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ENVIRONMENTAL MICROBIOLOGY

The Differential Vertical Distribution of the Airborne Biological Particles Reveals an Atmospheric Reservoir of Microbial Pathogens and Aeroallergens

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Abstract

The most abundant biological particles present in the air are bacteria, fungal propagules and pollen grains. Many of them are proved allergens or even responsible for airborne infectious diseases, which supports the increase of studies in recent years on their composition, diversity, and factors involved in their variability. However, most studies in urban areas are conducted close to ground level and a factor such as height is rarely taken into account. Thus, the information about how the composition of biological particles changes with this variable is scarce. Here, we examined the differential distribution of bacteria, fungi, and plants at four altitudes (up to ~ 250 m) in a metropolitan area using high-throughput DNA sequencing. Most taxa were present at all levels (common taxa). However, a transitional layer between 80 and 150 m seemed to affect the scattering of these bioaerosols. Taxa not present at all altitudes (non-common) showed an upward tendency of diversity for bacteria and plants with height, while the opposite trend was observed for fungi. Certain patterns were observed for fungi and specific plant genera, while bacterial taxa showed a more arbitrary distribution and no patterns were found. We detected a wide variety of aeroallergens and potential pathogens at all heights, which summed a substantial portion of the total abundance for fungi and plants. We also identified potential connections between the biological particles based on their abundances across the vertical section.

Keywords Urban airborne biodiversity · Next-generation sequencing · Height · Bacteria · Fungi · Pollen

Introduction

Human population in urban environments is daily exposed to an enormous variety of airborne biological particles that include microorganisms such as viruses, bacteria, archaea, fungi, and parts of higher organisms like pollen [1]. Some of them play a relevant role in human health causing allergic symptoms (mainly by fungal spores and pollen) [2] and airborne infectious diseases such as influenza, legionaries' disease, and tuberculosis [3–5]. The origin of these particles is very diverse (soil, plant surface, water sources, other organisms, etc.) [1], and their presence, abundance, and dispersion are highly influenced by meteorological factors [6–8], resulting in seasonal and daily variations [9–13].

The presence of biological entities has been described in the upper atmosphere (up to 77 km), with no clear limit beyond which life is not detected [14, 15]. Previous aerobiological studies addressing the study of distribution of fungal spores and pollen grains with height have revealed the complexity of the matter. For instance, a differential pattern was initially proposed for pollen depending on whether it is from trees or herbaceous sources, suggesting that pollen grains from the former are capable of reaching higher altitudes so total counts increase with height, while the opposite occurs with the latter [16, 17]. Further studies have shown that this is

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only partly true and under the influence of the pollen type studied and meteorological conditions [18–20]. Similarly, Khattab and Levetin [21] found that the fungal basidiospores counts were higher at ground level (e.g., *Penicillium/Aspergillus* type) while ascospores concentration increased with the height (e.g., *Alternaria* spp.), although this difference was not confirmed by further studies [22]. A recent study conducted by Damialis et al. at rural landscapes [23], which identified pollen and spores at different heights up to 2000 m, demonstrated different dispersion models depending on the taxa. Therefore, further studies to unravel both total diversity and patterns of distribution with height are still required.

In metropolitan areas, the knowledge on composition of the airborne biological particles and how they are dispersed in the urban atmosphere is particularly relevant to evaluate the real exposure to pathogenic organisms and aeroallergens [24–26]. However, most surveys are conducted within the maximum exposure area for human (< 55 m above ground level), so the real reservoir of microscopic biodiversity above this height is still poorly understood. Furthermore, the majority of studies have been conducted by microscopy or culture approaches, so the total diversity is usually underestimated.

In addition, microbial biodiversity can be associated to larger particles as $PM_{2.5}$ and PM_{10} in metropolitan areas [27–31]. In fact, an increase in the prevalence of allergic diseases by a synergistic effect of these air pollutants and pollen grains has been described [32, 33]. Likewise, pollen grains can develop a rich microbiome that influences their allergenicity [34–36], so other interactions between microscopic organisms present in the air may remain unnoticed even though they are of a particular importance from both ecological and health points of views.

Next-generation DNA sequencing (NGS) has become recently a promising technology in this field and has been successfully applied to airborne bacteria, fungi and plant pollen [37–40], solving additionally the bias of the culture-based analyses. Here, we examined the patterns of distribution by height of the microbial (bacteria and fungi) and plant diversity present in the urban atmosphere using NGS technology. We characterized the fundamental taxa and identified the exposure to allergens and potential pathogens in this environment. Furthermore, we also correlated the presence and abundance between the different organisms, identifying putative new interspecific relationships present in the original source or during transport and whose concomitant exposure may result in significant relevance for human health.

Materials and Methods

Location and Sampling Methodology

Sampling was carried out in "Torre CEPSA," the second tallest tower in Spain, sited in Madrid (40.475677° N, 3.687686° W). The building is located in an urban location, surrounded by high traffic streets, highways and a few gardens, and close to a train station and two hospitals.

Airborne particles samples were taken using a DUO SAS Super 360 (VWR), with an airflow rate of 180 L/min. The sampler was customized in production to overcome the time/volume limitation of the standard equipment. This device uses two Petri dishes simultaneously (biological replicates) that were covered with sterile petroleum jelly (Vaseline, *Interapothek*) in a biosafety cabinet using sterilized materials and kept closed until they were placed into the sampler. The heads of the sampler were autoclaved the day of the sampling, and soaked in ethanol 96% and dried out with sterilized paper after each sampling. On Thursday 9th March 2017, a total of 8 samples (4 paired samples or duplicates) were taken at four different heights in the following order: ground level (~ 647 m above sea level), 80 m, 150 m, and ~ 250 m, corresponding with the accesses to the exterior of the tower (external corridors) and the rooftop, both areas used by the staff only. "Torre CEPSA" is a glass windowed building, which is frequently cleaned, and the sampler was placed at a minimum distance of 1 m from the closest wall. Each sample is a 1-h collection (~ 10.8 m^3). The meteorological data are shown in Supplementary Information ESM1 as a description of the meteorological condition during the sampling time. An additional sample keeping the device off was taking as a negative control.

DNA Extraction and High-Throughput Sequencing

Petri dishes were kept at 4 °C after collection until the DNA extraction was performed the following day. Working in a biosafety cabinet, the petroleum jelly of each dish containing the particle collected was recovered using a sterilized razor and put into an extraction tube of DNeasy PowerSoil Kit (Qiagen). DNA was extracted and purified following the manufacturer's instructions. DNA libraries and high-throughput sequencing using Illumina® MiSeq platform (2 × 300 bp reads) were performed at "Parque Científico de Madrid" (Madrid, Spain). Amplicon libraries were obtained using a different set of universal primers for each group of the biological entity studied (Bacteria: Bakt_341 (F): 5′-CCTACGGGNGGCWGCAG-3′; Bakt_805 (R): 5′-GACTACHVGGGTATCTAATCC-3′ [41], for partial amplification of the V3–V4 hypervariable regions of the gene 16S rRNA; Fungi: ITS86 (F): 5′-GTGAATCATCGAATCTTTGAA-3′ [42]; ITS-4 (R): 5′-TCCTCCGCTTATTGATATGC-3′ [43], for the region 5.8S–ITS2; Plants: ITS-p3 (F): 5′-YGACTCTCGGCAACGGATA-3′ [44]; ITS-4 (R): 5′-TCCTCCGCTTATTGATATGC-3′ [43], for the region 5.8S–ITS2). DNA amplification was null for the negative control under the same conditions, but it was included in the sequencing batch to discard contaminations and sequencing issues.

Raw Sequence Data obtained in this study are available in the National Center for Biotechnology Information (NCBI), Sequence Read Archive (SRA), under the Accession number SRP140605 (Bioproject PRJNA450512).

