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Ants reign over a distinct microbiome in forest soil

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Abstract

Biotic and abiotic characteristics shape the microbial communities in the soil environment. Manipulation of soil, performed by ants when constructing their nests, radically changes the soil characteristics and creates a unique environment, which differs in its composition, frequency and abundance of microbial taxa, from those in the reference soils. We sampled nests of the mound-building ant *Formica exsecta*, and the surrounding reference soils over a three-month period, and generated NGS (Illumina MiSeq), and T-RFLP data of the bacterial and fungal communities. We used ordination techniques and network analysis to disclose the community structure, and we assessed the variation in diversity, evenness and enrichment of taxa between the two environments. We also used indicator analysis to identify the potential core microbiome of the nests. Our results show that the bacterial and fungal communities, in the rigorously curated nest environment, are significantly different from those in the reference soils, in terms of community structure and enrichment of characteristic indicator taxa. We demonstrate that the nests represent a niche, where microbial species can adapt and diverge from the communities in the surrounding soils. Our findings contribute to our understanding of the composition and function of microbiomes in fragmented habitats.

Key words

Microbial community structure, wood ant nests, indicator taxa, fragmented habitat, boreal forest

1. Introduction

In a forest landscape, the distribution of microbes varies both in spatial and temporal dimensions (Lladó et al., 2018; Männistö et al., 2018; Voříšková and Baldrian, 2013). The spatial distribution encompasses clustering across areas of some centimetres to several kilometres, as well as vertical clustering, beneath the litter layer, following the stratification of the soil (Kadowaki et al., 2014). The spatial variation of the upper soil layers are tightly interlinked with the temporal variation, caused by seasonal changes in temperature, precipitation, photosynthesis and litter production, (Žifčáková et al.,

2017). Furthermore, the distribution of microbes in soil is also affected by manipulation of soil, whether it is compaction carried out by humans (Hartmann et al., 2014) or bioturbation performed by animals (Nkem et al., 2000).

Many organisms actively modify the dynamics of their habitats to better suit their needs, thereby increasing the heterogeneity of their surroundings, changing the abiotic variables and their impact on the biotic communities. Organisms that actively modify the dynamics of their habitats are often referred to as ecosystem engineers (Hastings et al., 2007; Jones et al., 1994; Jouquet et al., 2006; Lavelle et al., 2006). By their engineering actions, these organisms also affect the availability of resources for other species (Hastings et al., 2007). For example, beavers profoundly change the prevailing hydrological characteristics by building their dams, creating large wetlands that provide suitable habitats for other species, such as otters or riparian plants (Rosell et al., 2005). On dry land many invertebrates, such as ants, engineer the ecosystem by redistributing and concentrating soil and litter while building nests for themselves, simultaneously creating suitable niches for other species (Boots et al., 2012; Dauber et al., 2001; Dignac et al., 2017; Frouz and Jílková, 2008; Jílková and Frouz, 2014; Jones et al., 1994).

Ants are ubiquitous and diverse, they occupy nearly every ecological niche on earth, and have an important impact on the soil ecosystem function (King, 2016). Many ant species have an intimate interaction with soil, and have evolved mechanisms to manipulate both the soil and the organisms in it (Vander Meer, 2012). Some ant species demonstrate their soil engineering skills by excavating their dwellings beneath the soil surface, whereas some build conspicuous mounds above ground. This manipulation of mineral and organic material carried out by ants creates a distinct soil chemistry, which shapes the communities of fellow invertebrates, plants and microbes (Dauber et al., 2001; Jouquet et al., 2006), through the level of pH, humidity and available nutrients in the habitat in question (Dostál et al., 2005). In addition, the species-specific feeding strategies and breeding habits of the host are expected to regulate the microbial communities in the nests (Boots et al., 2012; Dauber et al., 2001). For example, many species of the mound-building wood ants derive considerable amounts of honeydew from tree aphids and transport it into the nest for food. The sugar metabolism and the available surplus of sugar intensifies respiration and increases decomposition. The subsequent release of basic cations affects the microbial community through changes in the pH (Jílková et al., 2012). The release and concentration of carbon (Jílková and Frouz, 2014), nitrogen and phosphorus (Kilpeläinen et al., 2007; Lenoir et al., 2001) in the nests also differs from that in the surrounding soils.

Furthermore, some wood ants, especially those living in the sub-arctic regions, such as the Eurasian *Formica* s. str. (Czechowski et al., 2002), actively regulate the temperature inside their nests. For many ant species living in a climate where summers are short, a thermoregulated nest is essential for prolonging the period of breeding and foraging (Jurgensen et al., 2008). In early spring, the *Formica* workers generate heat by utilizing their lipid reserves, maintaining the nest temperature close to +30 °C, regardless of much lower ambient temperatures (Jílková et al., 2015; Rosengren et al., 1987). The nest mounds are mainly built in dry, sunlit spots, providing insolation and heat during the summer (Katzerke et al., 2010; Littlewood and Young, 2008). The high and steady nest temperature is further maintained by the decomposing process (Laakso and Setälä, 1998), keeping the nest drier than the outside environment (Domisch et al., 2008; Jílková and Frouz, 2014). The temperature (Hawkes et

al., 2011; Lladó et al., 2018), acidity (Frouz and Jílková, 2008; Jílková et al., 2015) and humidity (Barnard et al., 2013; Castro et al., 2010) are considered to be major drivers of distribution, composition and abundance of microbial communities in soil environments. In the nests of *Formica* wood ants, these drivers would be expected to diverge from those in the surrounding soils, due to the abiotic and biotic characteristics of the nest mound, and the specific activities of the ants. So far, most of the studies on the microbial communities in ants nests have been carried out on species typical of warmer temperate, or tropical climate, such as *Solenopsis* fire ants (Baird et al., 2007; Ishak et al., 2011; Woolfolk et al., 2016), or *Atta* leaf-cutting ants (Duarte et al., 2014; Rodrigues et al., 2005), leaving the microbes associated with the boreal ant species practically unexplored.

We hypothesized that the nest of a *Formica* ant represents a unique environment, containing bacterial and fungal taxa, which are specifically adapted to the nest environment. We expected this to manifest itself as a difference in the composition, frequency, and abundance of these taxa, compared to the ones in the background soil. We also hypothesized that there would be key characteristic taxa within the microbiome of the nest environment that remain constant during the ant-active season. To investigate the validity of our hypotheses, we analysed the microbial communities in the nest soil of the wood ant *Formica exsecta* (Nylander 1846), as well as in a reference environment, during a three month period. We generated NGS (Illumina MiSeq) and T-RFLP data, and compared the microbial communities of the two environments (nest vs. reference soils) by ordination techniques, and network analysis. Furthermore, we analysed the levels of functional patterns, and compared diversity and evenness between nests and reference soils, and assessed the enrichment of taxa between the two environments at the level of phylum and genus. Finally, we used indicator analysis to determine the identity, and potential function of taxa that were consistently and significantly characteristic to either environment, and analysed their occurrence patterns in the nests and the reference soils.

2. Methods

2.1. Study objects and sampling

The ant *Formica exsecta* inhabits meadows and dry woodlands, and prefers sunny openings (Czechowski et al., 2002), where they construct their above-ground nest mounds. The nests are built of materials gathered from the surroundings, mainly pine and spruce needles, small twigs, and pieces of moss, lichen etc. (Jurgensen et al., 2008). The average lifespan of a nest has been estimated at 6.5 years (Haag-Liautard et al., 2009), but a nest can stay active up to 30 years (Pamilo, 1991). At our study site (Fig. S1), on the islands of Furuskär and Joskär, close to the Tvärminne zoological station (59°84'196"N, 23° 20'182"E) on the SW coast of Finland, the *F. exsecta* populations have been monitored since 1994 (Sundström et al., 1996; Vitikainen et al., 2011). These two islands represent a typical diverse biotope for this area, with habitats that consist of pine and juniper thickets, rich in ericoid shrubs, alternating with smooth granite cliffs, dry meadows and lush grove like patches (Lindström et al., 2018). All the sampled nest mounds were void of live plants, regardless of the surrounding habitat.

We sampled the nest material of 20 active nests (nest environments) together with a sample from the soil surrounding each nest (reference soils), in May, June and August 2015, in total 120 nest and reference soil samples. Nest samples comprised ~0.2 l of material, sampled from the nest dome at a depth of 10 – 15 cm, and nest locations were recorded with a Garmin GPS map60 (Garmin, Olathe,

KS, U.S). The reference soil samples were taken from a spot resembling the environmental conditions of the nest (similar moisture and exposure to light or shade, and without perennial plant cover), 2.5 – 3 m away from the focal nest. The samples of the reference soils (~0.2 l/sample) were taken from the surface litter to a depth of 5 – 15 cm, depending on the thickness of the litter layer. As the nest mounds remain inhabited for several years, and therefore contain litter from a long period of time, we included material from the entire litter layer into the reference samples to gain comparable reference material. The sampling depths were approximately according to those in previous studies on *Formica* ants (in relation to soil fauna (Lenoir et al., 2003a), clear fells (Sorvari et al., 2016), detrital food webs (Laakso and Setälä, 1998) or CO₂ emission (Jílková and Frouz, 2014). The reference soil sample spots were marked with flags during the first sampling in May, for easy retrieval upon consecutive samplings. All samples were collected by hand, using sterile gloves, and stored in ziplock bags at -80° C, until further processing.

DNA was extracted from a ~0.25 g randomly taken subsample of nest material or reference soil, using the PowerSoil® DNA Isolation Kit (MoBio Laboratories Inc., Carlsbad, CA, U.S) as per the manufacturer's instructions, except that TissueLyser II (Qiagen GmbH, Hilden, Germany) was used for 3 min at 20000 rpm during the phase of cell lysis (Lindström et al., 2018). A subset of three randomly chosen samples from Furuskär, and three from Joskär, were submitted for sequencing by Illumina MiSeq. To get a comprehensive overview of the community dynamics of all sampled nests and reference soils, all 120 samples were subjected to T-RFLP analysis, and the results of the two analyses were used to inform each other, as in Lindström et al. (2018).

2.2. Laboratory procedures and bioinformatics

The subset of six nest samples and corresponding reference soil samples, from May, June and August (=36 samples) were submitted for sequencing by Illumina MiSeq. Library preparation, sequencing, and bioinformatics analyses were conducted as in Lindström et al., (2018). Briefly, the bacterial 16S region was amplified using the primers 27F (AGAGTTTGATC(A/C)TGGCTCAG, Chung et al., 2004; Weisburg et al., 1991), and pD' (GTATTACCGCGGCTGCTG, Edwards et al., 1989). The fungal ITS2 region was amplified with the primers ITS7 (GTGA(A/G)TCATCGAATCTTTG, Ihrmark et al., 2012), and ITS4 (TCCTCCGCTTATTGATATGC, White et al., 1990). Illumina MiSeq sequencing of the libraries in pair-end mode was carried out by the DNA Sequencing and Genomics Laboratory, Institute of Biotechnology, University of Helsinki (Helsinki, Finland). Read filtering and OTU clustering (at 97% identity) was performed using UPARSE v. 8.1 (Edgar, 2013). The SILVAv123 (Quast et al., 2013), and UNITE v7 (Kõljalg et al., 2013) databases were used as references for alignment of the bacterial and fungal sequences, respectively. Singletons, doubletons, and sequences not identified to the level of kingdom were removed prior to further analysis. The cyanobacteria/chloroplasts were not removed from the data, as they were expected to reveal details of the origin of the nest building material. The number of sequences (reads) was used as a proxy for the abundance of taxa. Furthermore, the pH was measured in water (pH_w) and in CaCl₂ (pH_{Ca}), from the samples in this subset. For each sample, an amount of approximately 2 ml of nest or reference soil material (comprising 0.5 - 1.0 g) was shaken in four ml of MQ-water for three minutes and left to settle for one minute, prior to measuring the pH_w-value. After the first measurement, 30 µl of CaCl₂ was added, the shaking was repeated and the pH_{Ca}-value was measured.

PCR and purification of soil DNA for T-RFLP analysis was performed as in Lindström et al. (2018), but with modifications to the processing of fungal samples. Instead of targeting only the fungal ITS2 area, the whole ITS area (both ITS1 and ITS2) was targeted with the TAMRA-tagged primers ITS1F (CTTGGTCATTTAGAGGAAGTAA, Gardes and Bruns, 1993), and ITS4 (TCCTCCGCTTATTGATATGC, White et al., 1990). For bacteria, the FAM-tagged forward primer 27F (AGAGTTTGATC(A/C)TGGCTCAG, Chung et al., 2004; Weisburg et al., 1991), and the reverse primer 1387R (GGGCGG(A/T)GTGTACAAGGC, Wade et al., 1998) were used. The digestion of the bacterial and fungal sequences was carried out by the enzymes HaeIII and MspI, as in Lindström et al., (2018). The labelled bacterial and fungal terminal restriction fragments (T-RFs) were separated on an ABI-3730 (Applied Biosystems, Life Technologies, Carlsbad, CA, U.S) with the internal size standard GeneScan 500 ROX (Life Technologies, Bleiswijk, NL), and peaks were scored with GeneMapper v.5 (Applied Biosystems, Life Technologies). Peak data of T-RFs within the range of 70 to 400 bp, and above a threshold of 100 fluorescence units were extracted from GeneMapper, and imported into T-rex (<http://trex.biohpc.org>) for noise filtering (to remove peaks not considered to comprise unique T-RFs), alignment and binning (Culman et al., 2009). The T-RF data was normalized with the package *vegan* in R, prior to statistical analysis (Oksanen et al., 2011), and the number of peaks were counted. A pilot analysis of the T-RFs showed similar results for the data generated by the enzymes HaeIII and MspI. Therefore, only data generated by MspI were used in the main analyses, for both bacteria and fungi.

2.3 Statistical analysis

From the Illumina MiSeq OTUs (hereafter referred to as OTUs or OTU data), the number of reads, the total number of OTUs, and the number of OTUs, which were unique to either environment (detected only among the nest samples or reference soil samples), were counted. Prior to analysis, the OTU data was rarefied to the lowest number of reads in samples using the function *rrarefy* in the package *vegan* in R (Oksanen et al., 2011). The rarefied abundance is hereafter referred to as “total abundance” of bacteria or fungi. The average number of OTUs, the Shannon diversity indices, and Pielou’s evenness estimates per sample were calculated with the package *vegan* (function *diversity*) in R. Differences between the environments in the average number of OTUs, diversity, evenness and pH were tested using a mixed-model ANOVA, with environment as a fixed factor, locID as a repeated random effect, and with a correction to account for multiple comparisons, implemented in the software (JMP v.13, SAS Institute Inc., Cary, NC, U.S).

To assess differences in the bacterial and fungal community compositions in the nest samples compared to the reference soil samples, Bray-Curtis inter-sample dissimilarity matrices were generated of the OTU and T-RF data, and plotted into a Principal Co-ordinates Analysis (PCoA, Legendre and Anderson, 1999). The Bray-Curtis matrices were also subjected to a permutational ANOVA (PERMANOVA) with 999 permutations to test the effect of environment (nest vs. reference soil), together with the effect of month, island and the physical location (locID) of each nest and reference soil pair, on the similarity of the bacterial and fungal communities in the samples. The PERMANOVA was performed using the locID of each nest and corresponding reference soil as strata, in order to constrain the permutations and account for the repeated measurement. The Bray-Curtis, PCoA and the PERMANOVA were carried out in R with the functions *vegdist*, *capscale* and *adonis2* in package *vegan* (Oksanen et al., 2011). PCoA and PERMANOVA were carried out on both

the Illumina MiSeq (OTU) data, and, to confirm the trends from the OTU data, on the more extensive T-RFLP data.

To explore the correlation patterns of the microbial communities across nests and reference soils, networks were constructed with the CoNet app (Faust et al., 2015) in Cytoscape v 3.5.1 (Shannon et al., 2003) on the OTU data. OTUs with fewer than 20 sequencing reads were discarded, and the data were normalized by column. Pearson correlations were generated, and only correlations (edges) significant at or below 0.001 (Fisher's Z score) after Bonferroni corrections for multiple tests, were retained. Networks were visualized with the prefuse force directed layout in Cytoscape, and OTUs with indicator values above 0.5 were used to colour the networks (detailed description of the indicator analysis below). Four descriptors for undirected networks were extracted for the whole networks, or the largest subnetworks, using the network analysis function in Cytoscape: clustering coefficient (number of actual edges in network divided by number of possible edges, averaged over the total network), network centralization (topology measure, from centralized to decentralized), network density (normalized measure for average connectivity of a node in the network) and network heterogeneity (tendency of hub nodes). Networks were initially generated separately for each month, and, subsequently, further split by environment for each month and kingdom. The level of functional organisation (*Fo*, sensu Marzorati et al, 2008) of the bacterial and fungal OTUs was determined by estimating the Pareto-Lorenz curves, where the cumulative normalized number of OTUs was plotted against their respective cumulative normalized abundance (Marzorati et al., 2008). This was performed in JMP v.13 (SAS Institute Inc).

