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Bacterial diversity and composition in the fluid of pitcher plants of the genus *Nepenthes*

Takeuchi, Yayoi ; Chaffron, Samuel ; Salcher, Michaela M ; Shimizu-Inatsugi, Rie ; Kobayashi, Masaki J
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Abstract: Pitchers are modified leaves used by carnivorous plants for trapping prey. Their fluids contain digestive enzymes from the plant and they harbor abundant microbes. In this study, the diversity of bacterial communities was assessed in *Nepenthes* pitcher fluids and the composition of the bacterial community was compared to that in other environments, including the phyllosphere of *Arabidopsis*, animal guts and another pitcher plant, *Sarracenia*. Diversity was measured by 454 pyrosequencing of 16S rRNA gene amplicons. A total of 232,823 sequences were obtained after chimera and singleton removal that clustered into 3260 distinct operational taxonomic units (OTUs) (3% dissimilarity), which were taxonomically distributed over 17 phyla, 25 classes, 45 orders, 100 families, and 195 genera. Pyrosequencing and fluorescence in situ hybridization yielded similar estimates of community composition. Most pitchers contained high proportions of unique OTUs, and only 22 OTUs (<0.6%) were shared by 14/16 samples, suggesting a unique bacterial assemblage in each pitcher at the OTU level. Diversity analysis at the class level revealed that the bacterial communities of both opened and unopened pitchers were most similar to that of *Sarracenia* and to that in the phyllosphere. Therefore, the bacterial community in pitchers may be formed by environmental filtering and/or by phyllosphere bacteria.

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1 **Supporting Information**

2 **Bacterial diversity and composition in the fluid of pitcher plants of the genus**

3 ***Nepenthes***

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38 *A.1. Sample collection*

39 The samples were collected in or around Lambir Hills National Park (LHNP), Sarawak,
40 Malaysia (4°2'N, 113°50'E; 150 m a.s.l.). *Nepenthes albomarginata* was collected near the
41 summit of Bukit Pantu (approximately 300 m a.s.l.), *N. ampullaria* was collected near a pond
42 in LHNP, *N. mirabilis* was collected at the edge of LHNP, and *N. hirsuta* was collected in
43 LHNP. We also used fluid collected from cultivated *N. albomarginata* and *N. ampullaria*
44 plants in a greenhouse in the Botanical Garden at the University of Zurich, Zurich,
45 Switzerland (47°21'N, 8°33'E; 440 m a.s.l.).

46 Field samples were collected in Borneo during October 2007 for *N. albomarginata*,
47 December 2007 for *N. ampullaria*, and March 2008 for *N. hirsuta* at LHNP. The plants
48 cultivated in Zurich were sampled in October 2008. We carefully transferred the pitcher fluid

49 in the field to Falcon tubes using a 5–10-ml pipette. For *N. ampullaria* in Borneo, the
50 unopened pitcher was opened carefully in the field using a razor, and the fluid was transferred
51 to a Falcon tube. To avoid contamination of *N. ampullaria* in Zurich, we brought an
52 unopened pitcher back to the laboratory and collected samples on a clean bench. All samples
53 of pitcher fluid were fixed with formaldehyde (2% final concentration) and stored at 4°C
54 until further processing.

55 A.2. Estimation of bacterial density in each sample

56 The pH values of all samples were measured using pH paper (Panpeha, pH 0–14, Schleicher
57 and Schuell, NH, USA; and pH 2.8–4.4, Toyo Roshi Co. Ltd, Japan), except *N. mirabilis*.
58 The total bacterial abundance was estimated as follows: 5–300 µl of formaldehyde-fixed
59 samples were stained with 4',6-diamidino-2-phenylindole (DAPI, 1 µg ml⁻¹ sample) [11],
60 filtered through black polycarbonate filters (0.22 µm pore size, Osmonics), and placed onto
61 cellulose nitrate support filters (0.45 µm pore size, Sartorius). Images of the preparations
62 were recorded automatically using a CCD camera (Zeiss Axiocam), which was mounted on
63 an epifluorescence microscope (Zeiss Axio Imager.Z1) equipped with a motorized stage, and
64 analysed with a custom-made automated counting routine programmed in Visual Basic for
65 Applications [13].

66 We confirmed that there was a high bacterial density in the sampled pitchers, with a mean
67 of 3.8×10^8 cells ml⁻¹ (Table 1). The density of AL2Z was the lowest (2.0×10^5 cells ml⁻¹,
68 Table 1), whereas that of HIB was the highest (4.8×10^9 cells ml⁻¹, Table 1). The unopened
69 pitchers, AMUB and AMUZ, also contained high densities of bacteria (1.7×10^6 and $9.6 \times$
70 10^5 cells ml⁻¹, respectively), although they were lower than a previous study of *N. alata* ($\sim 10^7$
71 cells ml⁻¹) [15]. The bacterial density was negatively correlated with the pH (GLM, $t = 2.3$, P
72 < 0.05), but it did not differ among the species (*N. albomarginata* or *N. ampullaria*),

73 locations (Borneo or Zurich), or developmental stages (unopened, mature, or dead) (GLM, $t =$
74 $-1.0, -0.3,$ and $-0.4,$ respectively, $P > 0.1$).

75 *A.3. DNA extraction*

76 DNA extractions were performed at the limnology station of the University of Zurich, Zurich,
77 Switzerland. Up to 4 ml of fluid (excluding macro-parts of insects) from each pitcher sample
78 was filtered through polycarbonate filters (0.22 μm pore size, Osmonics). We used all of the
79 fluid from pitchers that contained $< 600 \mu\text{l}$ of pitcher fluid. The filters were cut, and the DNA
80 was extracted using 2 ml bead-beating tubes containing beads from a Powersoil DNA
81 Isolation kit (MoBio; Madison, WI). The final DNA concentration was estimated by gel
82 electrophoresis.

83 *A.4. 454 Pyrosequencing*

84 Short fragments of the V5-V6 16S rRNA hypervariable regions (length in *E. coli* ~ 280 bp)
85 were amplified using primers for bacterial pyrosequencing, according to the method of
86 Stecher *et al.* [16]. The primers containing the adapters A and B (19 bp, each) for 454
87 sequencing at their 5'-end were B-V5 (5'-GCCTTGCCAGCCCGCTCAG ATT AGA TAC
88 CCY GGT AGT CC-3') and A-V6-TAGC (5'-GCCTCCCTCGCGCCATCAG [TAGC]
89 ACGAGCTGACGACARCCATG-3'), where the brackets contain 16 different 4-mer tag
90 identifiers i.e., [TAGC, TCGA, TCGC, TAGA, TGCA, ATCG, AGCT, AGCG, ATCT,
91 ACGT, GATC, GCTA, GCTC, GATA, GTCA, CAGT]. PCR reactions were performed in 50
92 μl reaction volumes that contained $1\times$ buffer, $2.5 \mu\text{M}$ MgCl_2 , $0.25 \mu\text{M}$ of each primer, 0.5
93 μM of each dNTP, 0.3 U ExTaq polymerase (Takara, Japan), and 1–10 ng DNA. The PCR
94 conditions were as follows: 94°C for 2 min, 30 cycles at 94°C for 30 s, 54°C for 30 s, 72°C
95 for 30 s, and a final extension at 72°C for 10 min. The amplified PCR products were loaded
96 onto an agarose gel and recovered using a QIAquick Gel Extraction Kit (QIAGEN). DNA

97 was quantified using a Qubit fluorometer (Invitrogen). Pyrosequencing was conducted using
98 a 454 Life Sciences Genome Sequencer FLX (Roche).