Sequence Assembly, Preprocessing, and Normalization

Bioinformatic processing of the next-generation sequencing (NGS) data was performed as described in Núñez et al. [38]. A first check of the total number of sequences per sample, sequence quality and length distribution was performed with FastQC software (version 0.11.3, Babraham Bioinformatics Group, Babraham Institute, UK [www.bioinformatics.babraham.ac.uk/projects/fastqc/]). Paired-ends sequences were assembled with PANDAseq ([45]; version 2.8, https://github.com/neufeld/pandaseq/wiki/PANDAseq-Assembler), filtering by Q-score quality (default 0.6), trimming the primer sequences and removing the sequences exceeding the length of the amplicon (bacteria: min 400 bp, max 500; plants: min 320, max 550). For fungal ITS library, as the sequencing protocol exceeded the length of the amplicon, we employed "read_fastq" from Biopieces (version 2.0, http://maasha.github.io/biopieces/) to remove the primer sequence followed by "fastq-join" ([46]; https://github.com/brwnj/fastq-join) to pair the reads. General processing of the sequences was carried out in Qiime suite environment [47]; version 1.9.1, http://qiime.org). Chimeras were subtracted using USEARCH v8.1 (https://drive5.com/usearch/) with default values. OTUs clustering and taxonomic assignments were performed with the default algorithm of Qiime (pick_open_reference_otus.py), using UCLUST for picking OTUs

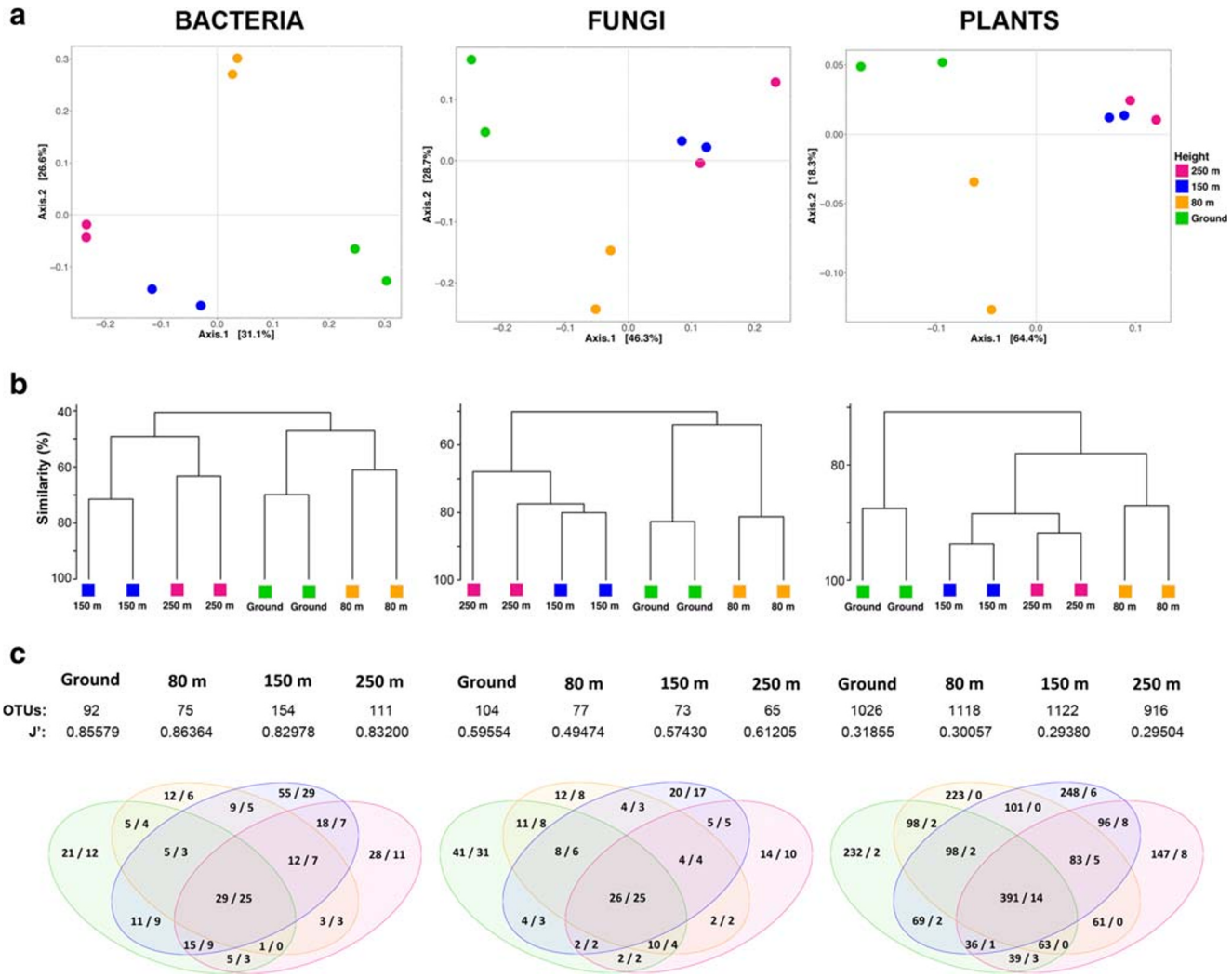
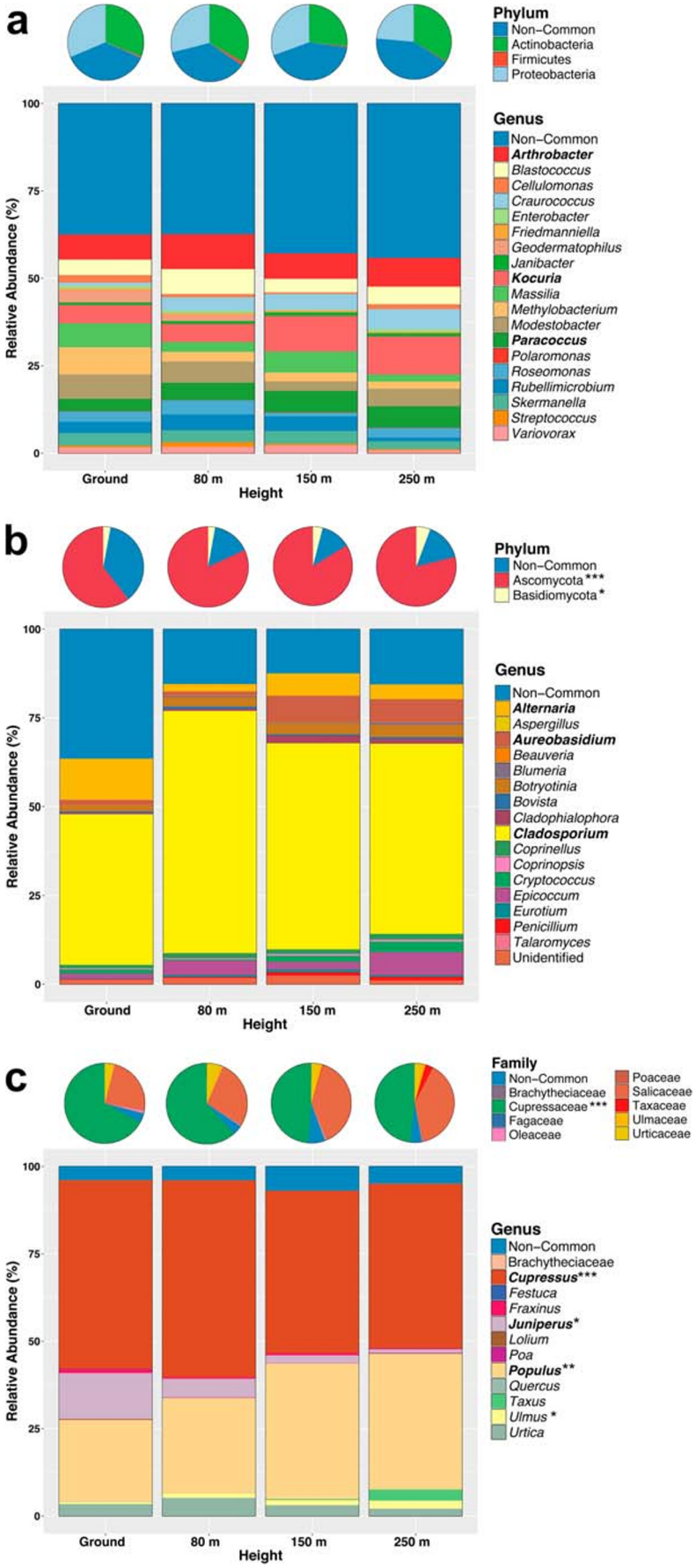