The number of bacterial and fungal reads at the level of phylum and genus were counted, and the effect of environment on the total abundance was analysed using a mixed-model ANOVA in JMP v.13 (SAS Institute Inc, USA), with locID as a repeated random effect, and a correction implemented into the software to account for multiple comparisons. In order to identify the OTUs that represent bacterial and fungal taxa, which are indicators for either environment, we computed Indicator values (Dufrêne and Legendre, 1997), separately for each sampled month, for both the bacterial and fungal OTUs. An indicator taxon is evenly abundant, and predominantly found in a specific environment or habitat type. The analysis calculates Indicator values between zero (no association with the specific environment), and one (strongly associated with the specific environment), and tests the significance of the association. The analysis was performed in R using the *indval* function in the *indicspecies* package (Cáceres and Legendre, 2009), with $p \leq 0.05$ as the cut-off. Based on the analysis, we further determined a core set of indicator taxa for each environment. This was done for bacteria by identifying the OTUs that gained indicator status in all three sampled months. Owing to the low number of fungal indicators, we relaxed the conditions to two months for fungi. The taxa represented by these OTUs were then considered as core indicators for their respective environments. In order to determine level of correspondence, we compared the indicators and the genera, which were significantly more abundant in the respective environment.

2.4. Accession numbers

The unprocessed sequences are available at NCBI Sequence Read Archive, Bioproject number PRJNA399258.

3. Results

The mean pH values for the nest material were pHw = 4.89 ±0.67, and pHCa = 4.06 ±0.74, and the corresponding values for the reference soils were 4.93 ±0.72 and 3.94 ±0.78, respectively. The difference between the two environments was not significant (pHw: $DF=1$, $F=0.09$ and $P=0.760$, pHCa $DF=1$, $F=2.31$ and $P=0.139$). Given the absence of significant differences, we did not include the pH as factors in the models.

3.1. Bacteria

The Illumina MiSeq sequencing produced in total 2404324 reads, 52% of which originated from the nest samples (Table S1). The reads clustered into 5579 OTUs, 4550 of which were present in the nest samples and 5054 in the reference soil. There were 512 OTUs unique to the nest environment and 1015 OTUs unique to the reference soils. The average number of bacterial OTUs per nest was 1163.2 ±327.9, significantly lower than that of reference soils (1434.4 ±332.8) (Table 1). Diversity was significantly lower in the nests (5.35 ±0.37) than in the reference soils (5.60 ±0.45), whereas the evenness of OTUs did not differ between two environments. The T-RFLP, and the restriction by enzyme MspI generated 75 bacterial T-RFs from the nest samples, and 59 T-RFs from the reference soils.

Table 1. The difference in the mean number of the bacterial and fungal OTUs, the mean value of the diversity index (Shannon-Wiener) and the mean estimate of evenness (Pielou's) between the nest and the reference soil environment. Bold face values are significant at $P<0.05$.

	BACTERIA					FUNGI				
	Mean	SD	df	F	p	Mean	SD	df	F	p
Nbr of OTUs										
Nest	1163.22	327.99	1.00	18.20	0.001	279.00	57.66	1.00	1.15	0.293
Ref. soils	1434.44	332.80				300.22	67.93			
Shannon										
Nest	5.35	0.37	1.00	6.81	0.014	3.55	0.72	1.00	3.89	0.058
Ref. soils	5.60	0.45				3.97	0.47			
Pielou's										
Nest	0.76	0.03	1.00	1.50	0.230	0.63	0.12	1.00	4.06	0.053
Ref. soils	0.77	0.04				0.70	0.06			

Based on the Bray-Curtis distances, the bacterial communities showed a significant difference in their composition between the nest and the reference soils environments, for both OTUs and the more comprehensive T-RF data, across most pairs of nests and reference soils. (Fig. 1, Table 2). For both the OTUs and the T-RFs, environment explained most of the variation of the dissimilarities, followed by location (OTUs), and month and location (T-RFs), respectively. The effect of island was significant only for the OTUs, whereas the effect of month was significant only for the T-RFs (Table 2). The effect of island was, however, confounded by the effect of location, due to the nested nature of the data.

Figure 1. Distribution of nests and reference soil communities according to Principal Coordinates analysis, (a) bacterial OTUs, n=36, (b) bacterial T-RFs, n=127, (c) fungal OTUs, n=36, and (d) fungal T-RFs, n=121. Different symbols represent the locID of each nest sample and corresponding reference soil sample. For the OTU data and the corresponding samples in the T-RF data, black symbols indicate the nest environment, and corresponding grey symbols indicate the reference soil environment. The closed grey circles represent the remaining T-RF samples of the nests, and the open grey circles represent the ones of the reference soils. The letters F and J indicate the name of the island (Furuskär or Joskär).

The network analysis also demonstrated a clear clustering according to environment and location, across all three months of sampling (Fig. 2), with low centralization (range 0.083-0.13) and high clustering (range 0.736-0.777), typical for a modular structure (Table S2). This suggests that communities in each environment and location assemble and function in similar ways. The Pareto-Lorenz curves of both the nests and the reference soil environment were similarly shaped, but the *Fo* value for the nest environment was slightly higher (0.92) than that for the reference soils (0.89) (Fig. 3).

Table 2. PERMANOVA test of the effects of environment (nest or reference soils), month, island and locID (location of nest and corresponding reference soil sample) on the Bray-Curtis distances of the microbial OTU and T-RF data. Bold face values are significant at $p < 0.05$.

Test effect	OTUs				T-RFs			
	<i>F</i>	<i>df</i>	<i>R</i> ²	<i>p</i>	<i>F</i>	<i>df</i>	<i>R</i> ²	<i>p</i>
BACTERIA								
environment	7.32	30	0.158	0.001	18.55	120	0.118	0.001
month	0.9	30	0.019	0.491	7.62	120	0.048	0.001
island	2.53	30	0.055	0.014	1.57	120	0.010	0.131
locID	4.84	30	0.105	0.001	2.99	120	0.019	0.009
FUNGI								
environment	5.22	30	0.124	0.001	15.14	114	0.109	0.001
month	0.59	30	0.014	0.950	1.09	114	0.008	0.329
island	2.46	30	0.058	0.003	2.46	114	0.018	0.002
locID	3.33	30	0.079	0.001	4.12	114	0.030	0.001

Figure 2. Monthly networks of nests and reference soils, constructed for bacteria and fungi (n=36). Red dots correspond to indicator OTUs in the nest environment, and blue dots to indicator OTUs in the reference soils. All other OTUs are coloured grey.

Figure 3. Functional organization (F_o) according to the Pareto-Lorenz curves of bacterial (a) and fungal (b) OTUs ($n=36$). The continuous black line represents the nest communities, the dashed line represents the communities of the reference soils. The F_o value equals the value projected at the y-axis, where the critical 20% at the x-axis (grey continuous line) intercepts with the Pareto-Lorenz curves.

3.1.1. Taxon distributions, indicator taxa, and core indicators

Eighteen different bacterial phyla were identified, covering 96% of the OTUs. Sixteen of these were present in the nest samples, and all 18 in the reference soils (Table 3). The four most abundant ones, Proteobacteria, Actinobacteria, Acidobacteria and Bacteroidetes, represented 91.3% of the total rarefied read abundance (total abundance). The remaining phyla represented 4.7% of the total abundance, whereas 4.0% remained unidentified at the level of phylum (Table 3).

We identified 51.2% of the total abundance to the level of genus, encompassing 266 different genera. Twenty-eight of these were significantly more abundant in the nest environment, and 47 were more abundant in the reference soils (Table S3). Of the most abundant genera (covering more than 0.9% of the total abundance), the *Burkholderia* and *Mycobacterium* were significantly more abundant in the nest environment, whereas the Acidobacteria Gp1, Gp2, *Caulobacter*, and *Rhizomicrobium* were more abundant in the reference soils.

Of the 5579 bacterial OTUs, 181 (15.51% of the total abundance) were classified as indicator taxa for the nest, and 288 (17.44% of the total abundance) for the reference soils. The indicator values ranged between 0.63 and 1 (Table S4). Of these were 72 OTUs, representing seven phyla, further classified as core indicators, 35 for the nest environment (3.74% of the total abundance), and 37 for the reference soils (4.43% of the total abundance) (Table 4). Two phyla (Actinobacteria and Cyanobacteria) were characterized as containing core indicators for the nest environment, whereas core indicators belonging to four phyla (Armatimonadetes, Bacteroidetes, Planctomycetes, and Verrucomicrobia) were absent in the nest environment, but present in the reference soils (Table 4). Lower taxa belonging to Acidobacteria and Proteobacteria were identified as core indicators for both environments.

Table 3. Comparison of read abundance in nests and reference soils of bacterial and fungal phyla, presented as percentages of the total abundance across both environments. Bold face values are significant at $p < 0.05$.

	Nest	Reference soils	<i>F</i>	<i>p</i>	No. of identified genera	
					In nests	In ref. soils
BACTERIAL phyla:						
Acidobacteria	9.49	10.94	2.63	0.116	13	15
Actinobacteria	13.41	7.67	9.20	0.005	65	61
Armatimonadetes	0.55	0.56	0.01	0.929	4	4
Bacteroidetes	2.80	3.65	2.47	0.127	28	30
BRC1	0.0002	0.01	6.38	0.017	1	1
Chloroflexi	0.05	0.06	0.22	0.641	5	5
Cyanobacteria/Chloroplast	0.63	0.07	11.17	0.002	4	3
Firmicutes	0.25	0.32	0.31	0.580	13	10
Gemmatimonadetes	0.16	0.35	8.47	0.007	1	1
Nitrospira	0.00009	0.01	1.41	0.244	1	1
OD1	0.0001	0.0003	0.71	0.407	1	1
Planctomycetes	0.10	0.26	14.76	0.001	6	6
Proteobacteria	20.52	22.83	3.30	0.080	103	104
Spirochaetes	-	0.02				1
SR1	-	0.0016				1
Tenericutes	0.0015	0.0011	0.08	0.779	2	1
TM7	0.33	0.25	1.01	0.323	1	1
Verrucomicrobia	0.11	0.58	40.96	0.001	3	3
Not identified	1.59	2.41	8.5	0.007		
Total	100				251	249
FUNGAL phyla:						
Ascomycota	46.84	38.12	29.46	0.001	118	114
Basidiomycota	1.58	6.67	25.5	0.001	35	46
Chytridiomycota	0.01	0	1.07	0.309	2	2
Glomeromycota	-	0.05				1
Mucoromycota	0.16	0.17	0.03	0.866	5	4
Not identified	1.42	4.98	14.76	0.001		
Total	100				160	167

Eight of the core indicators for the nest environment were identified to the level of genus, four Actinobacteria (*Actinomycetospora*, *Frondihabitans*, *Pseudonocardia*, and *Streptomyces*), three Proteobacteria (*Burkholderia*, *Brevundimonas*, and *Methylobacterium*), and one Cyanobacteria (*Chloroplasts*). Five genera were identified as core indicators for the reference soils, one each of Armatimonadetes (Gp5), Bacteroidetes (*Ferruginibacter*), Planctomycetes (*Zavarzinella*), Proteobacteria (*Acidisphaera*), and Verrucomicrobia (*Opitutus*) (Table 4). For Acidobacteria, Gp2,

Gp3, and Gp5 were identified as core indicators for the reference soils only, whereas Gp1 remained as representative of both environments (Table 4). All core indicators identified at the level of genus, with the exception of *Streptomyces*, corresponded with the significantly more abundant genera in their respective environment (Table S3).

Table 4. The bacterial and fungal core indicators; the number of OTUs, reads and percentage of the total abundance they represent.

Nest environment						Reference soil environment				
Phylum	Taxon	Level	OTUs	Reads	% of tot abund.	Taxon	Level	OTUs	Reads	% of tot abund.
BACTERIA										
Acidobacteria	Acidobacteria_Gp1	n.a.	2	13878	1.21	Acidobacteria_Gp1	n.a.	5	24263	2.11
Acidobacteria						Acidobacteria_Gp2	n.a.	3	2882	0.25
Acidobacteria						Acidobacteria_Gp3	n.a.	4	1630	0.14
Acidobacteria						Acidobacteria_Gp5	n.a.	1	121	0.01
Actinobacteria	Actinobacteria	Class	1	369	0.03					
Actinobacteria	Actinomycetales	Order	6	3610	0.31					
Actinobacteria	Microbacteriaceae	Family	3	1563	0.14					
Actinobacteria	Frondihabitans	Genus	2	696	0.06					
Actinobacteria	Actinomycetospora	Genus	1	874	0.08					
Actinobacteria	Pseudonocardia	Genus	1	541	0.05					
Actinobacteria	Streptomyces	Genus	1	1606	0.14					
Cyanobacteria	Chloroplast	Genus	1	259	0.02					
Armatimonadetes						Armatimonadetes Gp5	n.a.	1	180	0.02
Bacteroidetes						Bacteroidetes	Phylum	1	210	0.02
Bacteroidetes						Chitinophagaceae	Family	2	3516	0.31
Bacteroidetes						Ferruginibacter	Genus	1	203	0.02
Planctomycetes						Planctomycetaceae	Family	1	76	0.01
Planctomycetes						Zavarzinella	Genus	1	93	0.01
Proteobacteria	Alphaproteobacteria	Class	1	831	0.07	Alphaproteobacteria	Class	3	3810	0.33
Proteobacteria	Rhizobiales	Order	4	4123	0.36	Rhizobiales	Order	3	3324	0.29
Proteobacteria	Methylobacterium	Genus	2	2529	0.22					
Proteobacteria	Acetobacteraceae	Family	4	3755	0.33	Acetobacteraceae	Family	1	288	0.03
Proteobacteria						Acidisphaera	Genus	1	610	0.05
Proteobacteria	Caulobacteraceae	Family	1	287	0.02					
Proteobacteria	Brevundimonas	Genus	1	2443	0.21					
Proteobacteria						Burkholderiales	Order	1	265	0.02
Proteobacteria	Burkholderiaceae	Family	1	447	0.04					
Proteobacteria	Burkholderia	Genus	2	5003	0.44					
Proteobacteria						Deltaproteobacteria	Class	1	156	0.01
Proteobacteria						Gammaproteobacteria	Class	2	7335	0.64
Verrucomicrobia						Opitutus	Genus	3	1631	0.14
Not identified			1	147	0.01			2	334	0.03
Total		Tot.	35	42961	3.74			37	50927	4.43

FUNGI									
Ascomycota	Ascomycota	Phylum	3	3948	1.54	Ascomycota	Phylum	3	2250 0.88
Ascomycota	Coniochaetaceae	Family	1	250	0.10				
Ascomycota	Dothioraceae	Family	1	1646	0.64				
Ascomycota	Exophiala	Genus	1	291	0.11				
Ascomycota	Oidiodendron	Genus	2	4538	1.77				
Ascomycota	Scleroconidioma	Genus	1	349	0.14				
Ascomycota						Helotiales	Order	1	56 0.02
Ascomycota						Calycina	Genus	1	206 0.08
Ascomycota						Pochonia	Genus	1	214 0.08
Mucoromycota	Umbelopsis	Genus	1	286	0.11	Mortierella	Genus	1	84 0.03
Total		Tot.	10	11308	4.40			7	2810 1.09

3.2. Fungi

Illumina sequencing generated a total of fungal 894469 reads, 60% of which originated from the nests (Table S1). The reads clustered into 1854 OTUs, 1494 of which were found in the nest samples, 1625 in reference soils, and 1265 were shared between the two environments. Of these 229 OTUs were unique to the nests, and 360 unique to the reference soils, respectively. Neither the number of OTUs, nor the levels of diversity and evenness differed significantly between the nests, and the reference soils (Table 1). The T-RFLP analysis using MspI, generated 132 T-RFs from the soil samples, and 131 from the reference soils.