99 *A.5. Quality filtering and OTU definition*

100 We applied quality control to the 454 reads in order to avoid artificially inflating the
101 ecosystem diversity estimates [10]. Reads containing the consensus sequence
102 ('ACGAGCTGACGACA[AG]CCATG') of the V6 reverse primer were filtered based on
103 their length (length = 200–300 bp). Quality filtering was then applied to include sequences
104 that only contained one of the exact 4-nt tag sequences and a maximum of one ambiguous
105 nucleotide “N.” The latter criterion has been reported to be a good indicator of the sequence
106 quality in a single read [8].

107 To reduce the computational time and complexity, we constructed operational taxonomic
108 units (OTUs) using the complete filtered dataset, which included all of the nonredundant
109 reads from all samples. After OTU computation, the redundant sequences were considered in
110 the OTU abundance analysis. During the subsequent taxonomic classification, we included
111 additional quality-filtered 16S rRNA reference sequences, which were selected from the
112 Greengenes database
113 (http://greengenes.lbl.gov/Download/Sequence_Data/Greengenes_format/greengenes16SrRN
114 [Agenes.txt.gz](http://greengenes.lbl.gov/Download/Sequence_Data/Greengenes_format/greengenes16SrRN); release 01-29-2010) [2]. This reference database is based on full-length
115 nonchimerical sequences with a minimum length of 1100 bp (to include the entire V6 regions
116 of all entries). No archaeal sequences were included in the analysis.

117 The alignment of nonredundant reads from all pitchers and the reference database was
118 performed using the secondary structure-aware Infernal aligner (<http://infernal.janelia.org/>;
119 release 1.0) [5] based on the 16S rRNA bacterial covariance model of the RDP database
120 (<http://rdp.cme.msu.edu/>) [3]. Before defining OTUs, we removed reference sequences that
121 lacked successful alignments (Infernal bit-score < 0). The alignment was then processed

122 including an equivalent amount of information from each read. We identified the consensus
123 reverse primer sequence of the V6 region in the aligned sequence of *Escherichia coli* K12 as
124 a reference. The full alignment was then trimmed from the start position (defined by the *E.*
125 *coli* V6 reverse primer) and ended after 200 bp. This also limited the effect of
126 pyrosequencing errors by trimming the 3' end of each read, which is more prone to
127 sequencing errors [10]. OTUs were built using this alignment by hierarchical cluster analysis
128 at various distances (0.01, 0.03, 0.05, and 0.10) using the “complete linkage clustering” tool
129 in the RDP pyrosequencing pipeline (<http://pyro.cme.msu.edu/pyro/>) [3].

130 *A.6. Taxonomic assignment*

131 Initially, taxonomy was inferred for all reads using the stand-alone version of the RDP
132 classifier (<http://sourceforge.net/projects/rdp-classifier>; revision 2.0) [18]. Taxon-level
133 predictions were considered reliable when supported by a bootstrap value of > 80%. The
134 taxonomy of each OTU was predicted using any reference sequences present in a cluster or
135 the taxonomy of the reads present in the cluster, which were predicted by the RDP classifier.
136 We favoured any reference sequences over the reads, which increased the resolution of the
137 predictions. The taxonomy of each OTU was inferred by a simple majority vote; i.e., the
138 OTU was annotated as a specific taxon if > 50% of the reference sequences (or reads) in a
139 cluster agreed. When there were conflicts, we assigned a consensus taxon to a higher
140 phylogenetic level if the majority vote condition was met.

141 *A.7. Chimera estimation*

142 Deep sequencing using the 454 platform detected extensive bacterial diversity, which was
143 previously undetected using culture-dependent methods [14]. However, the sequencing data
144 generated from pools of PCR products should be interpreted carefully, and the limitations and
145 biases of the PCR technique need to be considered, or the bacterial diversity can be

146 overestimated, as reported recently [10, 12]. Moreover, chimeric sequences can be generated
147 during amplification.

148 Recombination points (recombination can occur with an incompletely extended primer or
149 via template switching) are extremely difficult to detect in short sequences. The PyroNoise
150 tool can be used to filter noise and to remove chimeras from 454 pyrosequencing data [12].
151 Thus, diversity estimates may be at least one order of magnitude too high because of
152 sequencing errors. To the best of our knowledge, no tools were available to detect chimeras
153 in short 454 read libraries at the time of the analysis. Therefore, we detected chimeras by
154 comparing the taxonomies assigned to the N-terminal and C-terminal read fragments using
155 BLASTn. To ensure a reasonable alignment length and a relatively high shared identity with
156 the matching reference sequences, we only analysed reads where both fragments had a
157 minimum identity of 95% and a minimum bit-score of 150 (these cut-offs were selected
158 heuristically). A given read was considered chimeric if the taxonomies of the best hits for
159 each half were not congruent (i.e., they differed at the phylum level). Our simple chimera
160 detection method gave a slightly higher chimera detection rate compared with the method of
161 Quince *et al.* [12] (~4.5% compared with ~3%), which suggested that our approach was at
162 least comparable in terms of stringency.

163 The estimated rate of chimera sequence reads detected (8.29%) was similar to a previous
164 report (~7%) that used the same detection method [16]. This chimera frequency was
165 relatively high given that we probably detected only a fraction of the chimeric reads using our
166 method (see Materials and methods).

167 *A.8. Comparison of bacterial diversity among pitcher plants and other environments*

168 The average rarefaction curves of the sequence data were constructed to estimate and
169 compare the bacterial diversity. We also compared the data in this study with 500 sequences
170 selected randomly from published studies; i.e., farm soil, termite gut, coastal seawater, human

171 gut, phyllosphere of *Arabidopsis thaliana* (which is similar to those of soybean and clover)
172 and mouse gut (see “*Non-metric multidimensional scaling (NMDS)*” in Materials & Methods).
173 The rarefaction curves of OTUs versus the sequence number were produced using the
174 function “specaccum” in the vegan package in R. However, it should be noted that only a
175 limited environmental range has been studied so far and that these published datasets were
176 acquired by shotgun sequencing and/or using different 16S rRNA primer sets. Despite these
177 methodological differences, it was useful to compare these environments with the pitcher
178 plant microbiota, particularly the microbiota found in animal guts, because they may have
179 interesting similarities.

180 The rarefaction curves indicated that the bacterial diversity of pitcher plants was lower than
181 that in the soil, termite gut, and the ocean, and similar to that in the *Arabidopsis* phyllosphere
182 and mouse gut, but higher than that in the human gut (Fig. 4). The oceanic bacterial
183 community is considered to allow free bacterial dispersal [6], whereas phyllosphere
184 communities will constrain the colonization or survival of external bacterial species [4].
185 Similar levels of diversity in the phyllosphere community might be explained by
186 environmental filtering on the bacterial community and/or a low bacterial migration rate in
187 the pitcher fluid.

188 *A.9. Possibility of contamination*

189 One of the common OTUs in the pitcher fluid was affiliated to the genus *Propionibacterium*
190 (Fig. 3), which is known to be a common contaminant [1], so there may have been a concern
191 about contamination of our samples. However, the overall percentage of these bacteria in the
192 samples was low, so we retained them in the analysis. In addition, we detected a high number
193 of unique OTUs in all samples, which also suggests that there were few artefacts in our
194 sequencing results.

195 A.10. Bacterial communities after the addition of prey

196 To examine the effect of prey addition to the bacterial community, we performed
197 supplementation experiments in the field using four pitchers from one individual *N. mirabilis*
198 collected from the edge of LHNP during March 2008. In 2/4 pitchers (MI1C and MI2C), an
199 ant (cleaned with 70% ethanol) was added to the fluid of each pitcher, whereas nothing was
200 added to the other two pitchers (i.e., no treatment for MI3A and MI4A). Each pitcher was
201 covered with a mesh bag and left for 24 h. We then collected 15 ml of fluid from each pitcher.