Fig. 1 Differential distribution of the biological airborne particles in height. **a** Principal coordinate Analyses (PCoA) showing the similarity of the biological composition between samples for the different communities. **b** Cluster analyses based on Bray-Curtis indices. **c** Richness (Observed OTUs), Evenness (*J'*) coefficients, and Venn diagrams showing the OTUs/phylotype distribution for the different heights


a
Phylum
Non−Common
Actinobacteria
Firmicutes
Proteobacteria
Genus
Non−Common
Arthrobacter
Blastococcus
Cellulomonas
Craurococcus
Enterobacter
Friedmanniella
Geodermatophilus
Janibacter
Kocuria
Massilia
Methylobacterium
Modestobacter
Paracoccus
Polaromonas
Roseomonas
Rubellimicrobium
Skermanella
Streptococcus
Variovorax
Relative Abundance (%)
100
75
50
25
0
Ground
80 m
150 m
250 m
Height
b
Phylum
Non−Common
Ascomycota ***
Basidiomycota *
Genus
Non−Common
Alternaria
Aspergillus
Aureobasidium
Beauveria
Blumeria
Botryotinia
Bovista
Cladophialophora
Cladosporium
Coprinellus
Coprinopsis
Cryptococcus
Epicoccum
Eurotium
Penicillium
Talaromyces
Unidentified
Relative Abundance (%)
Ground
80 m
150 m
250 m
Height
c
Family
Non−Common
Brachytheciaceae
Cupressaceae ***
Fagaceae
Oleaceae
Poaceae
Salicaceae
Taxaceae
Ulmaceae
Urticaceae
Genus
Non−Common
Brachytheciaceae
Cupressus***
Festuca
Fraxinus
Juniperus*
Lolium
Poa
Populus**
Quercus
Taxus
Ulmus *
Urtica
Relative Abundance (%)
Ground
80 m
150 m
250 m
Height

◀ **Fig. 2** Characterization of the common atmospheric biodiversity (present at all heights). Bar plots of the taxa associated to the common OTUs (core) for each community: bacteria (**a**), fungi (**b**), and pollen (**c**). The most abundant genera are highlighted in bold. Statistical differences of the abundance distribution (Wilcoxon signed-rank test) are indicated based on the level of significance: ***$p < 0.001$; **$p < 0.01$; *$p < 0.05$

[48], which were clustered with 97% similarity cutoff. Taxonomic assignments were performed applying UCLUST algorithm (minimum consensus 0.51, similarity > 0.9, max accepts 3) with SILVA database for bacteria ([49]; release_132), and UNITE ([50]; version 7.0, https://unite.ut.ee/) for fungi. A customized database was created for plants assignment as described previously in Núñez et al. [38].

The OTUs assigned to chloroplast and mitochondria in 16S analysis were filtered out. When the OTUs found in a library were assigned or identified to a different organism of that analyzed in the library (for instance, OTUs assigned to Plantae in Fungi library), and those that did not reach at least the taxonomic rank of Order were removed. As a part of the denoising process performed in R software environment ([51]; version V3.4.2, https://www.r-project.org/), we estimated a base threshold (detection limit) to consider a given OTU as detected. Firstly, we identified all the OTUs with a mix of zero and non-zero values in all the samples, and for each of these OTUs we took the smallest non-zero count value. The median of all these values was considered as our technical detection limit. Then, we filtered out the OTUs below this value (1 count for pollen, 5 for fungi, and 4 for bacteria). Finally, only the OTUs present in both samples of the same duplicate were taken into consideration. The differences in counts were then normalized with "metagenomeSeq" package [52] and subsequent analyses were performed using the package "phyloseq" ([53]; version 1.20.0). See Supplementary Material ESM2 for additional information and ESM4–6 for complete final records. The package "Tax4fun" [54] was used to explore the functional diversity of the bacterial communities.

Statistical Analyses

The statistical analyses were performed with different packages in R environment. Permutational multivariate analyses of variance (PERMANOVA) associated to PCoAs were performed with "vegan" package using the Bray-Curtis distance matrices and 999 permutations ("adonis" function). Evenness index (J') described by Pielou [55] and other diversity indexes (ESM3) were calculated subtracting the detection limit from all the counts, so the OTUs with one count above the detection limit are considered as singletons, and below as absent. Wilcoxon signed-rank test (paired test, two-sided, and confidence level at 0.95) was applied to evaluate the significance of the abundance distribution of the main taxa. Only those genera with > 3 observations (OTUs) were assessed. Spearman's rank correlations between organisms (two-sided, confidence level at 0.95, and p values adjusted using Benjamini-Hochberg correction) was performed using the matrix with the sum of relative abundance compiled by each genus from the core communities present in each sample, so a total of 8 observations per taxa were used in the test.

Results and Discussion

Differential Distribution of the Biological Airborne Particles in Height

As shown in Fig. 1a, the different biological particles showed a similar distribution, with differences fundamentally based on the height (PERMANOVA R2 values 0.730, 0.790, and 0.825 for bacteria, fungi, and plants, respectively, with associated p values < 0.01), indicating different composition between the levels. Similar ordinations were obtained when phylogenetic information based on Unifrac distance matrices was included, although fewer differences between samples were found (Supplementary Information ESM3). A particular tendency to cluster in two heights was observed in both cases (Fig. 1b and ESM3), suggesting the existence of a transitional layer between 80 and 150 m around which the biological entities showed a different community composition.

After merging the data of the replicates from each altitude, the OTUs distribution showed different patterns (Fig. 1c). In contrast to other studies performed at higher altitudes in non-urban areas [15, 56, 57], bacterial richness (number of OTUs) displayed an upward tendency with height, increasing above 80 m. This fact would explain the fast changes described in short periods by other authors [9, 58, 59], simply because the potential source is just a few meters above. On the contrary, the highest value for fungi was found at ground level, with a remarked decrease over this elevation. Other diversity indexes (Chao1, Shannon, Fisher) showed similar results (Supplementary Information ESM3). These results would suggest that bacteria are more easily dispersed in the atmosphere than fungal propagules, which tend to remain at lower heights. Size, shape, and the ease to get attached to other particles may explain these tendencies.

In the case of airborne plant DNA (mostly from pollen grains although the contribution of microscopic plant debris cannot be discarded), richness was very steady across the four heights.

Fundamental Biodiversity Present in a Vertical Section

The common OTUs (those found at all the heights) for bacteria represented 57–63% of the total abundance. This core was

formed by 12 different families and 19 genera (Fig. 2a), which belonged to the main phyla Actinobacteria (25–30%), Proteobacteria (25–30%), and Firmicutes (< 2%). *Kocuria*, *Arthrobacter*, and *Paracoccus* were the most abundant genera in all the samples, in accordance with the bacterial biodiversity described previously for this season and area [37]. Although the relative abundance of some taxa varied with the height, no pattern associated with this variable was found at any taxonomic rank examined ($p > 0.05$ for Wilcoxon tests). Additionally, the relative abundance of the non-common OTUs (those not present at all heights) is the greatest of the three communities (bacteria, fungi, or plant) analyzed (35–42% of the total abundance for each height).

