016880
B521	o_Babeliales,f_UBA12409	ERP016880
B522	o_Babeliales,f_Vermiphilaceae	ERP016880
B523	p_Elusimicrobia,o_Lineage IV	ERP016880
B524	p_Elusimicrobia,o_Lineage IIa	ERP016880
B525	o_Campylobacterales,f_Sulfurovaceae,g_Sulfurovum	ERP016880
B526	o_Campylobacterales,f_Thiovulaceae,g_Sulfuricurvum	ERP016880
B527	o_Fibrobacterales	ERP016880
B528	o_Fibrobacterales,f_Fibrobacteraceae	ERP016880
B529	o_Bacillales,f_Bacillaceae	ERP016880
B530	o_Bacillales,f_Bacillaceae,g_Anaerobacillus	ERP016880
B531	o_Bacillales,f_Bacillaceae,g_Geobacillus	ERP016880
B532	o_Lactobacillales,f_Lactobacillaceae,g_Lactobacillus	ERP016880
B533	o_Clostridiales,f_Clostridiaceae 2	ERP016880
B534	o_Clostridiales,f_Clostridiaceae 2,g_Alkaliphilus	ERP016880
B535	o_Clostridiales,f_Family XIV	ERP016880
B536	o_Clostridiales,f_Peptostreptococcaceae,g_Sporacetigenium	ERP016880
B537	o_Clostridiales,f_Syntrophomonadaceae,g_Dethiobacter	ERP016880
B538	o_Clostridiales,f_Syntrophomonadaceae	ERP016880
B539	o_Erysipelotrichales,f_Erysipelotrichaceae,g_Dubosiella	ERP016880
B540	o_Limnochordales,f_Limnochordaceae	ERP016880
B541	c_BD2-11 terrestrial group	ERP016880
B542	o_Gemmatimonadales,f_Gemmatimonadaceae	ERP016880
B543	o_Gemmatimonadales,f_Gemmatimonadaceae	ERP016880

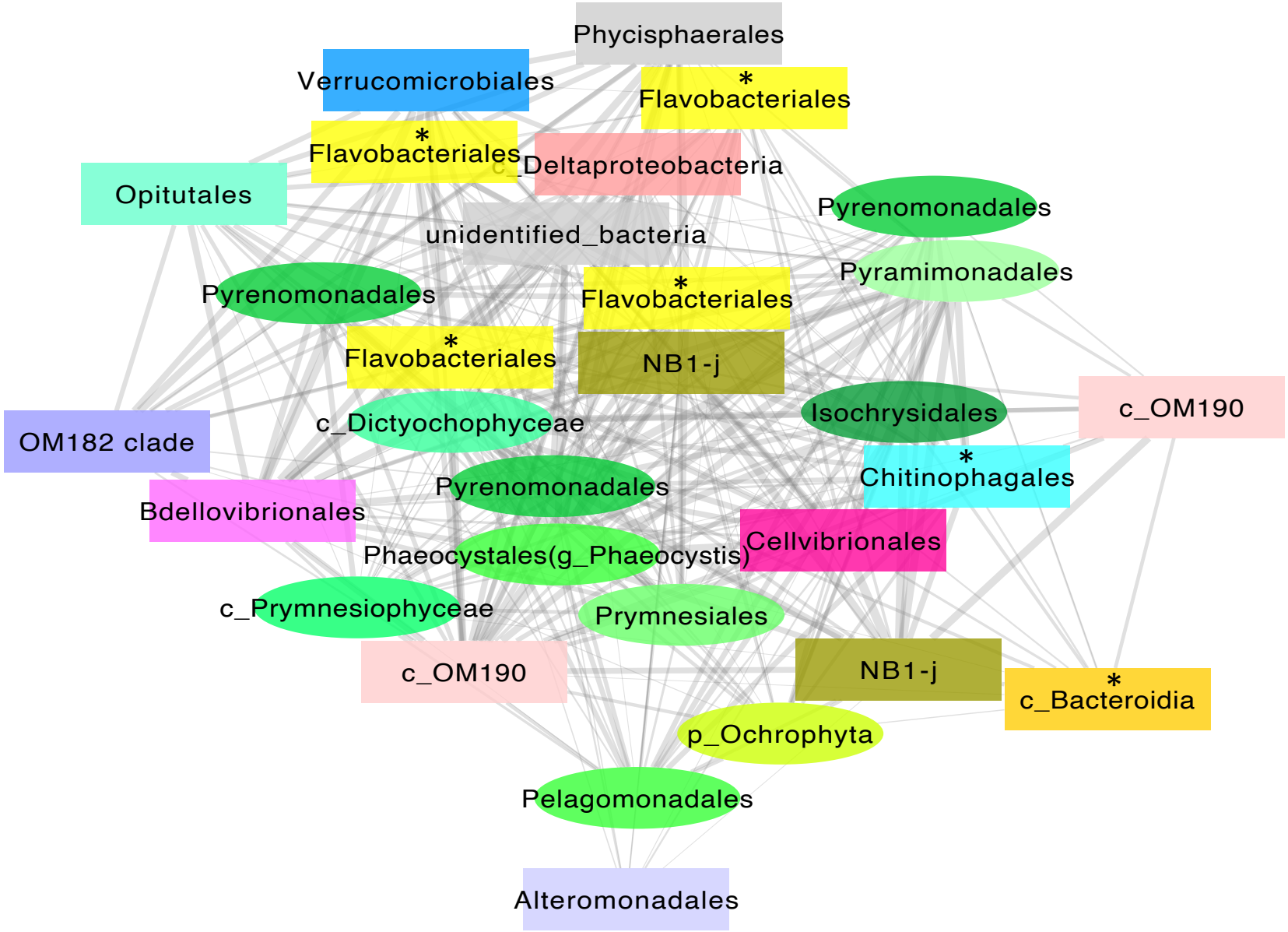