202 We found that one of two pitchers with added prey (MI4A) contained a high abundance of
203 Enterobacteriales, including members of the families Enterobacteriaceae and
204 Methylococcaceae (Table A.1). Enterobacteriaceae are common members of the animal gut
205 flora, while Methylococcaceae are major methanotrophs. A previous study of *Sarracenia*
206 *alata* [9] also reported that members of Enterobacteriaceae were present in the fluid of all *S.*
207 *alata* samples. This may suggest that supplementation with fresh prey affected the bacterial
208 community, particularly an increase in digestion-related microbes when prey was available.
209 However, more samples are required to confirm this hypothesis.

210 *N. mirabilis* samples had a different bacterial community compared with other pitchers
211 and the controls (Fig. 5b, Fig. A.2b). This may have been partly due to the processing method
212 because these samples were kept in the laboratory for 24 h prior to fixation. Higashi *et al.* [7]
213 reported that the bacterial density and pH of pitcher fluid increased dramatically after gelatin
214 addition in test tubes, whereas there was only a small change in living pitchers. Thus, our
215 results suggest that living pitcher plants might be able to control the bacterial density and
216 community composition of their fluids via enzyme secretion, although this hypothesis should
217 be tested experimentally with more samples.

218 In the pitchers used for prey supplementation experiments (*N. mirabilis*), the values of 1D
219 and 2D did not differ between the treatments (Table 1). However, these samples did not

220 cluster with the other pitchers (Fig. 5b, Fig. A.2b). Both pitchers with added prey were
221 dominated by Gammaproteobacteria, although each had a specific bacterial community
222 composition at the OTU level. For example, one pitcher with added prey (MI3A) was
223 dominated by Pseudomonadales (32%), a relatively common taxon in other mature pitchers,
224 whereas the other (MI4A) contained high amounts of Enterobacteriales (55%). The bacterial
225 community in one of the control pitchers (MI1C) was very different from all other pitchers
226 (Fig. 5b, Fig. A.2b), i.e., it was dominated by Clostridiales (99%), so we treated this as an
227 outlier sample. Another control sample (MI2C) contained high amounts of unclassified
228 bacteria (~55%).

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281 **Supplementary figure captions**

282 **Fig. A.1** Rank-abundance distribution of OTUs in each pitcher. The colored circles indicate
283 common 22 OTUs. The number of the common 22 OTUs included by each sample is shown.
284 The significance of whether the common OTUs are more abundant than the total OTUs was
285 examined by *t*-test followed by the Bonferroni correction, but none were significant.

286 **Fig. A.2 (a)** NMDS ordination of the bacterial class composition for 16 *Nepenthes* samples
287 and seven other environmental samples based on the Bray–Curtis index (abundance = 1000
288 resampling). The stress value is 10.3.

289 **(b)** NMDS ordination of the OTU composition for 16 *Nepenthes* samples based on the Bray–
290 Curtis index (abundance = 1000 resampling). The stress value is 14.3.

291

Table S1 Frequency of taxonomic groups in each sample. The mean percentage (\pm SD) was calculated based on 1000 resamplings without replacement (each sample size = 100)

Phylum	Class	Order	Family	Genus	AL1B	AL2B	AL1Z	AL2Z	AM1B	AM2B	AM1Z	AM2Z	AMDZ	AMUB	AMUZ	HIB	M11C	M12C	M13A	M14A			
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	Gp2	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.014 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00		
				Gp3	0 ± 0.00	0 ± 0.00	0.417 ± 0.07	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.259 ± 0.05	0 ± 0.00	0.02 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	
				Gp4	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.032 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Gp5	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.007 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.006 ± 0.01	0 ± 0.00	0.006 ± 0.01	3.044 ± 0.17	0 ± 0.00	0 ± 0.00	0.086 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Gp6	0 ± 0.00	0.613 ± 0.08	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.007 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.106 ± 0.03	0 ± 0.00	0.018 ± 0.01	0 ± 0.00
				Gp10	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.026 ± 0.02
Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	0.081 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.153 ± 0.04	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.028 ± 0.02	0.006 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	1.355 ± 0.11	0 ± 0.00	
				Brevibacterium	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.095 ± 0.03	0.183 ± 0.04	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.065 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.13 ± 0.04
				Corynebacterium	0 ± 0.00	0.393 ± 0.06	0 ± 0.00	0.087 ± 0.03	0 ± 0.00	0.819 ± 0.09	0.197 ± 0.04	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.038 ± 0.02	0.056 ± 0.02	1.039 ± 0.10	0 ± 0.00	0.366 ± 0.06	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Brachybacterium	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.44 ± 0.06	0 ± 0.00	0.437 ± 0.07	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.042 ± 0.02	0 ± 0.00	0 ± 0.00	0.283 ± 0.05	0 ± 0.00	0 ± 0.00	0.035 ± 0.02	0 ± 0.00
				Kytococcus	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.577 ± 0.08	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Actinotelluria	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.337 ± 0.06	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