The core of fungal diversity (Fig. 2b) was formed mainly by DNA sequences corresponding to the phylum Ascomycota (> 60% of each sample) and a minority to Basidiomycota (< 6%). Among the 13 different families and 16 genera that were identified, Davidiellaceae and the genus *Cladosporium*/*Davidiella* were clearly predominant (> 40% of the relative abundance in each height), followed by *Alternaria* (3–12%) and *Aureobasidium* (1–9%). Although no significant variation in the abundance of the constitutive genera was found between heights, the abundance of Ascomycota was significantly lower at ground level ($p < 0.001$), while the opposite tendency was observed for Basidiomycota ($p < 0.05$).

In the case of the plant diversity (Fig. 2c), the 391 OTUs in common compiled between 93 and 96% of the total abundance, which would explain the high similarity between the samples' composition (Fig. 1b, right panel). The plant core was formed by 8 families of vascular plants and 1 bryophyte, with a total of 11 different genera, and a high predominance of *Cupressus* spp. (Fig. 2c). Both the presence and the relative abundance of pollen detected by NGS are supported by the pollen calendar of the region and previous studies [37, 60]. The pollen of *Cupressus* spp. and *Juniperus* spp. would tend to accumulate in the area next to the base (ground and 80 m, $p < 0.001$ and $p < 0.05$, respectively, and family Cupressaceae $p < 0.001$) while the pollen of *Populus* spp. and *Ulmus* spp. (Ulmaceae) would follow the opposite tendency and be more abundant at 250 m ($p < 0.05$, respectively). We also evaluated if these differential patterns would be related to the size of the pollen grains. The plant genera were classified into "Small" (10–25 μm), "Medium" (26–51 μm), and "Large" (51–100 μm) according to the average size of their pollen grains (information extracted from http://www-saps.plantsci.cam.ac.uk/pollen/; https://pollenatlas.net/atlas/pollen-profiles; https://www.paldat.org; and technical documents from the aerobiological network of the region "Red Palinocam," http://www.comunidad.madrid/servicios/salud/polen). However, no significant correlation of this feature with height was found ($p > 0.05$ for the Kruskal-Wallis test, Supplementary Information ESM3). In fact, the plant genera with small pollen grains seemed to accumulate at the lower altitudes. A plausible explanation comes from the fact that many pollen grains are not completely spherical and present morphologies and some additional structures to help in their aerodynamics, so the size cannot be considered as a unique variable to explain the patterns observed across the vertical section.

Recently, Damialis et al. [23] found an increase of the diversity and concentration of fungal spores and many pollen types with height up to 2000 m. The number of OTUs and evenness index variations determined in our work suggested that the pollen diversity do not significantly change up to 250 m in the metropolitan areas, although we agree that particular differences exist for specific taxa.

Distribution of the Divergence Taxa Between Heights

A total of 69 bacterial genera, which mostly belonged to the phyla Actinobacteria and Proteobacteria (Fig. 3a), were differently distributed in the vertical section. Jointly, they gathered 25–31% of the total relative abundance in each height with no remarked difference between levels. Thirty-six genera were detected only in one height (19 at 150 m) but their contribution to the total abundance was marginal (< 6% of each sample jointly). In regard to fungi, 21 out of 53 genera were exclusively found at ground level (Fig. 3b), which mostly belonged to genera of the Phylum Basidiomycota (> 23% corresponded to *Strobilurus* spp.). For plants, the contribution of the non-common genera (32) represented a minor fraction (0.5–3.4% of the total abundance of each height sample), with a tendency to find more diversity when height increases (Fig. 3c). Unlike previously proposed [16, 17], we did not observe any correlation with the type of plant (herbaceous or tree) and height, finding DNA from several herbaceous species above the ground level (Fig. 2c) and at least 14 genera of this type were only detected over 150 m (Fig. 3c).

Pathogens and Allergenic Particles

Our results showed that urban population is widely exposed to fungal and pollen allergens at any height. Most of the diversity found in this work has been previously reported to have consequences in human health, acting as allergens or opportunistic pathogens [26, 61, 62]. Although a taxonomic resolution to species level would be required to be confident about the pathogenicity of the microbial genera we found, several genera are fundamentally associated to health issues. For instance, *Enterobacter* or *Streptococcus* were detected as part of the biodiversity core, and were found at all the heights (Table 1). Other genera related with the human microbiome included *Acinetobacter*, *Corynebacterium*, *Cutibacterium* (former *Propionibacterium*), *Klebsiella* and *Lactobacillus*, gathering ≤ 5% from each sample.

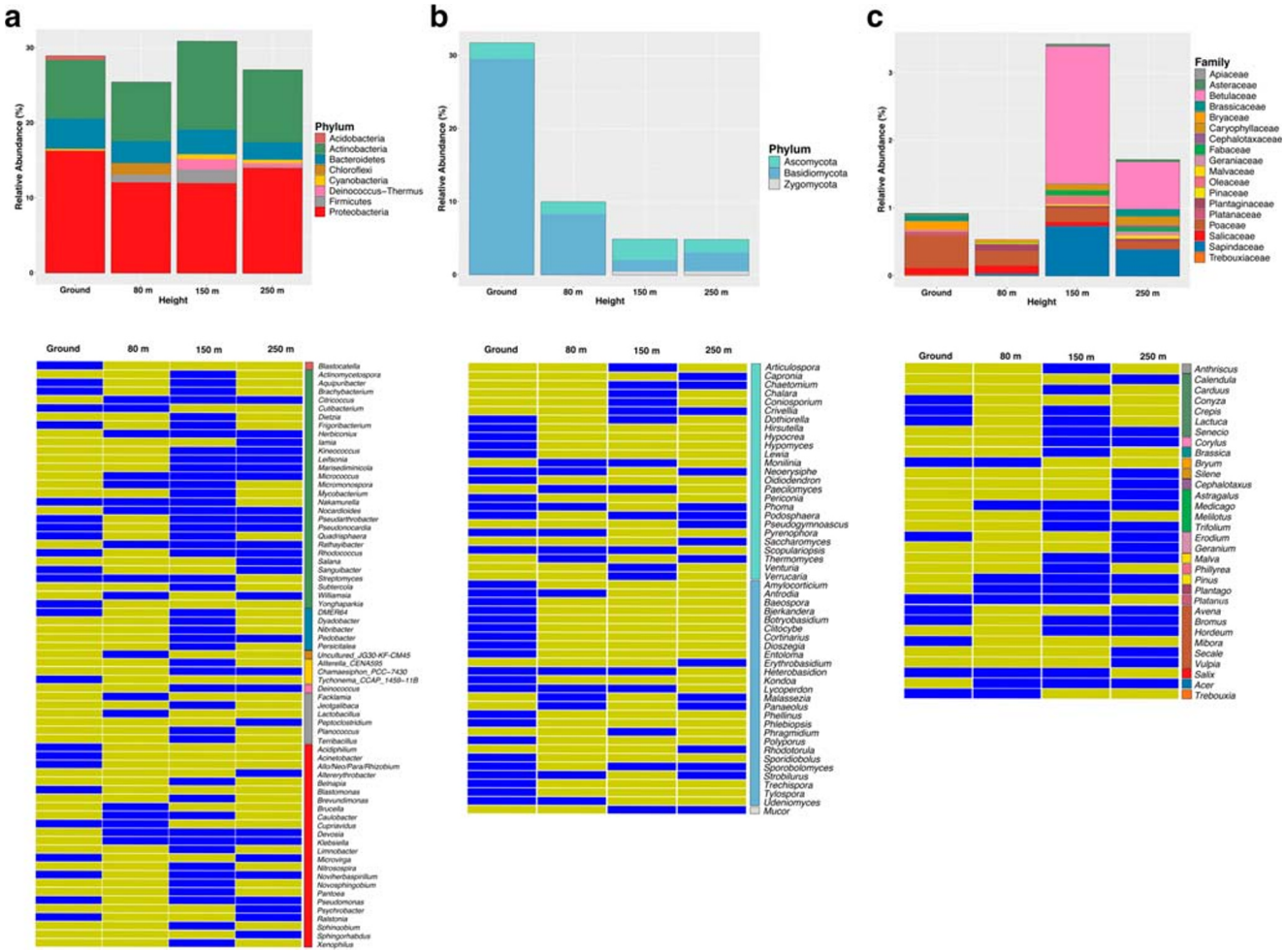


Fig. 3 Detailed description of the non-common taxa by height. Bar plots (relative abundance) and heatmap (presence/absence) representations of bacteria (**a**), fungi (**b**), and pollen (**c**)

