

# Soil Microbiome Diversity on Sable Island, Nova Scotia

By  
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## Abstract

The soil microbiome is essential for ecosystem functioning and influences both above- and below-ground communities. Sable Island is a sand bar with a large feral horse population, which has been shown to affect marram grasslands more than heathlands. Feral horses can have negative effects on soil microbiomes by reducing microbial diversity and abundance, but there has been no previous research on soil microbes on Sable Island. Determining the microbial composition and the driving factors of diversity is crucial for effective ecosystem management. Our goal was to determine differences in microbial  $\alpha$ -diversity and  $\beta$ -diversity across vegetation types, soil pH, organic matter, and phosphorous. This study also serves as an overall survey of bacterial and fungal diversity. We expected microbial  $\alpha$ -diversity to be lower in marram grasslands than in heathlands, and the microbial  $\beta$ -diversity to differ between vegetation types. Using eDNA from soil samples, we identified bacteria with 16S and fungi with ITS2 DNA barcodes and performed soil analyses from 80 samples from 16 sites on the island. We identified a total of 812 bacterial and 336 fungal ASVs. Our results indicate that bacterial  $\alpha$ -diversity was significantly ( $p < 0.05$ ) affected by the vegetation type, soil pH, and organic matter content, but not phosphorous concentration. In contrast, fungi were robust to variation in the environmental factors and fungal  $\alpha$ -diversity was not significantly affected by any variables. Microbial  $\alpha$ -diversity was not lower in marram grasslands than in heathlands, potentially due to horse activities damaging the vegetation types similarly and an increase in nutrient deposition in the marram. Microbial  $\beta$ -diversity of presence/absence was not significantly affected by any variable. Identifying drivers of soil microbiome diversity is important for effective ecosystem management in vulnerable ecosystems such as Sable Island.

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## Table of Contents

<b>1. Introduction</b> .....	<b>4</b>
<b>1.1 Microbes in the environment</b> .....	<b>4</b>
1.1.1 <i>Bacteria and Fungi</i> .....	5
<b>1.2 Grazer effects on the environment</b> .....	<b>7</b>
<b>1.3 Sable Island</b> .....	<b>9</b>
1.3.1 <i>Sable Island Biodiversity</i> .....	10
<b>1.4 Objectives and Hypotheses</b> .....	<b>11</b>
<b>2. Materials and Methods</b> .....	<b>12</b>
<b>2.1 Site Design</b> .....	<b>12</b>
<b>2.2 Soil Sampling and Analyses</b> .....	<b>13</b>
2.2.1 <i>eDNA</i> .....	13
2.2.2 <i>Soil Characteristics</i> .....	14
<b>2.3 eDNA Extraction, Metabarcoding, and Bioinformatics Processing</b> .....	<b>15</b>
<b>2.4 Statistical Analyses</b> .....	<b>16</b>
<b>3. Results</b> .....	<b>17</b>
<b>3.1 Overview</b> .....	<b>17</b>
<b>3.2 Relative Abundance</b> .....	<b>18</b>
<b>3.3 <math>\alpha</math>-Diversity</b> .....	<b>19</b>
<b>3.4 <math>\beta</math>-Diversity</b> .....	<b>22</b>
<b>4. Discussion</b> .....	<b>23</b>
<b>4.1 Effects of Vegetation Type on Microbial Diversity</b> .....	<b>24</b>
4.1.1 <i>Relative Abundance</i> .....	24
4.1.2 <i><math>\alpha</math>-Diversity</i> .....	25
4.1.3 <i><math>\beta</math>-Diversity</i> .....	26
<b>4.2 Effects of Soil Characteristics on Microbial Diversity</b> .....	<b>27</b>
4.2.1 <i><math>\alpha</math>-Diversity</i> .....	27
4.2.2 <i><math>\beta</math>-Diversity</i> .....	27
<b>4.3 Ecosystem Management</b> .....	<b>28</b>
<b>4.4 Limitations and Future Research</b> .....	<b>28</b>
<b>5. Conclusion</b> .....	<b>29</b>
<b>Acknowledgements</b> .....	<b>31</b>
<b>References</b> .....	<b>32</b>
<b>Appendix</b> .....	<b>40</b>
<b>Appendix A</b> .....	<b>40</b>
<b>Appendix B</b> .....	<b>42</b>
<b>Appendix C</b> .....	<b>45</b>
C.1. <i>Bacteria and Archaea</i> .....	45
C.2 <i>Fungi</i> .....	61

# 1. Introduction

## 1.1 Microbes in the environment

Microbes in the soil consist of bacteria, fungi, archaea, viruses, and protozoa; together these microbes form the soil microbiome (Fierer, 2017). Soil contains a high abundance of diverse taxa even though only approximately 0.000001% of the soil surface area is inhabited by microbes (Young & Crawford, 2004). Of the microbes that are present, only 0.1-5% are active at a given moment, and 10-60% can be activated within hours of stimuli (Blagodatskaya & Kuzyakov, 2013). This means that most microbes are dormant until conditions permit, at which point they become engaged in processes such as decomposition. The microbiome composition varies widely depending on many factors, including the vegetation type and soil characteristics such as aggregate size, texture, nutrient content, and pH; however, no particular factor is consistently an overarching determinant of the composition (Fierer, 2017).

The soil microbiome is fundamental to ecosystem functioning; it is responsible for nutrient cycling, decomposition, and carbon sequestration (Mishra et al., 2023). These three processes often work simultaneously when breaking down organic matter. Nitrogen is cycled by ammonification followed by nitrification; this is when organic nitrogen is converted to ammonia by one set of microorganisms, and then another group of microorganisms convert the ammonia into nitrites and nitrates (Mishra et al., 2023). Microorganisms convert phosphorous from an organic to an inorganic form which is soluble and more bioavailable to plants (Mishra et al., 2023). Microbes feed on the organic carbon in decomposing organic material to use it for their biomass. Additionally, the microbiome affects atmospheric carbon dioxide (CO<sub>2</sub>) concentrations despite their low cumulative biomass (Liang et al., 2017). Carbon sequestration occurs when autotrophic microbes take CO<sub>2</sub> from the atmosphere to build biomass or release non-gaseous carbon forms

into the rhizosphere (Jansson & Hofmockel, 2020). Dead microbial biomass, containing carbon, adheres to soil substrates and acts as a carbon sink (Liang et al., 2017). Some microbe species can also transform CO<sub>2</sub> into carbonate minerals that remain in the soil for extensive periods (Jiang et al., 2022). However, when the microbial pool is affected by increased temperature or nitrogen, the microbial contribution to the carbon sink is decreased which can result in a carbon source-sink imbalance (Liang & Balsler (2012).

Shifts in the microbial taxa can impact how the microbiome operates and what ecological function is served (Fierer, 2017). Diversity of the microbiome can depend on abiotic factors such as pH, soil nutrient concentrations, precipitation, and temperature; physical disturbance such as compaction and erosion; and anthropogenic factors such as pollutants, invasive species, and climate change (Mishra et al., 2023). As the soil microbiome is important for the functioning of ecosystems, impacts on the microbiome can lead to reduced functionality with downstream consequences.

### *1.1.1 Bacteria and Fungi*

Bacterial and fungal taxonomic diversity is affected by abiotic and biotic factors. As bacteria and fungi both live in similar environments, they are competing for the same resources (Bahram et al., 2018). Bacterial taxa differ among climatic regions suggesting niche specialization, which may make them more susceptible to climate change (Bahram et al., 2018). Bahram et al. (2018) suggested that fungi are more tolerant to nutrient and water limitations than bacteria, as they possess structures like hyphae which improve their ability to access water and can use more complex carbon sources. Both taxonomic groups have evolved mechanisms to increase their competitive advantage: fungi will express antimicrobial compounds, and in response, bacteria

express antibiotic-resistance genes (ARGs) (Bahram et al., 2018). Bacteria expressing ARGs are found more often when in competition with fungi than with other bacteria (Bahram et al., 2018).

The relative abundance of bacteria or fungi in the soil fluctuates based on environmental factors. This is often due to pH, nutrients, soil moisture, soil temperature, disturbance, and the presence of organic matter; however, the outcome of bacterial or fungal dominance can be inconsistent with the general expectations (Strickland & Rousk, 2010). This is likely due to both groups having similar functions in ecosystem processes, as they can be symbiotic with plants, break down organic matter, or cause disease (Clark, 2012; Money, 2016). Also, the high diversity within the microbiome can allow shifts in dominance depending on environmental conditions (i.e., saprophytic fungi decrease with nitrogen limitation, but mycorrhizal fungi are unaffected) (Strickland & Rousk, 2010). Bacterial or fungal dominance can not be directly related to functionality within the soil; the specific functional groups of bacteria or fungi must be compared to assess relevant dominances and functional shifts (Strickland & Rousk, 2010). However, determining the functionality of specific taxa remains a difficult task (Fierer, 2017).

Some taxa of bacteria and fungi form mutualistic associations that benefit both their plant host and the microbe itself. These associations help the plant and promote growth by providing nutrients that are difficult to access, making plants more stress tolerant and providing resistance to disease by pathogenic microbes (Amoo et al., 2023; Trillas & Segarra, 2009). Protection of the plant by a beneficial microorganism is done by parasitizing the pathogenic microorganism, antibiosis (i.e., production of antibiotics), or competition (Amoo et al., 2023).

The association some bacteria form with plants results in a nitrogen-carbon exchange. Two major groups of bacteria are nitrogen-fixing: rhizobia and *Frankia*; these bacteria form associations with plants and receive carbon while providing nitrogen to the plant (Franche et al.,

2009). Both groups of bacteria enter the plant through root hairs intracellularly or intercellularly, and once the infection is established the plant forms a nodule at that site (Vessey et al., 2004). Rhizobia forms a symbiosis with leguminous plants or non-leguminous *Parasponia* sp. where plants form root nodules for the bacteria to live in (Franche et al., 2009); the rhizobia give the plant ammonium and receive carbon in return (Prell & Poole, 2006). *Frankia* bacteria form a symbiosis with actinorhizal plants, leading to a similar exchange of nitrogen and carbon (Vessey et al., 2004).

Several types of fungi, such as endophytic and ectophytic, form beneficial associations with plants, which live in and outside the plant's body, respectively. Examples of endophytic fungi include arbuscular mycorrhizae and ericoid mycorrhizae. Arbuscular and ericoid mycorrhizae form associations via penetrating the plant cells by growing branched or coiled structures, respectively (Trillas & Segarra, 2009). Fungi that form an association without penetrating the host are known as ectomycorrhizal, or ectophytic, fungi which form structures around the root of the plant (Trillas & Segarra, 2009). Like rhizobia and *Frankia*, the associated fungi receive carbon from the host plant, while providing nutrients such as phosphorous, nitrogen, potassium, and other metals to the plant (Marschner & Dell, 1994). The colonization of the plant with the fungi elicits a defence response by the plant to prevent invasion into the endodermis and vessels by pathogenic microbes, and thereby help protect the plant from pathogenic fungi (Trillas & Segarra, 2009).

## **1.2 Grazer effects on the environment**

Terrestrial grazers are animals that feed on plants like grasses; often, these animals form herds such as cattle and horses. Grazers affect biotic and abiotic factors in their environment through activities such as grazing, trampling, and producing excrement (Eldridge et al., 2020). Biotic effects of grazing include the herbivory of plant species which reduces plant relative abundances, facilitates exotic species, and alters the plant community composition (e.g., grasslands

to shrublands) with increasing grazing intensity (Mikola et al., 2009; Eldridge et al., 2020; McSherry & Ritchie, 2013). Grazers also have biotic effects on the presence of soil macrofauna (e.g., nematodes, ants), and can induce the growth of mycorrhizal hyphae (Mikola et al., 2009; Eldridge et al., 2020; McSherry & Ritchie, 2013). Abiotic effects of grazing consist of increased soil pH, increased soil density (as trampling removes soil pores), increased soil moisture, increased erosion, and reduced litter cover and depth (Mikola et al., 2009; Eldridge et al., 2020). Grazers also cause nutrient patchiness due to herbivory; they remove plant biomass and thus nutrients, and later return the nutrients in patches through excrement (Mikola et al., 2009).

Depending on vegetation and soil type, the effects of grazers can differ. Intense grazing on sandy soils reduces vegetation, which can make the soil more vulnerable to erosion and potentially lead to net carbon release from the soil (McSherry & Ritchie, 2013). Whether plants use C<sub>3</sub> or C<sub>4</sub> photosynthesis affects whether the carbon is sequestered or released under grazing pressures. The C<sub>3</sub> and C<sub>4</sub> photosynthesis pathways differ in the enzymes (RuBP carboxylase vs. PEP carboxylase, respectively) and mechanisms used to create the sugar, allowing for different adaptations to their environments, such as cold tolerance (Pearcy & Ehleringer, 1984). Under heavy grazing intensity, C<sub>4</sub> grasses have a positive interaction by increasing soil carbon sequestration, this is in contrast to C<sub>3</sub> grasses which have a negative interaction by decreasing the soil carbon (McSherry & Ritchie, 2013). This may partly be due to mycorrhizal associations with C<sub>4</sub> grasses which enhance soil stability by fungal glomalin production (McSherry & Ritchie, 2013).

Detrimental environmental effects on the vegetation and soil are caused by overstocking grazing animals which leads to the over-utilization of land and food resources (Rickert, 1996). Horses spend more time foraging and travelling than cattle resulting in increased damage to vegetation and soil through their varied grazing and trampling at high stocking densities (Nolte et



al., 2017). Feral horses significantly negatively affect environmental quality by causing reductions in plant biomass, increases in erosion, reductions in animal richness, and reductions in microbial abundances which leads to ecosystem functioning disruptions (Eldridge et al., 2020).

### **1.3 Sable Island**

Sable Island is a sand bar southeast of Nova Scotia, Canada. The crescent-shaped island is approximately 40 km long and has a maximum width of 1.5 km, located at 43.9333 °N, -60.0000 °W in the North Atlantic Ocean (Eamer et al., 2022; Catling et al., 2009). As the island is a sand bar, there is accumulation and erosion of sediment, both of which affect the vegetation communities; currently, the island has more retreat occurring than sedimentation (Eamer et al., 2022). There is a possibility of eastward migration of the island due to how the sediment is accumulating, though the retreat trends are stronger which indicates the island is shrinking, rather than migrating (Eamer et al., 2022). Sable Island experiences strong winds averaging 25.7 km/h which help shape the dunescape as well as the vegetation communities (Byrne & McCann, 1995).

From 1553 to 1633, animals such as cattle and pigs were transported by Portuguese settlers to live on the island, but the animals were then removed and slaughtered by Acadians and New Englanders (Christie, 1980). Reverend Andrew Le Mercier brought cattle, sheep, hogs, and horses to the island in 1737, but abandoned them by 1753, and just before 1760, Thomas Hancock also brought horses, hogs, sheep, and goats to the island (Christie, 1980). Though many animals were taken to the island over the years, they were often stolen or sold, with only horses establishing long-term survival (Christie, 1980). Either the introduction of horses by Le Mercier or Hancock led to an established population of horses which persists today (Christie, 1980).

### 1.3.1 Sable Island Biodiversity

Sable Island is an important habitat on which a number of animal species, including birds and seals, depend. Bird species include the Least Sandpiper (*Calidris minutilla*), Spotted Sandpiper (*Actitis macularia*), Ipswich Sparrow (*Passerculus sandwichensis princeps*), and endangered Roseate Tern (*Sterna dougallii*) (Miller, 1983; Ross, 1980; Gochfeld, 1983). Herring Gulls (*Larus argentatus*) also frequent this island, although they are not native (Miller, 1983). This island is an important breeding ground for grey seals (*Halichoerus grypus*) and harbour seals (*Phoca vitulina*) (Freedman et al. 2011). One of the most prominent species is the introduced feral horse (*Equus caballus*). There are also at least 573 documented invertebrates, of which 480 are native (Chow, 2020). Therefore, Sable Island is home to a diverse array of animal species, some of which are endemic and highly dependent on the island.

Vegetation on Sable Island covers 40% of the surface area with the unvegetated portion consisting of bare fine-medium textured sand (Byrne & McCann, 1995). The island was previously thought to have been mostly covered by vegetation, but that has decreased since the establishment of horses in the 18<sup>th</sup> century (Byrne & McCann, 1995). There are 158 native species and 82 introduced species of flora (Catling et al., 1984; Catling et al., 2009) forming communities of marram and shrub heathland which dominate the island, alongside sandwort and pond-edge vegetation (Catling et al., 1984; Eamer et al., 2022). Marram grass grows in wind-blown sandy substrate, shrub heathland is in protected inland sites, sandwort is found closer to the ocean where it is prone to inundation and sea spray during storms, and pond-edge vegetation is found surrounding brackish or freshwater ponds (Catling et al., 1984). The distribution of these communities on Sable Island is related to distance from shore and the slope of the dune which is associated with sand erosion or accumulation (Tissier et al., 2013).

In dunescapes in Nova Scotia, marram grass (e.g., *Calamagrostis breviligulata*) is responsible for the stabilization of the sand which leads to the formation of sand ridges (Davis, 1996). Heathland vegetation (e.g., *Juniperus horizontalis*) can then form communities in the stabilized substrate after there is an increase in organic matter (Davis, 1996). Vegetation types that are sensitive to sand accumulation, such as heathlands, are inland and away from potential sand burial sites, and plants with salt adaptations are near brackish water or by the shore (Tissier et al., 2013). Although marram grasslands are the most tolerant to sand accumulation, they are the most susceptible to horse damage (Freedman et al., 2011).

The horse population was introduced to this island by humans but has been feral for generations and is genetically distinct from other breeds, though they are not considered a distinct breed (Freedman et al., 2011; Plante et al., 2007). As of 2019, the population consisted of approximately 590 horses (Johnsen, 2022). Given the island's small size and vulnerability to erosion, having such a significant number of horses grazing and trampling the soil can cause substantial damage. These horses have been extensively studied in terms of their history, foraging habits, gut microbiome, population genetics, and negative effects on the vegetation communities, especially the marram grasslands (Christie, 1980; Johnsen, 2022; Stothart et al., 2020; Lucas et al., 2009; Plante et al., 2007; Freedman et al., 2011). However, the effects of the horses on the soil microbiome on Sable Island remain unclear due to a lack of research on the soil microbiome.

#### **1.4 Objectives and Hypotheses**

We used eDNA metabarcoding to assess the differences in the microbiomes of Sable Island.  $\alpha$ -diversity and  $\beta$ -diversity were compared to assess differences in local species richness and the turnover in microbial communities across sites, respectively. Our objectives were to 1) assess the

effects of vegetation type (marram vs. heath), pH, organic matter, and phosphorous ( $P_2O_5$ ) on microbial  $\alpha$ -diversity and  $\beta$ -diversity, and 2) conduct an overall survey of bacteria and fungi.