B544	o_Halanaerobiales,f_Halobacteroidaceae,g_Halonatronum	ERP016880
B549	o_Oligosphaerales,f_Lenti-02	ERP016880
B550	o_Nitrospirales,f_Nitrospiraceae,g_Nitrospira	ERP016880
B551	c_Thermodesulfovibrionia	ERP016880
B553	p_Patescibacteria,c_CPR2	ERP016880
B554	c_Microgenomatia	ERP016880
B555	c_Parcubacteria	ERP016880
B556	o_Brocadiales,f_Brocadiaceae	ERP016880
B557	c_OM190	ERP016880
B558	c_Phycisphaerae,o_CCM11a	ERP016880
B559	c_Phycisphaerae,o_CCM11a	ERP016880
B560	c_Phycisphaerae,o_CCM11a	ERP016880
B561	c_Phycisphaerae,o_CCM11a	ERP016880
B562	o_Phycisphaerales,f_Phycisphaeraceae,g_AKYG587	ERP016880
B563	o_Phycisphaerales,f_Phycisphaeraceae	ERP016880
B564	c_Phycisphaerae,o_S-70	ERP016880
B565	o_Tepidisphaerales,f_WD2101 soil group	ERP016880
B566	o_Gemmatales,f_Gemmataceae	ERP016880
B567	o_Pirellulales,f_Pirellulaceae,g_Rubripirellula	ERP016880
B568	o_Planctomycetales,f_Rubinisphaeraceae,g_SH-PL14	ERP016880
B569	o_Planctomycetales	ERP016880
B570	o_Planctomycetales	ERP016880
B571	o_Planctomycetales	ERP016880
B572	o_Caedibacterales,f_Caedibacteraceae,g_Caedibacter	ERP016880
B573	o_Caulobacterales,f_Hyphomonadaceae,g_Litorimonas	ERP016880
B574	o_Caulobacterales,f_Hyphomonadaceae,g_SWB02	ERP016880
B575	o_Dongiales,f_Dongiaceae,g_Dongia	ERP016880
B576	o_Elsterales	ERP016880