Actinobacteria	Actinobacteria	Actinomycetales	Gordoniaceae	Gordonia	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.015 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00		
				Intrasporangiaceae	Knoellia	0 ± 0.00	0.401 ± 0.06	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.021 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	
				Terrabacter	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.014 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	
				Tetrasphaera	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.889 ± 0.09	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	
				Unclassified	0 ± 0.00	0.015 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	
				Microbacteriaceae	Cryobacterium	0 ± 0.00	0 ± 0.00	0.066 ± 0.03	0.024 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.012 ± 0.01	0.032 ± 0.02	0 ± 0.00	0.007 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Leifsonia	0.006 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.07 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.063 ± 0.03	0 ± 0.00	0 ± 0.00	0.786 ± 0.09	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00		
				Leucobacter	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.139 ± 0.04	0.168 ± 0.04	0.006 ± 0.01	0.068 ± 0.03	0 ± 0.00	0.018 ± 0.01	
				Microbacterium	0.957 ± 0.09	0.404 ± 0.06	2.019 ± 0.15	0.42 ± 0.06	0.238 ± 0.05	0.467 ± 0.07	0.164 ± 0.04	9.447 ± 0.29	3.732 ± 0.19	0 ± 0.00	0.139 ± 0.04	0.168 ± 0.04	0.006 ± 0.01	0.068 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	
				Subtercola	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.606 ± 0.08	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	
				Unclassified	0.199 ± 0.04	0 ± 0.00	0.004 ± 0.01	0.214 ± 0.05	0.007 ± 0.01	0 ± 0.00	0.026 ± 0.02	0.006 ± 0.01	0.361 ± 0.06	0 ± 0.00	0.021 ± 0.01	1.13 ± 0.11	0 ± 0.00	0.039 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	
				Micrococcaceae	Citricoccus	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.033 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Kocuria	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.063 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.176 ± 0.04	0 ± 0.00	0 ± 0.00		
				Micrococcus	0 ± 0.00	0 ± 0.00	0.004 ± 0.01	0.065 ± 0.03	0 ± 0.00	0.603 ± 0.08	0 ± 0.00	0 ± 0.00	0.128 ± 0.04	0.678 ± 0.08	0.091 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00		
				Rothia	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.072 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.13 ± 0.04	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	
				Unclassified	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.085 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	
				Mycobacteriaceae	Mycobacterium	0 ± 0.00	0 ± 0.00	7.519 ± 0.26	19.15 ± 0.40	0 ± 0.00	0 ± 0.00	0.008 ± 0.01	0 ± 0.00	0.598 ± 0.07	0 ± 0.00	0.057 ± 0.02	0 ± 0.00	0.057 ± 0.02	0 ± 0.00	0.034 ± 0.02	0 ± 0.00	0 ± 0.00	
				Unclassified	0.916 ± 0.09	1.029 ± 0.10	1.308 ± 0.11	2.537 ± 0.16	0.162 ± 0.04	0.499 ± 0.07	1.613 ± 0.12	0 ± 0.00	0.688 ± 0.08	0 ± 0.00	0 ± 0.00	6.347 ± 0.25	0.205 ± 0.05	0.194 ± 0.04	22.16 ± 0.41	0 ± 0.00	0 ± 0.00		
Actinobacteria	Actinobacteria	Actinomycetales	Nakamurellaceae	Nakamurella	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.155 ± 0.04	0 ± 0.00	0 ± 0.00			
				Nocardiaceae	Rhodococcus	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.055 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.471 ± 0.07	0 ± 0.00	0 ± 0.00	0.006 ± 0.01	0 ± 0.00	0 ± 0.00	2.835 ± 0.17	0 ± 0.00	0 ± 0.00		
				Nocardiodiaceae	Friedmanniella	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.032 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.194 ± 0.04	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00		
				Marmoricola	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.052 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00			
				Nocardioidea	Marmoricola	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.292 ± 0.06	0 ± 0.00	0.12 ± 0.04	0 ± 0.00	0 ± 0.00	0.648 ± 0.08	0 ± 0.00	0 ± 0.00	0.299 ± 0.05	0 ± 0.00	0 ± 0.00	0 ± 0.00		
				Propionimonas	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.007 ± 0.01	0 ± 0.00	5.568 ± 0.22	0 ± 0.00	0 ± 0.00	0 ± 0.00		
Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Brooklavia	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.029 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00			
				Propionibacterium	1.282 ± 0.12	1.148 ± 0.11	2.461 ± 0.16	1.327 ± 0.12	1.208 ± 0.12	1.378 ± 0.12	0.316 ± 0.06	0.704 ± 0.08	0.822 ± 0.09	0.608 ± 0.08	0.969 ± 0.09	1.273 ± 0.11	0 ± 0.00	0.625 ± 0.08	0 ± 0.00	0.523 ± 0.07			
				Pseudonocardiaceae	Amycolatopsis	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.161 ± 0.04	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00		
				Pseudonocardia	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.028 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00			
				Unclassified	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00		
				Unclassified	0.492 ± 0.07	2.228 ± 0.15	0.647 ± 0.08	2.629 ± 0.16	0.702 ± 0.08	1.057 ± 0.10	0.412 ± 0.06	1.658 ± 0.13	1.457 ± 0.12	0.557 ± 0.08	0.474 ± 0.07	2.517 ± 0.15	0.007 ± 0.01	0.372 ± 0.06	0.38 ± 0.06	0.419 ± 0.07			
Actinobacteria	Actinobacteria	Actinomycetales	Bifidobacteriales	Bifidobacteriaceae	Gardnerella	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.658 ± 0.08	0.138 ± 0.04	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00			
				Rubrobacteriales	Rubrobacteriaceae	Conexibacter	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.051 ± 0.02	0 ± 0.00	0 ± 0.00	0.063 ± 0.02	0 ± 0.00	0.194 ± 0.04	0 ± 0.00	0 ± 0.00			
				Unclassified	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	1.554 ± 0.13	0 ± 0.00	0 ± 0.00	0 ± 0.00				