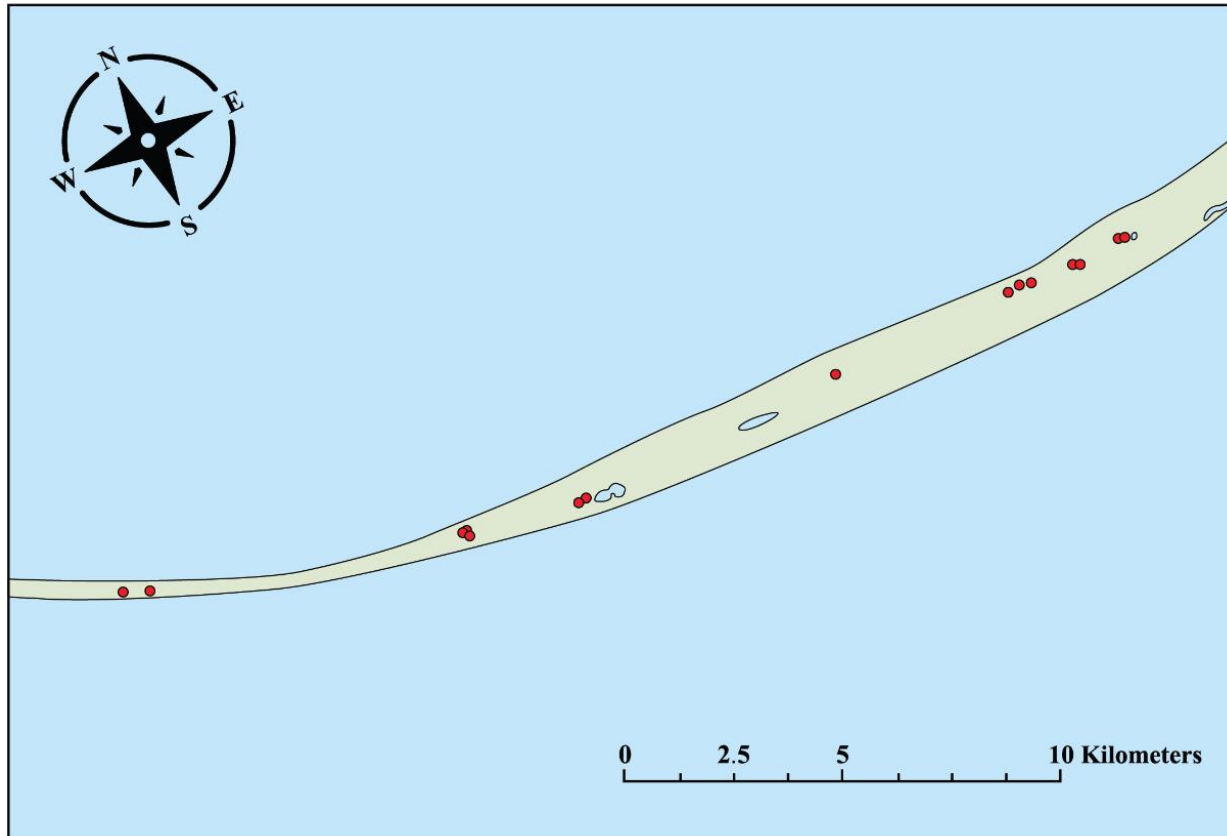
Plant species richness positively affects microbial biomass, activity, and composition in other grasslands (Strecker et al., 2015; Chung et al., 2007). Therefore, we hypothesized that the  $\alpha$ -diversity of the microbes would be lower in the marram grasslands than in the shrub heathlands due to the lower plant species richness, and the negative effects on marram by horses (Freedman et al., 2011). Similarly, as specific vegetation is expected to support different microbial taxa, and horse activity impacts the vegetation types differently, we hypothesized there would be more similarities in the microbial communities within the vegetation types than between them.

## 2. Materials and Methods

### 2.1 Site Design

In the spring of 2021, 16 sites were selected across Sable Island based on evidence of horse activity (e.g., grazing, trails, rubbing, or feces) (Figure 1). The plant communities and the geomorphology vary across sites, but each site was paired with a corresponding, similar site to create a total of eight pairs. The sites ranged in size from 0.25 ha to 2.36 ha, and five, 5 m x 5 m plots were evenly distributed within each site. The vegetation in these plots was categorized as marram grassland, heathland, intermediate, or unvegetated (marram  $n = 35$ , heath  $n = 31$ , intermediate  $n = 12$ , unvegetated  $n = 2$ ). Plots dominated with marram grass (*Calamagrostis breviligulata*) or beach pea (*Lathyrus japonicus*) were categorized as marram, while plots with dominant species such as bayberry (*Morella pensylvanica*) or crowberry (*Empetrum nigrum*) were categorized as heath. Plots dominated by yarrow (*Achillea millefolium*) or Kentucky bluegrass (*Poa pratensis*) were categorized as intermediate, and unvegetated plots were categorized as

unvegetated. The plots were placed at least 5 m from the edge of the site to account for edge effects. In total, 80 plots representing five replicate plots for each of the 16 sites across Sable Island were used in this study.



**Figure 1.** Locations of the 16 sites established on Sable Island, Nova Scotia in the spring of 2021. The size of each site ranged from 0.25 ha to 2.36 ha.

## 2.2 Soil Sampling and Analyses

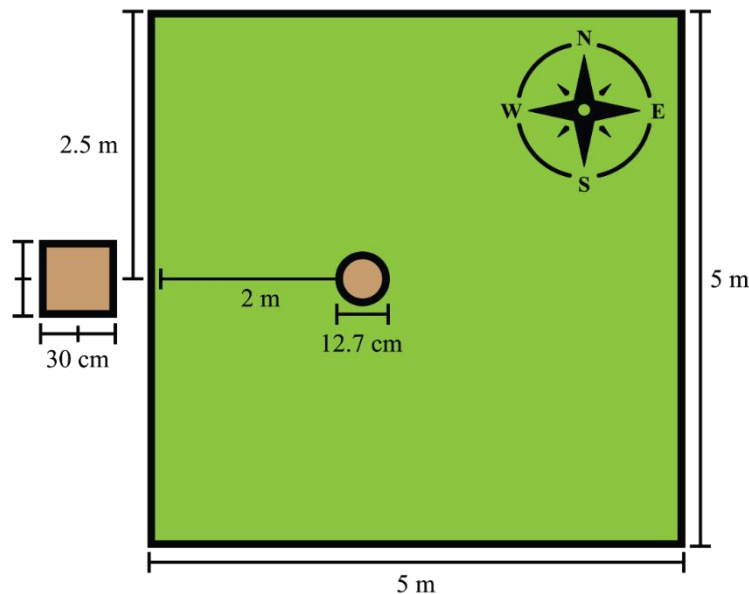
### 2.2.1 *eDNA*

Vegetation was removed with pruning shears from a circular patch, 26 cm in diameter, near the centre of each plot (Figure 2). A bulb planter (12.7 cm width x 12.7 cm depth) was then used to take a soil sample for *eDNA* analysis. The bulb planter was cleaned between samples with a dilute, unscented soap solution and a rag to prevent cross-contamination. The samples were stored

individually in resealable plastic bags, kept in a cooler while in the field, and then stored at  $-20\text{ }^{\circ}\text{C}$  for the duration of collection between mid-July and the end of August 2021. Samples were shipped to Dalhousie University and Saint Mary's University, NS where they were stored at  $-80\text{ }^{\circ}\text{C}$ .

### 2.2.2 Soil Characteristics

Immediately outside the centre of the western edge of the plot, vegetation was removed from a  $30\text{ cm} \times 30\text{ cm}$ ,  $900\text{ cm}^2$  area (Figure 2). A soil sample was taken with the same bulb planter ( $12.7\text{ cm}$  width  $\times$   $12.7\text{ cm}$  depth) for pH, phosphorous concentration (kg/ha) and organic matter (%) analysis. The bulb planter was cleaned between samples with a dilute, unscented soap solution to prevent cross-contamination. The samples were stored individually in resealable plastic bags and kept in a cooler while in the field, and then stored at  $-20\text{ }^{\circ}\text{C}$  for the duration of collection. Samples were shipped to the Department of Agriculture, Truro, NS for analysis. All soil samples were collected between mid-July and the end of August 2021.



**Figure 2.** Plot placement set up for Sable Island soil sampling. The sample for soil eDNA came from the  $12.7\text{ cm}$  diameter area inside the plot where vegetation was removed. The sample for soil characteristics (pH, phosphorous, and organic matter) came from the  $30\text{ cm} \times 30\text{ cm}$  area outside the west side of the plot where vegetation was removed. The measurements reported are accurate, but the figure is not to scale.

After the soil characteristics were analyzed, the samples were grouped into appropriately sized categories for analysis. For pH, the categories were 4.00-4.99 (n = 17), 5.00-5.99 (n = 33), and >6.00 (n = 28). For organic matter content (%) the categories were <1 (n = 48), 1-2 (n = 16), and >2 (n = 14). Finally, the phosphorous concentration (kg/ha) categories were 10-20 (n = 8), 21-30 (n = 53), and >30 (n = 17). One plot was not analyzed for any soil characteristics as no soil sample was taken. It was categorized as N/A (n = 1).

### **2.3 eDNA Extraction, Metabarcoding, and Bioinformatics Processing**

The soil samples for eDNA were stored at -80 °C and were thawed and homogenized before DNA extraction. Environmental DNA was extracted from approximately 0.25 g of soil with a DNeasy® PowerSoil® Pro Kit (QIAGEN) following their recommended protocols and using a QIAGEN TissueLyser II at 25 Hz for 10 minutes for cell lysis as recommended. After the DNA was isolated and eluted, the samples were stored at -80 °C until sequencing.

The extracted eDNA was sent to the Integrated Microbiome Resource lab at Dalhousie University (Halifax, NS) for sequencing and bioinformatics processing (Comeau, 2022; Comeau et al., 2017). Briefly, the targeted DNA was PCR-amplified with the Phusion Plus polymerase and separate primers designed to amplify bacteria and fungi (Comeau, 2022). For bacteria, the 16S V4-V5 region was amplified (forward primer: 515FB = GTGYCAGCMGCCGCGGTAA, reverse primer: 926R = CCGYCAATTYMTTTRAGTTT (Quince et al., 2011)). For fungi, the ITS2 region was amplified (forward primer: ITS86(F) = GTGAATCATCGAATCTTTGAA (Turenne et al., 1999), reverse primer: ITS4(R) = TCCTCCGCTTATTGATATGC (White et al., 1990)). The PCR began with an initial denaturation at 98 °C for 30 seconds, followed by 25 cycles of 98 °C for 10 s, 55 °C for 30 s, 72 °C for 30 s, a final extension at 72 °C for 4 min 30 s and then held at 4 °C (Comeau, 2022). PCR products were verified by the Hamilton Nimbus Select robot using Coastal

Genomics Analytical Gels and normalized with the Charm Biotech Just-a-Plate 96-well Normalization Kit (Comeau, 2022). PCR products were quantified fluorometrically with the Invitrogen Qubit dsDNA HS assay before sequencing on an Illumina MiSeq (v3 2 x 300 bp paired-end reads) (Comeau et al., 2017).

After sequencing was completed, the sequence reads were processed according to Comeau et al. (2017). Briefly, the paired-end reads were merged using PEAR (v0.9.10) and any low-quality sequences (quality score <30 in 90% of bases) were identified by FastQC (v0.11.5) and removed by FASTX-Toolkit (v0.0.14). Any potentially chimeric reads were removed with VSEARCH (v1.11.1). Then, open-reference ASV (amplicon sequence variant) picking was done with QIIME wrapper scripts (v1.91) by comparing the sequence reads obtained to reference sequences to identify an ASV for each amplicon when possible. An ASV for bacteria (16S) includes reads that have 97% similar sequence identity. ASVs that were less than 0.1% of the total number of sequences were removed. Finally, QIIME2 (Bolyen et al., 2019) was used to compare the diversity of taxa found across samples.

## **2.4 Statistical Analyses**

$\alpha$ -diversity of bacteria and fungi was determined using Shannon entropy which was performed using QIIME2 (Bolyen et al., 2019). Shannon entropy accounts for the evenness and abundance of taxa within a community by measuring the uncertainty and creating equivalencies which can be compared (Jost, 2006). Two communities which have the same entropy may differ in terms of evenness or abundance of taxa (Jost, 2006). The Shannon entropies were compared with a Kruskal-Wallis test to determine significance using QIIME2 (Bolyen et al., 2019).



The microbial community composition ( $\beta$ -diversity) of bacteria and fungi was determined by calculating Jaccard and Bray-Curtis distance matrixes and performing a Principal Coordinate Analysis (PCoA) using QIIME2 (Bolyen et al., 2019). Jaccard is based on presence/absence data and thus weights rare taxa equal to abundant taxa; Bray-Curtis is abundance-based and thus is less sensitive to changes in rare species (Jaccard, 1912; Bray & Curtis, 1957). The Jaccard index is the most robust to errors across indices, and Bray-Curtis is the most robust to errors for abundance-based indices (Schroeder & Jenkins, 2018). The variables' effects on the microbial communities were assessed with a permutational multivariate analysis of variance (PERMANOVA) using the Adonis2 function from the vegan package in R (Oksanen et al., 2022).

All data visualizations and the PERMANOVAs were performed in R v.4.3.2 (R Core Team, 2023) and R Studio v.2023.12.1+402 (Posit team, 2023). Packages not already stated are qiime2R (Bisanz, 2018) and phyloseq (McMurdie & Holmes, 2013) for reading qza files from QIIME2, tidyverse (Wickham et al., 2019) for data manipulation and visualizations, and RColorBrewer for colour-bind-friendly palettes (Neuwirth, 2022).

### **3. Results**

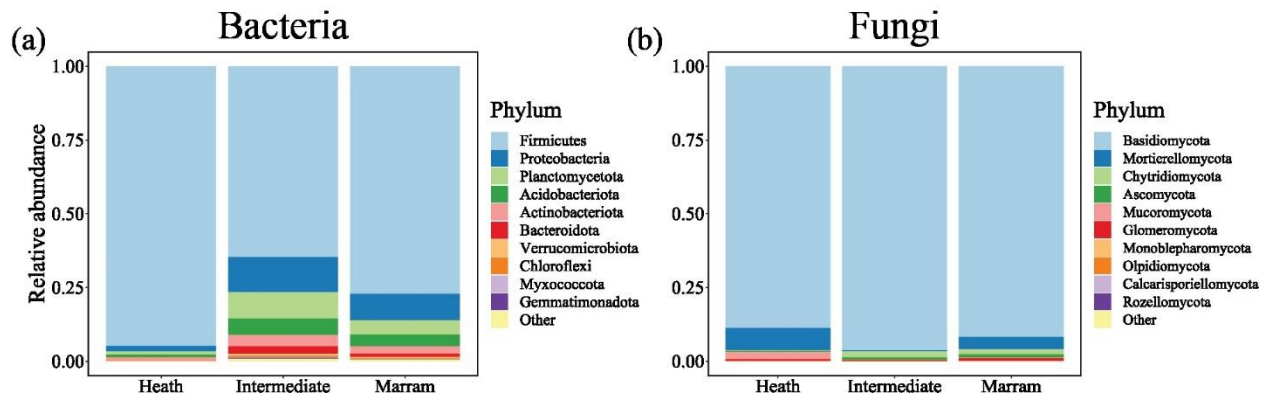
#### **3.1 Overview**

Across all 80 samples from the 16 sites on Sable Island, there were a total of 3,057,553, and 2,282,503 raw DNA sequence reads for bacteria and fungi respectively. From those reads, we identified 37 bacterial and 12 fungal phyla with a total of 812 and 336 bacterial and fungal ASVs, respectively (Appendix Tables C1 & C2). Of the 80 samples, one unvegetated sample failed to amplify for bacteria and fungi, and one marram sample failed to be sequenced for fungi (bacteria  $n = 79$ , fungi  $n = 78$ ). The bacterial communities had higher  $\alpha$ -diversity than the fungal

communities.  $\alpha$ -diversity of bacteria differed significantly ( $p < 0.05$ ) across vegetation types and between most environmental factors, whereas  $\alpha$ -diversity of fungi did not differ significantly.  $\beta$ -diversity in each vegetation type and across environmental factors were not significantly different for bacteria or fungi with the Jaccard distance. However, the  $\beta$ -diversity of bacterial taxa was significantly different across vegetation types with the Bray-Curtis distance.

### **3.2 Relative Abundance**

Across vegetation types, the relative abundance of bacterial and fungal phyla differed, however, the dominant phyla were similar. The two most abundant bacterial phyla were the same across all three vegetation types (Table 1). Firmicutes was the most abundant bacterial phylum in all vegetation types and was more relatively abundant in heath than marram and intermediate (Table 1, Figure 3). Similarly, Basidiomycota was the most abundant fungal phylum across all vegetation types (Table 1). However, Basidiomycota were more relatively abundant in the intermediate sites than marram and heath (Table 1, Figure 3). The same bacterial and fungal phyla were in the top six most relatively abundant phyla across the vegetation types but differed in their abundance rank depending on the vegetation type (Table 1). There were fewer similarities in the phyla relative abundance rank in fungi between vegetation types compared to bacteria (Table 1).



**Figure 3.** The relative abundances of taxa at the phylum classification in each vegetation type on Sable Island, NS. The most abundant 10 phyla are displayed, in order of decreasing relative abundance, with the remaining less abundant phyla grouped into the ‘Other’ category. **(a)** Bacterial taxa; **(b)** Fungal taxa.

**Table 1.** Ranking of the most relatively abundant bacteria and fungi phyla across the vegetation types on Sable Island, NS in 2021.