B577	o_Holosporales,f_Holosporaceae	ERP016880
B578	o_Micropepsales,f_Micropepsaceae	ERP016880
B579	o_Reyranellales,f_Reyranellaceae,g_Reyranella	ERP016880
B580	o_Rhizobiales,f_A0839	ERP016880
B581	o_Rhizobiales,f_KF-JG30-B3	ERP016880
B582	o_Rhizobiales,f_Rhizobiales Incertae Sedis,g_Bauldia	ERP016880
B583	o_Rhizobiales,f_Rhizobiales Incertae Sedis,g_Nordella	ERP016880
B584	o_Rhizobiales,f_Xanthobacteraceae,g_Bradyrhizobium	ERP016880
B585	o_Rhizobiales,f_Xanthobacteraceae,g_Pseudolabrys	ERP016880
B586	o_Rhodobacterales,f_Rhodobacteraceae,g_Pseudorhodobacter	ERP016880
B587	o_Rhodobacterales,f_Rhodobacteraceae,g_Rhodobacter	ERP016880
B588	o_Sphingomonadales,f_Sphingomonadaceae,g_Rhizorhapis	ERP016880
B589	c_Alphaproteobacteria	ERP016880
B590	o_Desulfobacterales,f_Desulfobacteraceae,g_Desulfatitalea	ERP016880

B591	o_Desulfobacterales,f_Desulfobacteraceae,g_Desulfonatronobacter	ERP016880
B592	o_Desulfobacterales,f_Desulfobacteraceae,g_Desulfosarcina	ERP016880
B593	o_Desulfobacterales,f_Desulfobacteraceae	ERP016880
B594	o_Desulfovibrionales,f_Desulfohalobiaceae,g_Desulfonatronospira	ERP016880
B595	o_Desulfuromonadales,f_Desulfuromonadaceae,g_Desulfuromonas	ERP016880
B596	o_Myxococcales,f_BIrii41	ERP016880
B597	o_Myxococcales,f_BIfdi19	ERP016880
B598	o_Myxococcales,f_Haliangiaceae,g_Haliangium	ERP016880