On the other hand, a total of 16 fungal genera with allergenic/pathogenic representatives were present in the atmosphere, with *Cladosporium* spp. dominating the relative abundance at all the heights, but relevant genera such as *Alternaria*, *Aspergillus*, *Epicoccum*, and *Penicillium* were also present. In addition, most pollen grains have an allergenic potential, especially the diversity found at this season. This was dominated by representatives from Cupressaceae (*Cupressus* spp. and *Juniperus* spp.) and Salicaceae (*Populus* spp.), so that > 99% of the abundance belonged to genera that may cause allergy symptoms [26].

Excepting fungi, which showed a lower abundance of pathogens/allergens at ground level, the exposure to relevant entities did not show important differences between the heights regarding diversity or abundance.

Potential Interaction Between Organisms

Microorganisms are hardly found isolated in an ecosystem. One interesting attempt is to elucidate the potential connections between the different entities by using their abundances as a quantitative variable. Therefore, we performed Spearman's rank correlations between the relative abundance of each organism of the core communities and the other taxa at genus level. As shown in Fig. 4, positive strong correlations ($rho > 0.7$) were resolved into two scenarios of connections, with no crossover interactions between them, which would suggest either a different source location or total independency. Some interactions have been previously confirmed by other methods. For instance, the presence of *Aspergillus* spp. in the leaf surface of *Ulmus* sp. (Fig. 4) was described by Levetin and Dorsey [63]. Also the most abundant bacteria, *Kocuria* (Actinobacteria), *Paracoccus* (Alphaproteobacteria), and the fungus *Aureobasidium* showed all positive correlations with the trees *Populus*, *Ulmus* and *Taxus*, associations described in former studies [63–66], coinciding with our results. However, in our study, most of these correlations failed to past the statistical significance test ($p > 0.05$), likely because of the shortage of observations (see Supplementary Material Dataset ESM7 and ESM8 for complete data).

Table 1 Potential allergenic/pathogenic genera and their relative abundance distribution by height

Organism	Genus	Relative abundance (%)			
		Ground	80 m	150 m	250 m
Bacteria	*Acinetobacter*	0.608	0.000	0.000	0.000
	Enterobacter	0.721	0.684	0.273	0.680
	Geodermatophilus	4.869	1.841	0.284	0.006
	Klebsiella	0.000	0.168	0.067	0.120
	Micromonospora	0.000	0.202	0.324	0.000
	Mycobacterium	0.000	0.000	0.191	0.000
	Pseudomonas	2.410	0.000	0.275	0.168
	Roseomonas	3.034	6.928	2.135	5.891
	Streptococcus	0.983	1.329	0.632	1.313
	Total	12.625	11.152	4.181	8.178
Fungi	*Alternaria*	12.498	2.983	6.759	4.639
	Aspergillus	0.084	0.231	0.547	0.978
	Aureobasidium	1.381	1.108	7.351	9.095
	Botryotinia	1.426	2.496	3.085	3.448
	Chaetomium	0.000	0.000	0.452	0.298
	Cladosporium	42.580	68.218	57.966	53.586
	Cryptococcus	2.000	1.044	4.140	3.491
	Epicoccum	1.710	4.094	2.135	8.264
	Eurotium	0.171	0.511	0.772	0.450
	Mucor	0.000	0.000	0.470	0.506
	Oidiodendron	0.036	0.000	0.000	0.000
	Paecilomyces	0.000	0.107	0.077	0.000
	Penicillium	0.400	0.515	1.703	1.702
	Phoma	0.029	0.043	0.000	0.029
	Scopulariopsis	0.040	0.247	0.312	0.000
	Talaromyces	0.065	0.143	0.183	0.038
	Total	62.420	81.740	85.952	86.524
Plants	*Acer*	0.000	0.030	0.738	0.395
	Corylus	0.000	0.000	2.028	0.694
	Cupressus	56.787	59.288	48.932	49.398
	Fraxinus	1.200	0.463	1.116	0.468
	Juniperus	13.161	5.396	2.296	1.041
	Poaceae[a]	0.868	0.374	0.316	0.468
	Pinus	0.000	0.019	0.022	0.010
	Platanus	0.054	0.001	0.001	0.000
	Populus	23.424	27.570	39.021	39.256
	Quercus	0.002	0.004	0.003	0.003
	Salix	0.099	0.112	0.059	0.000
	Taxus	0.063	0.061	0.295	3.185
	Ulmus	0.583	1.310	1.559	2.422
	Urtica	3.434	5.197	3.226	2.119
	Total	99.324	99.606	99.442	99.450

[a] Family Graminaceae/Poaceae includes the following detected genera: *Avena*, *Bromus*, *Festuca*, *Hordeum*, *Lolium*, *Mibora*, *Poa*, *Secale*, and *Vulpia*

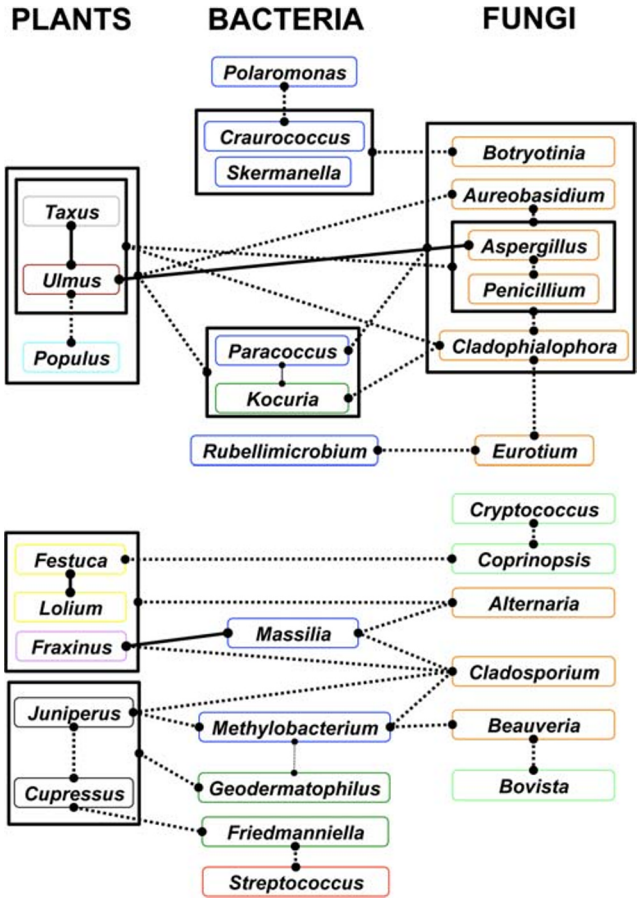


Fig. 4 Representation of the correlation between taxa. Color frames indicate taxonomic groups. Bacteria: (green box) Actinobacteria; (red box) Firmicutes; (blue box) Proteobacteria. Fungi: (orange box) Ascomycota; (green box) Basidiomycota. Plants: (black box) Cupressaceae; (purple box) Oleaceae; (yellow box) Poaceae; (turquoise box) Salicaceae; (gray box) Taxaceae; (brown box) Ulmaceae. Relations connected by dotted lines indicate p values > 0.05 while continuous lines indicate p values < 0.05. Only those with two or more correlations with a *rho* value > 0.7 are shown (see Supplementary Material EMS7 and EMS8 for complete results)

Some recent publications have reported that the combination of two or more allergenic particles like pollen grains with fungal spores or endotoxins can exacerbate the immune response [34, 35, 67]. Accordingly, we observed a positive correlation between grass pollen (*Festuca* spp. and *Lolium* spp., Poaceae) and the ash tree (*Fraxinus* spp., Oleaceae) with the also allergenic fungi *Alternaria* spp. These associations presented low statistical reliability ($p > 0.05$), but they point out a relationship to be confirmed in further studies due to its interest in allergy. On the other hand, the correlations between plant taxa would suggest a similar aerodynamics of the pollen grains or a close source location instead of real interspecific interactions of the individuals.