Abundance rank	Heath		Intermediate		Marram	
	Bacteria	Fungi	Bacteria	Fungi	Bacteria	Fungi
1	Firmicutes	Basidiomycota	Firmicutes	Basidiomycota	Firmicutes	Basidiomycota
2	Proteobacteria	Mortierellomycota	Proteobacteria	Chytridiomycota	Proteobacteria	Mortierellomycota
3	Acidobacteriota	Mucoromycota	Planctomycetota	Ascomycota	Planctomycetota	Chytridiomycota
4	Planctomycetota	Glomeromycota	Acidobacteriota	Mortierellomycota	Acidobacteriota	Ascomycota
5	Actinobacteriota	Ascomycota	Actinobacteriota	Glomeromycota	Actinobacteriota	Glomeromycota
6	Bacteroidota	Chytridiomycota	Bacteroidota	Mucoromycota	Bacteroidota	Mucoromycota
7	Verrucomicrobiota	Calcarisporiellomycota	Other	Olpidiomycota	Other	Monoblepharomycota
8	Other	Monoblepharomycota	Verrucomicrobiota	Monoblepharomycota	Verrucomicrobiota	Rozellomycota
9	Myxococcota	Other	Chloroflexi	Rozellomycota	Chloroflexi	Olpidiomycota
10	Chloroflexi	Olpidiomycota	Gemmatimonadota	Other	Myxococcota	Other
11	Gemmatimonadota	Rozellomycota	Myxococcota	Calcarisporiellomycota	Gemmatimonadota	Calcarisporiellomycota

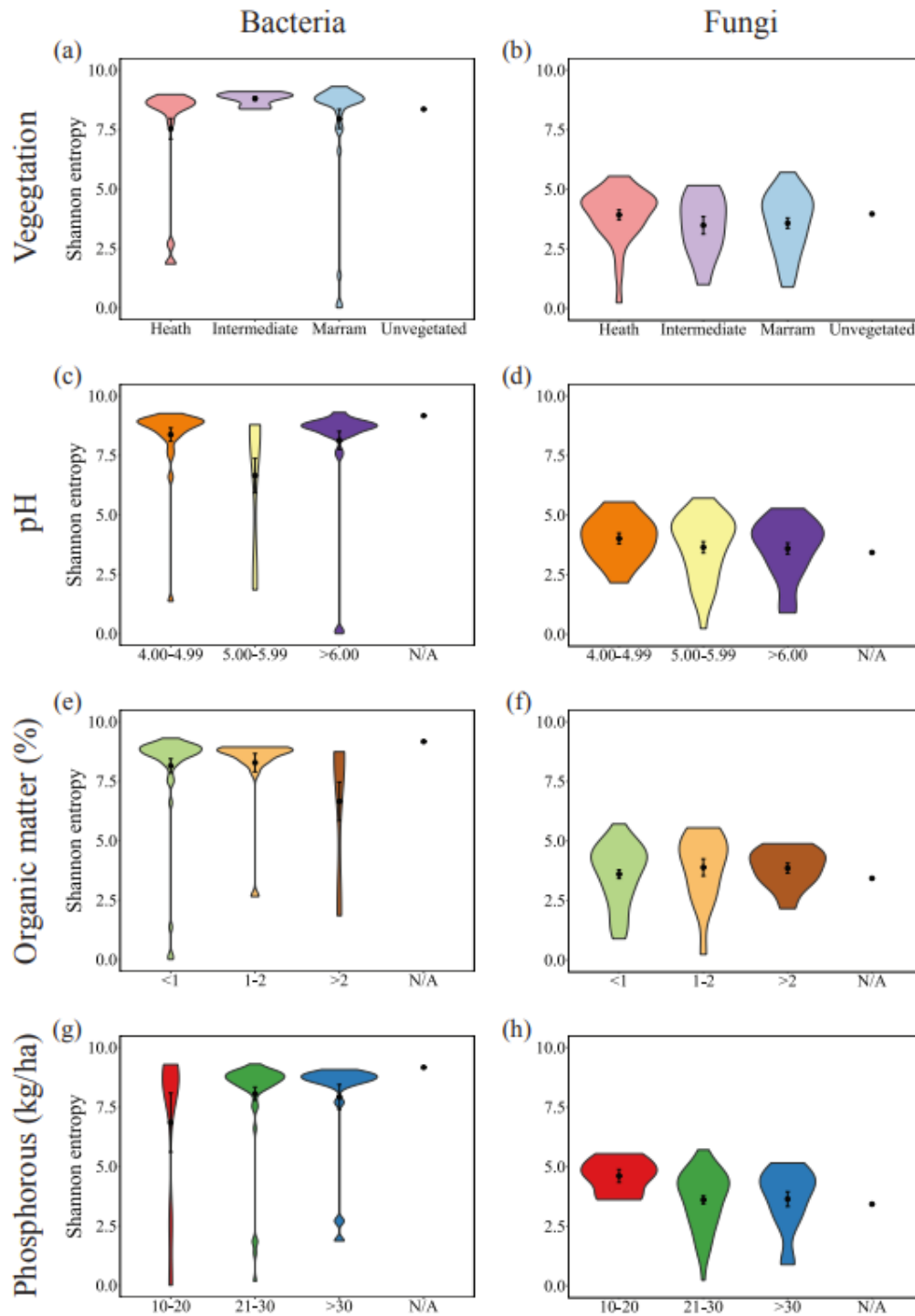
### 3.3 $\alpha$ -Diversity

The intermediate vegetation type had the highest bacterial  $\alpha$ -diversity, followed by the unvegetated, and then the marram (Figure 4a, Appendix Table A1). The heath bacterial diversity was significantly lower than the marram and the intermediate ( $p = 0.043$ ,  $p = 0.006$ ) (Figure 4a, Appendix Table A2). In fungi, the  $\alpha$ -diversity was not significantly different across the vegetation types ( $p = 0.61$ ) (Figure 4b, Appendix Table A1).

Bacterial  $\alpha$ -diversity was similar in soil samples with pH 4.00-4.99 and >6, with 4.00-4.99 being slightly higher; the lowest diversity was in pH 5.00-5.99 (Figure 4c, Appendix Table A1). There was a significant difference from pH 4.00-4.99 to both pH 5.00-5.99 and >6 ( $p = 0.008$ ,  $p = 0.004$ ) (Appendix Table A2). In fungi, the  $\alpha$ -diversity was not significantly affected by pH ( $p = 0.80$ ) (Figure 4d, Appendix Table A1).

The bacterial  $\alpha$ -diversity in soil samples with an organic matter content <1% and 1-2% was similar, with 1-2% being slightly higher (Figure 4e, Appendix Table A1). The bacterial diversity in organic matter >2% was significantly lower than <1% and 1-2% ( $p = 0.005$ ,  $p = 0.011$ ) (Figure 4e, Appendix Table A2). In fungi, the  $\alpha$ -diversity was not significantly affected by organic matter content ( $p = 0.73$ ) (Figure 4f, Appendix Table A1).

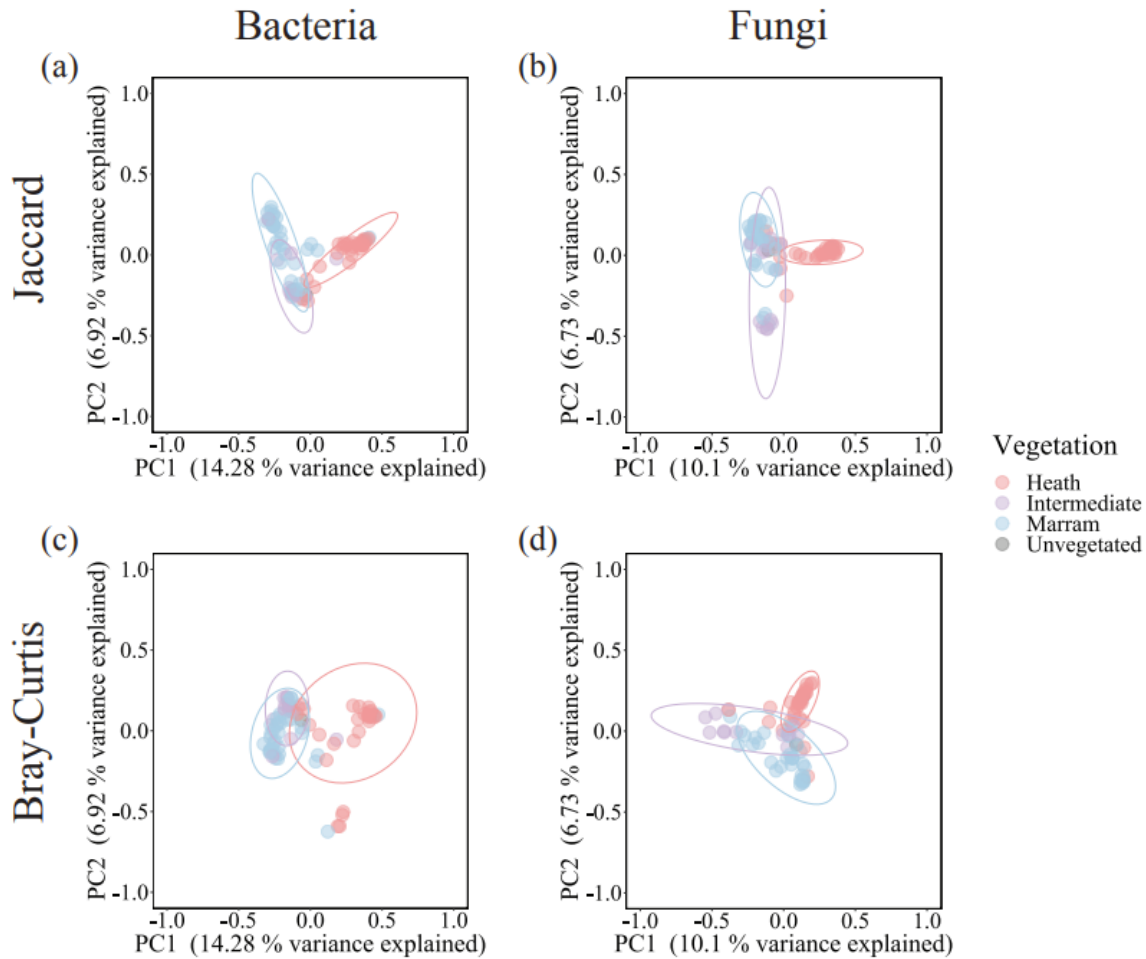
There were no significant differences in the  $\alpha$ -diversity for bacteria or fungi across phosphorous concentrations ( $p = 0.44$ ,  $p = 0.17$ ) (Figure 4g, h, Appendix Table A1).



**Figure 4.** The mean Shannon entropy ( $\alpha$ -diversity) of soil microbial communities in vegetation types and across environmental factors on Sable Island, NS. **(a, c, e, g)** Bacterial taxa; **(b, d, f, h)** Fungal taxa; **(a, b)** Vegetation types; **(c, d)** pH; **(e, f)** Organic matter content (%); **(g, h)** Phosphorous ( $P_2O_5$ ) (kg/ha). N/A represents plots where soil analyses were not completed. Error bars represent standard error.

### 3.4 $\beta$ -Diversity

$\beta$ -diversity was compared using two different dissimilarity methods with a PCoA. The PC1 axis explained 14.28% of the variation in bacterial communities, and PC2 explained 6.92%, compared to fungi where PC1 and PC2 explained 10.1% and 6.73% of the fungal diversity respectively. The microbial composition of vegetation types was not significantly different for either bacteria or fungi with the Jaccard distance ( $p = 0.076$ ,  $p = 0.85$ ) (Figure 5a, b, Appendix Table A3). However, with the Bray-Curtis distance, bacterial communities across vegetation types were significantly different, but not for fungi ( $p = 0.038$ ,  $p = 0.53$ ) (Figure 5c, d, Appendix Table A3). Both Jaccard and Bray-Curtis distances explained a low amount of variation (<5%) for bacteria and fungi (Appendix Table A3). The variance was not explained by the environmental factors (pH, organic matter, phosphorous) for Jaccard or Bray-Curtis distances for bacteria or fungi with all  $R^2$  below 0.03, and all p-values >0.05 (Appendix Table A3, Appendix Figure B1, B2, B3).



**Figure 5.** The beta diversity of soil microbes in vegetation types on Sable Island, NS with a principal coordinate analysis (PCoA) with a Jaccard (**a**, **b**), and a Bray-Curtis distance matrix (**c**, **d**). (**a**, **c**) Bacterial taxa; (**b**, **d**) Fungal taxa. N/A represents plots where soil analyses were not completed.

#### 4. Discussion

Bacterial diversity differed based on several factors whereas fungal diversity did not change across any factor. We found significant effects of vegetation types, soil pH, and organic matter content, but not phosphorous concentration, on bacterial  $\alpha$ -diversity. We found no significant effects of any factors on fungal  $\alpha$ -diversity. Additionally, for  $\beta$ -diversity, the bacterial and fungal taxa in each vegetation type, soil pH, organic matter content, and phosphorous category

were not significantly different, and each factor explained less than 5% of the variation observed. Although the bacterial taxa abundances differed significantly across vegetation types, the vegetation still explains a low amount (3.7%) of the variation. The most relatively abundant phyla of bacteria and fungi were the same in each vegetation type further reflecting the lack of significant differences.

## **4.1 Effects of Vegetation Type on Microbial Diversity**

### *4.1.1 Relative Abundance*

Firmicutes had the highest bacterial relative abundance in all vegetation types, likely due to their close association with plant roots in the endorhizosphere and rhizosphere soil (Hashmi et al., 2020). The most abundant family of Firmicutes found was *Bacillaceae* in both marram grasslands and heathlands. This family is tolerant to a variety of conditions including drought, salinity and other extremes allowing them to survive in the different soils in the different vegetation types (Mandic-Mulec et al., 2016). Proteobacteria also had a high relative abundance in marram grasslands and intermediate vegetation. In another study, proteobacteria were also common in the soil with grasses (Qiao et al., 2022). Some classes of proteobacteria are copiotrophic and thus found in nutrient-rich soils, and copiotrophs are more abundant in herbs than shrubs (Ma et al., 2023). However, marram grass grows in a sandy substrate rather than soil which is typically nutrient-limited by nitrogen and phosphorous, which would not be preferable for copiotrophs. However, fecal excrement by horses along with nutrient transfer mediated by grey seals movements would enrich the soils facilitating copiotrophic bacteria such as proteobacteria to flourish (Read, 1989; McLoughlin et al., 2016). Additionally, Acidobacteriota was more relatively abundant in heathland soils, potentially due to their acid-tolerance (Ward et al., 2009). The range of pH values across the vegetation types would allow Acidobacteriota to live in all environments



we sampled, thereby also explaining their high abundance in marram and intermediate vegetation types (Ward et al., 2009).

Basidiomycota had the highest relative abundance in all vegetation types by far. This may be due to their ability to form associations with plants and their saprotrophic ability allowing them to create symbioses with plants, and then continue to thrive after the plant has died (Watkinson, 2016). Arbuscular mycorrhizal fungi are from the phylum Glomeromycota and are associated with grasses often and trees, ectomycorrhizal fungi are from Basidiomycota and Ascomycota and are associated with trees, and ericoid mycorrhiza are from Ascomycota and are associated with heath plants (Watkinson, 2016). Based on those symbiotic relationships, we expected significant differences in the fungal phyla and their relative abundances between vegetation types; however, we found no significant differences. Though similar to our results, another study found a higher abundance of Ascomycota in grasslands and mixed vegetation sites (Qiao et al., 2022). Interestingly, there were no significant differences in fungal taxa turnover across vegetation types suggesting symbioses with plants may not be eliciting as much of an effect on fungi as previously expected.

#### *4.1.2 $\alpha$ -Diversity*

The vegetation type had significant effects on the bacterial  $\alpha$ -diversity but not in the way we hypothesized. Instead, the intermediate vegetation had the highest  $\alpha$ -diversity among the four vegetation types. One study also found that shrub-grass mixed communities had higher bacterial  $\alpha$ -diversity than grass communities (Qiao et al., 2022). This is potentially due to having a variety of plant functional groups in this community (i.e., both grasses and shrubs), allowing for a higher variety of different plant-microbe associations. In contrast, the marram grass vegetation type mainly contained grasses, while the heath vegetation type mainly contained shrubs.

Aside from the symbioses occurring between the plant and microbes, the bacterial diversity results could be explained by the effects of horse activities. We initially hypothesized that marram grasslands would have a decreased diversity due to horse activities such as frequent grazing, but our results show a lower diversity in heath than marram. The horses on Sable Island prefer to consume marram grass as it is a higher quality food, but when population density is high, heathlands are increasingly selected (Van Beest et al., 2013). This results in the horses foraging and thus trampling the soil and causing mechanical damage to the microbes in both marram and heathlands which was not accounted for previously. In unvegetated plots, there may be less trampling and damage which could contribute to the higher diversity in those plots.

#### *4.1.3 $\beta$ -Diversity*

We hypothesized the microbial communities would differ between the vegetation types, which was partially supported. Bacteria in vegetation types were significantly different in abundance, but not in community composition. This indicates some vegetation types were more favourable for certain taxa allowing their dominance over other taxa. Other studies have also found significant differences in the microbial communities in different vegetation types (e.g., Ma et al., 2023), though we did not see the same differences in fungi. Many of the bacterial and fungal taxa in our samples inhabit a wide range of environments which is why we saw them in all vegetation types (Hashmi et al., 2020; Tedersoo et al., 2014; He et al., 2022). Our soil samples contained bulk and rhizospheric soil which means we were unable to detect microbial community differences at a finer scale. This could partially explain the overall microbial community homogeneity observed.

## 4.2 Effects of Soil Characteristics on Microbial Diversity

### 4.2.1 $\alpha$ -Diversity

Bacterial  $\alpha$ -diversity was affected by the pH and organic matter content but not phosphorus. There were no significant effects of these factors on fungal  $\alpha$ -diversity. There was a significantly lower bacterial  $\alpha$ -diversity in soil with a pH of 5-5.99 than in the lower and higher pH category, which is different from another study in which the bacterial  $\alpha$ -diversity increased with pH from 3 to 9 (Griffiths et al., 2011). In other studies, fungal diversity also increased with increased pH from 3 to 6.5 (Liu et al., 2018). We also observed a lower bacterial  $\alpha$ -diversity in organic matter >2%, which differs from other studies where more organic matter leads to an increase in microbial diversity (Sul et al., 2013). We found bacterial and fungal  $\alpha$ -diversity were not affected by phosphorous, even though the taxa in our study were similar to a study which found an effect of phosphorus (Kuramae et al., 2011). Research has also shown that fungi tend to be more tolerant of environmental stressors than bacteria (Coleine et al., 2022). This could explain why there is a lack of significant effects on the fungal  $\alpha$ -diversity.

### 4.2.2 $\beta$ -Diversity

There were no significant differences in the turnover of bacteria or fungal communities across the various soil characteristics. Many of the bacterial and fungal taxa are ubiquitous in soil environments which is why we observed them across the full ranges of soil pH, organic matter content and phosphorous concentration (Hashmi et al., 2020; Ward et al., 2009; Tedersoo et al., 2014; He et al., 2022).

### **4.3 Ecosystem Management**

Our research found bacteria to be more variable than fungi across the abiotic and biotic environment on Sable Island. Soil microbes influence the health of plants and may encourage growth through symbioses thus improving soil quality and reducing erosion (Clark, 2012; Money, 2016; Normaniza et al., 2018). As the vegetation on Sable Island is affected by the horses (Freedman et al., 2011), understanding how the microbes are affected and implementing protection for them is essential for ecosystem functionality. The microbial communities are important for ecosystem management and can aid in the protection of vegetation, and resistance of the soil to erosion (Watkinson, 2016; Normaniza et al., 2018). The positive effects of microbes on vegetation and soil can also help vulnerable organisms such as the Roseate Terns, and the grey seals by protecting their nesting habitat from degradation.

### **4.4 Limitations and Future Research**

This study was able to identify a wide variety of bacterial and fungal diversity by using eDNA. This methodology can identify taxa which are low in abundance or are unculturable giving us a deeper insight into the community (Torsvik & Øvreås, 2002). However, it does detect taxa which are inactive and in their dormant state, which means there may be more differentiation in active microbial communities between vegetation types and soil characteristics than we were able to detect (Locey et al., 2020). Accounting for microbial dormancy is a common issue when dealing with microorganisms which calls for different methods of analyzing microbial communities (Locey, 2010). Also, we sampled with a soil core and homogenized the soil samples, which makes identifying fine-scale relationships difficult as microbial communities can differ between soil aggregates and between bulk soil and the rhizosphere (Fierer, 2017; Philippot et al., 2013). It is

important to keep in mind the complexity of the microbiome and that there are likely many interactions that were not identified.

Additionally, there may be more species that were not identified due to either sampling sites not encompassing enough areas to identify all taxa on Sable Island, or due to limitations of primers. Some taxa may not have been amplified consistently, or at all by the primers leading to a misrepresentation or a lack of representation overall. Even though some taxa may be left out or misrepresented, using DNA is still able to identify more than other methods such as culturing.

This study has resulted in a baseline survey of bacterial and fungal diversity across Sable Island, particularly on the microbiome diversity and composition between vegetation types. The next step for the microbiome on Sable Island is to investigate the direct and indirect effects the horses have on the microbiome and soil characteristics. As this study has found significant differences in the bacterial communities already, further determining the impacts of the horses on the microbiome will aid in ecosystem management to support the island's biodiversity.

## **5. Conclusion**

The soil microbiome is responsible for driving many ecosystem functions, affecting above-ground organisms, and it is also affected by abiotic and biotic factors (Mishra et al., 2023; Van Der Heijden et al., 2007; Fierer, 2017). The microbiome taxa can adapt to changes in the abiotic and biotic environment by shifting to exploit new resources and by forming symbioses or other interactions (Li et al., 2022). Our results indicate bacterial  $\alpha$ -diversity to be more variable than fungi due to environmental differences including vegetation types and soil characteristics. We found very few differences in the  $\beta$ -diversity of bacteria, and no differences in fungal diversity suggesting robust microbial communities or an indistinguishable variety of active and dormant

taxa. Many of the taxa identified on Sable Island are common throughout the soil and occupy a wide range of environmental conditions. Some of our results are consistent with other studies, particularly regarding plant-microbe associations, while other results regarding soil characteristics found no significance or inconsistent patterns compared to other studies. Sable Island has allowed a unique study of a soil microbiome which is not affected by anthropogenic activity directly but rather by feral horses. Further research can identify the direct impacts of the horses on the microbiome. Identifying the key players of the microbiome along with what is driving the diversity and composition is important for ecosystem management, especially in vulnerable ecosystems such as Sable Island (Fierer, 2017).