The Bray-Curtis distances in the nests differed significantly from the ones in the reference soils, both for OTUs and T-RFs. The effect of location on the dissimilarities of the communities was also significant, but confounded, as in the case of bacteria (Fig. 1, Table 2). The network analysis also showed a clear clustering according to environment and location (Fig 2), with high clustering values, ranging from 0.809–0.851, and low network centralities, ranging from 0.089–0.128 (Table S2). This suggests highly decentralized and modular network topologies, and similar structures of the communities in the two environments. The Pareto-Lorenz curves signalled high *Fo* values for both environments (0.92 and 0.88 for nests, and soils, respectively) (Fig. 3).

3.2.1. Taxon distributions, indicator taxa, and core indicators

Five fungal phyla were identified, covering 93.6% of the total abundance. Four of these, (Ascomycota, Basidiomycota, Chytridiomycota and Mucoromycota) were present in both environments, and one, Glomeromycota, only in reference soils (Table 3). The two most common phyla, Ascomycota and Basidiomycota accounted for 93.2% of the total abundance, whereas the remaining three phyla each represented less than 1% of the reads. (Table 3). We identified 41.0% of the total abundance to the level of genus, encompassing 181 genera. Fifteen of these were significantly more abundant in the nest environment, and 24 in the reference soils (Table S5). Of the most abundant genera (covering more than 0.7% of the total abundance), the genera *Cladophialophora*, *Oidiodendron* and *Thelebolus* were significantly more abundant in the nest environment, whereas *Meliniomyces* and *Piloderma* were more abundant in the reference soils.

Of the 1854 fungal OTUs, 31 (17.19% of the total abundance) were classified as indicator taxa for the nest, and 16 (2.01% of the total abundance) for the reference soils. The indicator values ranged between 0.67 and 1 (Table S6). Of these 17 OTUs, representing two phyla, Ascomycota and Mucoromycota, were further classified as core indicators, 10 for the nest environment (4.4% of the total abundance), and seven for the reference soils (1.09% of the total abundance). Four of the core indicators for the nest environment were identified to the level of genus, three in the phylum Ascomycota (*Exophiala*, *Oidiodendron* and *Scleroconidioma*), and one in Mucoromycota (*Umbelopsis*) (Table 4). For the reference soils, three core indicators were identified to the level of genus, two in Ascomycota (*Calycina* and *Pochonia*), and one in Mucoromycota (*Mortierella*) (Table 4). All core indicators identified to the level of genus, were also significantly more abundant in their respective environment (Table S5).

4. Discussion

In this study, we characterized the bacterial and fungal communities in the nest mounds of the ant *F. exsecta* and in the reference soils. We found that the nest environment, which is largely shaped by its inhabitants, harbours bacterial and fungal communities that are distinct from the surrounding top soil. As a whole, the enrichment of certain taxa could be distinguished already at the level of phylum, such as Actinobacteria and Ascomycota in the nests, or Basidiomycota and Verrucomicrobia in the reference soils. On lower taxonomic levels, we found significant differences in the community assembly of both bacteria and fungi between the two environments, suggesting different functional associations, based on the taxon-specific traits affiliated with the microbes in question. In particular, the nest-characteristic core indicators contained several potential Actinobacterial ant symbionts, whereas no potential ant-symbiotic taxa were seen among the most characteristic taxa in the reference soils.

Both the bacterial and the fungal nest communities of *F. exsecta* mounds were highly distinct from the reference soils throughout the sampling season, yet showed considerable similarity across the nest environments, regardless of location. This was clearly visible in the results of both the NGS and the more extensive T-RFLP data, rendering strong support for our hypothesis of dissimilar microbial communities in the nests compared to those in the reference soils. The network analysis provided further support for the hypothesis, as the nest environments formed modular sub-networks, largely separated from the reference soil networks, both for bacteria and fungi across the three sampling events. These results largely agree with earlier studies on intra-nest microbial communities of other ant species in other climatic zones, both for bacterial (Boots et al., 2012; Kellner et al., 2015; Lucas et al., 2017), and fungal communities (Boots and Clipson, 2013). We also found secondary effects of island, and the physical location of nests and corresponding reference soils. This was most likely due to differences in soil type and vegetation between the locations of each nest/reference soil pair. An evaluation of the reciprocal importance of location and island cannot be done, as these two effects are confounded, due to the nested structure of the study.

The functional organization of the communities indicated dominance by a few species in both the nest environment, and the reference soils. This can decisively reduce the resilience of a community, when resilience is defined as the tendency of a community to return to its original functional state before disturbance (Marzorati et al., 2008; Pimm, 1984; Shade et al., 2012; Wittebolle et al., 2009). Our analysis should, however, only be considered as a broad characterization of the functional

organization within the communities, as these consist of many taxonomically different, but functionally similar microbes (Burke et al., 2011). In some communities, function is linked with microbial composition, but not in others (Shade and Handelsman, 2012). Hence, a thorough evaluation of the resilience of the microbial organisation according to function or traits, and their variation between the nests and the reference soils, would require a separate study.

The abundance of several phyla differed significantly between the nests, and the reference soils, although most phyla were present in both environments. All the identified bacterial taxa, both in nests and reference soils, were typical of oligotrophic, moderately acidic soils of coniferous forests, in particular the most abundant Acidobacteria, Actinobacteria, and Proteobacteria (Baldrian et al., 2012). The abundances of these phyla vary considerably in forest soils, depending on soil components (Baldrian et al., 2012; Sietiö et al., 2018). The enrichment of Actinobacteria and Ascomycota in the nests may be due to activities of the ants, whereas the phylum Glomeromycota was detected only in the reference soils, likely because these mycorrhiza forming fungi prefer the plant rhizosphere (Young, 2012).

The indicators represented broadly the bacterial and fungal genera, which were enriched in the environment in question. Overall, our results were in agreement with earlier studies on soil microbes, both with respect to the number and taxonomy of the indicators, e.g. (Bach et al., 2018; Leff et al., 2018). Interestingly, we found that the fungal indicators of the nest environment covered 17.19% of the total abundance, whereas the reference soil indicators covered only 2.01% of the total abundance. By contrast, the corresponding difference for the bacterial indicators was negligible (15.51% vs. 17.44%). The higher percentage of total abundance covered by fungal nest indicators may be attributable to the high concentration of recalcitrant, coniferous litter in the nests, which is expected to attract fungal decomposers over bacterial ones (Haňáčková et al., 2015; Voříšková and Baldrian, 2013). Hence, the reference soils would not be expected to contain such stable clusters of specialized fungal decomposers.

Those indicator taxa, which were consistently present throughout the sampling period in either the nests or the reference soils, were identified as core indicators of their respective environment. Several of the bacterial core indicators of the nests encompassed taxa, which are significantly associated with, or symbiotic to, ants, such as the bacterial genera *Pseudonocardia* (Folgarait et al., 2011), *Streptomyces* (Sen et al., 2009) *Burkholderia*, *Methylobacterium* (Van Borm et al., 2002), and *Brevundimonas* (Jaffe et al., 2001), as well as the fungal core indicator *Exophiala* (Duarte et al., 2014). These may represent members of the microbiome that forms symbiotic relationships with the ants. The remaining core indicators of the nest, the three bacterial genera, *Fronidhabitans* (Han et al., 2016), *Methylobacterium* (Pirttilä et al., 2000), and Cyanobacteria/Chloroplast (Aschenbrenner et al., 2016), and three fungal genera, *Oidiodendron*, *Scleroconidioma* (Davey and Currah, 2006), and *Umbelopsis* (Santalahti et al., 2016), are frequently found in pine and spruce needles, moss and lichen (Laakso and Setälä, 1998; Lenoir et al., 2003b; Littlewood and Young, 2008), and may thus owe their presence in the nest to the nest material.

In the reference soil, the bacterial core indicators suggested associations with the rhizosphere, (*Ferruginibacter*, Timonen et al., 2017), with acidic environments, (*Acidisphaera*, Hiraishi et al., 2000), *Sphagnum* moss (*Zavarzinella*, Kulichevskaya et al., 2009), or plant roots (the fungal core indicator *Calycina*, Addy et al., 2005). The bacterium *Opitutus*, here classified as a core indicator of

the reference soils, but has also been found in association with *Cephalotes* ants (Kautz et al., 2013). Interestingly, the core indicators of the reference soils also encompassed the potentially entomopathogenic genera *Pochonia* (Lin et al., 2018), and *Mortierella* (Vega et al., 2012), which were mainly absent from the nests. This begs the question whether the nest environment and the ants represent a hostile environment to these fungi. Acidobacteria Gp1 was the only taxon, which was a core indicator of both the nest and the reference soil. This signals functional specificity at taxonomic levels lower than the ones we could identify in this study, such as species or strain level. The Gp1 has a broad range of enzymes related to sugar usage compared to other Acidobacterial groups (Kielak et al., 2016). Nests containing surplus honeydew (Jílková et al., 2018) may therefore favour the growth of certain specialized strains of Gp1, compared to the reference soils, where the resources are more diverse.

5. Conclusions

Taken together, the results support our hypothesis that the bacterial and fungal communities in the nests of mound-building ants are highly distinct compared to surrounding soils, regarding the community composition, but also regarding the enrichment of taxa. Furthermore, also in accordance with our hypothesis, we identified a small, but consistent, set of core indicators that encompass the potential core microbiome of the nest mounds. A core microbiome (sensu Shade and Handelsman, 2012) is a set of stable and consistent microbes shared across similar habitats, hypothesized to play a key role within the habitat. The presence of such a distinct and consistent microbiome, inside a shielded and constantly maintained environment, suggests a highly adapted microbial community (Koskella and Vos, 2015). Several of the core indicators of the nests were typical of the litter-based (Laakso and Setälä, 1998) nest soil, but some of the taxa we identified may be associated specifically with ants. We found no such patterns in the reference soils, as these were mainly enriched in taxa typical of the rhizosphere. Thus, our results suggest potential candidates for further studies, especially the Actinobacteria, and lower taxa therein.

Characterizing the core members of the community is crucial to understand which taxa play a pivotal role in ecosystem functions. Except for leaf-cutting ants (e.g. (Currie, 2001; Sen et al., 2009)), the microbes dwelling in ant nests are virtually uncharted, especially with respect to their variation in time and space, and in comparison with the surrounding soils. Our results show that the nest environment, which is rigorously curated and maintained by its host, provides an environment, where microbial species can adapt and diverge from the communities in the surrounding soils. Thus, our results contribute to our understanding of the composition and function of microbiomes in fragmented habitats, and suggests further avenues of exploration on microbes and their adaptation in secluded environments.

Data accessibility

The unprocessed sequences are available at NCBI Sequence Read Archive, Bioproject number PRJNA399258.

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Figure S1. The sampling area showing the two islands in Tvärminne archipelago.

Table S1. Read counts from the UPARSE pipeline.

	BACTERIA	FUNGI
Total reads (R1+R2)	9224540	6147738
Merged reads	2928489	3021162
Filtered reads	2166255	2250044
Reads in OTU table	2404410	894635
Reads (singletons and doubletons removed)	2404324	894469
Mean no. of reads / sample (<i>S.D.</i>)	66787 (17235)	24846 (10447)
Lowest no. of reads / sample	31931	7141

Table S2. Network descriptors for the monthly networks.

BACTERIA	May	June	August
Number of nodes in total network	2475	2173	2367
Number of subnetworks	1	2	1
Number of nodes in largest subnetwork	2475	2171	2367
Clustering coefficient	0.777	0.747	0.736
Network centrality	0.130	0.120	0.083
Network density	0.084	0.062	0.061
Network heterogeneity	0.713	0.761	0.599

FUNGI	May	June	August
Number of nodes in total network	714	711	779
Number of subnetworks	1	1	1
Number of nodes in largest subnetwork	714	711	779
Clustering coefficient	0.850	0.806	0.851
Network centrality	0.128	0.104	0.098
Network density	0.086	0.069	0.072
Network heterogeneity	0.760	0.643	0.599

Table S3. Comparison of bacterial read abundance in nest and reference soils, at the level of genera, presented as the percentage of TA across both environments. Only genera, which are significantly ($p \leq 0.05$) more abundant in either environment, are shown. ($DF = 1$, $DF_{Den} = 29$.)

Genus	<i>F</i>	<i>p</i>	Nest			Reference soils		
			reads	% of TA	Core indicator	reads	% of TA	Core indicator
Acidaminococcus	4.52	0.042	12	0.001		0	0	
Acidisoma	11.4	0.002	3565	0.31		1661	0.14	
Acidisphaera	35.86	0.001	51	0.004		663	0.06	yes
Aciditerrimonas	14.57	0.001	1621	0.14		3968	0.35	
Acidobacteria Gp1	8.68	0.006	30067	2.62	yes	56842	4.94	yes
Acidobacteria Gp13	8.26	0.008	12	0.001		197	0.02	
Acidobacteria Gp2	11.69	0.002	627	0.05		10002	0.87	yes
Acidobacteria Gp3	14.11	0.001	2848	0.25		5837	0.51	yes
Acidobacteria Gp5	5.16	0.031	10	0.001		452	0.04	yes
Acidobacteria Gp6	4.41	0.045	206	0.02		2148	0.19	
Acidobacteria Gp7	9.49	0.005	30	0.003		598	0.05	
Acidocella	4.26	0.048	5133	0.45		2917	0.25	
Actinocatenispora	4.58	0.041	126	0.01		2	0.0002	
Actinomycetospora	25.78	0.001	1143	0.1	yes	23	0.002	
Actinospica	5.92	0.021	274	0.02		1131	0.1	
Armatimonadetes_gp1	7.51	0.01	5354	0.47		3060	0.27	
Armatimonadetes_gp3	13.41	0.001	576	0.05		1322	0.12	
Armatimonadetes_gp4	5.7	0.024	27	0.002		95	0.01	
Armatimonadetes_gp5	31.32	0.001	429	0.04		1984	0.17	
Asticcacaulis	4.63	0.04	154	0.01		436	0.04	
Beijerinckia	17.4	0.001	361	0.03		19	0.002	
BRC1 Ls	5.35	0.028	5	0.0004		98	0.01	
Brevundimonas	22.35	0.001	3460	0.3	yes	828	0.07	
Burkholderia	12.36	0.002	24167	2.1	yes	10459	0.91	
Byssovorax	6.24	0.018	37	0.003		511	0.04	
Catenulispora	7.89	0.009	26	0.002		209	0.02	
Caulobacter	8.25	0.008	10261	0.89		13528	1.18	
Chitinophaga	4.66	0.039	73	0.01		340	0.03	
Chlorophyta	7.42	0.011	825	0.07		120	0.01	
Collimonas	5.91	0.022	6	0.001		305	0.03	
Conexibacter	7.84	0.009	1705	0.15		901	0.08	
Cryptosporangium	4.44	0.044	181	0.02		19	0.002	
Curvibacter	13.56	0.001	2	0.0002		101	0.01	
Demequina	4.92	0.035	19	0.002		242	0.02	
Dokdonella	6.01	0.021	105	0.01		2008	0.17	
Ferruginibacter	5.87	0.022	839	0.07		2056	0.18	yes
Fron dihabitans	12.24	0.002	796	0.07	yes	48	0.004	
Gemmata	11.52	0.002	56	0.005		245	0.02	
Gemmatimonas	8.31	0.007	1819	0.16		4004	0.35	
Gordonia	10.03	0.004	22	0.002		0	0	
Herbiconiux	5.74	0.023	3196	0.28		1781	0.15	

Ideonella	7.35	0.011	105	0.01		519	0.05	
Kineococcus	5.05	0.032	50	0.004		1	0.0001	
Kofleria	17.79	0.001	62	0.01		1402	0.12	
Labrys	5	0.033	160	0.01		314	0.03	
Marmoricola	5.79	0.023	5208	0.45		1086	0.09	
Massilia	5.6	0.025	7787	0.68		1678	0.15	
Methylobacterium	14.68	0.001	3925	0.34	yes	193	0.02	
Micrococcus	4.98	0.034	361	0.03		64	0.01	
Mycobacterium	14.89	0.001	28640	2.49		8061	0.7	
Nevskia	5.08	0.032	187	0.02		767	0.07	
Nitrosospora	4.35	0.046	141	0.01		40	0.003	
Nocardioides	4.34	0.046	3036	0.26		1338	0.12	
Novosphingobium	5.91	0.022	2484	0.22		1267	0.11	
Ohtaekwangia	5.46	0.027	183	0.02		2010	0.17	
Opitutus	44.73	0.001	1157	0.1		6338	0.55	yes
Pelomonas	8.18	0.008	53	0.005		529	0.05	
Phenylobacterium	6.61	0.016	3211	0.28		5579	0.49	
Phycisphaera	26.39	0.001	5	0.0004		414	0.04	
Planctomyces	4.71	0.038	5	0.0004		19	0.002	
Pseudonocardia	16.82	0.001	1959	0.17	yes	637	0.06	
Rhizomicrobium	9.41	0.005	12539	1.09		22876	1.99	
Rhodopila	6.97	0.013	697	0.06		117	0.01	
Rudaea	9.88	0.004	127	0.01		3391	0.29	
Schlesneria	11.63	0.002	15	0.001		279	0.02	
Sorangium	29.02	0.001	145	0.01		743	0.06	
Spirochaeta	5.29	0.029	0	0		190	0.02	
Sporichthya	6.66	0.015	101	0.01		415	0.04	
Stella	12.36	0.002	38	0.003		8	0.001	
Steroidobacter	15.07	0.001	250	0.02		1324	0.12	
Streptophyta	8.12	0.008	4600	0.4		382	0.03	
Terriglobus	14.32	0.001	1540	0.13		234	0.02	
Variovorax	7.57	0.01	985	0.09		2603	0.23	
Verrucomicrob.								
Subdiv3	16.3	0.001	2	0.0002		25	0.002	
Zavarzinella	41.03	0.001	7	0.001		176	0.02	yes
Not identified	0.95	0.338	275260	23.95		285242	24.81	

Table S5. Comparison of fungal read abundance in nest and reference soils, at the level of genera, presented as the percentage of TA across both environments. Only genera, which are significantly ($p \leq 0.05$) more abundant in either environment, are shown. ($DF=1$, $DF_{Den} = 29$.)