We also explored the functional diversity of the bacterial communities found in the air (Supplementary Information ESM3). No significant differences were observed between heights. The carbohydrate and amino acid metabolism

pathways and membrane transport were the main functional pathways at any level. Similar results were reported by Wei et al. [68] for airborne bacterial communities.

Conclusions and Final Remarks

Our work examined the concomitant presence of the main airborne biological particles present in an urban environment (bacteria, fungi, and plants) at different heights with DNA-based accuracy. Our results showed that the urban atmosphere is very rich in microscopic biodiversity, which is particularly steady in height for pollen but more fluctuating for fungi and bacteria. The divergences between the different heights analyzed are mainly due to minor representatives, excepting for bacteria, whose non-common taxa may exceed the 40% of the total diversity of one height. We also observed some trends on the distribution of the biological entities, with an increase of different taxa for bacteria and pollen at higher altitudes and the opposite tendency for fungi. Nonetheless, some additional variables besides height may influence the results, so this preliminary study must be confirmed with more extensive works. For instance, a comparative analysis with a building-independent sample to evaluate the contribution from the buildings surfaces would be interesting. Such samples could be collected employing unmanned aerial vehicles (drones) or helium balloons, although law restrictions to use these devices in metropolitan areas can make it difficult to conduct. Although the potential emissions from building walls are inherent to this type of study, to measure their relative contribution to the total diversity is something to consider, even when our study was carried out in a glass windowed building (frequently cleaned) and samples were taken at 1 m from the walls. The influence of the meteorological factors should be also taken into account. Our collection was conducted in a short period of time (≈ 5 h), which would show a minimal effect caused by these variables. However, some previous studies reported even intra-diurnal changes that may alter the patterns of abundance and distribution of the biological particles [69–71], although such patterns are still imprecise. Lighthart and Shaffer [69] reported several changes along a day time, with peaks during morning. Fang and colleagues [70] found the opposite pattern, and recently Gusareva et al. [71] reported changes day a night. Moreover, architecture and building design in the city may create main wind corridors or, contrary, obstructing barriers affecting to the exposure not only to the exposure of $PM_{2.5}$ as suggested by Zhang and colleagues [72] but also to biological particles.

Our results also showed that urban population is continuously exposed to a significant amount of aeroallergens and potentially harmful microorganisms, which would support a continuous monitoring. The correlations of the abundances between the organisms (co-occurrence) were hampered by the limited number of observations. Nonetheless, some of the associations found in our study have been previously described, and more thorough studies as those conducted by Manijaran et al. [73], Fan et al. [74], or Gusareva et al. [71] may set the spot on new bilateral relationships, which is particularly interesting from an ecological point of view as well as public health.

Finally, although this work shows a particular picture in time and place of the urban atmosphere, the observations are interesting enough to conduct further studies about the biological entities present at different scales in the cities in addition to the chemical pollution.

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Compliance with Ethical Standards

Conflict of Interest The authors declare that they have no conflict of interest.

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Table 1 Meteorological factors (average values during the sampling time).

Sampling time (Start-End)	**Barometric Pressure (kPa)**	**Relative Humidity (%)**	**T (ºC)**	**Wind Speed[a] (m/s)**	**NO_2 [a] (µg/m³)**	**$PM_{2.5}$ [a] (µg/m³)**	**PM_{10} [a] (µg/m³)**	**Samples**
09:20 - 10:20	94.2	64.6	17.2	0.5	56	11	15	Ground_1 Ground_2
10:40 - 11:40	93.3	48.7	19.5	1.2	50	11	16	80 m_1 80 m_2
12:20 -13:30	92.5	31.0	22.8	0.2	73	19	27	150 m_1 150 m_2
13:40 -14:40	91.4	26.3	26.5	0.6	82	24	33	250 m_1 250 m_2

[a] Measured at ground level.

Table S1. Sequence processing information.

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Samples	No. paired sequences	Total no. OTUs	No. OTUs Unassigned	No. OTUs assigned to "chloroplasts/ mitochondria"	No. OTUs with bacterial taxonomic assignment*	Final OTUs analyzed
Ground_1	72,317	784	12	401	371 (7)	92
Ground_2	75,106	832	12	413	407 (5)	
80 m_1	81,666	777	8	490	279 (1)	75
80 m_2	88,672	767	5	448	314 (2)	
150 m_1	72,350	931	7	423	483 (5)	154
150 m_2	57,402	934	9	406	519 (9)	
250 m_1	73,931	895	8	464	423 (2)	111
250 m_2	69,522	826	5	423	398 (2)	

FUNGI

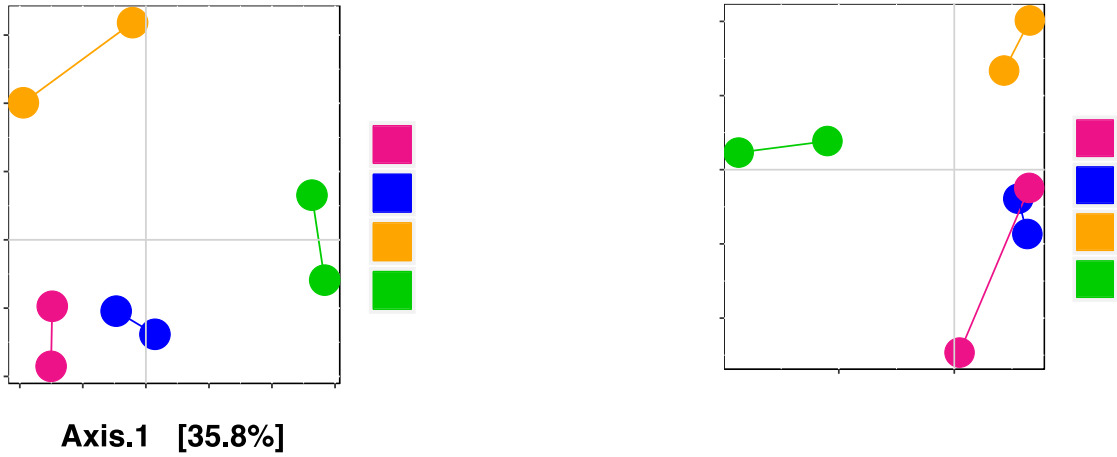
Samples	No. paired sequences	Total no. OTUs	No. OTUs "Unassigned/Plants"	No. OTUs with fungal taxonomic assignment*	Final OTUs analyzed
Ground_1	82,625	1,359	982	377 (56)	104
Ground_2	96,197	1,494	1,083	411 (62)	
80 m_1	77,540	1,364	1,099	265 (45)	77
80 m_2	81,524	1,425	1,159	266 (42)	
150 m_1	81,682	1,544	1,286	258 (41)	73
150 m_2	63,710	1,414	1,101	313 (55)	
250 m_1	70,342	1,361	1,129	232 (41)	65
250 m_2	78,773	1,395	1,157	238 (46)	