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## Appendix

### Appendix A

**Table A1.** Shannon entropy mean values for the vegetation types and environmental factors for each microbe. The *H* and *p* values are reported for each variable for bacteria and fungi. Significant *p* values are in bold ( $p < 0.05$ ).

Microbe	Variable	Shannon entropy	Standard error	<i>H</i>	<i>p</i> value
<b>Vegetation type</b>					
Bacteria	<i>Heath</i>	7.536	0.432	9.140	<b>0.027</b>
	<i>Intermediate</i>	8.803	0.075		
	<i>Marram</i>	7.949	0.403		
	<i>Unvegetated</i>	8.357			
Fungi	<i>Heath</i>	3.926	0.205	1.836	0.607
	<i>Intermediate</i>	3.488	0.367		
	<i>Marram</i>	3.576	0.216		
	<i>Unvegetated</i>	3.965			
<b>pH</b>					
Bacteria	4.00-4.99	8.374	0.281	12.240	<b>0.007</b>
	5.00-5.99	6.652	0.725		
	>6	8.130	0.378		
Fungi	4.00-4.99	4.019	0.226	1.027	0.795
	5.00-5.99	3.648	0.236		
	>6	3.594	0.233		
<b>Organic matter content (%)</b>					
Bacteria	<1	8.147	0.297	11.300	<b>0.010</b>
	1-2	8.280	0.382		
	>2	6.652	0.808		
Fungi	<1	3.607	0.183	1.314	0.726
	1-2	3.888	0.355		
	>2	3.855	0.210		
<b>Phosphorous (P<sub>2</sub>O<sub>5</sub>) (kg/ha)</b>					
Bacteria	10-20	6.850	1.238	2.690	0.442
	21-30	8.058	0.276		
	>30	7.927	0.521		
Fungi	10-20	4.616	0.269	4.992	0.172
	21-30	3.612	0.167		
	>30	3.644	0.310		



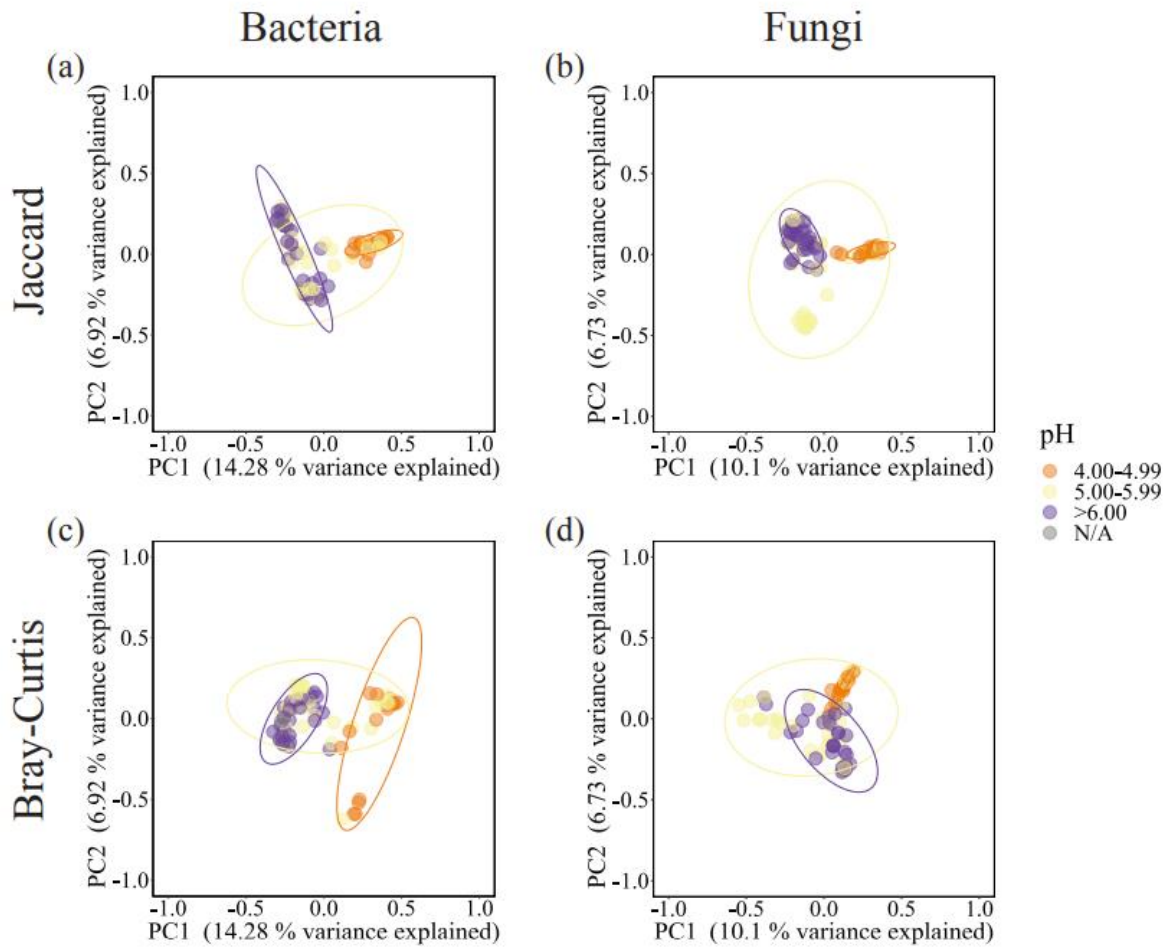
**Table A2.** Pair-wise Kruskal Wallis (post hoc) test results to determine significant differences within variables. The  $H$ ,  $p$  values, and  $q$  values (adjusted  $p$  value for false discovery rate) are reported for interactions within bacterial variables which were significant. Significant  $p$  values are in bold ( $p < 0.05$ ).

Variable		$H$	$p$ value	$q$ value
Group 1	Group 2			
<b>Vegetation type</b>				
<i>Unvegetated</i>	<i>Heath</i>	0.355	0.551	0.551
	<i>Intermediate</i>	2.570	0.109	0.218
	<i>Marram</i>	0.669	0.413	0.496
<i>Heath</i>	<i>Intermediate</i>	7.628	<b>0.006</b>	0.034
	<i>Marram</i>	4.100	<b>0.043</b>	0.129
<i>Intermediate</i>	<i>Marram</i>	1.101	0.294	0.441
<b>pH</b>				
4.00-4.99	5.00-5.99	7.030	<b>0.008</b>	0.024
	>6.00	8.427	<b>0.004</b>	0.022
5.00-5.99	>6.00	0.681	0.409	0.409
<b>Organic matter content (%)</b>				
<1	>2	7.901	<b>0.005</b>	0.030
	1-2	0.312	0.577	0.577
>2	1-2	6.430	<b>0.011</b>	0.034

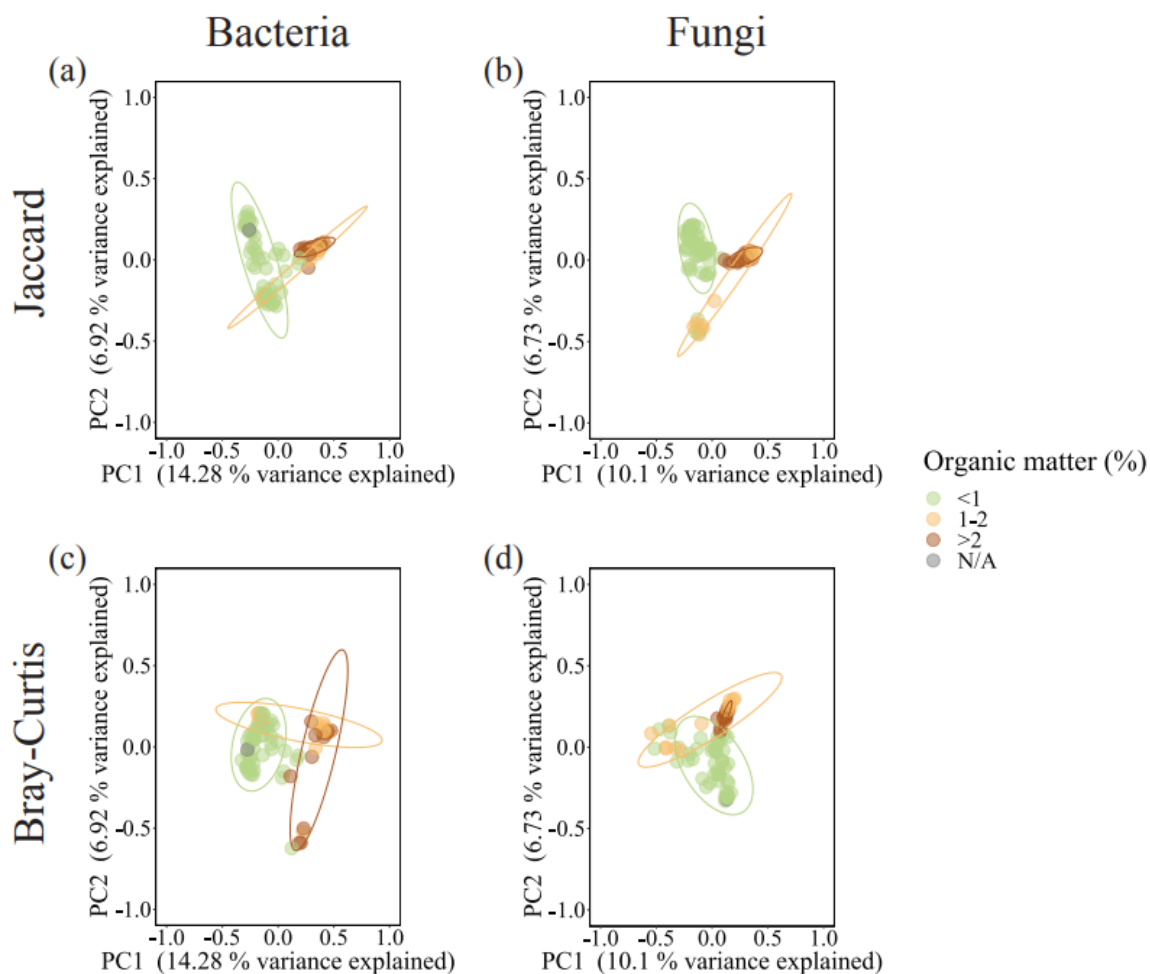
**Table A3.** Permutational multivariate analysis of variance results of  $F$ , variance explained ( $R^2$ ), and  $p$  value for each variable, each microbe and with Jaccard or Bray-Curtis distances. Significant  $p$  values are in bold ( $p < 0.05$ ).

Dissimilarity Measure	Microbe	Variable	$F$	$R^2$	$p$ value
Jaccard	Bacteria	Vegetation type	1.260	0.033	0.076
		pH	1.062	0.028	0.284
		Organic matter content	1.070	0.028	0.275
		Phosphorous	0.888	0.023	0.739
	Fungi	Vegetation type	0.880	0.023	0.851
		pH	0.866	0.023	0.890
		Organic matter content	1.066	0.028	0.252
Bray-Curtis	Bacteria	Vegetation type	1.454	0.037	<b>0.038</b>
		pH	1.036	0.027	0.366
		Organic matter content	0.986	0.026	0.459
		Phosphorous	0.657	0.017	0.988
	Fungi	Vegetation type	0.977	0.026	0.531
		pH	0.833	0.022	0.925
		Organic matter content	1.035	0.027	0.346
		Phosphorous	1.097	0.029	0.195

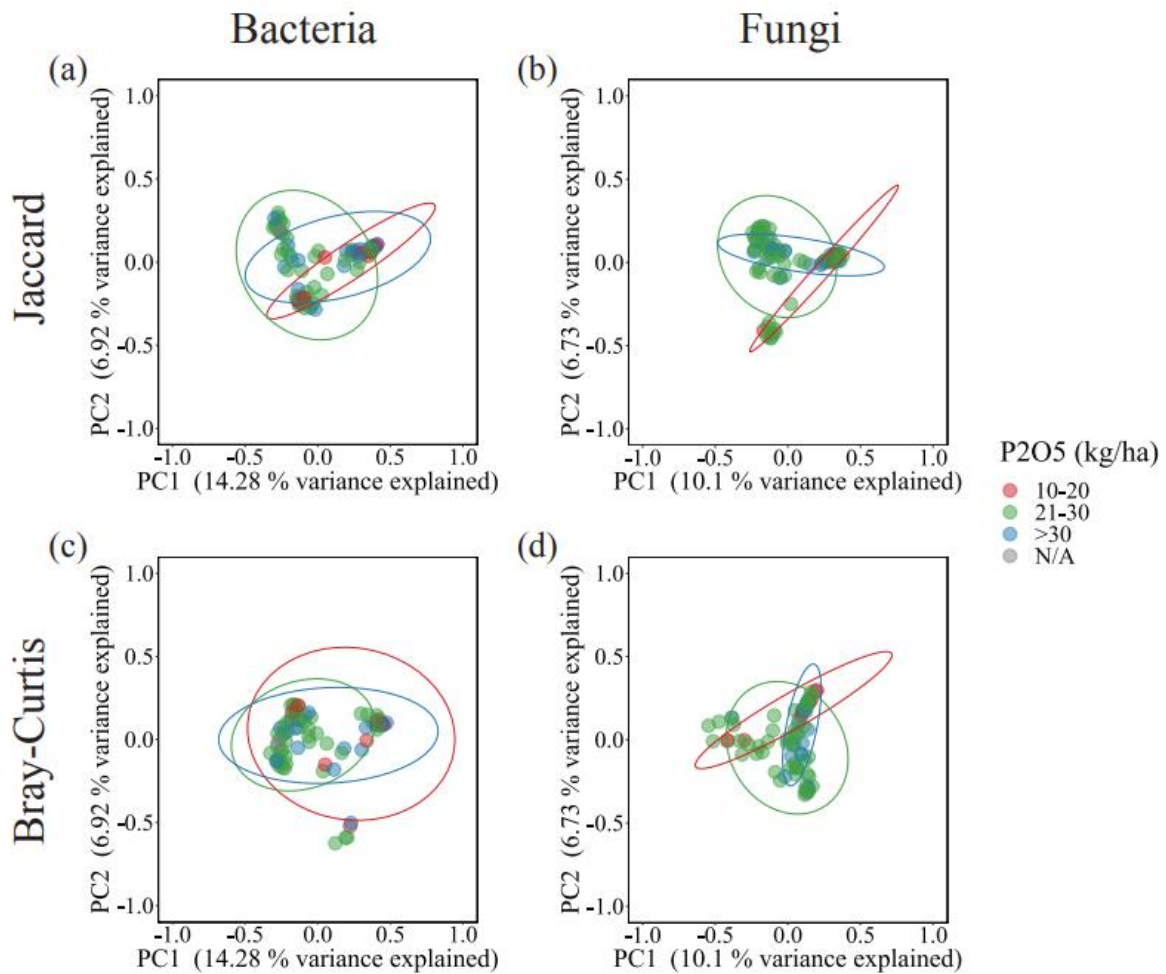
## Appendix B



**Figure B1.** The beta diversity of soil microbes in different soil pH on Sable Island, NS with a principal coordinate analysis (PCoA) with a Jaccard (**a**, **b**), and a Bray-Curtis distance matrix (**c**, **d**) for (**a**, **c**) Bacterial taxa and (**b**, **d**) Fungal taxa. N/A represents plots where soil analyses were not completed.



**Figure B2.** The beta diversity of soil microbes in different soil organic matter contents on Sable Island, NS with a principal coordinate analysis (PCoA) with a Jaccard (a, b), and a Bray-Curtis distance matrix (c, d) for (a, c) Bacterial taxa and (b, d) Fungal taxa. N/A represents plots where soil analyses were not completed.



**Figure B3.** The beta diversity of soil microbes in different soil phosphorous ( $P_2O_5$ ) concentrations on Sable Island, NS with a principle coordinate analysis (PCoA) with a Jaccard (**a**, **b**), and a Bray-Curtis distance matrix (**c**, **d**) for (**a**, **c**) Bacterial taxa and (**b**, **d**) Fungal taxa. N/A represents plots where soil analyses were not completed.