Genus	<i>F</i>	<i>p</i>	Nest			Reference soils		
			reads	% of TA	Core indicator	reads	% of TA	Core indicator
Bionectria	5.99	0.021	0	0		37	0.01	
Calycina	7.28	0.012	3	0.001		206	0.08	yes
Ceratobasidium	4.63	0.04	7	0.003		29	0.01	
Chaunopycnis	4.28	0.048	8	0.003		41	0.02	
Cladophialophora	14.09	0.001	5016	1.95		1186	0.46	
Cryptodiscus	5.7	0.024	245	0.1		1	0.0004	
Exobasidium	4.64	0.04	113	0.04		50	0.02	
Exophiala	7.08	0.013	350	0.14	yes	92	0.04	
Fellomyces	4.44	0.044	15	0.01		1	0.0004	
Galerina	4.75	0.038	2	0.001		76	0.03	
Gliomastix	5.64	0.024	2	0.001		15	0.01	
Hyaloscypha	22.51	0.001	1023	0.4		37	0.01	
Hymenoscyphus	4.35	0.046	0	0		12	0.005	
Hyphodiscus	5.5	0.026	64	0.02		598	0.23	
Infundichalara	5.38	0.028	61	0.02		4	0.002	
Inocybe	4.39	0.045	0	0		43	0.02	
Lactarius	5.35	0.028	1	0.0004		677	0.26	
Lecanicillium	7.18	0.012	1	0.0004		81	0.03	
Meliniomyces	14.55	0.001	215	0.08		1697	0.66	
Mollisia	5.21	0.03	89	0.03		399	0.16	
Mortierella	12.61	0.001	3	0.001		332	0.13	yes
Mycena	6.61	0.016	54	0.02		246	0.1	
Neonectria	12.26	0.002	12	0.005		241	0.09	
Oidiodendron	9.59	0.004	15303	5.95	yes	1990	0.77	
Penicillium	10.96	0.003	1006	0.39		140	0.05	
Phialocephala	30.71	0.001	153	0.06		1604	0.62	
Piloderma	7.5	0.01	0	0		1818	0.71	
Pochonia	16.92	0.001	18	0.01		242	0.09	yes
Rhizoscyphus	6.39	0.017	1067	0.42		372	0.14	
Rhodospiridium	16.03	0.001	19	0.01		0	0	
Russula	5.04	0.033	0	0		87	0.03	
Scleroconidioma	20.47	0.001	349	0.14	yes	1	0.0004	
Suillus	5.85	0.022	3	0.001		183	0.07	
Thelebolus	5.15	0.031	10222	3.98		112	0.04	
Tomentella	7.61	0.01	0	0		73	0.03	
Umbelopsis	5.59	0.025	388	0.15	yes	45	0.02	
Verticillium	8.49	0.007	7	0.003		104	0.04	
Xenochalara	4.54	0.042	706	0.27		225	0.09	
Not identified	15.19	0.001	66184	25.74		85602	33.3	

Table S4. The bacterial indicator OTUs.

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Otu	month	env	Indval	p	freq	phylum	class	order	family	genus
Otu181	5	nest	1	0.002	6	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium
Otu156	5	nest	1	0.003	6	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu191	5	nest	1	0.004	6	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu91	5	nest	1	0.001	6	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Pseudonocardia
Otu980	5	nest	1	0.004	6	Armatimonadetes	Armatimonadia	Armatimonadales	Armatimonadaceae	Armatimonadetes_gp1
Otu78	5	nest	1	0.004	6	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia
Otu827	5	nest	1	0.003	6	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Frondihabians
Otu3254	5	nest	1	0.002	6	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu245	5	nest	0.995780591	0.004	7	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Actinomycetospora
Otu139	5	nest	0.995495495	0.002	7	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	-
Otu283	5	nest	0.994181214	0.014	8	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces
Otu36	5	nest	0.993449782	0.01	9	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu1911	5	nest	0.993197279	0.002	7	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	-
Otu57	5	nest	0.990345937	0.004	11	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	-
Otu1077	5	nest	0.989473684	0.007	7	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu199	5	nest	0.988919668	0.001	10	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu59	5	nest	0.983548766	0.023	10	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium
Otu38	5	nest	0.98096533	0.001	12	Acidobacteria	Acidobacteria_Gp1	-	-	-
Otu112	5	nest	0.978658537	0.025	9	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium
Otu938	5	nest	0.973958333	0.005	10	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	-
Otu742	5	nest	0.972972973	0.005	7	Armatimonadetes	Armatimonadia	Armatimonadales	Armatimonadaceae	Armatimonadetes_gp1
Otu5290	5	nest	0.971014493	0.02	7	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu266	5	nest	0.968515742	0.028	12	Acidobacteria	Acidobacteria_Gp1	-	-	Terriglobus
Otu267	5	nest	0.967845659	0.024	11	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu110	5	nest	0.967741935	0.013	10	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu1488	5	nest	0.967032967	0.009	8	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu235	5	nest	0.965384615	0.003	10	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu4799	5	nest	0.959677419	0.036	10	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter
Otu1517	5	nest	0.958373669	0.028	11	Acidobacteria	Acidobacteria_Gp1	-	-	Granulicella
Otu413	5	nest	0.956923077	0.031	9	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter
Otu56	5	nest	0.955350269	0.016	11	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu745	5	nest	0.953846154	0.005	9	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu348	5	nest	0.947826087	0.013	7	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu1579	5	nest	0.947368421	0.016	8	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu70	5	nest	0.939313984	0.005	12	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Pseudonocardia
Otu196	5	nest	0.9375	0.009	10	Actinobacteria	Actinobacteria	Actinomycetales	Cryptosporangiaceae	-
Otu573	5	nest	0.93495935	0.004	9	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu2975	5	nest	0.934895833	0.005	11	Acidobacteria	Acidobacteria_Gp1	-	-	Granulicella
Otu20	5	nest	0.929602888	0.017	11	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia
Otu41	5	nest	0.921703297	0.011	12	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia
Otu158	5	nest	0.917266187	0.022	10	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	-
Otu15	5	nest	0.895652174	0.009	12	Actinobacteria	Actinobacteria	Solirubrobacterales	-	-
Otu262	5	nest	0.887892377	0.018	10	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	-
Otu95	5	nest	0.886308068	0.009	12	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu371	5	nest	0.874263261	0.004	12	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu142	5	nest	0.874100719	0.038	11	Actinobacteria	Actinobacteria	Acidimicrobiales	-	-
Otu1021	5	nest	0.869565217	0.019	8	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia
Otu295	5	nest	0.866242038	0.019	10	-	-	-	-	-
Otu92	5	nest	0.861833105	0.01	12	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	-
Otu2489	5	nest	0.857142857	0.007	12	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	-
Otu151	5	nest	0.855769231	0.013	11	Actinobacteria	Actinobacteria	Solirubrobacterales	-	-
Otu124	5	nest	0.85520362	0.017	12	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium
Otu559	5	nest	0.846938776	0.025	11	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu61	5	nest	0.844047619	0.023	11	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium
Otu77	5	nest	0.842696629	0.004	12	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	-
Otu201	5	nest	0.833333333	0.006	5	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia
Otu122	5	nest	0.833333333	0.012	5	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu277	5	nest	0.833333333	0.013	5	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu613	5	nest	0.833333333	0.02	5	Actinobacteria	Actinobacteria	Solirubrobacterales	-	-
Otu183	5	nest	0.833333333	0.019	5	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	-
Otu600	5	nest	0.833333333	0.019	5	-	-	-	-	-
Otu1485	5	nest	0.833333333	0.014	5	Proteobacteria	Alphaproteobacteria	-	-	-
Otu1409	5	nest	0.833333333	0.022	5	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu3731	5	nest	0.833333333	0.014	5	Proteobacteria	Alphaproteobacteria	Alphaproteobacteria_I.s-	-	Rhizomicrobium
Otu885	5	nest	0.833333333	0.022	5	TM7	-	-	-	TM7_genera_I.s
Otu1346	5	nest	0.833333333	0.022	5	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu1779	5	nest	0.833333333	0.013	5	Actinobacteria	Actinobacteria	-	-	-
Otu1035	5	nest	0.833333333	0.02	5	Proteobacteria	Alphaproteobacteria	-	-	-
Otu1329	5	nest	0.833333333	0.012	5	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Actinomycetospora
Otu4753	5	nest	0.833333333	0.007	5	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	-
Otu1677	5	nest	0.833333333	0.013	5	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Methylocystis
Otu79	5	nest	0.831924486	0.028	6	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1
Otu170	5	nest	0.831493745	0.025	6	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu324	5	nest	0.829846583	0.044	6	Actinobacteria	Actinobacteria	-	-	-
Otu163	5	nest	0.829145729	0.018	6	Acidobacteria	Acidobacteria_Gp1	-	-	-
Otu175	5	nest	0.8281893	0.04	7	Proteobacteria	Alphaproteobacteria	-	-	-
Otu29	5	nest	0.827292111	0.014	12	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium
Otu127	5	nest	0.825617284	0.03	6	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-

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Otu403	5	nest	0.821484992	0.02	6	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Fronidhabitans
Otu2528	5	nest	0.821078431	0.023	6	Acidobacteria	Acidobacteria_Gp1	-	-	-
Otu448	5	nest	0.819892473	0.032	6	Cyanobacteria	Chloroplast	-	Chloroplast	Chlorophyta
Otu336	5	nest	0.819444444	0.038	10	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	-
Otu3650	5	nest	0.818439716	0.01	12	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu166	5	nest	0.817843866	0.045	8	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu54	5	nest	0.816051552	0.009	12	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Herbiconiux
Otu439	5	nest	0.815217391	0.028	6	Proteobacteria	Betaproteobacteria	Burkholderiales	-	-
Otu4717	5	nest	0.813953488	0.032	11	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia
Otu385	5	nest	0.813648294	0.037	8	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu1649	5	nest	0.8125	0.04	6	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	-
Otu2587	5	nest	0.811403509	0.025	6	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	-
Otu375	5	nest	0.80952381	0.032	6	-	-	-	-	-
Otu247	5	nest	0.808950086	0.045	8	Actinobacteria	Actinobacteria	Solirubrobacterales	-	-
Otu240	5	nest	0.807407407	0.049	6	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
Otu2731	5	nest	0.807291667	0.027	6	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu499	5	nest	0.807291667	0.021	6	Cyanobacteria	Chloroplast	-	Chloroplast	-
Otu3	5	nest	0.803103264	0.037	11	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu2520	5	nest	0.798611111	0.011	6	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu153	5	nest	0.788416537	0.027	12	Acidobacteria	Acidobacteria_Gp1	-	-	-
Otu4069	5	nest	0.784313725	0.028	7	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium
Otu182	5	nest	0.782238443	0.03	12	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas
Otu797	5	nest	0.770992366	0.033	9	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu2359	5	nest	0.763888889	0.043	7	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
Otu30	5	nest	0.759962494	0.024	12	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	-
Otu1481	5	nest	0.759803922	0.031	6	TM7	-	-	-	TM7_genera_I.s.
Otu860	5	nest	0.748945148	0.047	7	Proteobacteria	Deltaproteobacteria	Myxococcales	-	-
Otu642	5	nest	0.735294118	0.038	7	Actinobacteria	Actinobacteria	Acidimicrobiales	Acidimicrobiaceae	Aciditerrimonas
Otu195	5	nest	0.719026549	0.034	8	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium
Otu517	5	nest	0.666666667	0.046	4	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	-
Otu794	5	nest	0.666666667	0.049	4	-	-	-	-	-
Otu368	5	nest	0.666666667	0.041	4	Cyanobacteria	Chloroplast	-	Chloroplast	-
Otu675	5	nest	0.666666667	0.05	4	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu569	5	nest	0.666666667	0.045	4	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	-
Otu546	5	nest	0.666666667	0.048	4	Cyanobacteria	Chloroplast	Chloroplast	-	-
Otu920	5	nest	0.666666667	0.048	4	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu1062	5	nest	0.666666667	0.05	4	Armatimonadetes	Armatimonadia	Armatimonadales	Armatimonadaceae	Armatimonadetes_gp1
Otu3875	5	nest	0.666666667	0.049	4	Proteobacteria	Alphaproteobacteria	-	-	-
Otu3231	5	nest	0.666666667	0.047	4	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Stella
Otu585	5	nest	0.658119658	0.049	5	Proteobacteria	Alphaproteobacteria	-	-	-
Otu2760	5	ref soils	1	0.002	6	Acidobacteria	Acidobacteria_Gp2	-	-	Gp2
Otu929	5	ref soils	1	0.004	6	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-
Otu1072	5	ref soils	1	0.003	6	Proteobacteria	-	-	-	-
Otu1852	5	ref soils	1	0.004	6	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-
Otu1269	5	ref soils	1	0.004	6	-	-	-	-	-
Otu5460	5	ref soils	1	0.006	6	Bacteroidetes	-	-	-	-
Otu3842	5	ref soils	1	0.005	6	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae	-
Otu459	5	ref soils	0.995951417	0.005	7	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu83	5	ref soils	0.995391705	0.004	7	Proteobacteria	Gammaproteobacteria	-	-	-
Otu656	5	ref soils	0.993791786	0.004	9	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1
Otu382	5	ref soils	0.990353698	0.003	7	Acidobacteria	Acidobacteria_Gp2	-	-	Gp2
Otu1250	5	ref soils	0.988095238	0.003	7	Bacteroidetes	-	-	-	-
Otu503	5	ref soils	0.987179487	0.006	7	-	-	-	-	-
Otu16	5	ref soils	0.985519591	0.03	10	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1
Otu128	5	ref soils	0.98543972	0.005	9	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-
Otu85	5	ref soils	0.984177215	0.027	10	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1
Otu40	5	ref soils	0.983852364	0.01	10	Acidobacteria	Acidobacteria_Gp2	-	-	Gp2
Otu62	5	ref soils	0.983022071	0.006	10	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1
Otu132	5	ref soils	0.979381443	0.037	9	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	-
Otu421	5	ref soils	0.977941176	0.004	8	Proteobacteria	Gammaproteobacteria	-	-	-
Otu467	5	ref soils	0.977011494	0.005	9	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu2477	5	ref soils	0.975609756	0.005	7	Proteobacteria	Alphaproteobacteria	-	-	-
Otu393	5	ref soils	0.965217391	0.004	9	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu638	5	ref soils	0.962711864	0.006	11	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu1426	5	ref soils	0.961748634	0.004	9	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu1818	5	ref soils	0.960784314	0.006	8	-	-	-	-	-
Otu5	5	ref soils	0.960339943	0.038	11	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu714	5	ref soils	0.96	0.011	8	Proteobacteria	Alphaproteobacteria	-	-	-
Otu1061	5	ref soils	0.955445545	0.014	10	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu64	5	ref soils	0.95194085	0.036	11	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu514	5	ref soils	0.951156812	0.004	11	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu1497	5	ref soils	0.95	0.006	7	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	Schlesneria
Otu231	5	ref soils	0.947368421	0.024	10	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu6	5	ref soils	0.946466809	0.009	11	Proteobacteria	Gammaproteobacteria	-	-	-
Otu669	5	ref soils	0.942386831	0.008	11	Proteobacteria	Alphaproteobacteria	-	-	-
Otu1527	5	ref soils	0.941176471	0.015	8	Proteobacteria	Alphaproteobacteria	-	-	-
Otu25	5	ref soils	0.936550492	0.002	12	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1
Otu341	5	ref soils	0.927631579	0.022	11	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu1076	5	ref soils	0.919354839	0.007	8	Proteobacteria	Alphaproteobacteria	-	-	-
Otu5381	5	ref soils	0.918918919	0.004	9	Actinobacteria	Actinobacteria	-	-	-
Otu612	5	ref soils	0.918454936	0.012	12	Proteobacteria	Gammaproteobacteria	-	-	-