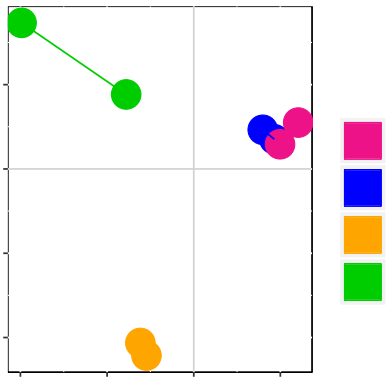
PLANTS

Samples	No. paired sequences	Total no. OTUs	No. OTUs Unassigned	No. OTUs with plant taxonomic assignment*	Final OTUs analyzed
Ground_1	122,595	3,194	327	2,867 (0)	1,026
Ground_2	108,126	2,783	329	2,454 (0)	
80 m_1	136,904	3,296	357	2,939 (1)	1,118
80 m_2	114,000	3,043	356	2,687 (0)	
150 m_1	147,447	3,341	384	2,957 (3)	1,122
150 m_2	119,605	2,298	336	2,662 (1)	
250 m_1	100,510	2,669	331	2,338 (1)	916
250 m_2	92,705	2,510	308	2,202 (2)	

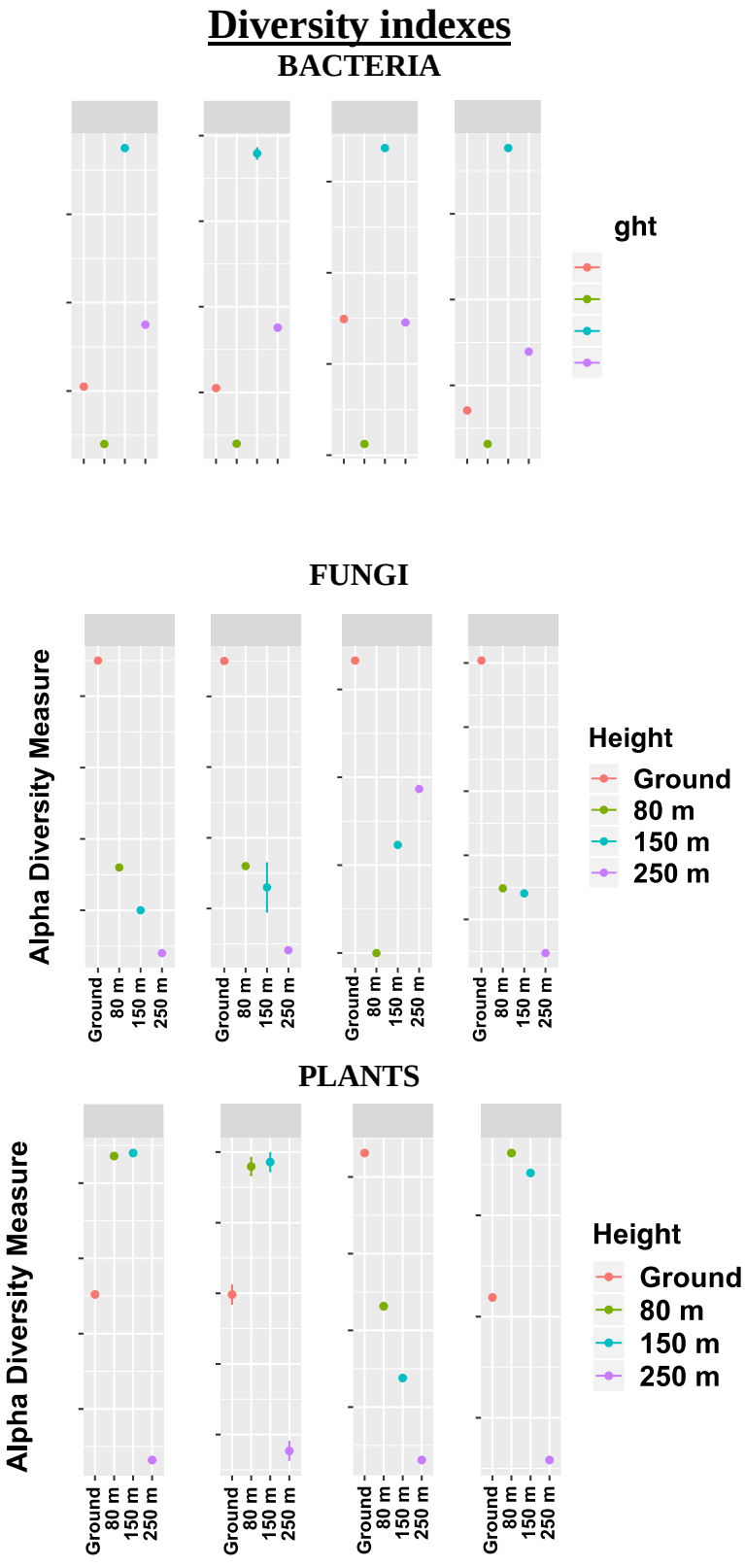
* *No. OTUs for which the taxonomic rank did not reach the Order rank in parenthesis*

Principal Coordinates Analyses (PCoA)



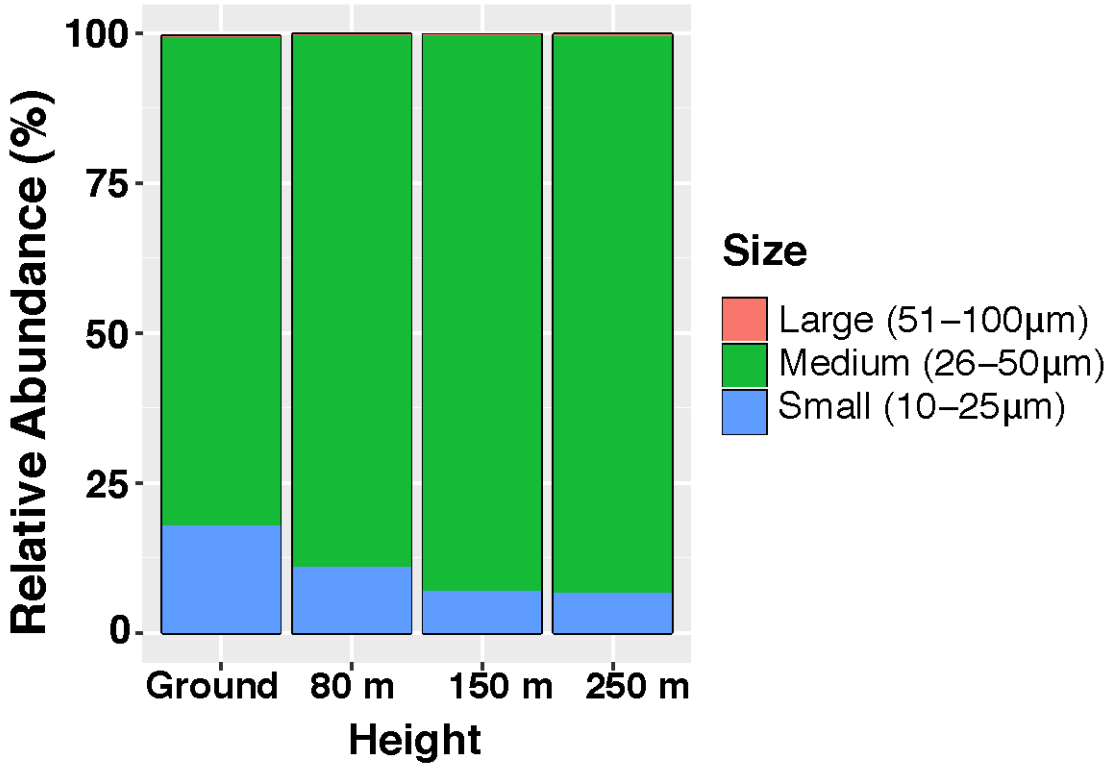


Principal Coordinates Analyses (PCoA) including phylogenetic information (Weighted Unifrac).