## Appendix C

### C.1. Bacteria and Archaea

**Table C1.** All archaeal and bacterial ASVs identified on Sable Island, NS in 2021 in alphabetical order.

Kingdom	Phylum	Family	Genus	Species
Archaea	Crenarchaeota	<i>Bathyarchaeia</i> <i>Group_1.1c</i> <i>Nitrosotaleaceae</i> <i>Nitrososphaeraceae</i>	<i>Bathyarchaeia</i> <i>Group_1.1c</i> <i>Candidatus_Nitrosotalea</i> <i>Candidatus_Nitrocosmicus</i>	<i>uncultured_methanogenic</i> <i>uncultured_crenarchaeote</i> <i>uncultured_archaeon</i> <i>uncultured_archaeon</i>
Bacteria	Abditibacteriota	<i>Abditibacteriaceae</i>	<i>Abditibacterium</i>	<i>usteinense</i> <i>bacterium</i> <i>bacterium_LY17</i> <i>metagenome</i> <i>uncultured_actinobacterium</i> <i>uncultured_bacterium</i>
Bacteria	Acidobacteriota	<i>Acidobacteriaceae_(Subgroup_1)</i>	<i>Acidicapsa</i>	<i>acidisoli</i> <i>borealis</i> <i>Acidicapsa_sp.</i>
			<i>Acidipila</i>	<i>Acidobacteria_bacterium</i> <i>metagenome</i> <i>uncultured_bacterium</i>
			<i>Bryocella</i>	<i>elongata</i> <i>uncultured_Acidobacteria</i> <i>uncultured_bacterium</i>
			<i>Edaphobacter</i>	<i>Edaphobacter_sp.</i> <i>uncultured_Acidobacterium</i>
			<i>Granulicella</i>	<i>bacterium_enrichment</i> <i>paludicola</i> <i>Granulicella_sp.</i>
			<i>Occallatibacter</i>	<i>bacterium_enrichment</i> <i>uncultured_bacterium</i> <i>uncultured_forest</i>
			<i>uncultured</i>	<i>Acidobacteria_bacterium</i> <i>uncultured_Acidobacterium</i> <i>uncultured_forest</i> <i>metagenome</i> <i>uncultured_Acidobacteria</i> <i>uncultured_bacterium</i> <i>uncultured_bacterium</i>
		<i>Acidobacteriae</i>	<i>Paludibaculum</i>	<i>uncultured_forest</i> <i>metagenome</i> <i>uncultured_Acidobacteria</i> <i>uncultured_bacterium</i> <i>uncultured_bacterium</i>
		<i>AKIW659</i> <i>Blastocatellaceae</i>	<i>AKIW659</i> <i>Aridibacter</i>	<i>uncultured_bacterium</i> <i>uncultured_bacterium</i>
		<i>Bryobacteraceae</i>	<i>Blastocatella</i> <i>Bryobacter</i>	<i>uncultured_organism</i> <i>Acidobacteria_bacterium</i> <i>Acidobacteriaceae_bacterium</i> <i>metagenome</i> <i>uncultured_eubacterium</i> <i>uncultured_Holophaga</i> <i>uncultured_Solibacteraceae</i>

Table C1. (Continued)

Kingdom	Phylum	Family	Genus	Species
		<i>DS-100</i>	<i>DS-100</i>	<i>uncultured_bacterium</i>
		<i>Holophagaceae</i>	<i>Holophagaceae</i>	<i>uncultured_bacterium</i>
		<i>Koribacteraceae</i>	<i>Candidatus_Koribacter</i>	<i>uncultured_Acidobacteria</i>
				<i>uncultured_bacterium</i>
		<i>Solibacteraceae</i>	<i>Candidatus_Solibacter</i>	<i>uncultured_eubacterium</i>
				<i>bacterium_Ellin7504</i>
				<i>uncultured_Acidobacteriaceae</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_forest</i>
		<i>Subgroup_12</i>	<i>Subgroup_12</i>	<i>uncultured_Holophaga</i>
		<i>Subgroup_13</i>	<i>Subgroup_13</i>	<i>uncultured_bacterium</i>
				<i>uncultured_bacterium</i>
		<i>Subgroup_17</i>	<i>Subgroup_17</i>	<i>uncultured_Holophaga</i>
		<i>Subgroup_2</i>	<i>Subgroup_2</i>	<i>metagenome</i>
				<i>bacterium_enrichment</i>
				<i>metagenome</i>
				<i>uncultured_Acidobacteria</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_eubacterium</i>
				<i>uncultured_forest</i>
		<i>Subgroup_5</i>	<i>Subgroup_5</i>	<i>uncultured_Holophaga</i>
		<i>Subgroup_7</i>	<i>Subgroup_7</i>	<i>uncultured_bacterium</i>
				<i>uncultured_Desulfovirga</i>
		<i>Thermoanaerobaculaceae</i>	<i>Subgroup_10</i>	<i>uncultured_proteobacterium</i>
				<i>Acidobacteria_bacterium</i>
				<i>Holophaga_sp.</i>
				<i>uncultured_soil</i>
			<i>Thermoanaerobaculum</i>	<i>uncultured_bacterium</i>
		<i>uncultured</i>	<i>uncultured</i>	<i>metagenome</i>
				<i>metagenome</i>
				<i>uncultured_Acidobacteriaceae</i>
				<i>uncultured_Acidobacteriales</i>
				<i>uncultured_Acidobacteriales</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_Candidatus</i>
				<i>uncultured_forest</i>
		<i>Vicinamibacteraceae</i>	<i>Vicinamibacteraceae</i>	<i>uncultured_Holophaga</i>
		<i>67-14</i>	<i>67-14</i>	<i>Acidobacteria_bacterium</i>
				<i>bacterium_enrichment</i>
				<i>metagenome</i>
				<i>Solirubrobacterales_bacterium</i>
				<i>uncultured_bacterium</i>
		<i>Acidothermaceae</i>	<i>Acidothermus</i>	<i>uncultured_Conexibacteraceae</i>
				<i>Actinomycetales_bacterium</i>
				<i>metagenome</i>
				<i>uncultured_Actinoallomurus</i>
				<i>uncultured_actinobacterium</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_soil</i>
				<i>uncultured_Thermomonosporaceae</i>

Table C1. (Continued)

Kingdom	Phylum	Family	Genus	Species
		<i>Actinospicaceae</i>	<i>Actinospica</i>	<i>Actinospica</i> _sp. <i>Persicaria</i> _minor uncultured_actinobacterium
		<i>Catenulisporaceae</i>	<i>Catenulispora</i>	uncultured_bacterium <i>Catenulispora</i> _acidiphila
		<i>Demequinaceae</i>	<i>Demequina</i>	<i>Catenulispora</i> _sp. globuliformis
		<i>Dermabacteraceae</i>	<i>Brachybacterium</i>	tyrofermentans
		<i>Dermacoccaceae</i>	<i>Flexivirga</i>	alba
		<i>Frankiaceae</i>	<i>Jatrophihabitans</i>	bacterium_Ellin6090 <i>Jatrophihabitans</i> _sp. metagenome uncultured_actinobacterium uncultured_bacterium metagenome
		<i>Gaiellaceae</i>	<i>Gaiella</i>	uncultured_Acidimicrobiales
		<i>Iamiaceae</i>	<i>Iamia</i>	<i>Aquihabitans</i> _daechungensis
		<i>Ilumatobacteraceae</i>	<i>CL500-29_marine_group</i>	<i>Hevea</i> _brasiliensis metagenome
			<i>Ilumatobacter</i>	nonamiensis
			uncultured	uncultured_Actinomycetales uncultured_bacterium
		<i>IMCC26256</i>	<i>IMCC26256</i>	actinobacterium_BGR bacterium_enrichment uncultured_Acidimicrobiia uncultured_Acidothermaceae uncultured_actinobacterium uncultured_Ferrimicrobium
		<i>Kineosporiaceae</i>	<i>Kineosporia</i>	<i>Kineosporia</i> _aurantiaca uncultured_Kineosporiaceae
		<i>MB-A2-108</i>	<i>Quadrisphaera</i> <i>MB-A2-108</i>	granulorum metagenome
		<i>Microbacteriaceae</i>	<i>Agrococcus</i>	jejuensis uncultured_bacterium
		<i>Micromonosporaceae</i>	<i>Amnibacterium</i> <i>Actinocatenispora</i>	<i>Actinocatenispora</i> _rupis uncultured_bacterium
			<i>Dactyloporangium</i>	metagenome
		<i>Microtrichaceae</i>	<i>Luedemannella</i> uncultured	uncultured_Acidimicrobiia metagenome
		<i>Microtrichales</i>	<i>Microtrichales</i>	uncultured_Nakamurellaceae
		<i>Nakamurellaceae</i>	<i>Nakamurella</i>	uncultured_organism
		<i>Nocardiaceae</i>	<i>Rhodococcus</i>	aerolatus
		<i>Nocardioideaceae</i>	<i>Marmoricola</i> <i>Nocardioides</i>	uncultured_bacterium <i>Kribbella</i> _sp. dilutus halotolerans
		<i>Propionibacteriaceae</i>	<i>Aestuariimicrobium</i> <i>Friedmanniella</i> uncultured	uncultured_organism actinobacterium_MH3-4 uncultured_bacterium uncultured_endolithic
		<i>Pseudonocardiaceae</i>	<i>Amycolatopsis</i>	balhimycina

Table C1. (Continued)

Kingdom	Phylum	Family	Genus	Species
			<i>Pseudonocardia</i>	<i>saalfeldensis</i>
				<i>spinosispora</i>
		<i>Solirubrobacteraceae</i>	<i>Conexibacter</i>	<i>uncultured_bacterium</i>
				<i>woesei</i>
				<i>Rubrobacterineae_bacterium</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_Conexibacteraceae</i>
			<i>JCM_18997</i>	<i>Conexibacter_sp.</i>
			<i>uncultured</i>	<i>Phytoplasma_sp.</i>
		<i>Sporichthyaceae</i>	<i>uncultured</i>	<i>Solirubrobacterales_bacterium</i>
		<i>uncultured</i>	<i>uncultured</i>	<i>uncultured_bacterium</i>
				<i>bacterium_Ellin6515</i>
				<i>bacterium_Ellin6517</i>
				<i>Gaiella_sp.</i>
				<i>metagenome</i>
				<i>uncultured_Conexibacter</i>
				<i>uncultured_forest</i>
				<i>uncultured_Pseudonocardiaceae</i>
Bacteria	Armatimonadota	<i>Armatimonadales</i>	<i>Armatimonadales</i>	<i>uncultured_Armatimonadetes</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_Chloroflexi</i>
				<i>uncultured_eubacterium</i>
				<i>uncultured_soil</i>
		<i>Chthonomonadaceae</i>	<i>Chthonomonas</i>	<i>uncultured_Armatimonadetes</i>
				<i>uncultured_bacterium</i>
		<i>Chthonomonadales</i>	<i>Chthonomonadales</i>	<i>unidentified_marine</i>
		<i>Fimbriimonadaceae</i>	<i>Fimbriimonadaceae</i>	<i>uncultured_bacterium</i>
				<i>metagenome</i>
		<i>uncultured</i>	<i>uncultured</i>	<i>uncultured_bacterium</i>
				<i>metagenome</i>
				<i>uncultured_actinobacterium</i>
				<i>uncultured_bacterium</i>
Bacteria	Bacteroidota	<i>37-13</i>	<i>37-13</i>	<i>uncultured_Chitinophagaceae</i>
		<i>AKYH767</i>	<i>AKYH767</i>	<i>metagenome</i>
		<i>Chitinophagaceae</i>	<i>Arachidicoccus</i>	<i>uncultured_Bacteroidetes</i>
			<i>Aurantisolimonas</i>	<i>Arachidicoccus_sp.</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_soil</i>
			<i>Chitinophaga</i>	<i>metagenome</i>
			<i>Dinghuibacter</i>	<i>silviterrae</i>
			<i>Edaphobaculum</i>	<i>uncultured_bacterium</i>
				<i>uncultured_Bacteroidetes</i>
				<i>uncultured_Chitinophaga</i>
				<i>uncultured_Chitinophagaceae</i>
			<i>Filimonas</i>	<i>Filimonas_sp.</i>
			<i>Heliimonas</i>	<i>uncultured_bacterium</i>
			<i>Niabella</i>	<i>hibiscisoli</i>
			<i>Niastella</i>	<i>koreensis</i>
				<i>metagenome</i>



Table C1. (Continued)

Kingdom	Phylum	Family	Genus	Species
			<i>Parafilimonas</i>	metagenome uncultured_bacterium uncultured_Bacteroidetes
			<i>Pseudoflavitalea</i>	metagenome uncultured_bacterium
			<i>Puia</i>	metagenome
			<i>Rurimicrobium</i>	uncultured_bacterium
			<i>Segetibacter</i>	aerophilus uncultured_bacterium uncultured_Chitinophagaceae
			<i>Taibaiella</i>	smilacinae
			<i>Terrimonas</i>	metagenome
			uncultured	<i>Panacibacter_ginsenosidivorans</i> <i>Panacibacter_sp.</i> uncultured_Chitinophaga uncultured_Ferruginibacter
			<i>UTBCD1</i>	uncultured_bacterium
		<i>Crocinitomicaceae</i>	<i>Fluviicola</i>	<i>Fluviicola_sp.</i> uncultured_bacterium
		<i>CWT_CU03-E12</i>	<i>CWT_CU03-E12</i>	bacterium_enrichment uncultured_bacterium uncultured_Bacteroidetes
		<i>Cytophagaceae</i>	<i>Cytophaga</i>	metagenome uncultured_bacterium
			<i>Cytophagaceae</i>	uncultured_bacterium
			<i>Sporocytophaga</i>	myxococcoides
		<i>env.OPS_17</i>	<i>env.OPS_17</i>	metagenome
		<i>FFCH9454</i>	<i>FFCH9454</i>	uncultured_bacterium
		<i>Flavobacteriaceae</i>	<i>Flavobacterium</i>	hauense ceti uncultured_Flavobacteriaceae
			<i>Sediminicola</i>	uncultured_Flavobacteriaceae
			<i>Vitellibacter</i>	uncultured_Aequorivita
		<i>Hymenobacteraceae</i>	<i>Adhaeribacter</i>	uncultured_bacterium
			<i>Hymenobacter</i>	algoricola metagenome psychrophilus <i>Siccationidurans_ginsengisoli</i> uncultured_bacterium
		<i>Ignavibacteriaceae</i>	<i>Ignavibacterium</i>	uncultured_Chlorobi
		<i>Kapabacteriales</i>	<i>Kapabacteriales</i>	uncultured_bacterium uncultured_soil
		<i>KD3-93</i>	<i>KD3-93</i>	metagenome
		<i>Microscillaceae</i>	<i>Chryseolinea</i>	metagenome uncultured_bacterium
			<i>Ohtaekwangia</i>	metagenome
			<i>OLB12</i>	uncultured_bacterium
			uncultured	<i>Algoriphagus_sp.</i> <i>Cytophagales_bacterium</i> <i>Musa_ABB</i>

Table C1. (Continued)

Kingdom	Phylum	Family	Genus	Species
				<i>uncultured_Flammeovirgaceae</i>
				<i>uncultured_Flexibacter</i>
				<i>uncultured_Flexibacteraceae</i>
		<i>NS9_marine_group</i>	<i>NS9_marine_group</i>	<i>metagenome</i>
		<i>Paludibacteraceae</i>	<i>Paludibacter</i>	<i>uncultured_bacterium</i>
		<i>Rhodothermaceae</i>	<i>Rubrivirga</i>	<i>uncultured_bacterium</i>
			<i>uncultured</i>	<i>uncultured_bacterium</i>
		<i>S15-21</i>	<i>S15-21</i>	<i>uncultured_bacterium</i>
		<i>Saprospiraceae</i>	<i>uncultured</i>	<i>wastewater_metagenome</i>
		<i>SB-5</i>	<i>SB-5</i>	<i>uncultured_soil</i>
		<i>SJA-28</i>	<i>SJA-28</i>	<i>uncultured_bacterium</i>
				<i>uncultured_Ignavibacterium</i>
		<i>Sphingobacteriaceae</i>	<i>Mucilaginibacter</i>	<i>calamicampi</i>
			<i>Olivibacter</i>	<i>solii</i>
			<i>Pedobacter</i>	<i>arcticus</i>
				<i>heparinus</i>
				<i>Sphingobacteria_bacterium</i>
				<i>fermentans</i>
		<i>Spirosomaceae</i>	<i>Dyadobacter</i>	<i>Dyadobacter_sp.</i>
			<i>Persicitalea</i>	<i>uncultured_bacterium</i>
			<i>Spirosoma</i>	<i>fluminis</i>
				<i>hortii</i>
				<i>jeollabukense</i>
				<i>linguale</i>
				<i>luteum</i>
				<i>spitsbergense</i>
				<i>uncultured_bacterium</i>
				<i>unidentified</i>
			<i>uncultured</i>	<i>uncultured_Bacteroidetes</i>
		<i>uncultured</i>	<i>uncultured</i>	<i>uncultured_bacterium</i>
				<i>uncultured_Bacteroidetes</i>
				<i>uncultured_Cyclobacteriaceae</i>
		<i>Weeksellaceae</i>	<i>Chryseobacterium</i>	<i>piscium</i>
Bacteria	Bdellovibrionota	<i>Bdellovibrionaceae</i>	<i>OM27_clade</i>	<i>uncultured_bacterium</i>
		<i>0319-6G20</i>	<i>0319-6G20</i>	<i>marine_metagenome</i>
				<i>uncultured_gamma</i>
				<i>uncultured_Syntrophobacteraceae</i>
		<i>Bdellovibrionaceae</i>	<i>Bdellovibrio</i>	<i>uncultured_bacterium</i>
				<i>unidentified</i>
		<i>Silvanigrellaceae</i>	<i>Silvanigrella</i>	<i>metagenome</i>
		<i>Oligoflexales</i>	<i>Oligoflexus</i>	<i>Thymallus_thymallus</i>
				<i>uncultured_bacterium</i>
Bacteria	Chloroflexi	<i>A4b</i>	<i>A4b</i>	<i>metagenome</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_soil</i>
				<i>wastewater_metagenome</i>
		<i>AD3</i>	<i>AD3</i>	<i>uncultured_Chloroflexi</i>
				<i>uncultured_soil</i>
		<i>AKIW781</i>	<i>AKIW781</i>	<i>uncultured_bacterium</i>
				<i>uncultured_Kouleoethrix</i>
		<i>Anaerolineaceae</i>	<i>Leptolinea</i>	<i>uncultured_soil</i>

Table C1. (Continued)

Kingdom	Phylum	Family	Genus	Species
		<i>Anaerolineae</i> <i>C0119</i>	<i>Anaerolineae</i> <i>C0119</i>	<i>uncultured_Bellilinea</i> <i>uncultured_bacterium</i>
		<i>Elev-1554</i> <i>JG30-KF-AS9</i>	<i>Elev-1554</i> <i>JG30-KF-AS9</i>	<i>uncultured_Chloroflexi</i> <i>uncultured_bacterium</i> <i>Chloroflexi_bacterium</i>
		<i>JG30-KF-CM45</i>	<i>JG30-KF-CM45</i>	<i>uncultured_bacterium</i> <i>metagenome</i> <i>uncultured_bacterium</i> <i>uncultured_soil</i> <i>uncultured_Sphaerobacter</i> <i>uncultured_Thermomicrobium</i>
		<i>JG30-KF-CM66</i> <i>Ktedonobacteraceae</i>	<i>JG30-KF-CM66</i> <i>1959-1</i> <i>Ktedonobacter</i> <i>Thermosporothrix</i> <i>uncultured</i>	<i>uncultured_Caldilinea</i> <i>uncultured_bacterium</i> <i>uncultured_Chloroflexi</i> <i>uncultured_bacterium</i> <i>uncultured_bacterium</i> <i>uncultured_soil</i> <i>uncultured_bacterium</i> <i>metagenome</i> <i>metagenome</i>
Bacteria	Cloacimonadota	<i>Roseiflexaceae</i> <i>S085</i> <i>TK10</i> <i>PBS-18</i>	<i>uncultured</i> <i>S085</i> <i>TK10</i> <i>PBS-18</i>	<i>uncultured_bacterium</i> <i>metagenome</i> <i>metagenome</i> <i>uncultured_bacterium</i>
Bacteria	Cyanobacteria	<i>Gastranaerophilales</i> <i>Leptolyngbyaceae</i> <i>Nostocaceae</i> <i>Obscuribacteraceae</i>	<i>Gastranaerophilales</i> <i>Leptolyngbya_PCC-6306</i> <i>Anabaena_PCC-7122</i> <i>Candidatus_Obscuribacter</i> <i>Obscuribacteraceae</i>	<i>uncultured_bacterium</i> <i>Plectolyngbya_hodgsonii</i> <i>Anabaena_sp.</i> <i>uncultured_bacterium</i> <i>metagenome</i> <i>uncultured_bacterium</i> <i>metagenome</i>
		<i>Sericytochromatia</i>	<i>Sericytochromatia</i>	<i>uncultured_bacterium</i> <i>metagenome</i>
		<i>Vampirovibrionaceae</i>	<i>Vampirovibrio</i>	<i>uncultured_bacterium</i> <i>metagenome</i> <i>uncultured_bacterium</i>
Bacteria	Deinococcota	<i>Deinococcaceae</i>	<i>Vampirovibrionaceae</i> <i>Deinococcus</i>	<i>uncultured_bacterium</i> <i>bacterium_Ellin510</i> <i>aerolatus</i> <i>aerophilus</i> <i>alpinitundrae</i> <i>irradiatisoli</i> <i>persicinus</i> <i>radiomollis</i> <i>radioresistens</i> <i>ruber</i> <i>swuensis</i>
Bacteria	Dependentiae	<i>Babeliaceae</i> <i>Babeliales</i> <i>UBA12409</i> <i>Vermiphilaceae</i>	<i>Babeliaceae</i> <i>Babeliales</i> <i>UBA12409</i> <i>Vermiphilaceae</i>	<i>uncultured_Candidatus</i> <i>uncultured_bacterium</i> <i>uncultured_bacterium</i> <i>uncultured_bacterium</i>
Bacteria	Desulfobacterota	<i>Desulfobulbaceae</i> <i>Desulfosarcinaceae</i> <i>Syntrophorhabdaceae</i>	<i>uncultured</i> <i>Desulfatirhabdium</i> <i>Syntrophorhabdus</i>	<i>uncultured_bacterium</i> <i>uncultured_bacterium</i> <i>uncultured_bacterium</i>
Bacteria	Elusimicrobiota	<i>uncultured</i> <i>Endomicrobiaceae</i>	<i>uncultured</i> <i>Endomicrobium</i>	<i>uncultured_delta</i> <i>uncultured_Dongia</i> <i>uncultured_bacterium</i>