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Otu103	5	ref soils	0.914786967	0.018	10	Proteobacteria	Alphaproteobacteria Rhizobiales	-	-
Otu4438	5	ref soils	0.913385827	0.018	9	Proteobacteria	Gammaproteobacteria	-	-
Otu3829	5	ref soils	0.913043478	0.012	7	-	-	-	-
Otu26	5	ref soils	0.911674347	0.006	11	Proteobacteria	Alphaproteobacteria	-	-
Otu89	5	ref soils	0.904552129	0.022	10	Acidobacteria	Acidobacteria_Gp1	-	Gp1
Otu28	5	ref soils	0.900985453	0.007	12	Proteobacteria	Alphaproteobacteria Rhizobiales	-	-
Otu357	5	ref soils	0.890909091	0.017	10	Proteobacteria	Deltaproteobacteria Myxococcales	-	-
Otu389	5	ref soils	0.890756303	0.012	10	Acidobacteria	Acidobacteria_Gp3	-	Gp3
Otu387	5	ref soils	0.884654995	0.026	11	Acidobacteria	Acidobacteria_Gp1	-	Gp1
Otu2355	5	ref soils	0.88	0.022	8	Proteobacteria	-	-	-
Otu67	5	ref soils	0.876113826	0.011	12	Acidobacteria	Acidobacteria_Gp1	-	Gp1
Otu641	5	ref soils	0.873239437	0.014	9	Proteobacteria	Alphaproteobacteria	-	-
Otu916	5	ref soils	0.863157895	0.022	10	Actinobacteria	Actinobacteria	-	-
Otu1001	5	ref soils	0.85915493	0.025	10	-	-	-	-
Otu4470	5	ref soils	0.848167539	0.03	11	Proteobacteria	Alphaproteobacteria Rhodospirillales	Acetobacteraceae	-
Otu1555	5	ref soils	0.84375	0.033	8	Bacteroidetes	Sphingobacteria Sphingobacteriales	Chitinophagaceae	Segetibacter
Otu113	5	ref soils	0.837362637	0.033	12	Proteobacteria	Alphaproteobacteria Caulobacterales	Caulobacteraceae	-
Otu363	5	ref soils	0.833333333	0.019	5	Proteobacteria	Alphaproteobacteria Rhodospirillales	-	-
Otu523	5	ref soils	0.833333333	0.018	5	Proteobacteria	Alphaproteobacteria Rhodospirillales	Acetobacteraceae	-
Otu190	5	ref soils	0.833333333	0.023	5	Acidobacteria	Acidobacteria_Gp2	-	Gp2
Otu212	5	ref soils	0.833333333	0.02	5	Proteobacteria	Betaproteobacteria	-	-
Otu1759	5	ref soils	0.833333333	0.011	5	Acidobacteria	Acidobacteria_Gp3	-	Gp3
Otu1137	5	ref soils	0.833333333	0.02	5	Proteobacteria	Deltaproteobacteria Myxococcales	Cystobacteraceae	-
Otu648	5	ref soils	0.833333333	0.013	5	Acidobacteria	Acidobacteria_Gp2	-	Gp2
Otu876	5	ref soils	0.833333333	0.009	5	Acidobacteria	Acidobacteria_Gp2	-	Gp2
Otu430	5	ref soils	0.833333333	0.017	5	Proteobacteria	Betaproteobacteria Burkholderiales	Oxalobacteraceae	Collimonas
Otu1117	5	ref soils	0.833333333	0.019	5	Acidobacteria	Acidobacteria_Gp5	-	Gp5
Otu436	5	ref soils	0.833333333	0.02	5	Verrucomicrobia	Opitutae	Opitutales	Opitutus
Otu2967	5	ref soils	0.833333333	0.017	5	Proteobacteria	Alphaproteobacteria Rhodospirillales	-	-
Otu1261	5	ref soils	0.833333333	0.018	5	-	-	-	-
Otu100	5	ref soils	0.833333333	0.015	5	Bacteroidetes	Bacteroidetes_l.s	-	Ohtaekwangia
Otu2091	5	ref soils	0.833333333	0.016	5	Proteobacteria	Alphaproteobacteria	-	-
Otu1626	5	ref soils	0.833333333	0.017	5	Verrucomicrobia	Opitutae	Opitutales	Opitutus
Otu690	5	ref soils	0.833333333	0.02	5	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae
Otu3147	5	ref soils	0.833333333	0.013	5	Proteobacteria	Deltaproteobacteria Myxococcales	Polyangiaceae	Zavarzinella
Otu2212	5	ref soils	0.833333333	0.012	5	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae
Otu1210	5	ref soils	0.833333333	0.02	5	Bacteroidetes	Sphingobacteria	Sphingobacteriales	-
Otu3938	5	ref soils	0.833333333	0.014	5	Bacteroidetes	-	-	-
Otu1598	5	ref soils	0.833333333	0.014	5	Armatimonadetes	-	-	Armatimonadetes_gp5
Otu2605	5	ref soils	0.833333333	0.014	5	-	-	-	-
Otu1295	5	ref soils	0.833333333	0.008	5	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae
Otu2270	5	ref soils	0.833333333	0.017	5	Proteobacteria	Alphaproteobacteria Rhodospirillales	Acetobacteraceae	Acidisphaera
Otu4928	5	ref soils	0.833333333	0.007	5	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae
Otu3268	5	ref soils	0.833333333	0.007	5	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae
Otu4531	5	ref soils	0.833333333	0.018	5	Proteobacteria	Alphaproteobacteria	-	-
Otu408	5	ref soils	0.830823293	0.014	6	Verrucomicrobia	Opitutae	Opitutales	Opitutus
Otu94	5	ref soils	0.830058939	0.026	6	Proteobacteria	Alphaproteobacteria	Alphaproteobacteria_l.sRhizomicrobium	-
Otu513	5	ref soils	0.828828829	0.014	6	Acidobacteria	Acidobacteria_Gp1	-	Gp1
Otu1289	5	ref soils	0.827067669	0.017	6	-	-	-	-
Otu2262	5	ref soils	0.826330532	0.033	6	Proteobacteria	Betaproteobacteria Burkholderiales	-	-
Otu184	5	ref soils	0.825958702	0.042	7	Proteobacteria	Deltaproteobacteria Myxococcales	-	-
Otu532	5	ref soils	0.825925926	0.036	11	Proteobacteria	Alphaproteobacteria Rhodospirillales	Acetobacteraceae	-
Otu586	5	ref soils	0.82460733	0.017	7	Acidobacteria	Acidobacteria_Gp1	-	Gp1
Otu2928	5	ref soils	0.824275362	0.013	6	Proteobacteria	Alphaproteobacteria	-	-
Otu105	5	ref soils	0.822404372	0.044	9	Verrucomicrobia	Opitutae	Opitutales	Opitutus
Otu1052	5	ref soils	0.822222222	0.012	11	Proteobacteria	Alphaproteobacteria Rhodospirillales	Acetobacteraceae	-
Otu215	5	ref soils	0.821371611	0.02	7	Proteobacteria	Alphaproteobacteria Rhodospirillales	Acetobacteraceae	Acidisphaera
Otu1207	5	ref soils	0.820895522	0.031	6	Proteobacteria	Deltaproteobacteria	-	-
Otu682	5	ref soils	0.820707071	0.014	6	Proteobacteria	Alphaproteobacteria Rhizobiales	-	-
Otu1610	5	ref soils	0.820707071	0.034	6	Bacteroidetes	-	-	-
Otu712	5	ref soils	0.820610687	0.042	7	Verrucomicrobia	Opitutae	Opitutales	Opitutus
Otu1405	5	ref soils	0.815972222	0.022	6	Acidobacteria	Acidobacteria_Gp3	-	Gp3
Otu417	5	ref soils	0.815085158	0.034	7	Proteobacteria	Alphaproteobacteria	-	-
Otu1042	5	ref soils	0.814814815	0.015	6	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae
Otu144	5	ref soils	0.814176245	0.041	7	Acidobacteria	Acidobacteria_Gp2	-	Gp2
Otu752	5	ref soils	0.813253012	0.039	6	Proteobacteria	Betaproteobacteria	-	-
Otu986	5	ref soils	0.811403509	0.017	6	Acidobacteria	Acidobacteria_Gp3	-	Gp3
Otu463	5	ref soils	0.810961969	0.021	7	Verrucomicrobia	Opitutae	Opitutales	Opitutus
Otu1679	5	ref soils	0.809178744	0.018	7	Proteobacteria	Alphaproteobacteria	-	-
Otu951	5	ref soils	0.802469136	0.023	6	-	-	-	-
Otu1011	5	ref soils	0.798611111	0.025	7	Armatimonadetes	-	-	Armatimonadetes_gp5
Otu1249	5	ref soils	0.798611111	0.029	6	Proteobacteria	Betaproteobacteria	-	-
Otu1571	5	ref soils	0.791666667	0.031	6	-	-	-	-
Otu743	5	ref soils	0.790598291	0.049	8	Acidobacteria	Acidobacteria_Gp3	-	Gp3
Otu894	5	ref soils	0.790598291	0.043	6	Acidobacteria	Acidobacteria_Gp3	-	Gp3
Otu1594	5	ref soils	0.785714286	0.03	7	-	-	-	-
Otu1487	5	ref soils	0.784883721	0.035	7	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae
Otu3871	5	ref soils	0.772058824	0.043	7	Acidobacteria	Acidobacteria_Gp3	-	Gp3
Otu1504	5	ref soils	0.761904762	0.046	7	Proteobacteria	Alphaproteobacteria	-	-
Otu3329	5	ref soils	0.722222222	0.04	7	Proteobacteria	Gammaproteobacteria	-	-
Otu2077	5	ref soils	0.714285714	0.045	7	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae

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Otu65	5	ref soils	0.701760325	0.049	12	Proteobacteria	Alphaproteobacteria	Caulobacteriales	Caulobacteraceae	Caulobacter
Otu1469	5	ref soils	0.666666667	0.05	4	Acidobacteria	Acidobacteria_Gp6	-	-	Gp6
Otu819	5	ref soils	0.666666667	0.043	4	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu1017	5	ref soils	0.642857143	0.047	5	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1
Otu183	6	nest	1	0.004	6	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	-
Otu122	6	nest	1	0.003	6	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu1409	6	nest	1	0.003	6	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu368	6	nest	1	0.002	6	Cyanobacteria	Chloroplast	-	Chloroplast	-
Otu827	6	nest	1	0.005	6	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Frondihabians
Otu79	6	nest	0.996261682	0.011	10	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1
Otu156	6	nest	0.990196078	0.002	8	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu322	6	nest	0.990196078	0.006	7	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu794	6	nest	0.987341772	0.003	7	-	-	-	-	-
Otu490	6	nest	0.976470588	0.009	8	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu191	6	nest	0.975409836	0.004	7	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu36	6	nest	0.974358974	0.004	9	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu385	6	nest	0.97080292	0.001	9	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu245	6	nest	0.964444444	0.008	8	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardaceae	Actinomycetospora
Otu143	6	nest	0.964401294	0.035	10	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu335	6	nest	0.96097561	0.002	8	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia
Otu1531	6	nest	0.957894737	0.01	8	Acidobacteria	Acidobacteria_Gp1	-	-	Granulicella
Otu109	6	nest	0.956175299	0.01	9	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	-
Otu338	6	nest	0.95505618	0.022	9	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu139	6	nest	0.953571429	0.015	8	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	-
Otu247	6	nest	0.952380952	0.008	11	Actinobacteria	Actinobacteria	Solirubrobacterales	-	-
Otu675	6	nest	0.952380952	0.003	7	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu166	6	nest	0.94966443	0.026	10	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu112	6	nest	0.949333333	0.027	9	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium
Otu739	6	nest	0.946236559	0.007	9	Acidobacteria	Acidobacteria_Gp1	-	-	-
Otu147	6	nest	0.944903581	0.029	10	Cyanobacteria	Chloroplast	-	Chloroplast	Streptophyta
Otu403	6	nest	0.944444444	0.018	9	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Frondihabians
Otu24	6	nest	0.940414508	0.024	10	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium
Otu303	6	nest	0.93989071	0.009	7	-	-	-	-	-
Otu20	6	nest	0.938695652	0.002	12	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia
Otu324	6	nest	0.9375	0.01	8	Actinobacteria	Actinobacteria	-	-	-
Otu4103	6	nest	0.931623932	0.023	10	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu938	6	nest	0.931174089	0.009	9	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	-
Otu57	6	nest	0.923371648	0.006	8	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	-
Otu5447	6	nest	0.923076923	0.013	7	Actinobacteria	Actinobacteria	Solirubrobacterales	-	-
Otu38	6	nest	0.921503958	0.017	12	Acidobacteria	Acidobacteria_Gp1	-	-	-
Otu545	6	nest	0.921052632	0.01	7	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu745	6	nest	0.912280702	0.008	10	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu980	6	nest	0.911392405	0.02	10	Armatimonadetes	Armatimonadetes	Armatimonadales	Armatimonadaceae	Armatimonadetes_gp1
Otu110	6	nest	0.908227848	0.006	11	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu235	6	nest	0.899543379	0.004	10	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu267	6	nest	0.898734177	0.022	10	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu1492	6	nest	0.894736842	0.008	8	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia
Otu4717	6	nest	0.884615385	0.009	9	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia
Otu41	6	nest	0.872655479	0.026	12	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia
Otu181	6	nest	0.868131868	0.014	8	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium
Otu188	6	nest	0.859756098	0.044	10	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	Mucilagibacter
Otu3	6	nest	0.858514961	0.014	12	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu573	6	nest	0.856060606	0.018	8	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu158	6	nest	0.855614973	0.03	11	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	-
Otu666	6	nest	0.853080569	0.041	10	Proteobacteria	Alphaproteobacteria	Caulobacteriales	Caulobacteraceae	Brevundimonas
Otu266	6	nest	0.851963746	0.046	12	Acidobacteria	Acidobacteria_Gp1	-	-	Terriglobus
Otu1974	6	nest	0.836689038	0.029	12	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia
Otu456	6	nest	0.833333333	0.032	12	TM7	-	-	-	TM7_genera_I.s
Otu845	6	nest	0.833333333	0.019	5	TM7	-	-	-	M7_genera_I.s
Otu585	6	nest	0.833333333	0.015	5	Proteobacteria	Alphaproteobacteria	-	-	-
Otu855	6	nest	0.833333333	0.009	5	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu3254	6	nest	0.833333333	0.016	5	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu2055	6	nest	0.833333333	0.012	5	-	-	-	-	-
Otu1173	6	nest	0.833333333	0.018	5	Proteobacteria	Deltaproteobacteria	Myxococcales	-	-
Otu510	6	nest	0.833333333	0.017	5	Cyanobacteria	Chloroplast	-	Chloroplast	Chlorophyta
Otu4126	6	nest	0.833333333	0.013	5	Proteobacteria	Betaproteobacteria	Burkholderiales	-	-
Otu517	6	nest	0.833333333	0.017	5	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	-
Otu23	6	nest	0.830969267	0.026	7	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu237	6	nest	0.827338129	0.029	6	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu97	6	nest	0.823195458	0.031	6	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu600	6	nest	0.82278481	0.016	6	-	-	-	-	-
Otu1911	6	nest	0.821678322	0.02	7	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	-
Otu236	6	nest	0.8203125	0.019	6	-	-	-	-	-
Otu1012	6	nest	0.815602837	0.021	6	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu867	6	nest	0.815412186	0.037	7	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu375	6	nest	0.814814815	0.022	7	-	-	-	-	-
Otu604	6	nest	0.812757202	0.017	7	-	-	-	-	-
Otu1077	6	nest	0.810185185	0.026	6	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu91	6	nest	0.80952381	0.04	7	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardaceae	Pseudonocardia
Otu571	6	nest	0.808823529	0.026	7	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu3525	6	nest	0.808695652	0.02	12	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-