B599	o_Oligoflexales,f_Oligoflexaceae,g_Silvanigrella	ERP016880
B600	o_Betaproteobacteriales,f_A21b	ERP016880
B601	o_Betaproteobacteriales,f_Burkholderiaceae,g_Burkholderia-Caballeronia-Paraburkholderia	ERP016880
B602	o_Betaproteobacteriales,f_Methylophilaceae,g_Methylotenera	ERP016880
B603	o_Betaproteobacteriales,f_Nitrosomonadaceae	ERP016880
B604	o_Betaproteobacteriales,f_Nitrosomonadaceae,g_DSSD61	ERP016880
B605	o_Betaproteobacteriales,f_Nitrosomonadaceae,g_IS-44	ERP016880
B606	o_Betaproteobacteriales,f_Nitrosomonadaceae,g_MND1	ERP016880
B607	o_Betaproteobacteriales,f_Rhodocyclaceae,g_Sulfuritalea	ERP016880
B608	o_Betaproteobacteriales,f_SC-I-84	ERP016880
B609	c_Gammaproteobacteria,o_CCM19a	ERP016880
B610	o_Competibacterales,f_Competibacteraceae,g_Candidatus Competibacter	ERP016880
B611	o_Diplorickettsiales,f_Diplorickettsiaceae,g_Aquicella	ERP016880
B612	o_Diplorickettsiales,f_Diplorickettsiaceae	ERP016880
B613	o_Ectothiorhodospirales,f_Ectothiorhodospiraceae,g_Thioalkalivibrio	ERP016880
B614	o_Enterobacteriales,f_Enterobacteriaceae	ERP016880
B615	o_Gammaproteobacteria Incertae Sedis	ERP016880
B616	o_Gammaproteobacteria Incertae Sedis	ERP016880
B617	c_Gammaproteobacteria,o_JG36-TzT-191	ERP016880
B618	c_Gammaproteobacteria,o_PLTA13	ERP016880