Table C1. (Continued)

Kingdom	Phylum	Family	Genus	Species
		<i>Lineage_IIa</i>	<i>Lineage_IIa</i>	<i>uncultured_actinobacterium</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_soil</i>
		<i>Lineage_IIb</i>	<i>Lineage_IIb</i>	<i>uncultured_bacterium</i>
		<i>Lineage_IV</i>	<i>Lineage_IV</i>	<i>uncultured_Termite</i>
Bacteria	FCPU426	<i>FCPU426</i>	<i>FCPU426</i>	<i>uncultured_bacterium</i>
Bacteria	Fibrobacterota	<i>B122</i>	<i>B122</i>	<i>uncultured_bacterium</i>
		<i>Fibrobacteraceae</i>	<i>uncultured</i>	<i>bacterium_enrichment</i>
				<i>metagenome</i>
			<i>possible_genus_04</i>	<i>Juncus_effusus</i>
				<i>metagenome</i>
		<i>uncultured</i>	<i>uncultured</i>	<i>uncultured_bacterium</i>
Bacteria	Firmicutes	<i>Alicyclobacillaceae</i>	<i>Tumebacillus</i>	<i>uncultured_bacterium</i>
				<i>avium</i>
		<i>Bacillaceae</i>	<i>Bacillus</i>	<i>Tumebacillus_sp.</i>
				<i>murimartini</i>
				<i>psychrosaccharolyticus</i>
		<i>Caloramatoraceae</i>	<i>Fonticella</i>	<i>thermoamylovorans</i>
		<i>Clostridia_vadinBB60_group</i>	<i>Clostridia_vadinBB60_group</i>	<i>uncultured_bacterium</i>
		<i>Clostridiaceae</i>	<i>Clostridium_sensu_stricto_12</i>	<i>uncultured_bacterium</i>
			<i>Clostridium_sensu_stricto_9</i>	<i>Clostridium_akagii</i>
			<i>uncultured</i>	<i>uncultured_Clostridium</i>
		<i>Erysipelotrichaceae</i>	<i>Turicibacter</i>	<i>uncultured_bacterium</i>
			<i>ZOR0006</i>	<i>uncultured_bacterium</i>
		<i>Ethanoligenenaceae</i>	<i>Incertae_Sedis</i>	<i>uncultured_organism</i>
		<i>Hungateiclostridiaceae</i>	<i>uncultured</i>	<i>uncultured_bacterium</i>
		<i>Lachnospiraceae</i>	<i>Tyzzereella</i>	<i>uncultured_Ruminococcaceae</i>
		<i>Paenibacillaceae</i>	<i>Paenibacillus</i>	<i>uncultured_Clostridium</i>
				<i>alvei</i>
				<i>dajejonensis</i>
				<i>kobensis</i>
				<i>lautus</i>
				<i>oryzae</i>
				<i>pectinilyticus</i>
				<i>populi</i>
				<i>turicensis</i>
				<i>uliginis</i>
				<i>xylanilyticus</i>
		<i>Planococcaceae</i>	<i>Domibacillus</i>	<i>uncultured_actinobacterium</i>
		<i>Sporomusaceae</i>	<i>Dendrosporobacter</i>	<i>metagenome</i>
				<i>unidentified_eubacterium</i>
		<i>Thermoactinomycetaceae</i>	<i>Pelosinus</i>	<i>uncultured_bacterium</i>
		<i>type_III</i>	<i>Pasteuria</i>	<i>uncultured_Firmicutes</i>
		<i>uncultured</i>	<i>type_III</i>	<i>uncultured_Mollicutes</i>
		<i>GAL15</i>	<i>uncultured</i>	<i>low_GC</i>
Bacteria	GAL15	<i>GAL15</i>	<i>GAL15</i>	<i>uncultured_Firmicutes</i>
Bacteria	Gemmatimonadota	<i>Gemmatimonadaceae</i>	<i>Gemmatimonas</i>	<i>bacterium_Ellin5290</i>
				<i>Gemmatimonadetes_bacterium</i>
				<i>uncultured_Gemmatimonadaceae</i>
				<i>uncultured_soil</i>
			<i>Roseisolibacter</i>	<i>Gemmatirosa_kalamazonesis</i>
				<i>agri</i>

Table C1. (Continued)

Kingdom	Phylum	Family	Genus	Species
				<i>uncultured_bacterium</i>
				<i>uncultured_forest</i>
			<i>uncultured</i>	<i>Gemmatimonadetes_bacterium</i>
				<i>metagenome</i>
				<i>uncultured_Alphaproteobacteria</i>
				<i>uncultured_proteobacterium</i>
Bacteria	Methylomirabilota	<i>Longimicrobiaceae</i>	<i>Longimicrobiaceae</i>	<i>uncultured_bacterium</i>
Bacteria	Myxococcota	<i>Methylomirabilaceae</i>	<i>Sh765B-TzT-35</i>	<i>uncultured_bacterium</i>
		<i>Amb-16S-1034</i>	<i>Amb-16S-1034</i>	<i>uncultured_Polyangiaceae</i>
		<i>Blrii41</i>	<i>Blrii41</i>	<i>metagenome</i>
		<i>Haliangiaceae</i>	<i>Haliangium</i>	<i>myxobacterium_AT3-03</i>
				<i>uncultured_Myxococcales</i>
				<i>uncultured_Nannocystineae</i>
				<i>uncultured_proteobacterium</i>
		<i>mle1-27</i>	<i>mle1-27</i>	<i>uncultured_Polyangiaceae</i>
		<i>Myxococcaceae</i>	<i>KD3-10</i>	<i>metagenome</i>
			<i>uncultured</i>	<i>uncultured_bacterium</i>
				<i>metagenome</i>
				<i>uncultured_delta</i>
		<i>Nannocystaceae</i>	<i>Nannocystis</i>	<i>unidentified</i>
		<i>Phaselicystidaceae</i>	<i>Phaselicystis</i>	<i>uncultured_bacterium</i>
		<i>Polyangiaceae</i>	<i>Aetherobacter</i>	<i>uncultured_bacterium</i>
			<i>Minicystis</i>	<i>uncultured_bacterium</i>
			<i>Pajaroellobacter</i>	<i>Sorangiineae_bacterium</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_Polyangiaceae</i>
				<i>uncultured_proteobacterium</i>
		<i>Sandaracinaceae</i>	<i>uncultured</i>	<i>delta_proteobacterium</i>
				<i>metagenome</i>
Bacteria	Nitrospirota	<i>Nitrospiraceae</i>	<i>Nitrospira</i>	<i>uncultured_soil</i>
				<i>moscoviensis</i>
				<i>uncultured_Green</i>
				<i>uncultured_Nitrospirales</i>
Bacteria	Patescibacteria	<i>uncultured</i>	<i>uncultured</i>	<i>uncultured_bacterium</i>
		<i>Parcubacteria</i>	<i>Parcubacteria</i>	<i>uncultured_bacterium</i>
Bacteria	Planctomycetota	<i>Saccharimonadales</i>	<i>Saccharimonadales</i>	<i>uncultured_bacterium</i>
		<i>BD7-11</i>	<i>BD7-11</i>	<i>uncultured_bacterium</i>
		<i>CPla-3_termite_group</i>	<i>CPla-3_termite_group</i>	<i>metagenome</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_planctomycete</i>
		<i>Gemmataceae</i>	<i>Fimbrioglobus</i>	<i>Gemmata_sp.</i>
				<i>metagenome</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_Gemmata</i>
			<i>Gemmata</i>	<i>bacterium_enrichment</i>
				<i>Gemmata_sp.</i>
				<i>metagenome</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_Planctomycetaceae</i>
				<i>uncultured_Planctomycetales</i>

Table C1. (Continued)

Kingdom	Phylum	Family	Genus	Species
				<i>uncultured_planctomycete</i>
				<i>uncultured_soil</i>
			<i>uncultured</i>	<i>bacterium_enrichment</i>
				<i>metagenome</i>
				<i>Planctomycetaceae_bacterium</i>
				<i>planctomycete_WY69</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_planctomycete</i>
				<i>uncultured_Planctomycetia</i>
				<i>uncultured_sludge</i>
				<i>uncultured_thermal</i>
				<i>uncultured_Zavarzinella</i>
			<i>Zavarzinella</i>	<i>uncultured_bacterium</i>
				<i>Zavarzinella_formosa</i>
		<i>Gimesiaceae</i>	<i>uncultured</i>	<i>uncultured_bacterium</i>
		<i>Isosphaeraceae</i>	<i>Aquisphaera</i>	<i>uncultured_bacterium</i>
				<i>uncultured_planctomycete</i>
			<i>Candidatus_Nostocoida</i>	<i>Candidatus_Nostocoida</i>
				<i>uncultured_bacterium</i>
			<i>Paludisphaera</i>	<i>metagenome</i>
				<i>Paludisphaera_borealis</i>
				<i>uncultured_bacterium</i>
			<i>Singulisphaera</i>	<i>Isosphaera_sp.</i>
				<i>acidiphila</i>
				<i>rosea</i>
				<i>uncultured_Planctomycetales</i>
				<i>uncultured_planctomycete</i>
			<i>Tundrisphaera</i>	<i>metagenome</i>
				<i>lichenicola</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_eubacterium</i>
				<i>uncultured_Planctomycetaceae</i>
				<i>uncultured_planctomycete</i>
			<i>uncultured</i>	<i>Isosphaera_sp.</i>
				<i>metagenome</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_Planctomycetaceae</i>
				<i>uncultured_Planctomycetales</i>
				<i>uncultured_Singulisphaera</i>
		<i>OM190</i>	<i>OM190</i>	<i>uncultured_bacterium</i>
				<i>uncultured_soil</i>
		<i>Phycisphaeraceae</i>	<i>I-8</i>	<i>uncultured_bacterium</i>
			<i>Phycisphaera</i>	<i>uncultured_bacterium</i>
			<i>SM1A02</i>	<i>metagenome</i>
			<i>uncultured</i>	<i>metagenome</i>
		<i>Pirellulaceae</i>	<i>Blastopirellula</i>	<i>marina</i>
			<i>Pir4_lineage</i>	<i>metagenome</i>

Table C1. (Continued)

Kingdom	Phylum	Family	Genus	Species
				<i>uncultured_bacterium</i>
				<i>uncultured_Planctomycetaceae</i>
				<i>uncultured_Planctomycetales</i>
				<i>uncultured_soil</i>
			<i>Pirellula</i>	<i>agricultural_soil</i>
				<i>metagenome</i>
				<i>Pirellula_sp.</i>
				<i>Planctomycetes_bacterium</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_Pasteuria</i>
				<i>uncultured_Planctomycetaceae</i>
				<i>uncultured_Planctomycetales</i>
			<i>Rhodopirellula</i>	<i>planctomycete_str.</i>
				<i>uncultured_Planctomycetaceae</i>
			<i>uncultured</i>	<i>bacterium_enrichment</i>
				<i>metagenome</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_Firmicutes</i>
				<i>uncultured_Planctomycetaceae</i>
				<i>uncultured_Planctomycetales</i>
				<i>uncultured_sludge</i>
		<i>Rubinisphaeraceae</i>	<i>Planctomicrobium</i>	<i>uncultured_bacterium</i>
			<i>SH-PL14</i>	<i>metagenome</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_Planctomycetaceae</i>
				<i>uncultured_planctomycete</i>
		<i>Schlesneriaceae</i>	<i>Planctopirus</i>	<i>metagenome</i>
				<i>uncultured_bacterium</i>
			<i>Schlesneria</i>	<i>metagenome</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_planctomycete</i>
				<i>uncultured_Schlesneria</i>
		<i>Tepidisphaeraceae</i>	<i>Tepidisphaeraceae</i>	<i>uncultured_bacterium</i>
				<i>uncultured_planctomycete</i>
		<i>uncultured</i>	<i>uncultured</i>	<i>agricultural_soil</i>
				<i>metagenome</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_Planctomyces</i>
				<i>uncultured_soil</i>
		<i>vadinHA49</i>	<i>vadinHA49</i>	<i>uncultured_bacterium</i>
		<i>WD2101_soil_group</i>	<i>WD2101_soil_group</i>	<i>Planctomycetales_bacterium</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_eubacterium</i>
				<i>uncultured_Planctomycetaceae</i>
				<i>uncultured_Planctomycetales</i>
				<i>uncultured_planctomycete</i>

Table C1. (Continued)

Kingdom	Phylum	Family	Genus	Species
Bacteria	Proteobacteria	A0839	A0839	uncultured_soil metagenome
				uncultured_Phyllobacteriaceae
		A21b	A21b	uncultured_proteobacterium uncultured_bacterium
		Acetobacteraceae	Acetobacteraceae	uncultured_soil
			Acidicaldus	Acidisphaera_sp.
			Acidiphilium	uncultured_forest metagenome
				uncultured_bacterium
				uncultured_eubacterium
				uncultured_soil
			Acidisoma	tundrae
				uncultured_bacterium
			Acidisphaera	metagenome
				uncultured_soil
			Acidocella	uncultured_bacterium
			Belnapia	uncultured_bacterium
			Rhodopila	uncultured_bacterium
			Rhodovastum	Acetobacteraceae_bacterium metagenome
				uncultured_bacterium
			Roseomonas	arctica lacus ludipueritiae uncultured_organism
			uncultured	metagenome
		Amb-16S-1323	Amb-16S-1323	uncultured_soil
		Beijerinckiaceae	1174-901-12	uncultured_bacterium Methyloferula_sp. Rhizobiales_bacterium
				uncultured_Alphaproteobacteria
				uncultured_bacterium
				uncultured_Rhizobiales
				uncultured_soil
			alphaI_cluster	Alsobacter_sp.
			Beijerinckiaceae	Chelatococcus_asaccharovorans
			Camelimonas	uncultured_bacterium
			Methylobacterium-Methylorubrum	Methylobacterium_adhaesivum Methylobacterium_aerolatum Methylobacterium_cerastii Methylobacterium_komagatae uncultured_organism
			Methylocapsa	uncultured_bacterium
			Methylocella	Methylocella_palustris
			Methylocystis	uncultured_bacterium
			Methylorosula	Beijerinckia_sp.



Table C1. (Continued)

Kingdom	Phylum	Family	Genus	Species
				<i>uncultured_bacterium</i>
			<i>Methylovirgula</i>	<i>uncultured_bacterium</i>
			<i>Psychroglaciacicola</i>	<i>Psychroglaciacicola_arctica</i>
				<i>uncultured_bacterium</i>
			<i>Rhodoblastus</i>	<i>uncultured_bacterium</i>
			<i>Roseiarcus</i>	<i>uncultured_Alphaproteobacteria</i>
				<i>uncultured_bacterium</i>
			<i>uncultured</i>	<i>Methylobacterium_sp.</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_forest</i>
		<i>Burkholderiaceae</i>	<i>Limmobacter</i>	<i>metagenome</i>
			<i>Pandoraea</i>	<i>Burkholderia_sp.</i>
		<i>Caulobacteraceae</i>	<i>Asticcacaulis</i>	<i>uncultured_bacterium</i>
			<i>Brevundimonas</i>	<i>abyssalis</i>
			<i>Caulobacter</i>	<i>uncultured_soil</i>
			<i>Phenylobacterium</i>	<i>Afipia_genosp.</i>
			<i>uncultured</i>	<i>uncultured_Alphaproteobacteria</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_Caulobacteraceae</i>
		<i>CCD24</i>	<i>CCD24</i>	<i>metagenome</i>
		<i>Cellvibrionaceae</i>	<i>Cellvibrio</i>	<i>uncultured_bacterium</i>
		<i>Comamonadaceae</i>	<i>Aquabacterium</i>	<i>citratiphilum</i>
			<i>Variovorax</i>	<i>solii</i>
		<i>Coxiellaceae</i>	<i>Coxiella</i>	<i>uncultured_bacterium</i>
				<i>uncultured_Coxiellaceae</i>
		<i>Devosiaceae</i>	<i>Devosia</i>	<i>neptuniae</i>
		<i>Diplorickettsiaceae</i>	<i>Aquicella</i>	<i>metagenome</i>
				<i>uncultured_bacterium</i>
			<i>uncultured</i>	<i>metagenome</i>
				<i>Rickettsiella_sp.</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_Coxiellaceae</i>
		<i>Dongiaceae</i>	<i>Dongia</i>	<i>metagenome</i>
				<i>uncultured_Rhodospirillaceae</i>
		<i>Elsteraceae</i>	<i>Aliidongia</i>	<i>dinghuensis</i>
			<i>uncultured</i>	<i>uncultured_bacterium</i>
		<i>Geminococcaceae</i>	<i>Candidatus_Alysiosphaera</i>	<i>metagenome</i>
			<i>Candidatus_Alysiosphaera</i>	<i>uncultured_bacterium</i>
			<i>Geminococcus</i>	<i>uncultured_bacterium</i>
		<i>Granulosicoccaceae</i>	<i>Granulosicoccus</i>	<i>marinus</i>
		<i>Holosporaceae</i>	<i>uncultured</i>	<i>uncultured_bacterium</i>
		<i>Hyphomicrobiaceae</i>	<i>Hyphomicrobium</i>	<i>methylovorum</i>
				<i>Hyphomicrobium_sp.</i>
		<i>Hyphomonadaceae</i>	<i>Hirschia</i>	<i>metagenome</i>
			<i>SWB02</i>	<i>metagenome</i>
		<i>Inquilinaceae</i>	<i>Inquilinus</i>	<i>uncultured_Alphaproteobacteria</i>
				<i>uncultured_eubacterium</i>
		<i>JG36-TzT-191</i>	<i>JG36-TzT-191</i>	<i>uncultured_bacterium</i>
				<i>uncultured_proteobacterium</i>
		<i>KF-JG30-C25</i>	<i>KF-JG30-C25</i>	<i>uncultured_gamma</i>

Table C1. (Continued)