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Otu175	6	nest	0.808491418	0.032	8	Proteobacteria	Alphaproteobacteria-	-	-
Otu1595	6	nest	0.807291667	0.027	6	Proteobacteria	Alphaproteobacteria Rhizobiales	-	-
Otu199	6	nest	0.806451613	0.015	11	Actinobacteria	Actinobacteria Actinomycetales	-	-
Otu120	6	nest	0.803255485	0.049	7	Acidobacteria	Acidobacteria_Gp1	-	-
Otu70	6	nest	0.8	0.036	12	Actinobacteria	Actinobacteria Actinomycetales	Pseudonocardaceae	Pseudonocardia
Otu277	6	nest	0.794270833	0.017	7	Actinobacteria	Actinobacteria Actinomycetales	-	-
Otu283	6	nest	0.781835206	0.034	6	Actinobacteria	Actinobacteria Actinomycetales	Streptomycetaceae	Streptomyces
Otu613	6	nest	0.779569892	0.034	6	Actinobacteria	Actinobacteria Solirubrobacterales	-	-
Otu151	6	nest	0.778026906	0.04	12	Actinobacteria	Actinobacteria Solirubrobacterales	-	-
Otu2183	6	nest	0.75	0.032	11	Planctomycetes	Planctomycetacia Planctomycetales	Planctomycetaceae	Singulisphaera
Otu2489	6	nest	0.744186047	0.011	12	Proteobacteria	Alphaproteobacteria Caulobacterales	Caulobacteraceae	-
Otu198	6	nest	0.740740741	0.046	7	Cyanobacteria/Chloroplast	Chloroplast	Chloroplast	-
Otu1239	6	nest	0.737179487	0.04	6	Proteobacteria	Alphaproteobacteria-	-	-
Otu182	6	nest	0.718343195	0.007	12	Proteobacteria	Alphaproteobacteria Caulobacterales	Caulobacteraceae	Brevundimonas
Otu4069	6	nest	0.702614379	0.038	6	Actinobacteria	Actinobacteria Actinomycetales	Mycobacteriaceae	Mycobacterium
Otu1244	6	nest	0.666666667	0.048	6	Proteobacteria	Alphaproteobacteria Rhodospirillales	Acetobacteraceae	-
Otu129	6	nest	0.666666667	0.048	4	Proteobacteria	Alphaproteobacteria-	-	-
Otu558	6	nest	0.666666667	0.049	4	Proteobacteria	Alphaproteobacteria Rhodospirillales	Rhodospirillaceae	-
Otu885	6	nest	0.666666667	0.049	4	TM7	-	-	TM7_genera_incertae_sedis
Otu2239	6	nest	0.666666667	0.043	4	-	-	-	-
Otu3850	6	nest	0.666666667	0.049	4	-	-	-	-
Otu5356	6	nest	0.666666667	0.043	4	-	-	-	-
Otu988	6	ref soils	1	0.006	6	Proteobacteria	Deltaproteobacteria Myxococcales	-	-
Otu1049	6	ref soils	1	0.008	6	Armatimonadetes	-	-	Armatimonadetes_gp5
Otu690	6	ref soils	1	0.006	6	Planctomycetes	Planctomycetacia Planctomycetales	Planctomycetaceae	Zavarzinella
Otu4161	6	ref soils	1	0.004	6	Proteobacteria	Alphaproteobacteria-	-	-
Otu193	6	ref soils	0.98828125	0.01	7	Proteobacteria	Deltaproteobacteria Myxococcales	Polyangiaceae	Byssovorax
Otu202	6	ref soils	0.986486486	0.006	9	Proteobacteria	Betaproteobacteria Burkholderiales	-	-
Otu2262	6	ref soils	0.983870968	0.002	8	Proteobacteria	Betaproteobacteria Burkholderiales	-	-
Otu2760	6	ref soils	0.97761194	0.008	8	Acidobacteria	Acidobacteria_Gp2	-	Gp2
Otu242	6	ref soils	0.977011494	0.003	9	Bacteroidetes	Sphingobacteria Sphingobacteriales	Chitinophagaceae	-
Otu213	6	ref soils	0.976331361	0.033	8	Bacteroidetes	Sphingobacteria Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter
Otu1042	6	ref soils	0.975	0.008	7	Bacteroidetes	Sphingobacteria Sphingobacteriales	Chitinophagaceae	Ferruginibacter
Otu215	6	ref soils	0.973451327	0.001	8	Proteobacteria	Alphaproteobacteria Rhodospirillales	Acetobacteraceae	Acidisphaera
Otu83	6	ref soils	0.971175166	0.002	9	Proteobacteria	Gammaproteobacteria-	-	-
Otu1011	6	ref soils	0.970588235	0.01	7	Armatimonadetes	-	-	Armatimonadetes_gp5
Otu40	6	ref soils	0.970123023	0.004	10	Acidobacteria	Acidobacteria_Gp2	-	Gp2
Otu1117	6	ref soils	0.958333333	0.006	7	Acidobacteria	Acidobacteria_Gp5	-	Gp5
Otu132	6	ref soils	0.956228956	0.043	10	Actinobacteria	Actinobacteria Actinomycetales	Microbacteriaceae	-
Otu513	6	ref soils	0.951388889	0.024	8	Acidobacteria	Acidobacteria_Gp1	-	Gp1
Otu330	6	ref soils	0.949044586	0.031	9	Acidobacteria	Acidobacteria_Gp1	-	-
Otu1061	6	ref soils	0.946236559	0.005	9	Acidobacteria	Acidobacteria_Gp3	-	Gp3
Otu128	6	ref soils	0.945632799	0.005	9	Bacteroidetes	Sphingobacteria Sphingobacteriales	Chitinophagaceae	-
Otu85	6	ref soils	0.943462898	0.004	10	Acidobacteria	Acidobacteria_Gp1	-	Gp1
Otu1171	6	ref soils	0.941176471	0.011	7	Proteobacteria	Deltaproteobacteria Myxococcales	Polyangiaceae	Sorangium
Otu1852	6	ref soils	0.935483871	0.002	8	Bacteroidetes	Sphingobacteria Sphingobacteriales	Chitinophagaceae	-
Otu743	6	ref soils	0.933333333	0.006	8	Acidobacteria	Acidobacteria_Gp3	-	Gp3
Otu656	6	ref soils	0.931166348	0.006	10	Acidobacteria	Acidobacteria_Gp1	-	Gp1
Otu646	6	ref soils	0.926829268	0.002	9	Bacteroidetes	Flavobacteria Flavobacteriales	Flavobacteriaceae	-
Otu64	6	ref soils	0.912225705	0.012	11	Proteobacteria	Alphaproteobacteria Rhizobiales	-	-
Otu408	6	ref soils	0.911564626	0.007	8	Verrucomicrobia	Opitutae Opitutales	Opitutaceae	Opitutus
Otu105	6	ref soils	0.909502262	0.02	11	Verrucomicrobia	Opitutae Opitutales	Opitutaceae	Opitutus
Otu467	6	ref soils	0.908163265	0.028	9	Acidobacteria	Acidobacteria_Gp3	-	Gp3
Otu1207	6	ref soils	0.902439024	0.02	9	Proteobacteria	Deltaproteobacteria-	-	-
Otu62	6	ref soils	0.897923875	0.028	10	Acidobacteria	Acidobacteria_Gp1	-	Gp1
Otu103	6	ref soils	0.893243243	0.005	12	Proteobacteria	Alphaproteobacteria Rhizobiales	-	-
Otu714	6	ref soils	0.888157895	0.03	9	Proteobacteria	Alphaproteobacteria-	-	-
Otu190	6	ref soils	0.885416667	0.012	8	Acidobacteria	Acidobacteria_Gp2	-	Gp2
Otu364	6	ref soils	0.885245902	0.014	9	Proteobacteria	Deltaproteobacteria Myxococcales	Polyangiaceae	-
Otu940	6	ref soils	0.881818182	0.007	10	Actinobacteria	Actinobacteria Acidimicrobiales	Acidimicrobiaceae	Aciditerrimonas
Otu514	6	ref soils	0.879310345	0.004	10	Proteobacteria	Alphaproteobacteria Rhizobiales	-	-
Otu911	6	ref soils	0.879032258	0.033	9	-	-	-	-
Otu459	6	ref soils	0.86746988	0.01	10	Acidobacteria	Acidobacteria_Gp3	-	Gp3
Otu682	6	ref soils	0.865671642	0.018	9	Proteobacteria	Alphaproteobacteria Rhizobiales	-	-
Otu5	6	ref soils	0.86011657	0.044	12	Proteobacteria	Alphaproteobacteria Rhizobiales	-	-
Otu16	6	ref soils	0.858229599	0.032	12	Acidobacteria	Acidobacteria_Gp1	-	Gp1
Otu203	6	ref soils	0.846153846	0.017	12	Proteobacteria	Alphaproteobacteria Rhodospirillales	Acetobacteraceae	-
Otu874	6	ref soils	0.844919786	0.009	10	Proteobacteria	Alphaproteobacteria Rhizobiales	-	-
Otu66	6	ref soils	0.843817787	0.027	11	Acidobacteria	Acidobacteria_Gp2	-	Gp2
Otu268	6	ref soils	0.843648208	0.006	11	-	-	-	-
Otu641	6	ref soils	0.835051546	0.019	11	Proteobacteria	Alphaproteobacteria-	-	-
Otu100	6	ref soils	0.833333333	0.017	5	Bacteroidetes	Bacteroidetes_Is	Ohtaekwangia	-
Otu1400	6	ref soils	0.833333333	0.014	5	-	-	-	-
Otu1626	6	ref soils	0.833333333	0.014	5	Verrucomicrobia	Opitutae Opitutales	Opitutaceae	Opitutus
Otu971	6	ref soils	0.833333333	0.016	5	Acidobacteria	Acidobacteria_Gp2	-	Gp2
Otu1251	6	ref soils	0.833333333	0.01	5	Actinobacteria	Actinobacteria Solirubrobacterales	-	-
Otu2006	6	ref soils	0.833333333	0.017	5	Proteobacteria	Deltaproteobacteria Myxococcales	Cystobacteraceae	-
Otu2422	6	ref soils	0.833333333	0.02	5	-	-	-	-
Otu2073	6	ref soils	0.833333333	0.01	5	Proteobacteria	Deltaproteobacteria Myxococcales	-	-
Otu2945	6	ref soils	0.833333333	0.023	5	Bacteroidetes	-	-	-
Otu2212	6	ref soils	0.833333333	0.011	5	Planctomycetes	Planctomycetacia Planctomycetales	Planctomycetaceae	-

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Otu4742	6	ref soils	0.833333333	0.017	5	-	-	-	-	-
Otu3938	6	ref soils	0.833333333	0.015	5	Bacteroidetes	-	-	-	-
Otu2448	6	ref soils	0.833333333	0.012	5	Proteobacteria	-	-	-	-
Otu74	6	ref soils	0.82934927	0.036	7	Proteobacteria	Alphaproteobacteria	Rhodospirillales	-	-
Otu134	6	ref soils	0.829099307	0.032	12	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-
Otu523	6	ref soils	0.825688073	0.021	6	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu409	6	ref soils	0.825346113	0.047	6	Proteobacteria	Gammaproteobacteria	-	-	-
Otu503	6	ref soils	0.825	0.019	6	-	-	-	-	-
Otu363	6	ref soils	0.822368421	0.019	6	Proteobacteria	Alphaproteobacteria	Rhodospirillales	-	-
Otu1250	6	ref soils	0.817307692	0.024	6	Bacteroidetes	-	-	-	-
Otu26	6	ref soils	0.812138728	0.016	11	Proteobacteria	Alphaproteobacteria	-	-	-
Otu759	6	ref soils	0.811965812	0.011	6	Acidobacteria	Acidobacteria_Gp2	-	-	Gp2
Otu2480	6	ref soils	0.80952381	0.031	6	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu2301	6	ref soils	0.807692308	0.036	8	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter
Otu1487	6	ref soils	0.806878307	0.028	6	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-
Otu1610	6	ref soils	0.804597701	0.031	6	Bacteroidetes	-	-	-	-
Otu1369	6	ref soils	0.802469136	0.02	6	Proteobacteria	-	-	-	-
Otu1076	6	ref soils	0.8	0.032	10	Proteobacteria	Alphaproteobacteria	-	-	-
Otu67	6	ref soils	0.785930663	0.015	12	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1
Otu1014	6	ref soils	0.784132841	0.048	7	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiales_Ls	-
Otu565	6	ref soils	0.783505155	0.036	11	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus
Otu341	6	ref soils	0.782258065	0.015	10	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu1594	6	ref soils	0.777027027	0.049	8	-	-	-	-	-
Otu1081	6	ref soils	0.777027027	0.035	6	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Rudaea
Otu6	6	ref soils	0.776859504	0.016	12	Proteobacteria	Gammaproteobacteria	-	-	-
Otu844	6	ref soils	0.773809524	0.019	6	-	-	-	-	-
Otu2180	6	ref soils	0.769230769	0.045	8	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter
Otu1939	6	ref soils	0.763888889	0.036	6	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu592	6	ref soils	0.757575758	0.047	7	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Pelomonas
Otu238	6	ref soils	0.757142857	0.035	12	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu2632	6	ref soils	0.756756757	0.042	8	Proteobacteria	Alphaproteobacteria	-	-	-
Otu326	6	ref soils	0.748945148	0.046	7	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	Nevskia
Otu1697	6	ref soils	0.689655172	0.048	7	Armatimonadetes	-	-	-	Armatimonadetes_gp5
Otu3030	6	ref soils	0.666666667	0.048	4	Proteobacteria	Deltaproteobacteria	Myxococcales	-	-
Otu951	6	ref soils	0.666666667	0.05	4	-	-	-	-	-
Otu1295	6	ref soils	0.666666667	0.05	4	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-
Otu1261	6	ref soils	0.666666667	0.046	4	-	-	-	-	-
Otu2326	6	ref soils	0.666666667	0.042	4	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-
Otu65	6	ref soils	0.637189794	0.03	12	Proteobacteria	Alphaproteobacteria	Caulobacteriales	Caulobacteraceae	Caulobacter
Otu1329	8	nest	1	0.003	6	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Actinomycetospora
Otu201	8	nest	0.999289773	0.005	7	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia
Otu78	8	nest	0.998245614	0.008	7	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia
Otu79	8	nest	0.995043047	0.01	8	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1
Otu122	8	nest	0.992125984	0.008	8	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu245	8	nest	0.990074442	0.001	7	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Actinomycetospora
Otu191	8	nest	0.987113402	0.002	9	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu643	8	nest	0.983050847	0.016	8	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-
Otu181	8	nest	0.979539642	0.003	9	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium
Otu156	8	nest	0.979338843	0.005	8	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu794	8	nest	0.974358974	0.003	7	-	-	-	-	-
Otu5290	8	nest	0.973684211	0.01	8	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu129	8	nest	0.973568282	0.014	9	Proteobacteria	Alphaproteobacteria	-	-	-
Otu59	8	nest	0.973194341	0.048	12	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium
Otu573	8	nest	0.973154362	0.004	9	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu450	8	nest	0.972477064	0.018	9	-	-	-	-	-
Otu175	8	nest	0.967914439	0.009	9	Proteobacteria	Alphaproteobacteria	-	-	-
Otu675	8	nest	0.961290323	0.008	8	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu110	8	nest	0.956937799	0.001	12	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu139	8	nest	0.956923077	0.003	10	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	-
Otu1911	8	nest	0.95483871	0.02	10	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	-
Otu36	8	nest	0.949644226	0.012	11	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu545	8	nest	0.943089431	0.017	10	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu2036	8	nest	0.93814433	0.012	8	Acidobacteria	Acidobacteria_Gp1	-	-	-
Otu385	8	nest	0.9375	0.012	11	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu10	8	nest	0.934791414	0.039	11	Cyanobacteria	Chloroplast	-	Chloroplast	Streptophyta
Otu403	8	nest	0.931558935	0.025	9	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Frondihabitans
Otu2568	8	nest	0.928571429	0.015	7	Proteobacteria	Deltaproteobacteria	-	-	-
Otu112	8	nest	0.922619048	0.046	12	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium
Otu745	8	nest	0.92251816	0.013	12	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu1312	8	nest	0.915966387	0.007	8	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu3525	8	nest	0.911917098	0.015	12	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu38	8	nest	0.907180385	0.003	12	Acidobacteria	Acidobacteria_Gp1	-	-	-
Otu827	8	nest	0.895833333	0.013	7	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Frondihabitans
Otu1595	8	nest	0.888888889	0.026	8	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu2489	8	nest	0.886666667	0.001	12	Proteobacteria	Alphaproteobacteria	Caulobacteriales	Caulobacteraceae	-
Otu4717	8	nest	0.866666667	0.013	9	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia
Otu182	8	nest	0.860692771	0.004	12	Proteobacteria	Alphaproteobacteria	Caulobacteriales	Caulobacteraceae	Brevundimonas
Otu235	8	nest	0.84981685	0.014	12	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu2731	8	nest	0.846153846	0.033	11	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu499	8	nest	0.843373494	0.042	10	Cyanobacteria	Chloroplast	Chloroplast	Chloroplast	-
Otu517	8	nest	0.833333333	0.017	5	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	-