B619	o_Salinisphaerales,f_Solimonadaceae,g_Polycyclovorans	ERP016880
B620	o_Steroidobacterales,f_Steroidobacteraceae	ERP016880
B621	o_Steroidobacterales,f_Steroidobacteraceae,g_Steroidobacter	ERP016880
B622	c_Gammaproteobacteria	ERP016880
B623	c_Gammaproteobacteria	ERP016880
B624	c_Gammaproteobacteria,o_WD260	ERP016880
B625	o_Xanthomonadales,f_Xanthomonadaceae,g_Arenimonas	ERP016880
B626	o_Haloplasmatales,f_Haloplasmataceae,g_Haloplasma	ERP016880
B627	o_Chthoniobacterales,f_Chthoniobacteraceae,g_Candidatus Udaeobacter	ERP016880
B628	o_Chthoniobacterales,f_Chthoniobacteraceae,g_Chthoniobacter	ERP016880
B629	o_Chthoniobacterales,f_Xiphinematobacteraceae,g_Candidatus Xiphinematobacter	ERP016880

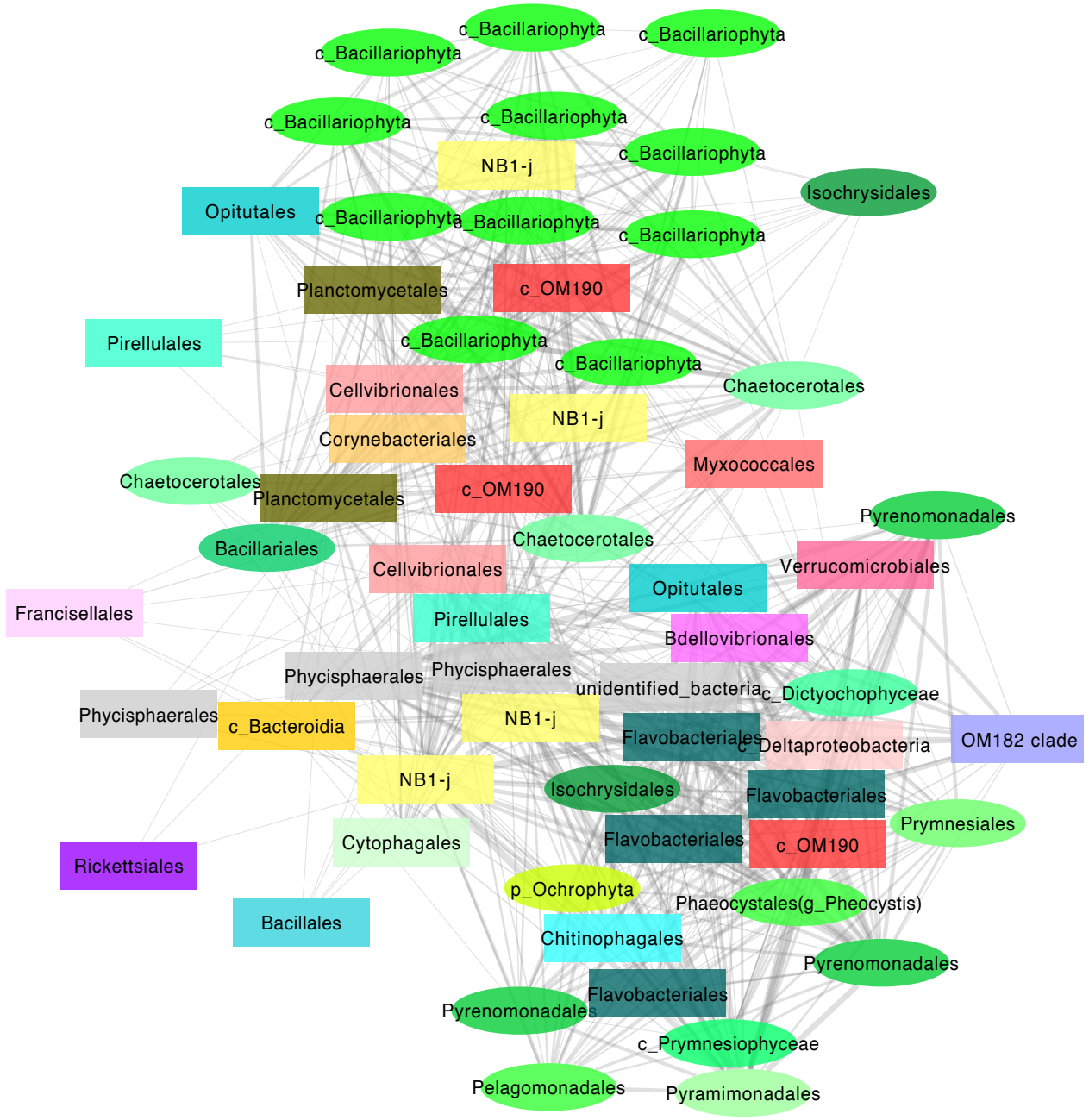
B630	o_Methylacidiphilales,f_Methylacidiphilaceae	ERP016880
B631	o_Pedosphaerales,f_Pedosphaeraceae	ERP016880
B632	o_Pedosphaerales,f_Pedosphaeraceae	ERP016880
B633	o_Pedosphaerales,f_Pedosphaeraceae,g_Pedosphaera	ERP016880
B634	o_Pedosphaerales,f_Pedosphaeraceae	ERP016880
B635	c_Verrucomicrobiae,o_S-BQ2-57 soil group	ERP016880
B636	o_Verrucomicrobiales,f_DEV007	ERP016880
B637	o_Verrucomicrobiales,f_Verrucomicrobiaceae,g_Verrucomicrobium	ERP016880


A
No.of nodes
200
180
160
140
120
100
80
60
40
20
0
190
99
50
44
38
38
30
30
28
18
7
6
5
5
5
4
3
3
2