Kingdom	Phylum	Family	Genus	Species
		<i>Labraceae</i>	<i>Labrys</i>	<i>uncultured_soil</i> <i>methylaminiphilus</i> <i>uncultured_Phyllobacteriaceae</i> <i>Xanthobacteraceae_bacterium</i>
		<i>Legionellaceae</i>	<i>Legionella</i>	<i>uncultured_bacterium</i>
		<i>Magnetospirillaceae</i>	<i>uncultured</i>	<i>uncultured_bacterium</i>
		<i>Methyloligellaceae</i>	<i>uncultured</i>	<i>metagenome</i>
		<i>Methylomonadaceae</i>	<i>Crenothrix</i>	<i>uncultured_bacterium</i>
		<i>Methylophilaceae</i>	<i>uncultured</i>	<i>metagenome</i>
		<i>Methylotenera</i>	<i>Methylotenera</i>	<i>uncultured_bacterium</i>
		<i>Methylophilaceae</i>	<i>Albibacter</i>	<i>Methylopila_sp.</i>
		<i>Micropepsaceae</i>	<i>Micropepsaceae</i>	<i>uncultured_Hyphomicrobiaceae</i> <i>uncultured_proteobacterium</i> <i>uncultured_bacterium</i>
			<i>Micropepsis</i>	<i>uncultured_bacterium</i>
			<i>Rhizomicrobium</i>	<i>uncultured_bacterium</i>
			<i>uncultured</i>	<i>bacterium_enrichment</i> <i>metagenome</i> <i>uncultured_Acidobacterium</i> <i>uncultured_bacterium</i> <i>uncultured_Hyphomicrobiaceae</i> <i>uncultured_proteobacterium</i> <i>alimentarius</i> <i>metagenome</i>
		<i>Moraxellaceae</i>	<i>Psychrobacter</i>	<i>alpha_proteobacterium</i>
		<i>Nitrosomonadaceae</i>	<i>Ellin6067</i>	<i>uncultured_bacterium</i>
			<i>GOUTA6</i>	<i>metagenome</i>
			<i>IS-44</i>	<i>uncultured_Rhodocyclaceae</i>
			<i>mle1-7</i>	<i>metagenome</i>
			<i>MND1</i>	<i>metagenome</i>
		<i>Oxalobacteraceae</i>	<i>uncultured</i>	<i>metagenome</i>
		<i>Paracaedibacteraceae</i>	<i>Massilia</i>	<i>albidiflava</i>
		<i>Pleomorphomonadaceae</i>	<i>Candidatus_Paracaedibacter</i>	<i>uncultured_bacterium</i>
		<i>Pseudomonadaceae</i>	<i>uncultured</i>	<i>uncultured_Rhizobiales</i>
		<i>R7C24</i>	<i>Pseudomonas</i>	<i>marincola</i>
			<i>R7C24</i>	<i>metagenome</i> <i>uncultured_bacterium</i> <i>metagenome</i>
		<i>Reyranellaceae</i>	<i>Reyranella</i>	<i>uncultured_Alphaproteobacteria</i> <i>thiogangeticum</i>
		<i>Rhizobiaceae</i>	<i>uncultured</i>	<i>Phyllobacteriaceae_bacterium</i> <i>Rhodospirillales_bacterium</i>
			<i>Mesorhizobium</i>	<i>uncultured_bacterium</i> <i>metallidurans</i> <i>metagenome</i> <i>uncultured_bacterium</i> <i>uncultured_Methylocystaceae</i> <i>uncultured_proteobacterium</i> <i>uncultured_bacterium</i> <i>metagenome</i> <i>uncultured_Alphaproteobacteria</i> <i>uncultured_Dokdonella</i> <i>uncultured_Dyella</i>
		<i>Rhizobiales_Incertae_Sedis</i>	<i>Tianweitania</i>	
			<i>Alsobacter</i>	
			<i>Bauldia</i>	
			<i>Nordella</i>	
			<i>uncultured</i>	
		<i>Rhodanobacteraceae</i>	<i>Dokdonella</i>	
			<i>Dyella</i>	

Table C1. (Continued)

Kingdom	Phylum	Family	Genus	Species
			<i>Luteibacter</i>	<i>Luteibacter_sp.</i>
			<i>Mizugakiibacter</i>	<i>uncultured_Xanthomonadaceae</i>
			<i>Rhodanobacter</i>	<i>uncultured_Dokdonella</i>
				<i>uncultured_Rudaea</i>
				<i>uncultured_Xanthomonadaceae</i>
			<i>Rudaea</i>	<i>uncultured_gamma</i>
		<i>Rhodobacteraceae</i>	<i>Amaricoccus</i>	<i>tamworthensis</i>
				<i>uncultured_bacterium</i>
		<i>Rhodocyclaceae</i>	<i>Uliginosibacterium</i>	<i>metagenome</i>
		<i>Rhodomicrobiaceae</i>	<i>Rhodomicrobium</i>	<i>uncultured_Hyphomicrobiaceae</i>
		<i>Rhodospirillaceae</i>	<i>uncultured</i>	<i>uncultured_bacterium</i>
		<i>SC-I-84</i>	<i>SC-I-84</i>	<i>metagenome</i>
				<i>uncultured_Nitrosomonadaceae</i>
		<i>Solimonadaceae</i>	<i>Alkanibacter</i>	<i>uncultured_soil</i>
				<i>gamma_proteobacterium</i>
				<i>metagenome</i>
			<i>Nevskia</i>	<i>Persicaria_minor</i>
				<i>uncultured_bacterium</i>
			<i>Polycyclovorans</i>	<i>uncultured_bacterium</i>
				<i>uncultured_Xanthomonadaceae</i>
			<i>uncultured</i>	<i>uncultured_bacterium</i>
		<i>Sphingomonadaceae</i>	<i>Altererythrobacter</i>	<i>bacterium</i>
				<i>Porphyrobacter_mercurialis</i>
				<i>uncultured_Altererythrobacter</i>
			<i>Hephaestia</i>	<i>uncultured_bacterium</i>
			<i>Novosphingobium</i>	<i>rosa</i>
				<i>uncultured_soil</i>
			<i>Parablastomonas</i>	<i>uncultured_bacterium</i>
			<i>Plot4-2H12</i>	<i>uncultured_Sphingomonadaceae</i>
			<i>Polymorphobacter</i>	<i>uncultured_Sphingomonas</i>
			<i>Qipengyuania</i>	<i>uncultured_bacterium</i>
			<i>Rhizorhapis</i>	<i>Sphingomonas_gotjawalisoli</i>
			<i>Sphingobium</i>	<i>Sphingomonas_azotoformans</i>
				<i>sufflavum</i>
			<i>Sphingomonas</i>	<i>Afipia_sp.</i>
				<i>crusticola</i>
				<i>ginsengisoli</i>
				<i>oligoaromativorans</i>
				<i>panacis</i>
				<i>phyllosphaerae</i>
				<i>polyaromaticivorans</i>
				<i>uncultured_eubacterium</i>
			<i>Sphingopyxis</i>	<i>baekryungensis</i>
				<i>taejonensis</i>
		<i>Steroidobacteraceae</i>	<i>Steroidobacter</i>	<i>bacterium_MI-37</i>
				<i>bacterium_MI-8</i>
			<i>uncultured</i>	<i>Hypsibius_dujardini</i>
				<i>metagenome</i>

Table C1. (Continued)

Kingdom	Phylum	Family	Genus	Species
		<i>Suterellaceae</i>	AAP99	metagenome
		<i>uncultured</i>	<i>uncultured</i>	<i>uncultured_bacterium</i>
		<i>uncultured</i>	<i>uncultured</i>	metagenome
				metagenome
				<i>Rhodospirillaceae_bacterium</i>
				<i>uncultured_Alphaproteobacteria</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_Bradyrhizobiaceae</i>
				<i>uncultured_forest</i>
				<i>uncultured_Hyphomicrobiaceae</i>
				<i>uncultured_proteobacterium</i>
				<i>uncultured_Rhizobiales</i>
				<i>uncultured_Rhodospirillaceae</i>
				<i>uncultured_soil</i>
		<i>Unknown_Family</i>	<i>Acidibacter</i>	metagenome
				<i>Steroidobacter_sp.</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_gamma</i>
				<i>uncultured_proteobacterium</i>
				<i>uncultured_Steroidobacter</i>
				<i>uncultured_Xanthomonadales</i>
			<i>Candidatus_Berkiella</i>	<i>uncultured_Thiotrichales</i>
				<i>uncultured_bacterium</i>
			<i>Candidatus_Ovatusbacter</i>	<i>uncultured_bacterium</i>
			<i>Unknown_Family</i>	<i>uncultured_soil</i>
		WD260	WD260	<i>uncultured_bacterium</i>
		<i>Xanthobacteraceae</i>	<i>Afipia</i>	<i>uncultured_Rhodopseudomonas</i>
			<i>Rhodoplanes</i>	<i>uncultured_Hyphomicrobiaceae</i>
			<i>uncultured</i>	<i>uncultured_Bradyrhizobiaceae</i>
				<i>uncultured_forest</i>
			<i>Xanthobacteraceae</i>	<i>Rhizobiales_bacterium</i>
		<i>Xanthomonadaceae</i>	<i>Pseudoxanthomonas</i>	<i>Pseudomonas_sp.</i>
			<i>Stenotrophomonas</i>	<i>rhizophila</i>
			<i>uncultured</i>	<i>uncultured_bacterium</i>
Bacteria	RCP2-54	<i>Yersiniaceae</i>	<i>Serratia</i>	<i>symbiotica</i>
		<i>RCP2-54</i>	<i>RCP2-54</i>	<i>uncultured_bacterium</i>
				<i>uncultured_Syntrophobacterales</i>
Bacteria	Spirochaetota	<i>Spirochaetaceae</i>	<i>Spirochaeta</i>	<i>Spirochaeta_sp.</i>
			<i>Spirochaeta_2</i>	metagenome
			<i>uncultured</i>	<i>uncultured_soil</i>
Bacteria	Sumerlaeota	V2072-189E03	V2072-189E03	<i>uncultured_Spirochaetales</i>
		<i>Sumerlaeaceae</i>	<i>Sumerlaea</i>	<i>uncultured_Acidobacteria</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_Desulfocaldus</i>
Bacteria	Verrucomicrobiota	<i>Chthoniobacteraceae</i>	<i>Candidatus_Udaeobacter</i>	<i>uncultured_Verrucomicrobia</i>
			<i>Chthoniobacter</i>	<i>bacterium_Ellin506</i>
				<i>bacterium_Ellin507</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_soil</i>

Table C1. (Continued)

Kingdom	Phylum	Family	Genus	Species
			<i>Chthoniobacteraceae</i>	<i>Verrucomicrobia_bacterium</i>
				<i>uncultured_bacterium</i>
			<i>LD29</i>	<i>uncultured_bacterium</i>
		<i>Methylacidiphilaceae</i>	<i>uncultured</i>	<i>uncultured_bacterium</i>
		<i>Omnitrophaceae</i>	<i>Candidatus_Omnitrophus</i>	<i>uncultured_planctomycete</i>
		<i>Omnitrophales</i>	<i>Omnitrophales</i>	<i>uncultured_planctomycete</i>
		<i>Opiritaceae</i>	<i>uncultured</i>	<i>uncultured_bacterium</i>
		<i>Pedosphaeraceae</i>	<i>ADurb.Bin063-1</i>	<i>uncultured_bacterium</i>
			<i>Ellin516</i>	<i>metagenome</i>
				<i>uncultured_bacterium</i>
			<i>Pedosphaera</i>	<i>uncultured_bacterium</i>
			<i>Pedosphaeraceae</i>	<i>bacterium_enrichment</i>
			<i>uncultured</i>	<i>bacterium_enrichment</i>
				<i>uncultured_bacterium</i>
		<i>Pumiceococcaceae</i>	<i>Cerasicoccus</i>	<i>uncultured_organism</i>
		<i>S-BQ2-57_soil_group</i>	<i>S-BQ2-57_soil_group</i>	<i>uncultured_Verrucomicrobia</i>
		<i>Verrucomicrobiaceae</i>	<i>Roseimicrobium</i>	<i>metagenome</i>
			<i>uncultured</i>	<i>uncultured_soil</i>
		<i>Xiphinematobacteraceae</i>	<i>Candidatus_Xiphinematobacter</i>	<i>uncultured_Verrucomicrobia</i>
				<i>uncultured_Xiphinematobacteriaceae</i>
Bacteria	WPS-2	WPS-2	WPS-2	<i>hydrothermal_vent</i>
				<i>metagenome</i>
				<i>uncultured_bacterium</i>
				<i>uncultured_Firmicutes</i>
				<i>uncultured_forest</i>
Bacteria	WS2	WS2	WS2	<i>uncultured_soil</i>

## C.2 Fungi

Table C2. All fungal ASVs identified on Sable Island, NS in 2021 in alphabetical order.

Phylum	Family	Genus	Species
Ascomycota	<i>Celotheliaceae</i>	<i>Celotheliaceae_gen_Incertae_sedis</i>	<i>Celotheliaceae_sp</i>
	<i>Clavicipitaceae</i>	<i>Clavicipitaceae_gen_Incertae_sedis</i>	<i>Clavicipitaceae_sp</i>
		<i>Metapochonia</i>	<i>suchlasporia</i>
	<i>Cyphellophoraceae</i>	<i>Cyphellophoraceae_gen_Incertae_sedis</i>	<i>Cyphellophoraceae_sp</i>
	<i>Herpotrichiellaceae</i>	<i>Exophiala</i>	<i>moniliae</i>
			<i>opportunistica</i>
			<i>quercina</i>
	<i>Hypocreaceae</i>	<i>Hypocreaceae_gen_Incertae_sedis</i>	<i>Hypocreaceae_sp</i>
	<i>Hypocreales_fam_Incertae_sedis</i>	<i>Hypocreales_gen_Incertae_sedis</i>	<i>Hypocreales_sp</i>
	<i>Ophiocordycipitaceae</i>	<i>Drechmeria</i>	<i>campanulata</i>
		<i>Hirsutella</i>	<i>rostrata</i>
		<i>Perennicordyceps</i>	<i>paracuboidea</i>
	<i>Orbiliales_fam_Incertae_sedis</i>	<i>Orbiliales_gen_Incertae_sedis</i>	<i>Orbiliales_sp</i>
	<i>Pezizales_fam_Incertae_sedis</i>	<i>Pezizales_gen_Incertae_sedis</i>	<i>Pezizales_sp</i>

Table C2. (Continued)

Phylum	Family	Genus	Species
		<i>Coprotus</i>	<i>Coprotus_sp</i>
	<i>Pezizomycotina_fam_Incertae_sedis</i>	<i>Cytosporella</i>	<i>Cytosporella_sp</i>
	<i>Saccharomycetales_fam_Incertae_sedis</i>	<i>Candida</i>	<i>Candida_fluviatilis</i>
	<i>Taphrinaceae</i>	<i>Taphrina</i>	<i>inositophila</i>
			<i>Taphrina_sp</i>
Basidiobolomycota	<i>Basidiobolaceae</i>	<i>Basidiobolus</i>	<i>Basidiobolus_sp</i>
Basidiomycota	<i>Agaricaceae</i>	<i>Coprinus</i>	<i>foetidellus</i>
			<i>vosoustii</i>
	<i>Agaricales_fam_Incertae_sedis</i>	<i>Agaricales_gen_Incertae_sedis</i>	<i>Agaricales_sp</i>
	<i>Agaricomycetes_fam_Incertae_sedis</i>	<i>Agaricomycetes_gen_Incertae_sedis</i>	<i>Agaricomycetes_sp</i>
	<i>Agaricostilbales_fam_Incertae_sedis</i>	<i>Agaricostilbales_gen_Incertae_sedis</i>	<i>Agaricostilbales_sp</i>
	<i>Atheliaceae</i>	<i>Athelia</i>	<i>acrosspora</i>
			<i>Athelia_sp</i>
	<i>Auriculariales_fam_Incertae_sedis</i>	<i>Auriculariales_gen_Incertae_sedis</i>	<i>Auriculariales_sp</i>
		<i>Oliveonia</i>	<i>Oliveonia_pauxilla</i>
	<i>Bolbitiaceae</i>	<i>Panaeolus</i>	<i>fimiputris</i>
			<i>papilionaceus</i>
	<i>Boletales_fam_Incertae_sedis</i>	<i>Hydnomerulius</i>	<i>pinastri</i>
		<i>Leucogyrophana</i>	<i>olivascens</i>
	<i>Buckleyzymaceae</i>	<i>Buckleyzyma</i>	<i>aurantiaca</i>
	<i>Byssocorticiaceae</i>	<i>Athelopsis</i>	<i>lembospora</i>
	<i>Camptobasidiaceae</i>	<i>Camptobasidium</i>	<i>Camptobasidium_sp</i>
	<i>Cantharellales_fam_Incertae_sedis</i>	<i>Cantharellales_gen_Incertae_sedis</i>	<i>Cantharellales_sp</i>
	<i>Ceratobasidiaceae</i>	<i>Ceratobasidiaceae_gen_Incertae_sedis</i>	<i>Ceratobasidiaceae_sp</i>
		<i>Ceratobasidium</i>	<i>Ceratobasidium_sp</i>
		<i>Ceratorhiza</i>	<i>rhizodes</i>
		<i>Thanatephorus</i>	<i>cucumeris</i>
		<i>Thanatephorus</i>	<i>Thanatephorus_sp</i>
	<i>Chionosphaeraceae</i>	<i>Ballistosporomyces</i>	<i>sasicola</i>
		<i>Kurtzmanomyces</i>	<i>Kurtzmanomyces_sp</i>
	<i>Chrysozymaceae</i>	<i>Bannozyma</i>	<i>yamatoana</i>
		<i>Chrysozyma</i>	<i>Chrysozyma_sp</i>
		<i>Chrysozymaceae_gen_Incertae_sedis</i>	<i>Chrysozymaceae_sp</i>
		<i>Oberwinklerozyma</i>	<i>silvestris</i>
		<i>Pseudohyphozyma</i>	<i>bogoriensis</i>
		<i>Slooffia</i>	<i>cresolica</i>
		<i>Slooffia</i>	<i>tsugae</i>
	<i>Classiculaceae</i>	<i>Classicula</i>	<i>sinensis</i>
	<i>Clathraceae</i>	<i>Camarophyllopsis</i>	<i>Camarophyllopsis_sp</i>
		<i>Clathrus</i>	<i>Clathrus_sp</i>
		<i>Clavaria</i>	<i>argillacea</i>
			<i>falcata</i>

Table C2. (Continued)

Phylum	Family	Genus	Species
			<i>griseoilacina</i>
			<i>Clavaria_sp</i>
			<i>sphagnicola</i>
		<i>Clavariaceae_gen_Incertae_sedis</i>	<i>Clavariaceae_sp</i>
		<i>Clavulinopsis</i>	<i>corniculata</i>
			<i>fusiformis</i>
			<i>helvola</i>
			<i>laeticolor</i>
			<i>luteoalba</i>
			<i>Clavulinopsis_sp</i>
		<i>Ramariopsis</i>	<i>crocea</i>
			<i>flavescens</i>
			<i>Ramariopsis_sp</i>
	<i>Colacogloeaceae</i>	<i>Colacogloea</i>	<i>Colacogloea_sp</i>
		<i>Coleosporium</i>	<i>solidaginis</i>
	<i>Coniophoraceae</i>	<i>Coniophora</i>	<i>Coniophora_sp</i>
	<i>Corticaceae</i>	<i>Laetisaria</i>	<i>Laetisaria_fuciformis</i>
		<i>Limonomyces</i>	<i>roseipellis</i>
			<i>Limonomyces_sp</i>
	<i>Cortinariaceae</i>	<i>Cortinarius</i>	<i>spilomeus</i>
	<i>Cryptococcaceae</i>	<i>Cryptococcus</i>	<i>watticus</i>
	<i>Cyphellaceae</i>	<i>Rectipilus</i>	<i>Rectipilus_sp</i>
	<i>Cystobasidiaceae</i>	<i>Cystobasidium</i>	<i>finetarium</i>
			<i>minuta</i>
			<i>slooffiae</i>
		<i>Occultifur</i>	<i>externus</i>
			<i>kilbournensis</i>
			<i>mephitis</i>
			<i>Occultifur_sp</i>
	<i>Cystobasidiomycetes_fam_Incertae_sedis</i>	<i>Cystobasidiomycetes_gen_Incertae_sedis</i>	<i>Cystobasidiomycetes_sp</i>
	<i>Cystofilobasidiaceae</i>	<i>Cystofilobasidium</i>	<i>capitatum</i>
	<i>Entolomataceae</i>	<i>Clitopilus</i>	<i>baronii</i>
			<i>passeeckerianus</i>
			<i>Clitopilus_sp</i>
		<i>Entocybe</i>	<i>nitida</i>
		<i>Entoloma</i>	<i>brunneosericeum</i>
			<i>conferendum</i>
			<i>cuspidiferum</i>
			<i>foliomarginatum</i>
			<i>lampropus</i>
			<i>longistriatum</i>
			<i>paraconferendum</i>