Phylum	Class	Order	Family	Genus	AL1B	AL2B	AL1Z	AL2Z	AM1B	AM2B	AM1Z	AM2Z	AMDZ	AMUB	AMUZ	H1B	M1C	M1C	M1A	M1A	
Chloroflexi	Caldilineae	Caldilineales	Unclassified		0 ± 0.00	0 ± 0.00	0.615 ± 0.08	2.418 ± 0.15	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.005 ± 0.01	0.007 ± 0.01	0.264 ± 0.05	0 ± 0.00	0 ± 0.00	
			Caldilineaceae	Caldilinea	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.047 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
Cyanobacteria	Cyanobacteria	Unclassified	Unclassified		0 ± 0.00	0.186 ± 0.04	1.037 ± 0.10	2.236 ± 0.14	0.213 ± 0.05	0.346 ± 0.06	2.868 ± 0.17	0.006 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	2.995 ± 0.17	0.834 ± 0.09	0 ± 0.00	6.693 ± 0.27	0 ± 0.00	0.235 ± 0.05
			Deinococcus-Thermus	Deinococci	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.338 ± 0.06	0 ± 0.00	0.021 ± 0.01	0.174 ± 0.04	0 ± 0.00	0 ± 0.00	1.902 ± 0.14
Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	0.006 ± 0.01	0 ± 0.00	15.05 ± 0.36	0 ± 0.00	0 ± 0.00	0.473 ± 0.07	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.351 ± 0.06	0.365 ± 0.06	0.025 ± 0.02	0.155 ± 0.04	0 ± 0.00	0.078 ± 0.03
				Geobacillus	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.017 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Unclassified	0 ± 0.00	0 ± 0.00	0.739 ± 0.08	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.129 ± 0.04	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.014 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				IncertaeSedisX	0.266 ± 0.05	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				IncertaeSedisXII	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.079 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.042 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Listeriaeae	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.198 ± 0.04	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Paenibacillaceae	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.304 ± 0.06	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.007 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Cohnella	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.312 ± 0.06	0.032 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Paenibacillus	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.271 ± 0.05	0.269 ± 0.05	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Unclassified	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.017 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Staphylococcaceae	0 ± 0.00	0 ± 0.00	0.004 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.056 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Salinicoccus	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.077 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Staphylococcus	0.018 ± 0.01	1.471 ± 0.12	0.518 ± 0.07	0.333 ± 0.06	0.493 ± 0.07	0.594 ± 0.08	0.174 ± 0.04	0 ± 0.00	0.394 ± 0.06	0.491 ± 0.07	0.278 ± 0.05	0.028 ± 0.02	0 ± 0.00	1.083 ± 0.10	0 ± 0.00	0.332 ± 0.06	0 ± 0.00
				Unclassified	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.041 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.019 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Thermoactinomycetaceae	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.07 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Unclassified	4.055 ± 0.21	4.046 ± 0.21	2.812 ± 0.17	0.989 ± 0.10	0 ± 0.00	2.035 ± 0.14	0.321 ± 0.06	0 ± 0.00	0.641 ± 0.08	0.365 ± 0.06	0.441 ± 0.07	2.048 ± 0.14	0.019 ± 0.01	1.185 ± 0.11	0 ± 0.00	0.228 ± 0.05	0 ± 0.00
			Lactobacillales	Aerococcaceae	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.07 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.403 ± 0.06	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Carnobacteriaceae	0 ± 0.00	0 ± 0.00	0.016 ± 0.01	0.08 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Lactobacillaceae	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.127 ± 0.04	0 ± 0.00	0 ± 0.00	0.243 ± 0.05	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Streptococcaceae	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.091 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.136 ± 0.04	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Streptococcus	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.176 ± 0.04	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.434 ± 0.07	0.347 ± 0.06	0 ± 0.00	0.069 ± 0.03	0.198 ± 0.05	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.035 ± 0.02	0 ± 0.00
			Clostridia	Clostridiales	Clostridiaceae	Anaerobacter	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.823 ± 0.09	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	2.185 ± 0.15	0 ± 0.00	0.007 ± 0.01	0 ± 0.00
						Clostridium	0 ± 0.00	0 ± 0.00	0.017 ± 0.01	0 ± 0.00	0 ± 0.00	0.313 ± 0.06	14.73 ± 0.35	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	25 ± 0.45	0.02 ± 0.01	4.286 ± 0.20	0 ± 0.00
						Unclassified	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	8.391 ± 0.28	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	64 ± 0.50	0.058 ± 0.02	1.51 ± 0.12	0 ± 0.00	
						IncertaeSedisXI	0 ± 0.00	1.407 ± 0.12	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.087 ± 0.03	
						Finogoldia	0.154 ± 0.04	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	
						Peptoniphilus	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.119 ± 0.03	0 ± 0.00	0 ± 0.00	0.06 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	
						IncertaeSedisXII	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.557 ± 0.08	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00		
						IncertaeSedisXIII	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	1.347 ± 0.12	11.01 ± 0.32	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.452 ± 0.06	0 ± 0.00	0 ± 0.00		
						Mogibacterium	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.057 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00		
						Lachnospiraceae	Lachnospira	0 ± 0.00	0.164 ± 0.04	0 ± 0.00	0 ± 0.00	0.229 ± 0.05	7.695 ± 0.27	0 ± 0.00	0 ± 0.00	0.014 ± 0.01	0.294 ± 0.05	0.012 ± 0.01	0 ± 0.00	0 ± 0.00	
						Unclassified	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.551 ± 0.07	12.2 ± 0.32	0 ± 0.00	0.008 ± 0.01	0 ± 0.00	0.007 ± 0.01	0.006 ± 0.01	0.642 ± 0.08	0.262 ± 0.05	0.651 ± 0.08	0.165 ± 0.04
						Peptococcaceae	Desulfosporosinus	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	1.4 ± 0.12	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	
						Unclassified	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	1.211 ± 0.11	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.058 ± 0.02	0.342 ± 0.06	0 ± 0.00	0.211 ± 0.05	
						Peptostreptococcaceae	Peptostreptococcus	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.523 ± 0.07	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	
						Unclassified	0.285 ± 0.05	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00		
						Sporacetigenium	0 ± 0.00	0.517 ± 0.07	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.296 ± 0.05	0 ± 0.00	0 ± 0.00	
						Ruminococcaceae	Ethanoligenens	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.197 ± 0.05	0 ± 0.00	0.639 ± 0.08	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.289 ± 0.05	0 ± 0.00	0 ± 0.00	
						Faecalibacterium	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.828 ± 0.09	0 ± 0.00	
						Unclassified	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	1.441 ± 0.12	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.138 ± 0.04	0 ± 0.00	0.051 ± 0.02		
						Veillonellaceae	Anaerosinus	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.471 ± 0.07	0.976 ± 0.10	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.126 ± 0.04	0 ± 0.00	0 ± 0.00	
						Propionispira	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.013 ± 0.01	0 ± 0.00	0 ± 0.00		
						Sporomusa	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.192 ± 0.04	0.116 ± 0.03	0 ± 0.00	0 ± 0.00		