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Otu183	8	nest	0.833333333	0.02	5	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	-
Otu1824	8	nest	0.833333333	0.007	5	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu1409	8	nest	0.833333333	0.014	5	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu2136	8	nest	0.833333333	0.019	5	-	-	-	-	-
Otu2162	8	nest	0.833333333	0.016	5	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu1239	8	nest	0.833333333	0.024	5	Proteobacteria	Alphaproteobacteria	-	-	-
Otu2735	8	nest	0.833333333	0.017	5	Proteobacteria	Deltaproteobacteria	-	-	-
Otu4037	8	nest	0.833333333	0.015	5	-	-	-	-	-
Otu3364	8	nest	0.833333333	0.017	5	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	Singulisphaera
Otu41	8	nest	0.829749104	0.036	12	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia
Otu283	8	nest	0.829383886	0.035	6	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces
Otu1677	8	nest	0.825545171	0.02	6	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Methylocystis
Otu277	8	nest	0.82537155	0.047	8	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu4126	8	nest	0.820707071	0.033	6	Proteobacteria	Betaproteobacteria	Burkholderiales	-	-
Otu722	8	nest	0.811594203	0.037	12	Proteobacteria	Alphaproteobacteria	-	-	-
Otu368	8	nest	0.810606061	0.045	7	Cyanobacteria/Chloroplast	Chloroplast	Chloroplast	Chloroplast	-
Otu2587	8	nest	0.808823529	0.022	10	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	-
Otu166	8	nest	0.806781046	0.038	7	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu2975	8	nest	0.803370787	0.033	11	Acidobacteria	Acidobacteria_Gp1	-	-	Granulicella
Otu1604	8	nest	0.801282051	0.023	6	TM7	-	-	-	TM7_genera_I.s
Otu1481	8	nest	0.801282051	0.04	6	TM7	-	-	-	TM7_genera_I.s
Otu2349	8	nest	0.8	0.025	10	Actinobacteria	Actinobacteria	Solirubrobacterales	-	-
Otu303	8	nest	0.794797688	0.05	8	-	-	-	-	-
Otu3254	8	nest	0.78125	0.049	6	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu91	8	nest	0.781032078	0.043	8	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardaceae	Pseudonocardia
Otu2151	8	nest	0.773809524	0.014	6	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	Singulisphaera
Otu324	8	nest	0.772569444	0.041	8	Actinobacteria	Actinobacteria	-	-	-
Otu195	8	nest	0.763656633	0.034	8	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium
Otu153	8	nest	0.761862131	0.05	12	Acidobacteria	Acidobacteria_Gp1	-	-	-
Otu92	8	nest	0.736111111	0.01	12	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	-
Otu1832	8	nest	0.666666667	0.045	4	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces
Otu1742	8	nest	0.666666667	0.048	4	-	-	-	-	-
Otu236	8	nest	0.664215686	0.042	5	-	-	-	-	-
Otu1539	8	nest	0.631578947	0.049	5	-	-	-	-	-
Otu242	8	ref soils	1	0.002	6	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-
Otu1042	8	ref soils	1	0.004	6	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Ferruginibacter
Otu929	8	ref soils	1	0.002	6	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-
Otu193	8	ref soils	1	0.006	6	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Byssovorax
Otu1759	8	ref soils	1	0.003	6	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu808	8	ref soils	1	0.003	6	-	-	-	-	-
Otu1497	8	ref soils	1	0.005	6	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	Schlesneria
Otu503	8	ref soils	1	0.003	6	-	-	-	-	-
Otu1117	8	ref soils	1	0.005	6	Acidobacteria	Acidobacteria_Gp5	-	-	Gp5
Otu986	8	ref soils	1	0.004	6	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu3026	8	ref soils	1	0.004	6	Armatimonadetes	Armatimonadia	Armatimonadales	Armatimonadaceae	Armatimonadetes_gp1
Otu3738	8	ref soils	1	0.003	6	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	-
Otu2006	8	ref soils	1	0.004	6	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacteraceae	-
Otu1296	8	ref soils	1	0.004	6	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-
Otu1249	8	ref soils	1	0.004	6	Proteobacteria	Betaproteobacteria	-	-	-
Otu776	8	ref soils	1	0.003	6	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-
Otu596	8	ref soils	1	0.002	6	Proteobacteria	Alphaproteobacteria	-	-	-
Otu3694	8	ref soils	1	0.005	6	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Armatimonadetes_gp3
Otu1982	8	ref soils	1	0.002	6	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	Gemmata
Otu306	8	ref soils	0.993670886	0.006	7	Proteobacteria	Deltaproteobacteria	Myxococcales	Kofleriaceae	Kofleria
Otu4382	8	ref soils	0.99122807	0.002	7	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-
Otu83	8	ref soils	0.988970588	0.004	9	Proteobacteria	Gammaproteobacteria	-	-	-
Otu1365	8	ref soils	0.9875	0.002	7	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1
Otu2077	8	ref soils	0.987341772	0.002	7	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	Schlesneria
Otu694	8	ref soils	0.986842105	0.001	8	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Ferruginibacter
Otu1852	8	ref soils	0.985915493	0.007	7	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-
Otu246	8	ref soils	0.985294118	0.005	7	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-
Otu2928	8	ref soils	0.983050847	0.003	7	Proteobacteria	Alphaproteobacteria	-	-	-
Otu149	8	ref soils	0.982608696	0.034	9	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu377	8	ref soils	0.981132075	0.002	7	Proteobacteria	Deltaproteobacteria	Myxococcales	-	-
Otu765	8	ref soils	0.978723404	0.005	8	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Sorangium
Otu641	8	ref soils	0.978723404	0.002	9	Proteobacteria	Alphaproteobacteria	-	-	-
Otu467	8	ref soils	0.974193548	0.003	8	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu128	8	ref soils	0.972519084	0.006	11	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-
Otu26	8	ref soils	0.968512486	0.004	11	Proteobacteria	Alphaproteobacteria	-	-	-
Otu1250	8	ref soils	0.967741935	0.007	7	Bacteroidetes	-	-	-	-
Otu2534	8	ref soils	0.967741935	0.004	7	Actinobacteria	Actinobacteria	Actinomycetales	-	-
Otu1527	8	ref soils	0.966666667	0.002	8	Proteobacteria	Alphaproteobacteria	-	-	-
Otu1061	8	ref soils	0.964285714	0.005	8	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu451	8	ref soils	0.96350365	0.002	9	Proteobacteria	Alphaproteobacteria	Alphaproteobacteria_I.s	-	Rhizomicrobium
Otu911	8	ref soils	0.962732919	0.003	10	-	-	-	-	-
Otu1426	8	ref soils	0.961325967	0.002	9	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu479	8	ref soils	0.96	0.006	8	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Labrys
Otu851	8	ref soils	0.958333333	0.006	7	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	Nevskia
Otu2288	8	ref soils	0.958333333	0.01	7	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	Singulisphaera
Otu2900	8	ref soils	0.956521739	0.008	7	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	Gemmata
Otu1102	8	ref soils	0.954545455	0.007	7	Armatimonadetes	-	-	-	Armatimonadetes_gp5

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Otu357	8	ref soils	0.953736655	0.002	10	Proteobacteria	Deltaproteobacteria	Myxococcales	-	-	-
Otu743	8	ref soils	0.952380952	0.012	8	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3	-
Otu656	8	ref soils	0.950576606	0.006	10	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1	-
Otu85	8	ref soils	0.949675325	0.008	10	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1	-
Otu84	8	ref soils	0.947666195	0.039	9	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	-	-
Otu1600	8	ref soils	0.942857143	0.016	9	Actinobacteria	Actinobacteria	Actinomycetales	Catenulsporaceae	Catenulispora	-
Otu459	8	ref soils	0.942028986	0.004	9	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3	-
Otu40	8	ref soils	0.940184049	0.028	9	Acidobacteria	Acidobacteria_Gp2	-	-	Gp2	-
Otu215	8	ref soils	0.93956044	0.007	8	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Acidisphaera	-
Otu317	8	ref soils	0.935828877	0.03	11	Proteobacteria	Gammaproteobacteria	-	-	-	-
Otu268	8	ref soils	0.931558935	0.017	10	-	-	-	-	-	-
Otu644	8	ref soils	0.928888889	0.02	9	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Rudaea	-
Otu103	8	ref soils	0.923428571	0.008	9	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-	-
Otu227	8	ref soils	0.922413793	0.008	10	Acidobacteria	Acidobacteria_Gp1	-	-	-	-
Otu2396	8	ref soils	0.92	0.015	8	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	-	-
Otu3871	8	ref soils	0.918367347	0.04	9	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3	-
Otu638	8	ref soils	0.917197452	0.029	11	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-	-
Otu785	8	ref soils	0.914529915	0.031	10	-	-	-	-	-	-
Otu134	8	ref soils	0.911147011	0.006	11	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-	-
Otu16	8	ref soils	0.91053787	0.027	10	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1	-
Otu1422	8	ref soils	0.909090909	0.008	8	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-	-
Otu214	8	ref soils	0.908847185	0.016	11	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-	-
Otu1207	8	ref soils	0.904761905	0.015	8	Proteobacteria	Deltaproteobacteria	-	-	-	-
Otu287	8	ref soils	0.903846154	0.007	11	Actinobacteria	Actinobacteria	Actinomycetales	Sporichthyaceae	Sporichthya	-
Otu62	8	ref soils	0.898969072	0.006	9	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1	-
Otu565	8	ref soils	0.894736842	0.009	11	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus	-
Otu67	8	ref soils	0.89071618	0.008	11	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1	-
Otu387	8	ref soils	0.887733888	0.036	11	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1	-
Otu3449	8	ref soils	0.884615385	0.011	7	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter	-
Otu43	8	ref soils	0.882352941	0.036	10	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter	-
Otu87	8	ref soils	0.88185654	0.033	9	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Telmatosporillum	-
Otu25	8	ref soils	0.881795196	0.007	11	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1	-
Otu421	8	ref soils	0.88	0.015	11	Proteobacteria	Gammaproteobacteria	-	-	-	-
Otu6	8	ref soils	0.87661895	0.01	11	Proteobacteria	Gammaproteobacteri	-	-	-	-
Otu2477	8	ref soils	0.875	0.008	8	Proteobacteria	Alphaproteobacteria	-	-	-	-
Otu972	8	ref soils	0.873563218	0.016	11	Actinobacteria	Actinobacteria	Acidimicrobiales	Iamiaceae	Iamia	-
Otu566	8	ref soils	0.869565217	0.008	10	Proteobacteria	Alphaproteobacteria	-	-	-	-
Otu238	8	ref soils	0.868471954	0.004	12	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-	-
Otu431	8	ref soils	0.865591398	0.038	9	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1	-
Otu89	8	ref soils	0.858483755	0.02	11	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1	-
Otu203	8	ref soils	0.85046729	0.014	10	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-	-
Otu1189	8	ref soils	0.848605578	0.021	10	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-	-
Otu68	8	ref soils	0.841269841	0.032	11	Actinobacteria	Actinobacteria	Actinomycetales	-	-	-
Otu399	8	ref soils	0.83974359	0.019	11	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	-
Otu1014	8	ref soils	0.833333333	0.016	5	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiales_Ls	-	-
Otu1011	8	ref soils	0.833333333	0.019	5	Armatimonadetes	-	-	-	Armatimonadetes_gp5	-
Otu619	8	ref soils	0.833333333	0.013	5	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacteraceae	Anaeromyxobacter	-
Otu752	8	ref soils	0.833333333	0.008	5	Proteobacteria	Betaproteobacteria	-	-	-	-
Otu2717	8	ref soils	0.833333333	0.018	5	Proteobacteria	Deltaproteobacteria	Myxococcales	-	-	-
Otu3083	8	ref soils	0.833333333	0.019	5	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	-	-
Otu712	8	ref soils	0.833333333	0.017	5	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus	-
Otu2262	8	ref soils	0.833333333	0.013	5	Proteobacteria	Betaproteobacteria	Burkholderiales	-	-	-
Otu1710	8	ref soils	0.833333333	0.02	5	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	-	-
Otu1072	8	ref soils	0.833333333	0.012	5	Proteobacteria	-	-	-	-	-
Otu1218	8	ref soils	0.833333333	0.01	5	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	-	-
Otu526	8	ref soils	0.833333333	0.018	5	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	-	-
Otu3064	8	ref soils	0.833333333	0.018	5	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	Schlesneria	-
Otu2073	8	ref soils	0.833333333	0.014	5	Proteobacteria	Deltaproteobacteria	Myxococcales	-	-	-
Otu798	8	ref soils	0.833333333	0.021	5	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-	-
Otu1701	8	ref soils	0.833333333	0.019	5	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	-	-
Otu3150	8	ref soils	0.833333333	0.013	5	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	Singulisphaera	-
Otu4022	8	ref soils	0.833333333	0.018	5	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3	-
Otu2322	8	ref soils	0.833333333	0.019	5	Armatimonadetes	-	-	-	Armatimonadetes_gp5	-
Otu1504	8	ref soils	0.833333333	0.014	5	Proteobacteria	Alphaproteobacteria	-	-	-	-
Otu2172	8	ref soils	0.833333333	0.018	5	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	-	-
Otu1330	8	ref soils	0.833333333	0.016	5	Proteobacteria	Alphaproteobacteria	Caulobacteriales	Caulobacteraceae	Asticcacaulis	-
Otu2632	8	ref soils	0.833333333	0.016	5	Proteobacteria	Alphaproteobacteria	-	-	-	-
Otu1377	8	ref soils	0.833333333	0.013	5	Bacteroidetes	-	-	-	-	-
Otu1522	8	ref soils	0.833333333	0.021	5	Proteobacteria	Alphaproteobacteria	-	-	-	-
Otu1626	8	ref soils	0.833333333	0.017	5	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus	-
Otu2374	8	ref soils	0.833333333	0.021	5	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-	-
Otu1054	8	ref soils	0.833333333	0.016	5	Planctomycetes	Phycisphaerae	Phycisphaerales	Phycisphaeraceae	Phycisphaera	-
Otu3268	8	ref soils	0.833333333	0.015	5	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	-	-
Otu5588	8	ref soils	0.833333333	0.023	5	-	-	-	-	-	-
Otu4463	8	ref soils	0.833333333	0.014	5	Proteobacteria	Alphaproteobacteria	Rhodospirillales	-	-	-
Otu3215	8	ref soils	0.833333333	0.021	5	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	Gemmata	-
Otu4952	8	ref soils	0.833333333	0.017	5	Acidobacteria	Acidobacteria_Gp2	-	-	Gp2	-
Otu2272	8	ref soils	0.833333333	0.011	5	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	Gemmata	-
Otu3736	8	ref soils	0.833333333	0.016	5	-	-	-	-	-	-
Otu2351	8	ref soils	0.833333333	0.011	5	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	-	-
Otu874	8	ref soils	0.831050228	0.01	9	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-	-