Table C2. (Continued)

Phylum	Family	Genus	Species
			<i>pleopodium</i>
			<i>porphyrogriseum</i>
			<i>Entoloma_sp</i>
		<i>Inocephalus</i>	<i>murrayi</i>
		<i>Rhodocybe</i>	<i>cistetorum</i>
	<i>Entylomataceae</i>	<i>Entyloma</i>	<i>magnusii</i>
	<i>Eocronartiaceae</i>	<i>Eocronartium</i>	<i>Eocronartium_sp</i>
	<i>Erythrobasidiaceae</i>	<i>Erythrobasidium</i>	<i>hasegawae</i>
	<i>Erythrobasidiales_fam_Incertae_sedis</i>	<i>Erythrobasidiales_gen_Incertae_sedis</i>	<i>Erythrobasidiales_sp</i>
	<i>Exobasidiaceae</i>	<i>Exobasidium</i>	<i>rostrupii</i>
	<i>Filobasidiaceae</i>	<i>Filobasidium</i>	<i>globosum</i>
			<i>magnum</i>
			<i>Filobasidium_sp</i>
			<i>wieringae</i>
		<i>Goffeauzyna</i>	<i>agrionensis</i>
		<i>Goffeauzyna</i>	<i>gastrica</i>
		<i>Heterocephalacria</i>	<i>Heterocephalacria_sp</i>
		<i>Naganishia</i>	<i>diffluens</i>
	<i>Filobasidiales_fam_Incertae_sedis</i>	<i>Filobasidiales_gen_Incertae_sedis</i>	<i>Filobasidiales_sp</i>
	<i>Ganodermataceae</i>	<i>Ganoderma</i>	<i>applanatum</i>
	<i>Geastraceae</i>	<i>Nidulariopsis</i>	<i>iowensis</i>
	<i>Glomosporiaceae</i>	<i>Thecaphora</i>	<i>Thecaphora_sp</i>
	<i>GS29_fam_Incertae_sedis</i>	<i>GS29_gen_Incertae_sedis</i>	<i>GS29_sp</i>
	<i>Hydnaceae</i>	<i>Sistotrema</i>	<i>oblongisporum</i>
			<i>Sistotrema_sp</i>
	<i>Hydnodontaceae</i>	<i>Brevicellicium</i>	<i>Brevicellicium_sp</i>
		<i>Gliophorus</i>	<i>Gliophorus_sp</i>
			<i>irrigatus</i>
			<i>laetus</i>
		<i>Humidicutis</i>	<i>marginata</i>
		<i>Hygrocybe</i>	<i>cantharellus</i>
			<i>chlorophana</i>
			<i>flavescens</i>
			<i>helobia</i>
			<i>insipida</i>
			<i>miniata</i>
			<i>turunda</i>
		<i>Luellia</i>	<i>cystidiata</i>
		<i>Trechispora</i>	<i>caucasica</i>
			<i>invisitata</i>
			<i>Trechispora_sp</i>
			<i>stellulata</i>



Table C2. (Continued)

Phylum	Family	Genus	Species
			<i>stevensonii</i>
			<i>verruculosa</i>
	<i>Hygrophoropsidaceae</i>	<i>Hygrophoropsis</i>	<i>aurantiaca</i>
			<i>Hygrophoropsis_sp</i>
	<i>Hymenochaetales_fam_Incertae_sedis</i>	<i>Hymenochaetales_gen_Incertae_sedis</i>	<i>Hymenochaetales_sp</i>
	<i>Hyphodermataceae</i>	<i>Hyphoderma</i>	<i>Hyphoderma_sp</i>
	<i>Kriegeriaceae</i>	<i>Phenoliferia</i>	<i>Phenoliferia_sp</i>
	<i>Kriegeriales_fam_Incertae_sedis</i>	<i>Kriegeriales_gen_Incertae_sedis</i>	<i>Kriegeriales_sp</i>
	<i>Leucosporidiaceae</i>	<i>Leucosporidium</i>	<i>creatinivorum</i>
			<i>fragarium</i>
			<i>golubevii</i>
			<i>Leucosporidium_sp</i>
	<i>Leucosporidiales_fam_Incertae_sedis</i>	<i>Leucosporidiales_gen_Incertae_sedis</i>	<i>Leucosporidiales_sp</i>
	<i>Lyophyllaceae</i>	<i>Sagaranelia</i>	<i>Sagaranelia_sp</i>
	<i>Marasmiaceae</i>	<i>Marasmius</i>	<i>curreyi</i>
	<i>Microbotryales_fam_Incertae_sedis</i>	<i>Microbotryales_gen_Incertae_sedis</i>	<i>Microbotryales_sp</i>
	<i>Microbotryomycetes_fam_Incertae_sedis</i>	<i>Curvibasidium</i>	<i>cygneicollum</i>
		<i>Microbotryomycetes_gen_Incertae_sedis</i>	<i>Microbotryomycetes_sp</i>
	<i>Microsporomycetaceae</i>	<i>Microsporomycetaceae_gen_Incertae_sedis</i>	<i>Microsporomycetaceae_sp</i>
	<i>Microstromatales_fam_Incertae_sedis</i>	<i>Pseudomicrostroma</i>	<i>phylloplanum</i>
	<i>Mrakiaceae</i>	<i>Mrakia</i>	<i>aquatica</i>
			<i>Mrakia_sp</i>
	<i>Mycenaceae</i>	<i>Mycena</i>	<i>abramsii</i>
			<i>albidolilacea</i>
			<i>filopes</i>
			<i>galericulata</i>
			<i>griseoviridis</i>
			<i>leptocephala</i>
			<i>metata</i>
			<i>pura</i>
			<i>rubromarginata</i>
			<i>sanguinolenta</i>
			<i>Mycena_sp</i>
			<i>stylobates</i>
	<i>Omphalotaceae</i>	<i>Collybiopsis</i>	<i>hasanskyensis</i>
		<i>Gymnopus</i>	<i>earleae</i>
			<i>impudicus</i>
		<i>Marasmiellus</i>	<i>paspali</i>
		<i>Mycetinis</i>	<i>scorodonius</i>
		<i>Rhodocollybia</i>	<i>Rhodocollybia_butyracea_f_asema</i>
	<i>Phallaceae</i>	<i>Mutinus</i>	<i>ravenelii</i>
			<i>Mutinus_sp</i>

Table C2. (Continued)

Phylum	Family	Genus	Species
	<i>Phallales_fam_Incertae_sedis</i>	<i>Phallales_gen_Incertae_sedis</i>	<i>Phallales_sp</i>
	<i>Piskurozymaceae</i>	<i>Piskurozyma</i>	<i>fildesensis</i> <i>silvicola</i> <i>Piskurozyma_sp</i> <i>taiwanensis</i>
		<i>Solicoccozyma</i>	<i>terricola</i> <i>zizaniae</i>
	<i>Platyglloeales_fam_Incertae_sedis</i>	<i>Platyglloeales_gen_Incertae_sedis</i>	<i>Platyglloeales_sp</i>
	<i>Podoscyphaceae</i>	<i>Hypochnicium</i>	<i>Hypochnicium_sp</i>
	<i>Polyporales_fam_Incertae_sedis</i>	<i>Polyporales_gen_Incertae_sedis</i>	<i>Polyporales_sp</i>
	<i>Psathyrellaceae</i>	<i>Coprinellus</i>	<i>brevisetulosus</i> <i>curtus</i>
		<i>Coprinopsis</i>	<i>babosiae</i> <i>filamentifera</i> <i>pseudofriesii</i> <i>radiata</i> <i>Coprinopsis_sp</i> <i>villosa</i>
		<i>Parasola</i>	<i>misera</i>
		<i>Psathyrella</i>	<i>fimiseda</i>
	<i>Pucciniaceae</i>	<i>Puccinia</i>	<i>graminis</i> <i>striiformis</i>
	<i>Pucciniastraceae</i>	<i>Pucciniastraceae_gen_Incertae_sedis</i>	<i>Pucciniastraceae_sp</i>
	<i>Rhynchogastremataceae</i>	<i>Papiliotrema</i>	<i>fusca</i>
	<i>Rickenellaceae</i>	<i>Peniophorella</i>	<i>pallida</i>
	<i>Russulales_fam_Incertae_sedis</i>	<i>Russulales_gen_Incertae_sedis</i>	<i>Russulales_sp</i>
	<i>Sakaguchiaceae</i>	<i>Sakaguchia</i>	<i>dacryoidea</i> <i>Sakaguchia_sp</i>
	<i>Schizoporaceae</i>	<i>Lyomyces</i>	<i>Lyomyces_sp</i>
	<i>Serendipitaceae</i>	<i>Serendipita</i>	<i>Serendipita_sp</i> <i>herbamans</i> <i>vermifera</i>
		<i>Serendipitaceae_gen_Incertae_sedis</i>	<i>Serendipitaceae_sp</i>
	<i>Sphaerobolaceae</i>	<i>Sphaerobolus</i>	<i>ingoldii</i> <i>Sphaerobolus_sp</i>
	<i>Spiculogloeales_fam_Incertae_sedis</i>	<i>Meniscomyces</i>	<i>layueensis</i>
	<i>Sporidiobolaceae</i>	<i>Rhodotorula</i>	<i>graminis</i> <i>kratochvilovae</i> <i>mucilaginoso</i> <i>sphaerocarpa</i>
		<i>Sporidiobolaceae_gen_Incertae_sedis</i>	<i>Sporidiobolaceae_sp</i>
		<i>Sporidiobolus</i>	<i>salmonicolor</i>

Table C2. (Continued)

Phylum	Family	Genus	Species
		<i>Sporobolomyces</i>	<i>roseus</i>
	<i>Sporidiobolales_fam_Incertae_sedis</i>	<i>Sporidiobolales_gen_Incertae_sedis</i>	<i>Sporidiobolales_sp</i>
	<i>Stephanosporaceae</i>	<i>Cristinia</i>	<i>helvetica</i>
			<i>Cristinia_sp</i>
		<i>Lindmeria</i>	<i>Lindmeria_sp</i>
	<i>Strophariaceae</i>	<i>Agrocybe</i>	<i>pediades</i>
		<i>Deconica</i>	<i>phillipsii</i>
		<i>Galerina</i>	<i>marginata</i>
			<i>Galerina_sp</i>
			<i>venenata</i>
		<i>Hypholoma</i>	<i>capnoides</i>
			<i>lateritium</i>
		<i>Protostropharia</i>	<i>semiglobata</i>
		<i>Psilocybe</i>	<i>semilanceata</i>
	<i>Symmetrosporaceae</i>	<i>Symmetrospora</i>	<i>symmetrica</i>
			<i>gracilis</i>
	<i>Thelephorales_fam_Incertae_sedis</i>	<i>Thelephorales_gen_Incertae_sedis</i>	<i>Thelephorales_sp</i>
	<i>Tilletiariaceae</i>	<i>Tilletiaria</i>	<i>anomala</i>
	<i>Trechisporales_fam_Incertae_sedis</i>	<i>Trechisporales_gen_Incertae_sedis</i>	<i>Trechisporales_sp</i>
	<i>Tremellales_fam_Incertae_sedis</i>	<i>Tremellales_gen_Incertae_sedis</i>	<i>Tremellales_sp</i>
	<i>Tremellodendropsidales_fam_Incertae_sedis</i>	<i>Tremellodendropsidales_gen_Incertae_sedis</i>	<i>Tremellodendropsidales_sp</i>
	<i>Tremellomycetes_fam_Incertae_sedis</i>	<i>Tremellomycetes_gen_Incertae_sedis</i>	<i>Tremellomycetes_sp</i>
	<i>Tricholomataceae</i>	<i>Ampulloclitocybe</i>	<i>clavipes</i>
		<i>Clitocybe</i>	<i>dealbata</i>
		<i>Delicatula</i>	<i>integrella</i>
		<i>Flagelloscypha</i>	<i>minutissima</i>
			<i>Flagelloscypha_sp</i>
		<i>Lachnella</i>	<i>Lachnella_sp</i>
		<i>Leucoinocybe</i>	<i>Leucoinocybe_sp</i>
		<i>Ripartites</i>	<i>Ripartites_sp</i>
	<i>Tubulicrinaceae</i>	<i>Butlerelfia</i>	<i>eustacei</i>
	<i>Typhulaceae</i>	<i>Typhula</i>	<i>Typhula_sp</i>
	<i>Ustilaginaceae</i>	<i>Farysia</i>	<i>Farysia_acheniorum</i>
		<i>Kalmanozyma</i>	<i>Kalmanozyma_fusififormata</i>
		<i>Moesziomyces</i>	<i>aphidis</i>
			<i>bullatus</i>
		<i>Sporisorium</i>	<i>graminicola</i>
			<i>Sporisorium_sp</i>
		<i>Tranzscheliella</i>	<i>yupeitaniae</i>
		<i>Ustilago</i>	<i>kummeri</i>
			<i>Ustilago_sp</i>
	<i>Ustilentylomataceae</i>	<i>Bauerago</i>	<i>Bauerago_sp</i>

Table C2. (Continued)

Phylum	Family	Genus	Species
		<i>Ustilentyloma</i>	<i>graminis</i>
			<i>Ustilentyloma_sp</i>
Calcarisporiellomycota	<i>Calcarisporiellaceae</i>	<i>Calcarisporiella</i>	<i>Calcarisporiella_sp</i>
Chytridiomycota	<i>Alphamycetaceae</i>	<i>Betamyces</i>	<i>Betamyces_sp</i>
	<i>Chytridiomycota_fam_Incertae_sedis</i>	<i>Chytridiomycota_gen_Incertae_sedis</i>	<i>Chytridiomycota_sp</i>
	<i>Chytriomycetaceae</i>	<i>Rhizidium</i>	<i>Rhizidium_sp</i>
	<i>GS13_fam_Incertae_sedis</i>	<i>GS13_gen_Incertae_sedis</i>	<i>GS13_sp</i>
	<i>Powellomycetaceae</i>	<i>Fimicolochytrium</i>	<i>jonesii</i>
			<i>Fimicolochytrium_sp</i>
		<i>Geranomyces</i>	<i>variabilis</i>
		<i>Powellomyces</i>	<i>Powellomyces_sp</i>
		<i>Powellomycetaceae_gen_Incertae_sedis</i>	<i>Powellomycetaceae_sp</i>
	<i>Rhizophlyctidaceae</i>	<i>Rhizophlyctis</i>	<i>rosea</i>
			<i>Rhizophlyctis_sp</i>
	<i>Rhizophlyctidales_fam_Incertae_sedis</i>	<i>Rhizophlyctidales_gen_Incertae_sedis</i>	<i>Rhizophlyctidales_sp</i>
	<i>Rhizophydiaceae</i>	<i>Rhizophydiaceae_gen_Incertae_sedis</i>	<i>Rhizophydiaceae_sp</i>
	<i>Rhizophydiales_fam_Incertae_sedis</i>	<i>Rhizophydiales_gen_Incertae_sedis</i>	<i>Rhizophydiales_sp</i>
	<i>Sonoraphlyctidaceae</i>	<i>Sonoraphlyctis</i>	<i>ranzonii</i>
			<i>Sonoraphlyctis_sp</i>
	<i>Spizellomycetaceae</i>	<i>Spizellomyces</i>	<i>pseudodichotomus</i>
	<i>Spizellomycetales_fam_Incertae_sedis</i>	<i>Spizellomycetales_gen_Incertae_sedis</i>	<i>Spizellomycetales_sp</i>
Fungi_phy_Incertae_sedis	<i>Fungi_fam_Incertae_sedis</i>	<i>Fungi_gen_Incertae_sedis</i>	<i>Fungi_sp</i>
Glomeromycota	<i>Acaulosporaceae</i>	<i>Acaulospora</i>	<i>lacunosa</i>
	<i>Archaeosporaceae</i>	<i>Archaeospora</i>	<i>ecuadoriana</i>
			<i>trappei</i>
	<i>Archaeosporales_fam_Incertae_sedis</i>	<i>Archaeosporales_gen_Incertae_sedis</i>	<i>Archaeosporales_sp</i>
	<i>Claroideoglomeraceae</i>	<i>Claroideoglomus</i>	<i>Claroideoglomus_sp</i>
	<i>Glomeraceae</i>	<i>Glomeraceae_gen_Incertae_sedis</i>	<i>Glomeraceae_sp</i>
		<i>Rhizoglomus</i>	<i>vesiculiferum</i>
		<i>Rhizophagus</i>	<i>intraradices</i>
			<i>irregularis</i>
			<i>Rhizophagus_sp</i>
	<i>Glomeromycota_fam_Incertae_sedis</i>	<i>Glomeromycota_gen_Incertae_sedis</i>	<i>Glomeromycota_sp</i>
Monoblepharomycota	<i>Harpochytriaceae</i>	<i>Harpochytrium</i>	<i>Harpochytrium_sp</i>
	<i>Monoblepharidales_fam_Incertae_sedis</i>	<i>Monoblepharidales_gen_Incertae_sedis</i>	<i>Monoblepharidales_sp</i>
Mortierellomycota	<i>Mortierellaceae</i>	<i>Dissophora</i>	<i>globulifera</i>
		<i>Entomortierella</i>	<i>beljakovae</i>
		<i>Gryganskiella</i>	<i>cystojenkini</i>
		<i>Linnemannia</i>	<i>amoeboidea</i>
			<i>hyalina</i>
			<i>zychae</i>
		<i>Mortierella</i>	<i>alliacea</i>

Table C2. (Continued)

Phylum	Family	Genus	Species
			<i>alpina</i>
			<i>angusta</i>
			<i>basiparvispora</i>
			<i>echinula</i>
			<i>elongatula</i>
			<i>exigua</i>
			<i>fluviae</i>
			<i>formicae</i>
			<i>gemmafera</i>
			<i>macrocystis</i>
			<i>pulchella</i>
			<i>samyensis</i>
			<i>Mortierella_sp</i>
			<i>tsukubaensis</i>
			<i>turficola</i>
		<i>Mortierellaceae_gen_Incertae_sedis</i>	<i>Mortierellaceae_sp</i>
		<i>Podila</i>	<i>humilis</i>
			<i>minutissima</i>
	<i>Mortierellales_fam_Incertae_sedis</i>	<i>Mortierellales_gen_Incertae_sedis</i>	<i>Mortierellales_sp</i>
Mucoromycota	<i>Cunninghamellaceae</i>	<i>Absidia</i>	<i>glauca</i>
			<i>Absidia_sp</i>
		<i>Cunninghamella</i>	<i>elegans</i>
	<i>Endogonales_fam_Incertae_sedis</i>	<i>Endogonales_gen_Incertae_sedis</i>	<i>Endogonales_sp</i>
	<i>GS22_fam_Incertae_sedis</i>	<i>GS22_gen_Incertae_sedis</i>	<i>GS22_sp</i>
	<i>Umbelopsidaceae</i>	<i>Umbelopsis</i>	<i>isabellina</i>
			<i>ramanniana</i>
Olpidiomycota	<i>Olpidiomycota_fam_Incertae_sedis</i>	<i>Olpidiomycota_gen_Incertae_sedis</i>	<i>Olpidiomycota_sp</i>
Rozellomycota	<i>GS05_fam_Incertae_sedis</i>	<i>GS05_gen_Incertae_sedis</i>	<i>GS05_sp</i>