Phylum	Class	Order	Family	Genus	AL1B	AL2B	AL1Z	AL2Z	AM1B	AM2B	AM1Z	AM2Z	AMDZ	AMUB	AMUZ	H1B	M1C	M2C	M3A	M4A						
			Methylobacteriaceae	Methylobacterium	0 ± 0.00	0 ± 0.00	0.36 ± 0.06	0 ± 0.00	0.008 ± 0.01	0 ± 0.00	0 ± 0.00	0.006 ± 0.01	0.293 ± 0.05	0 ± 0.00	9.854 ± 0.30	0.092 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00					
			Methylocystaceae	Pleomorphomonas	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.247 ± 0.05	0.842 ± 0.09	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00			
				Nitritoreductor	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.018 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00		
				Rhizobiaceae	Rhizobium	0.179 ± 0.04	0 ± 0.00	2.757 ± 0.17	0 ± 0.00	0 ± 0.00	0.117 ± 0.03	0.138 ± 0.04	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.087 ± 0.03	0 ± 0.00		
				Unclassified		0 ± 0.00	0 ± 0.00	0.801 ± 0.09	0.279 ± 0.05	0 ± 0.00	0.405 ± 0.07	0.877 ± 0.09	0.29 ± 0.05	0.317 ± 0.06	0 ± 0.00	0.084 ± 0.03	0.321 ± 0.06	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00		
			Rhodobacterales	Rhodobacteraceae		Paracoccus	0 ± 0.00	0 ± 0.00	0.004 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.502 ± 0.07	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	
						Rhodobacter	0 ± 0.00	0 ± 0.00	0.976 ± 0.10	0.251 ± 0.05	0.453 ± 0.07	1.117 ± 0.10	0.008 ± 0.01	0.006 ± 0.01	0.623 ± 0.08	0 ± 0.00	0.028 ± 0.02	0.184 ± 0.04	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.018 ± 0.01	0 ± 0.00	
						Roseovarius	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.007 ± 0.01	0 ± 0.00	0 ± 0.00	0.007 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.051 ± 0.02	0 ± 0.00	0 ± 0.00	0.01 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
						Rubellimicrobium	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.036 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.808 ± 0.09	0.292 ± 0.06	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
						Silicibacter	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.08 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
Rhodospirillales	Acetobacteraceae		Craurococcus	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.034 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	2.457 ± 0.15	0.916 ± 0.09	0.036 ± 0.02				
			Unclassified	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.064 ± 0.03	0 ± 0.00	0 ± 0.00	0.069 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.107 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00			
Sphingomonadales	Sphingomonadaceae		Blastomonas	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.034 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00				
			Erythrobracter	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.056 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00			
			Novosphingobium	0 ± 0.00	0 ± 0.00	3.154 ± 0.17	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.284 ± 0.05	0 ± 0.00	0.248 ± 0.05	0 ± 0.00	0.006 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00			
			Sphingobium	0.238 ± 0.05	0 ± 0.00	0 ± 0.00	0.055 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.02 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00			
			Sphingomonas	0 ± 0.00	0 ± 0.00	0.847 ± 0.10	0.157 ± 0.04	0 ± 0.00	1.179 ± 0.11	0.113 ± 0.03	9.928 ± 0.30	0.707 ± 0.09	0.739 ± 0.08	6.011 ± 0.24	0.011 ± 0.01	0 ± 0.00	0.302 ± 0.06	1.103 ± 0.11	0.323 ± 0.06	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00			
			Sphingopyxis	0.549 ± 0.08	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.486 ± 0.07	0.077 ± 0.03	0 ± 0.00	0.008 ± 0.01	0.39 ± 0.06	4.007 ± 0.19	0.583 ± 0.08	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.35 ± 0.06	0 ± 0.00	0 ± 0.00			
			Unclassified	0.031 ± 0.02	0 ± 0.00	0.008 ± 0.01	0.046 ± 0.02	0 ± 0.00	0.122 ± 0.04	0.018 ± 0.01	0.007 ± 0.01	0 ± 0.00	0.065 ± 0.03	6.68 ± 0.25	0.034 ± 0.02	0 ± 0.00	0.009 ± 0.01	0 ± 0.00	0.069 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00			
			Unclassified	0.012 ± 0.01	0 ± 0.00	0.381 ± 0.06	0.381 ± 0.06	0.92 ± 0.10	0.335 ± 0.06	0.086 ± 0.03	0.104 ± 0.03	0.387 ± 0.06	0.161 ± 0.04	1.452 ± 0.12	0.093 ± 0.03	0 ± 0.00	0.019 ± 0.01	0 ± 0.00	0.097 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00			
Betaproteobacteria	Burkholderiales	Alcaligenaceae		Achromobacter	0 ± 0.00	0 ± 0.00	0.907 ± 0.09	0.008 ± 0.01	0 ± 0.00	0.007 ± 0.01	0 ± 0.00	0 ± 0.00	0.201 ± 0.04	0 ± 0.00	0 ± 0.00	0.017 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00					
				Sutterella	0 ± 0.00	0.474 ± 0.07	0 ± 0.00	0.079 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.243 ± 0.05	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.068 ± 0.03			
				Unclassified	0 ± 0.00	0 ± 0.00	0.017 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00		
		Burkholderiaceae		Burkholderia	0.013 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00			
				Chitinimonas	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.04 ± 0.02	0 ± 0.00	0.007 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.011 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00			
				Cupriavidus	0.536 ± 0.07	0.506 ± 0.07	0.755 ± 0.09	1.4 ± 0.12	0.653 ± 0.08	3.193 ± 0.18	0.221 ± 0.05	1.324 ± 0.12	1.549 ± 0.12	0 ± 0.00	0.511 ± 0.07	3.005 ± 0.16	0 ± 0.00	0.507 ± 0.07	0 ± 0.00	0.106 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00			
				Polynucleobacter	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.033 ± 0.02	0.179 ± 0.04	0.015 ± 0.01	0 ± 0.00	0 ± 0.00	0.04 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00			
				Ralstonia	0 ± 0.00	0 ± 0.00	0.008 ± 0.01	0.055 ± 0.02	0.036 ± 0.02	0.029 ± 0.02	0.009 ± 0.01	0.012 ± 0.01	0.016 ± 0.01	0 ± 0.00	0.007 ± 0.01	0.08 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00			
				Unclassified	0.006 ± 0.01	0 ± 0.00	0.005 ± 0.01	0.016 ± 0.01	0.007 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.008 ± 0.01	0.04 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00			
				Comamonadaceae	Acidovorax	0.702 ± 0.08	1.878 ± 0.13	2.553 ± 0.16	0.381 ± 0.06	0.135 ± 0.04	1.236 ± 0.11	0.38 ± 0.06	1.609 ± 0.12	0.387 ± 0.06	0 ± 0.00	0.134 ± 0.04	1.051 ± 0.10	0.007 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.114 ± 0.03	0 ± 0.00			
			Comamonas	0.228 ± 0.05	0 ± 0.00	0 ± 0.00	0.07 ± 0.03	0 ± 0.00	1.529 ± 0.12	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00					
			Curvibacter	0 ± 0.00	0 ± 0.00	0.52 ± 0.07	0.133 ± 0.04	0.176 ± 0.04	0 ± 0.00	0.042 ± 0.02	0.838 ± 0.09	0 ± 0.00	0.062 ± 0.02	0.533 ± 0.08	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.12 ± 0.04	0 ± 0.00					
			Delftia	4.549 ± 0.21	0.586 ± 0.08	1.278 ± 0.11	0.891 ± 0.09	0.565 ± 0.08	1.613 ± 0.13	0.189 ± 0.04	0 ± 0.00	0.696 ± 0.09	0 ± 0.00	1.654 ± 0.13	0.007 ± 0.01	1.319 ± 0.11	0 ± 0.00	0.326 ± 0.06	0 ± 0.00	0 ± 0.00	0 ± 0.00					
			Polaromonas	0.247 ± 0.05	0 ± 0.00	0.013 ± 0.01	0.127 ± 0.04	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.024 ± 0.02	0 ± 0.00	0.032 ± 0.02	0.014 ± 0.01	0.035 ± 0.02	0 ± 0.00	0.254 ± 0.05	0.028 ± 0.02	0 ± 0.00	0 ± 0.00						
			Rhodoferrax	1.111 ± 0.10	0 ± 0.00	0.067 ± 0.02	0.681 ± 0.08	0 ± 0.00	0.868 ± 0.09	0.217 ± 0.05	0 ± 0.00	0.624 ± 0.07	0 ± 0.00	0.327 ± 0.06	1.626 ± 0.12	0 ± 0.00	0.139 ± 0.04	3.625 ± 0.18	0.327 ± 0.06	0 ± 0.00	0 ± 0.00					
			Variovorax	5.928 ± 0.23	0 ± 0.00	0.773 ± 0.09	1.062 ± 0.11	0 ± 0.00	0.465 ± 0.07	0 ± 0.00	0.849 ± 0.09	0.041 ± 0.02	0.771 ± 0.09	0.514 ± 0.07	0.49 ± 0.07	0.006 ± 0.01	6.717 ± 0.25	0.518 ± 0.07	0 ± 0.00	0 ± 0.00						
			Unclassified	0.578 ± 0.08	0.032 ± 0.02	0.093 ± 0.03	0.51 ± 0.07	0.014 ± 0.01	1.658 ± 0.13	0.13 ± 0.04	1.178 ± 0.11	0.307 ± 0.05	0.058 ± 0.02	0.312 ± 0.06	0.827 ± 0.09	0 ± 0.00	0.271 ± 0.05	0.134 ± 0.04	0.07 ± 0.03	0 ± 0.00						
			Incertaedis5	Aquabacterium	0.067 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.353 ± 0.06	0 ± 0.00	0.044 ± 0.02	0 ± 0.00	0.0719 ± 0.08	0 ± 0.00	0.083 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00					
				Leptothrix	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00					
				Paucibacter	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00					
				Pelomonas	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.691 ± 0.08	0 ± 0.00	0.383 ± 0.06	0.034 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.07 ± 0.03					
				Tepidimonas	0.167 ± 0.04	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0																