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Otu9	8	ref soils	0.830463576	0.004	12	Proteobacteria	Alphaproteobacteria	Alphaproteobacteria_I.s	-	Rhizomicrobium
Otu53	8	ref soils	0.830353596	0.028	7	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Rudaea
Otu219	8	ref soils	0.828544061	0.02	6	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	-
Otu28	8	ref soils	0.826385224	0.023	12	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu190	8	ref soils	0.826210826	0.017	6	Acidobacteria	Acidobacteria_Gp2	-	-	Gp2
Otu340	8	ref soils	0.826210826	0.043	6	-	-	-	-	-
Otu212	8	ref soils	0.825757576	0.019	6	Proteobacteria	Betaproteobacteria	-	-	-
Otu905	8	ref soils	0.825617284	0.039	6	Proteobacteria	Deltaproteobacteria	Myxococcales	Kofleriaceae	Kofleria
Otu1037	8	ref soils	0.824175824	0.036	10	Proteobacteria	Alphaproteobacteria	-	-	-
Otu113	8	ref soils	0.824013158	0.023	11	Proteobacteria	Alphaproteobacteria	Caulobacteriales	Caulobacteraceae	-
Otu612	8	ref soils	0.823529412	0.023	11	Proteobacteria	Gammaproteobacteria	-	-	-
Otu364	8	ref soils	0.822873082	0.027	8	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	-
Otu1289	8	ref soils	0.822222222	0.019	6	-	-	-	-	-
Otu358	8	ref soils	0.822134387	0.026	12	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Armatimonadetes_gp3
Otu1197	8	ref soils	0.821678322	0.025	6	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus
Otu682	8	ref soils	0.821428571	0.018	6	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu988	8	ref soils	0.820895522	0.024	6	Proteobacteria	Deltaproteobacteria	Myxococcales	-	-
Otu184	8	ref soils	0.820512821	0.032	7	Proteobacteria	Deltaproteobacteria	Myxococcales	-	-
Otu304	8	ref soils	0.820413437	0.02	7	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-
Otu1187	8	ref soils	0.819892473	0.02	6	Bacteroidetes	-	-	-	-
Otu2	8	ref soils	0.818473609	0.004	12	Proteobacteria	Alphaproteobacteria	Alphaproteobacteria_I.s	-	Rhizomicrobium
Otu72	8	ref soils	0.818467129	0.04	7	Proteobacteria	Alphaproteobacteria	-	-	-
Otu1369	8	ref soils	0.817610063	0.017	6	Proteobacteria	-	-	-	-
Otu623	8	ref soils	0.817307692	0.043	6	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu1220	8	ref soils	0.817307692	0.019	6	Proteobacteria	Deltaproteobacteria	Myxococcales	-	-
Otu514	8	ref soils	0.815964523	0.025	11	Proteobacteria	Alphaproteobacteria	Rhizobiales	-	-
Otu4104	8	ref soils	0.815217391	0.024	6	Proteobacteria	-	-	-	-
Otu535	8	ref soils	0.814814815	0.026	7	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus
Otu528	8	ref soils	0.814814815	0.025	6	Proteobacteria	Alphaproteobacteria	-	-	-
Otu669	8	ref soils	0.813492063	0.022	6	Proteobacteria	Alphaproteobacteria	-	-	-
Otu483	8	ref soils	0.811403509	0.03	6	Proteobacteria	Betaproteobacteria	-	-	-
Otu1049	8	ref soils	0.810397554	0.019	7	Armatimonadetes	-	-	-	Armatimonadetes_gp5
Otu326	8	ref soils	0.809636651	0.023	7	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	Nevskia
Otu1081	8	ref soils	0.80952381	0.05	6	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Rudaea
Otu417	8	ref soils	0.808270677	0.039	7	Proteobacteria	Alphaproteobacteria	-	-	-
Otu2075	8	ref soils	0.808080808	0.032	6	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Sorangium
Otu1120	8	ref soils	0.806451613	0.033	9	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	-
Otu690	8	ref soils	0.804093567	0.012	6	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	Zavarzinella
Otu2760	8	ref soils	0.803571429	0.033	6	Acidobacteria	Acidobacteria_Gp2	-	-	Gp2
Otu105	8	ref soils	0.803357314	0.03	7	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus
Otu104	8	ref soils	0.803044719	0.011	12	Proteobacteria	Alphaproteobacteria	Alphaproteobacteria_I.s	-	Rhizomicrobium
Otu1594	8	ref soils	0.802469136	0.019	6	-	-	-	-	-
Otu1405	8	ref soils	0.8	0.016	6	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu2348	8	ref soils	0.798611111	0.036	6	Armatimonadetes	-	-	-	Armatimonadetes_gp5
Otu968	8	ref soils	0.796703297	0.041	8	Bacteroidetes	-	-	-	-
Otu69	8	ref soils	0.794915254	0.021	11	-	-	-	-	-
Otu408	8	ref soils	0.794444444	0.046	8	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus
Otu146	8	ref soils	0.794270833	0.046	6	Acidobacteria	Acidobacteria_Gp1	-	-	Gp1
Otu1597	8	ref soils	0.787878788	0.026	10	Proteobacteria	Alphaproteobacteria	-	-	-
Otu4438	8	ref soils	0.786163522	0.022	11	Proteobacteria	Gammaproteobacteria	-	-	-
Otu1052	8	ref soils	0.78358209	0.023	10	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu899	8	ref soils	0.782828283	0.024	7	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	-
Otu2480	8	ref soils	0.78125	0.032	6	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu523	8	ref soils	0.78042328	0.034	6	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu1186	8	ref soils	0.78030303	0.047	10	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia
Otu5310	8	ref soils	0.778508772	0.043	8	Proteobacteria	Alphaproteobacteria	Alphaproteobacteria_I.s	-	Rhizomicrobium
Otu382	8	ref soils	0.775529865	0.045	8	Acidobacteria	Acidobacteria_Gp2	-	-	Gp2
Otu714	8	ref soils	0.773809524	0.038	8	Proteobacteria	Alphaproteobacteria	-	-	-
Otu1939	8	ref soils	0.76754386	0.034	6	Acidobacteria	Acidobacteria_Gp3	-	-	Gp3
Otu532	8	ref soils	0.766203704	0.047	11	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu74	8	ref soils	0.763888889	0.041	7	Proteobacteria	Alphaproteobacteria	Rhodospirillales	-	-
Otu502	8	ref soils	0.763888889	0.036	6	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-
Otu37	8	ref soils	0.761041903	0.037	12	Proteobacteria	Alphaproteobacteria	Caulobacteriales	Caulobacteraceae	Phenyllobacterium
Otu2212	8	ref soils	0.758928571	0.041	7	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	-
Otu1280	8	ref soils	0.755208333	0.018	7	Armatimonadetes	Armatimonadia	Armatimonadales	Armatimonadaceae	Armatimonadetes_gp1
Otu4470	8	ref soils	0.751824818	0.024	12	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	-
Otu531	8	ref soils	0.751262626	0.05	7	Actinobacteria	Actinobacteria	Acidimicrobiales	Acidimicrobiaceae_I.s	Aciditerrimonas
Otu2342	8	ref soils	0.744047619	0.044	7	-	-	-	-	-
Otu1870	8	ref soils	0.738993711	0.046	7	Armatimonadetes	Armatimonadia	Armatimonadales	Armatimonadaceae	Armatimonadetes_gp1
Otu673	8	ref soils	0.738636364	0.042	7	TM7	-	-	-	TM7_I.s
Otu310	8	ref soils	0.735191638	0.043	12	Proteobacteria	-	-	-	-
Otu3427	8	ref soils	0.729166667	0.041	6	Proteobacteria	-	-	-	-
Otu1165	8	ref soils	0.725806452	0.032	7	-	-	-	-	-
Otu22	8	ref soils	0.713432836	0.034	12	Proteobacteria	Alphaproteobacteria	-	-	-
Otu355	8	ref soils	0.708229426	0.048	12	Proteobacteria	Gammaproteobacteria	-	-	-
Otu860	8	ref soils	0.695652174	0.049	8	Proteobacteria	Deltaproteobacteria	Myxococcales	-	-
Otu1230	8	ref soils	0.666666667	0.049	4	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Chitinophaga
Otu1680	8	ref soils	0.666666667	0.048	4	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	-
Otu1965	8	ref soils	0.666666667	0.049	4	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	-
Otu2068	8	ref soils	0.666666667	0.047	4	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	-
Otu2270	8	ref soils	0.666666667	0.047	4	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Acidisphaera

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Otu3984	8	ref soils	0.666666667	0.042	4	-	-	-	-
Otu2355	8	ref soils	0.666666667	0.048	4	Proteobacteria	-	-	-
Otu1	8	ref soils	0.641086102	0.018	12	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae
Otu1468	8	ref soils	0.637681159	0.043	5	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae

Table S6. The fungal indicator OTUs.

Otu	month	env	Indval	p	freq	phylum	class	order	family	genus
Otu337	5	nest	1	0.002	6	Zygomycota	Mucoromycotina_I.s	Mucorales	Umbelopsidaceae	Umbelopsis
Otu41	5	nest	0.833333333	0.015	5	Ascomycota	Dothideomycetes	Dothideomycetes_I.s	Myxotrichaceae	Oidiodendron
Otu105	5	nest	0.833333333	0.023	5	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Exophiala
Otu596	5	nest	0.833333333	0.019	5	Ascomycota	Dothideomycetes	Dothideomycetes_I.s	Myxotrichaceae	Oidiodendron
Otu360	5	nest	0.828719723	0.044	8	Ascomycota	Dothideomycetes	Dothideomycetes_I.s	Myxotrichaceae	Oidiodendron
Otu179	5	nest	0.821759259	0.017	6	Ascomycota	Sordariomycetes	Coniochaetales	Coniochaetaceae	-
Otu6	5	nest	0.805976431	0.05	6	Ascomycota	-	-	-	-
Otu9	5	nest	0.783169533	0.042	7	Ascomycota	Dothideomycetes	Pleosporales	Venturiaceae	-
Otu560	5	nest	0.666666667	0.038	4	Ascomycota	-	-	-	-
Otu455	5	nest	0.666666667	0.05	4	Ascomycota	-	-	-	-
Otu400	5	ref soils	0.833333333	0.029	5	Zygomycota	Mucoromycotina_I.s	Mortierellales	Mortierellaceae	Mortierella
Otu112	5	ref soils	0.824242424	0.039	6	Ascomycota	-	-	-	-
Otu305	5	ref soils	0.81871345	0.018	6	Ascomycota	Leotiomyces	Helotiales	Hyaloscyphaceae	Calycina
Otu1083	5	ref soils	0.777777778	0.018	6	Ascomycota	Leotiomyces	Helotiales	-	-
Otu360	6	nest	0.980904523	0.01	11	Ascomycota	Dothideomycetes	Dothideomycetes_I.s	Myxotrichaceae	Oidiodendron
Otu3	6	nest	0.977127173	0.016	11	Ascomycota	Dothideomycetes	Dothideomycetes_I.s	Myxotrichaceae	Oidiodendron
Otu337	6	nest	0.954545455	0.005	10	Zygomycota	Mucoromycotina_I.s	Mucorales	Umbelopsidaceae	Umbelopsis
Otu560	6	nest	0.945454545	0.006	8	Ascomycota	-	-	-	-
Otu76	6	nest	0.901960784	0.033	8	Ascomycota	Pezizomycotina_I.s	Pezizomycotina_I.s	Pezizomycotina_I.s	Xenochalara
Otu20	6	nest	0.870503597	0.044	12	Ascomycota	Dothideomycetes	Dothideales	Dothioraceae	-
Otu41	6	nest	0.833333333	0.022	5	Ascomycota	Dothideomycetes	Dothideomycetes_I.s	Myxotrichaceae	Oidiodendron
Otu25	6	nest	0.833333333	0.011	5	Ascomycota	Leotiomyces	Helotiales	-	-
Otu1631	6	nest	0.833333333	0.021	5	Ascomycota	Dothideomycetes	Pleosporales	Venturiaceae	Venturia
Otu105	6	nest	0.833333333	0.012	5	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Exophiala
Otu2	6	nest	0.832702657	0.027	7	Ascomycota	Dothideomycetes	Pleosporales	Venturiaceae	-
Otu6	6	nest	0.831882797	0.02	7	Ascomycota	-	-	-	-
Otu103	6	nest	0.826446281	0.016	6	Ascomycota	Dothideomycetes	Dothideomycetes_I.s	Dothideomycetes_I.s	Scleroconidioma
Otu165	6	nest	0.820707071	0.017	6	-	-	-	-	-
Otu38	6	nest	0.81970405	0.016	7	Ascomycota	Leotiomyces	Helotiales	Hyaloscyphaceae	Hyaloscypha
Otu12	6	nest	0.778267254	0.05	9	Ascomycota	-	-	-	-
Otu697	6	nest	0.745614035	0.033	6	Ascomycota	Eurotiomycetes	Eurotiales	Trichomaceae	Penicillium
Otu258	6	nest	0.666666667	0.048	4	Ascomycota	-	-	-	-
Otu112	6	ref soils	0.993630573	0.004	7	Ascomycota	-	-	-	-
Otu89	6	ref soils	0.884615385	0.027	12	Ascomycota	-	-	-	-
Otu124	6	ref soils	0.86875	0.04	9	Ascomycota	-	-	-	-
Otu199	6	ref soils	0.861538462	0.008	10	Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	Pochonia
Otu1083	6	ref soils	0.833333333	0.011	5	Ascomycota	Leotiomyces	Helotiales	-	-
Otu187	6	ref soils	0.833333333	0.019	5	-	-	-	-	-
Otu606	6	ref soils	0.833333333	0.02	5	Zygomycota	Mucoromycotina_I.s	Mortierellales	Mortierellaceae	Mortierella
Otu305	6	ref soils	0.827338129	0.021	6	Ascomycota	Leotiomyces	Helotiales	Hyaloscyphaceae	Calycina
Otu1036	6	ref soils	0.824275362	0.025	6	Ascomycota	Eurotiomycetes	-	-	-
Otu564	6	ref soils	0.807291667	0.041	6	Ascomycota	Sordariomycetes	Hypocreales	-	-
Otu179	8	nest	1	0.003	6	Ascomycota	Sordariomycetes	Coniochaetales	Coniochaetaceae	-
Otu455	8	nest	1	0.004	6	Ascomycota	-	-	-	-
Otu41	8	nest	0.993243243	0.007	7	Ascomycota	Dothideomycetes	Dothideomycetes_I.s	Myxotrichaceae	Oidiodendron
Otu321	8	nest	0.972222222	0.008	7	Ascomycota	Eurotiomycetes	Eurotiales	Trichomaceae	Penicillium
Otu20	8	nest	0.969814241	0.045	11	Ascomycota	Dothideomycetes	Dothideales	Dothioraceae	-
Otu43	8	nest	0.852941176	0.022	11	Ascomycota	Leotiomyces	Rhytismatales	Rhytismataceae	Lophodermium
Otu105	8	nest	0.833333333	0.016	5	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Exophiala
Otu103	8	nest	0.833333333	0.012	5	Ascomycota	Dothideomycetes	Dothideomycetes_I.s	Dothideomycetes_I.s	Scleroconidioma
Otu379	8	nest	0.833333333	0.013	5	Basidiomycota	Exobasidiomycetes	Exobasidiales	Exobasidiaceae	Exobasidium
Otu586	8	nest	0.833333333	0.012	5	Ascomycota	-	-	-	-
Otu718	8	nest	0.833333333	0.014	5	Ascomycota	-	-	-	-
Otu731	8	nest	0.833333333	0.012	5	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Exophiala
Otu21	8	nest	0.831056466	0.031	6	Ascomycota	-	-	-	-
Otu360	8	nest	0.827228327	0.015	6	Ascomycota	Dothideomycetes	Dothideomycetes_I.s	Myxotrichaceae	Oidiodendron
Otu102	8	nest	0.810810811	0.049	7	Ascomycota	Eurotiomycetes	Eurotiales	Trichomaceae	Penicillium
Otu278	8	nest	0.666666667	0.05	4	Ascomycota	-	-	-	-
Otu400	8	ref soils	1	0.002	6	Zygomycota	Mucoromycotina_I.s	Mortierellales	Mortierellaceae	Mortierella
Otu112	8	ref soils	0.989130435	0.005	7	Ascomycota	-	-	-	-
Otu124	8	ref soils	0.970178926	0.034	10	Ascomycota	-	-	-	-
Otu199	8	ref soils	0.950413223	0.015	9	Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	Pochonia
Otu19	8	ref soils	0.886792453	0.04	11	-	-	-	-	-
Otu89	8	ref soils	0.827794562	0.023	11	Ascomycota	-	-	-	-
Otu52	8	ref soils	0.826771654	0.025	6	Ascomycota	Leotiomyces	Helotiales	Hyaloscyphaceae	Lachnum
Otu138	8	ref soils	0.826558266	0.025	6	Ascomycota	Leotiomyces	Helotiales	Vibrissaceae	Phialocephala
Otu79	8	ref soils	0.785714286	0.024	10	-	-	-	-	-
Otu80	8	ref soils	0.75	0.04	9	-	-	-	-	-