2
2
2
2
2
1
1
1
1
1
1
Proteobacteria
Bacteroidetes
Actinobacteria
Verrucomicrobia
Acidobacteria
Planctomycetes
Chloroflexi
Firmicutes
Patescibacteria
Cyanobacteria
Dependentiae
Spirochaetes
Chlamydiae
Epsilonbacteraeota
Gemmatimonadetes
Armatimonadetes
Elusimicrobia
Fibrobacteres
Caldiserica
Dadabacteria
Kiritimatiellaeota
Nitrospirae
Rokubacteria
Tenericutes
Atribacteria
Calditrichaeota
Entotheonellaeota
Fusobacteria
Halanaerobiaeota
Lentisphaerae
Phylum

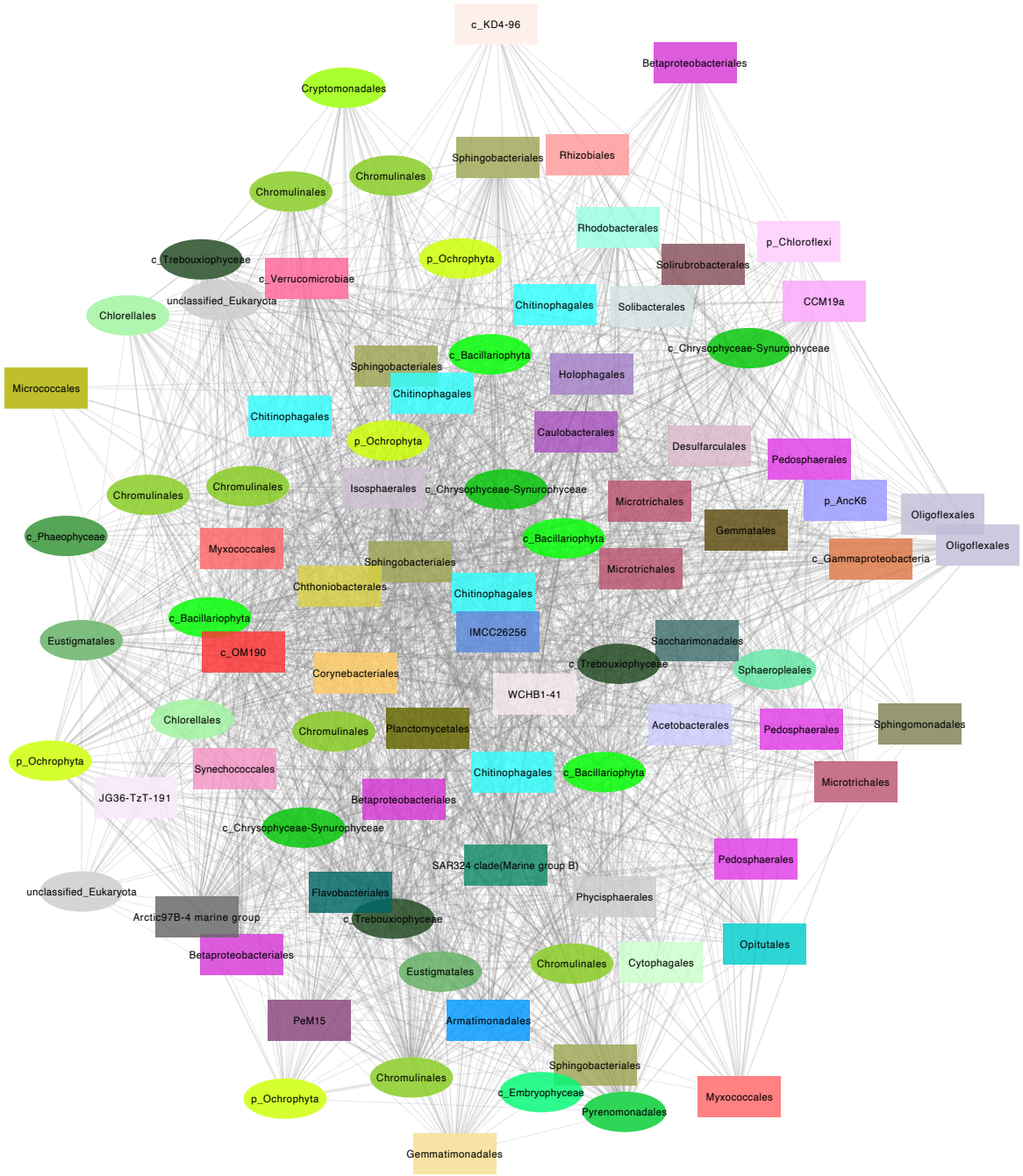

B
No. of nodes
40
35
30
25
20
15
10
5
0
37
14
8
5
3
3
2
2
2
Proteobacteria
Bacteroidetes
Planctomycetes
Verrucomicrobia
Firmicutes
Marinimicrobia (SAR406 clade)
Chloroflexi
Actinobacteria
Cyanobacteria
Phylum

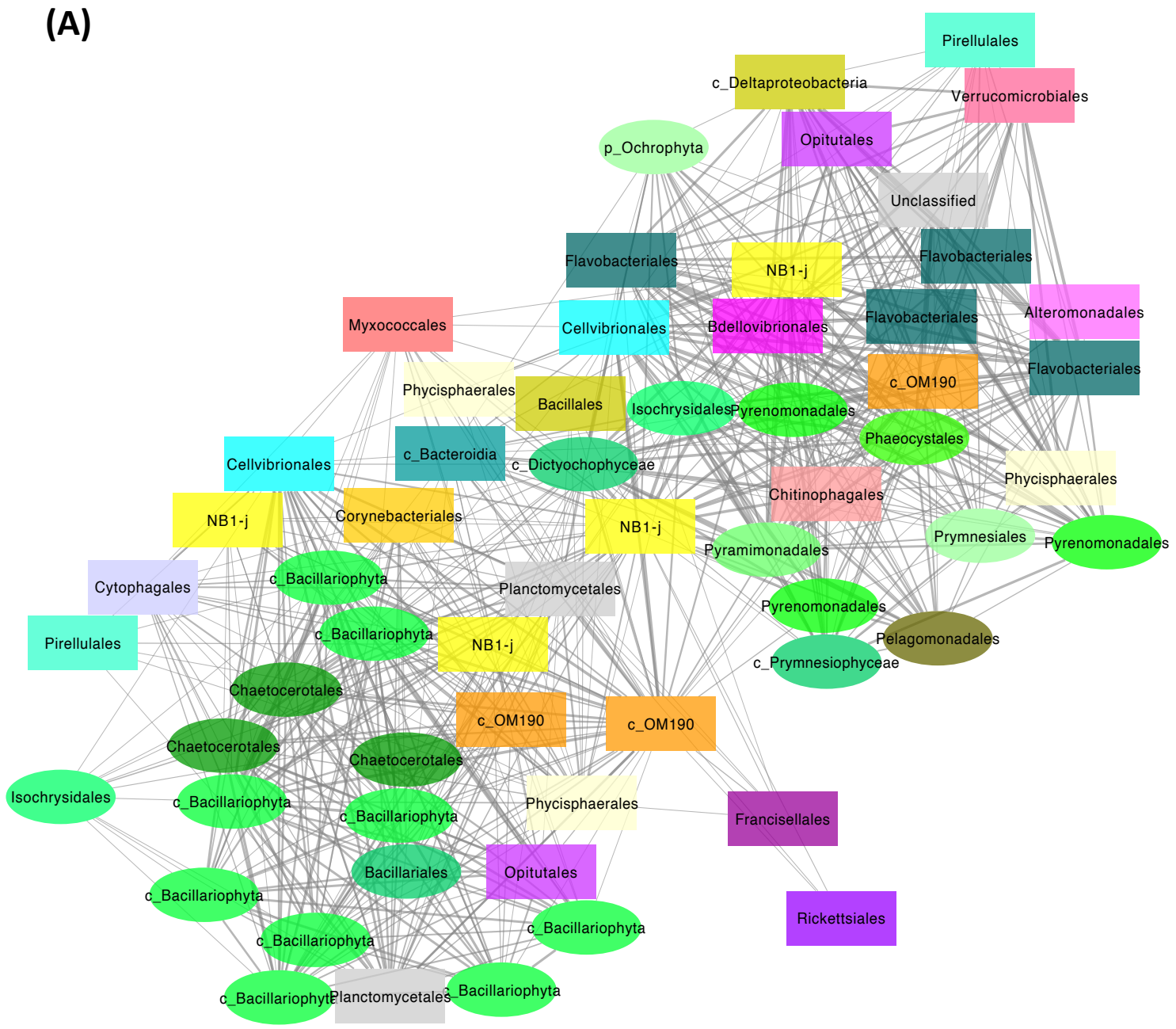

Phycisphaerales
Verrucomicrobiales
*
Flavobacteriales
*
Flavobacteriales
c_Deltaproteobacteria
Opitutales
Pyrenomonadales
unidentified_bacteria
Pyramimonadales
Pyrenomonadales
*
Flavobacteriales
*
Flavobacteriales
NB1-j
Isochrysidales
c_OM190
OM182 clade
c_Dictyochophyceae
*
Chitinophagales
Pyrenomonadales
Bdellovibrionales
Cellvibrionales
Phaeocystales(g_Phaeocystis)
c_Prymnesiophyceae
Prymnesiales
c_OM190
NB1-j
*
c_Bacteroidia
p_Ochrophyta
Pelagomonadales
Alteromonadales

(A) Interactions of OM190 in a marine environment