Phylum	Class	Order	Family	Genus	AL1B	AL2B	AL1Z	AL2Z	AM1B	AM2B	AM1Z	AM2Z	AMDZ	AMUB	AMUZ	HIB	M11C	M12C	M13A	M14A	
				Serratia	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.048 ± 0.02	0 ± 0.00	0.36 ± 0.06	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.006 ± 0.01	0 ± 0.00	0.005 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.017 ± 0.01
				Shigella	0.281 ± 0.05	0.307 ± 0.05	0 ± 0.00	1.186 ± 0.11	0.76 ± 0.09	0.772 ± 0.09	0.103 ± 0.03	0.753 ± 0.09	0.608 ± 0.08	1.611 ± 0.13	0.063 ± 0.03	0.006 ± 0.01	0 ± 0.00	0 ± 0.00	0.748 ± 0.09	0.331 ± 0.06	
				Unclassified	1.201 ± 0.11	6.133 ± 0.24	0 ± 0.00	0.586 ± 0.08	0.178 ± 0.04	1.2 ± 0.11	0.745 ± 0.09	0.025 ± 0.02	0.032 ± 0.02	0.655 ± 0.08	0.027 ± 0.02	0.389 ± 0.06	0 ± 0.00	0.01 ± 0.01	0.006 ± 0.01	54.52 ± 0.50	
		Legionellales	Coxiellaceae	Aquicella	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.016 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Rickettsiella	0 ± 0.00	0 ± 0.00	0.13 ± 0.04	0.008 ± 0.01	0 ± 0.00	0 ± 0.00	0.009 ± 0.01	0 ± 0.00	0 ± 0.00	0.039 ± 0.02	0 ± 0.00	0.005 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
			Legionellaceae	Fluoribacter	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.033 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Legionella	0 ± 0.00	0 ± 0.00	0.087 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Unclassified	0 ± 0.00	0 ± 0.00	0.567 ± 0.08	2.063 ± 0.14	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.317 ± 0.05	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.006 ± 0.01	0 ± 0.00	0.01 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00
		Methylococcales	Methylococcaceae	Methylobacter	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.008 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.036 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	13.24 ± 0.35	
				Methylomonas	0.55 ± 0.08	1.147 ± 0.10	0 ± 0.00	0.112 ± 0.03	0.415 ± 0.06	0 ± 0.00	0.224 ± 0.05	0 ± 0.00	0.259 ± 0.05	0 ± 0.00	0 ± 0.00	0.139 ± 0.04	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.168 ± 0.04	
				Unclassified	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.386 ± 0.06	
		Oceanospirillales	Oceanospirillaceae	Marinomonas	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.008 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.016 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Nitriicola	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.007 ± 0.01	0 ± 0.00	0 ± 0.00	0.041 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Unclassified	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.055 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.048 ± 0.02	0.275 ± 0.05	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
		Pseudomonadales	Incertaesedis6	Enhydrobacter	0 ± 0.00	0 ± 0.00	0.896 ± 0.09	0.056 ± 0.02	0.056 ± 0.02	0.467 ± 0.07	0 ± 0.00	0 ± 0.00	0.66 ± 0.08	0 ± 0.00	0.027 ± 0.02	0.239 ± 0.05	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.052 ± 0.02	
			Moraxellaceae	Acinetobacter	31.07 ± 0.48	16.16 ± 0.37	19.12 ± 0.40	2.865 ± 0.17	4.706 ± 0.21	18.95 ± 0.38	5.603 ± 0.24	10.36 ± 0.31	46.84 ± 0.49	13.56 ± 0.34	1.179 ± 0.11	12.66 ± 0.34	0.032 ± 0.02	4.009 ± 0.20	27.23 ± 0.43	10.33 ± 0.29	
				Alkanindiges	1.687 ± 0.13	2.027 ± 0.14	0 ± 0.00	0.11 ± 0.03	0.099 ± 0.03	0.173 ± 0.04	0.165 ± 0.04	0 ± 0.00	0.106 ± 0.03	0.311 ± 0.05	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Unclassified	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.039 ± 0.02	0 ± 0.00	0.006 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
			Pseudomonadaceae	Cellvibrio	0 ± 0.00	0 ± 0.00	0.461 ± 0.07	0 ± 0.00	0 ± 0.00	0.225 ± 0.05	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.007 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Flavimonas	0 ± 0.00	0 ± 0.00	0.029 ± 0.02	0 ± 0.00	0.035 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.012 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Pseudomonas	7.839 ± 0.27	14.65 ± 0.34	6.013 ± 0.24	2.572 ± 0.16	2.69 ± 0.17	4.249 ± 0.20	0.704 ± 0.09	0 ± 0.00	2.53 ± 0.16	6.067 ± 0.24	0.328 ± 0.06	7.813 ± 0.27	0.013 ± 0.01	5.228 ± 0.23	5.14 ± 0.22	1.033 ± 0.10	
				Unclassified	0.193 ± 0.04	0.274 ± 0.05	0.126 ± 0.03	0.12 ± 0.03	0.107 ± 0.03	0.205 ± 0.05	0.009 ± 0.01	0 ± 0.00	0.073 ± 0.03	0.092 ± 0.03	0.007 ± 0.01	0.167 ± 0.04	0 ± 0.00	0.116 ± 0.03	0.007 ± 0.01	0.131 ± 0.04	
			Unclassified	Unclassified	0.006 ± 0.01	0.047 ± 0.02	0.049 ± 0.02	0.024 ± 0.02	0 ± 0.00	0.045 ± 0.02	0.042 ± 0.02	0 ± 0.00	0.105 ± 0.03	0.012 ± 0.01	0 ± 0.00	0.023 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.009 ± 0.01
		Vibrionales	Vibrionaceae	Allomonas	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.015 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.008 ± 0.01	0.006 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.007 ± 0.01	0 ± 0.00	0 ± 0.00
				Photobacterium	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.008 ± 0.01	0 ± 0.00	0.029 ± 0.02	0 ± 0.00	0 ± 0.00	0.008 ± 0.01	0.006 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.007 ± 0.01	0 ± 0.00
				Vibrio	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.311 ± 0.05	0.171 ± 0.04	3.317 ± 0.18	0.206 ± 0.05	1.484 ± 0.12	0.855 ± 0.10	1.209 ± 0.11	0.007 ± 0.01	0.011 ± 0.01	0 ± 0.00	0.194 ± 0.04	4.298 ± 0.21	0 ± 0.00	0 ± 0.00
				Unclassified	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.033 ± 0.02	0 ± 0.00	0.095 ± 0.03	0.008 ± 0.01	0.483 ± 0.07	0 ± 0.00	0.052 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.01 ± 0.01	0.216 ± 0.05	0 ± 0.00	0 ± 0.00
		Xanthomonadales	Xanthomonadaceae	Lysobacter	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.049 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Stenotrophomonas	0 ± 0.00	1.17 ± 0.10	0.881 ± 0.09	0 ± 0.00	0 ± 0.00	0.319 ± 0.06	0.042 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.007 ± 0.01	0 ± 0.00	0 ± 0.00	0.246 ± 0.05	0 ± 0.00	0.097 ± 0.03	
				Xanthomonas	0.025 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Unclassified	0 ± 0.00	0.016 ± 0.01	0 ± 0.00	0 ± 0.00	0.007 ± 0.01	0 ± 0.00	0.07 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.073 ± 0.03	0.008 ± 0.01	
		Unclassified	Unclassified	Unclassified	0.086 ± 0.03	0.919 ± 0.09	1.289 ± 0.12	0.675 ± 0.08	0.228 ± 0.05	0.661 ± 0.08	0.463 ± 0.07	2.907 ± 0.17	0.657 ± 0.08	1.078 ± 0.10	0.049 ± 0.02	0.91 ± 0.09	0 ± 0.00	0.07 ± 0.03	0.081 ± 0.03	2.309 ± 0.15	
		Unclassified	Unclassified	Unclassified	0.196 ± 0.05	0.452 ± 0.07	1.283 ± 0.12	1.159 ± 0.10	0.319 ± 0.06	0.844 ± 0.09	0.232 ± 0.05	0.047 ± 0.02	1.494 ± 0.12	0.878 ± 0.09	0.619 ± 0.08	1.943 ± 0.14	0 ± 0.00	0.165 ± 0.04	0 ± 0.00	2.818 ± 0.16	
		TM7	TM7 genera incertae sedis	Unclassified	0.35 ± 0.06	0 ± 0.00	1.001 ± 0.10	0.753 ± 0.09	0 ± 0.00	1.583 ± 0.13	0.043 ± 0.02	0.146 ± 0.04	0.155 ± 0.04	0.058 ± 0.02	0 ± 0.00	0.041 ± 0.02	0.045 ± 0.02	0.117 ± 0.03	0.587 ± 0.07	0.131 ± 0.04	
		Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Opiritaceae	Opiritus	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.106 ± 0.03	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Verrucomicrobiaceae	Verrucomicrobium	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.008 ± 0.01	0 ± 0.00	0 ± 0.00	0.013 ± 0.01	0 ± 0.00	0.208 ± 0.04	0 ± 0.00	0.023 ± 0.02	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00
				Unclassified	Unclassified	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.388 ± 0.06	0 ± 0.00	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.006 ± 0.01	0 ± 0.00	0 ± 0.00	0.009 ± 0.01	0 ± 0.00	0 ± 0.00	0 ± 0.00	
				Xiphinematobacteriaceae	Unclassified	0 ± 0.00	0 ± 0.00	0 ± 0.00	0.071 ± 0.03	0 ± 0.00	0.376 ± 0.06	0 ± 0.00	0.509 ± 0.07	0 ± 0.00	0.71 ± 0.08	0 ± 0.00	0.824 ± 0.09	0 ± 0.00	0.108 ± 0.03	0 ± 0.00	0 ± 0.00
		Unclassified	Unclassified	Unclassified	6.433 ± 0.25	11.82 ± 0.32	3.746 ± 0.19	15.77 ± 0.35	39.75 ± 0.50	11.34 ± 0.33	6.365 ± 0.24	9.678 ± 0.30	8.203 ± 0.28	13.14 ± 0.34	6.15 ± 0.25	9.599 ± 0.28	0.108 ± 0.03	55.51 ± 0.50	3.758 ± 0.19	2.712 ± 0.16	