(B) Interactions of OM190 in a freshwater environment




(A)
Pirellulales
c_Deltaproteobacteria
Verrucomicrobiales
p_Ochrophyta
Opitutales
Unclassified
Flavobacteriales
NB1-j
Flavobacteriales
Myxococcales
Cellvibrionales
Bdellovibrionales
Flavobacteriales
Alteromonadales
Flavobacteriales
Phycisphaerales
Bacillales
Isochrysidales
Pyrenomonadales
c_OM190
Phaeocystales
Cellvibrionales
c_Bacteroidia
c_Dictyochophyceae
Phycisphaerales
Chitinophagales
NB1-j
Corynebacteriales
NB1-j
Pyramimonadales
Prymnesiales
Pyrenomonadales
Cytophagales
c_Bacillariophyta
Planctomycetales
Pyrenomonadales
Pirellulales
c_Bacillariophyta
NB1-j
Pelagomonadales
c_Prymnesiophyceae
Chaetocerotales
c_OM190
c_OM190
Chaetocerotales
Chaetocerotales
Isochrysidales
c_Bacillariophyta
c_Bacillariophyta
Phycisphaerales
Francisellales
Bacillariales
Opitutales
c_Bacillariophyta
Rickettsiales
c_Bacillariophyta
c_Bacillariophyta
c_Bacillariophyta
Planctomycetales
c_Bacillariophyta
(B)
Isochrysidales
Pirellulales
Rhodobacterales
Rickettsiales
Verrucomicrobiales
Flavobacteriales
Flavobacteriales
Flavobacteriales
Flavobacteriales
Flavobacteriales
Bolidomonadales
Prymnesiales
NB1-j
Pyrenomonadales
c_Bacillariophyta
Prymnesiales
Pyrenomonadales
Pyrenomonadales
Florenciellales
Prymnesiales
Pyrenomonadales
c_Bacillariophyta