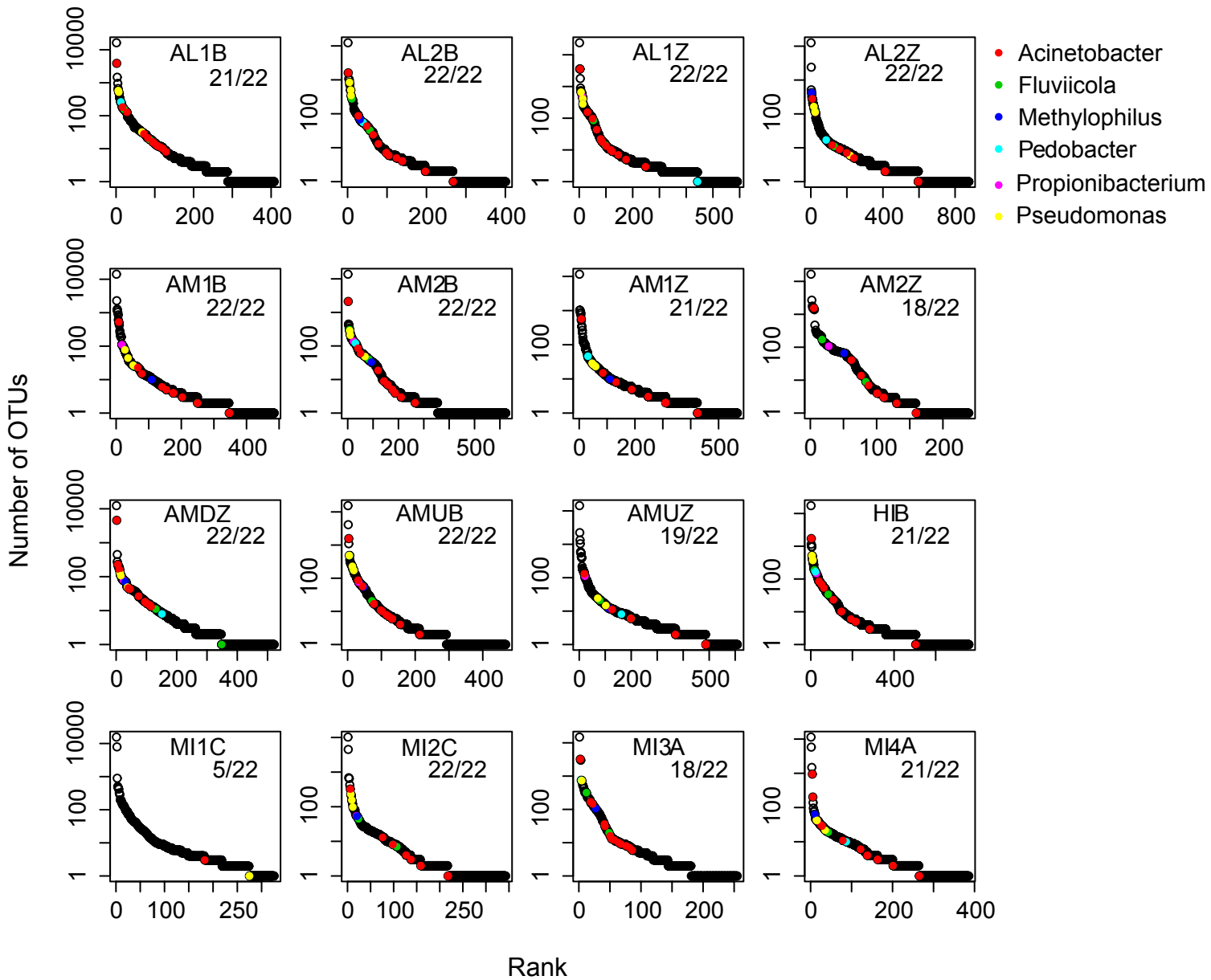


Figure A. 1

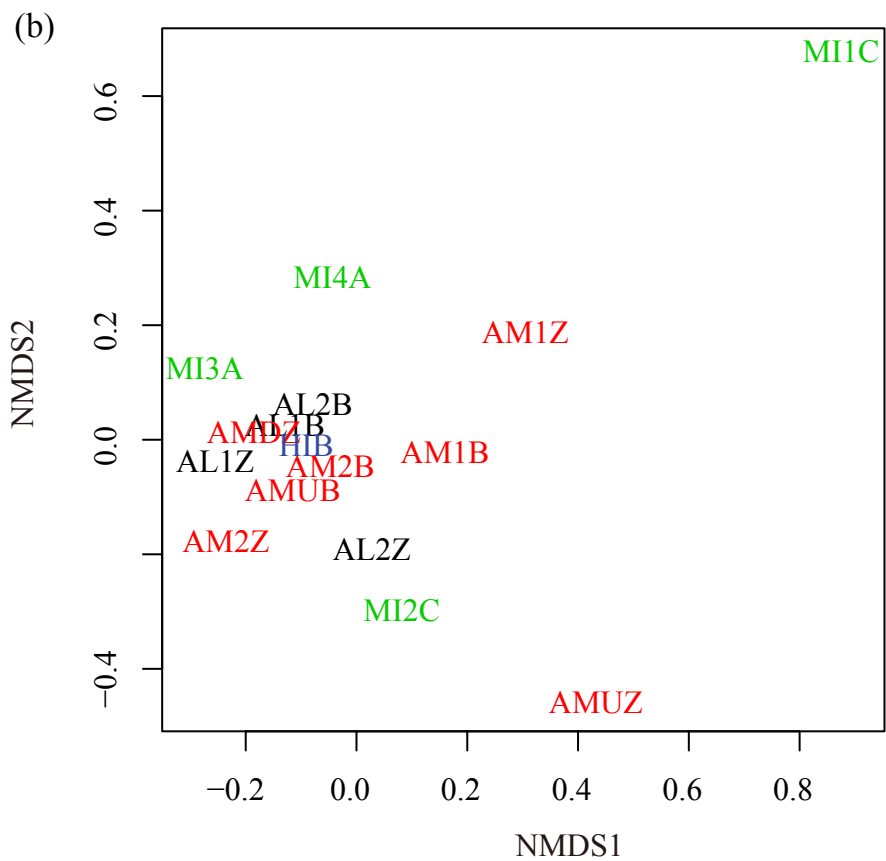
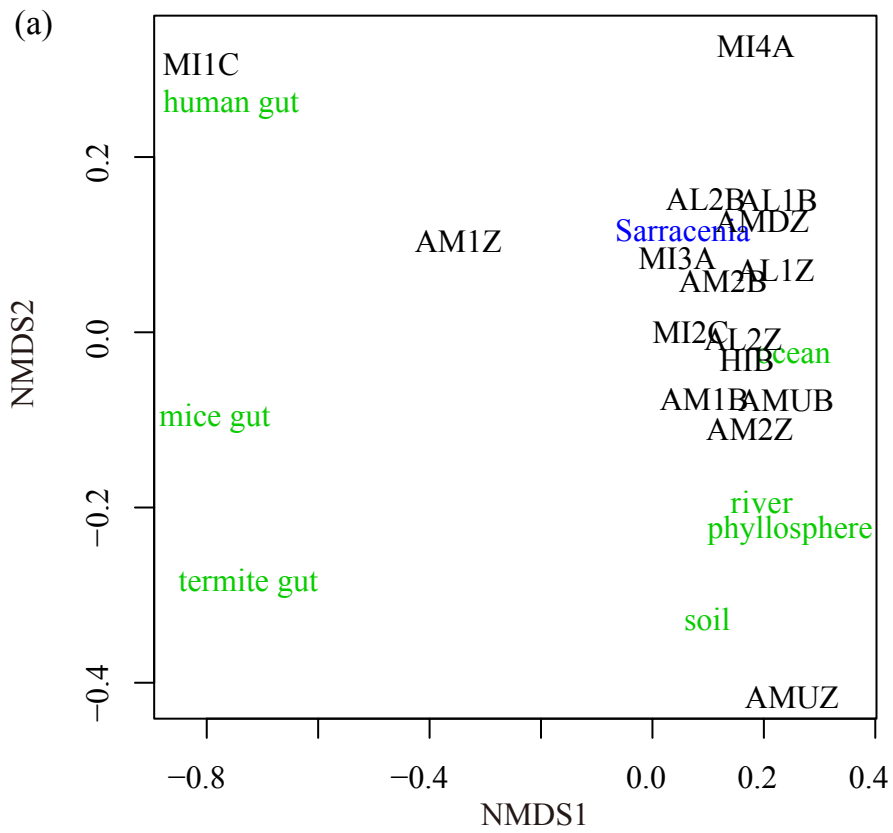


Figure A.2