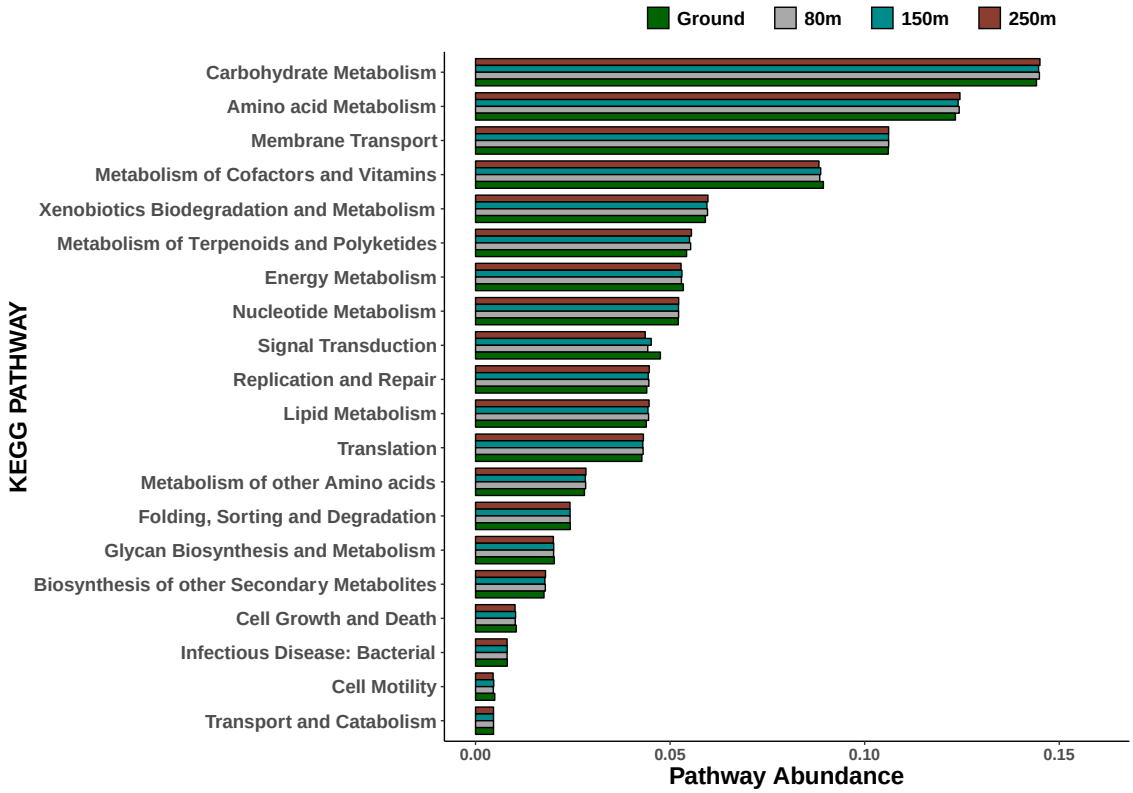
Alpha diversity indexes for the bacterial, fungal and plant communities at different heights.

Pollen grain distribution by height



Pollen grain distribution at the four altitudes based on their average size.

Functional pathways by height



OTU_ID	Ground_1	Ground_2	80m_1	80m_2	150m_1	150m_2	250m_1	250m_2	Kingdom	Phylum	Class	Order	Family	Genus	Species
OTU1	13	30	0	0	0	0	0	0	Bacteria	Acidobacteria	Blastocatellia_(Subgroup_4)	Blastocatellales	Blastocatellaceae	Blastocatella	uncultured_bacterium
OTU2	30	1	0	0	0	0	0	0	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Yonghaparkia	
OTU3	0	0	18	30	0	0	19	1	Bacteria	Actinobacteria	Actinobacteria	Corynebacteriales	Nocardiaceae	Williamsia	
OTU4	3	36	0	0	0	0	0	0	Bacteria	Actinobacteria	Actinobacteria	Frankiales	uncultured	uncultured_bacterium	
OTU5	0	0	0	0	4	6	0	0	Bacteria	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured_bacterium	
OTU6	6	22	0	0	0	0	0	0	Bacteria	Actinobacteria	Acidimicrobiia	Microtrichales	Ilumatobacteraceae	uncultured	uncultured_bacterium
OTU7	0	0	0	0	5	9	0	0	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Subtercola	Subtercola_boreus
OTU8	85	24	4	59	33	18	0	0	Bacteria	Actinobacteria	Actinobacteria	Streptomycetales	Streptomycetaceae	Streptomyces	
OTU9	15	18	0	0	0	0	32	9	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Sanguibacteraceae	Sanguibacter	
OTU10	0	0	0	0	0	0	3	4	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Beutenbergiaceae	Salana	
OTU11	27	33	0	0	42	23	35	11	Bacteria	Actinobacteria	Actinobacteria	Corynebacteriales	Nocardiaceae	Rhodococcus	Rhodococcus_corynebacterioides
OTU12	0	0	0	0	1	7	0	0	Bacteria	Actinobacteria	Actinobacteria	Corynebacteriales	Nocardiaceae	Rhodococcus	
OTU13	0	0	17	15	12	48	45	26	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Rathayibacter	
OTU14	0	0	0	0	1	2	5	8	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Rathayibacter	
OTU15	0	0	0	0	6	7	0	0	Bacteria	Actinobacteria	Actinobacteria	Kineosporiales	Kineosporiaceae	Quadrisphaera	uncultured_bacterium
OTU16	13	18	0	0	1	3	0	0	Bacteria	Actinobacteria	Actinobacteria	Kineosporiales	Kineosporiaceae	Quadrisphaera	
OTU17	0	0	0	0	3	7	0	0	Bacteria	Actinobacteria	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Pseudonocardia	uncultured_bacterium
OTU18	0	0	0	0	0	0	22	4	Bacteria	Actinobacteria	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Pseudonocardia	
OTU19	9	15	0	0	46	45	29	21	Bacteria	Actinobacteria	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Pseudonocardia	
OTU20	24	45	0	0	63	98	52	35	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Pseudarthrobacter	
OTU21	0	0	0	0	0	0	7	1	Bacteria	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	Nocardioides	
OTU22	0	0	0	0	17	12	33	1	Bacteria	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	Nocardioides	
OTU23	0	0	21	26	20	22	52	27	Bacteria	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	Nocardioides	uncultured_bacterium
OTU24	0	0	0	0	6	34	20	22	Bacteria	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	Nocardioides	uncultured_bacterium
OTU25	0	0	0	0	1	10	31	1	Bacteria	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	Nocardioides	uncultured_bacterium
OTU26	0	0	0	0	0	0	19	16	Bacteria	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	Nocardioides	uncultured_bacterium
OTU27	0	0	0	0	4	7	11	6	Bacteria	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	Nocardioides	
OTU28	0	0	0	0	0	0	7	1	Bacteria	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	Nocardioides	
OTU29	27	25	1	16	40	45	0	0	Bacteria	Actinobacteria	Actinobacteria	Frankiales	Nakamurellaceae	Nakamurella	uncultured_bacterium
OTU30	0	0	0	0	5	2	0	0	Bacteria	Actinobacteria	Actinobacteria	Frankiales	Nakamurellaceae	Nakamurella	uncultured_bacterium
OTU31	0	0	0	0	5	12	0	0	Bacteria	Actinobacteria	Actinobacteria	Corynebacteriales	Mycobacteriaceae	Mycobacterium	
OTU32	0	0	22	48	66	23	0	0	Bacteria	Actinobacteria	Actinobacteria	Frankiales	Geodermatophilaceae	Modestobacter	uncultured_bacterium
OTU33	3	8	1	3	2	2	4	4	Bacteria	Actinobacteria	Actinobacteria	Frankiales	Geodermatophilaceae	Modestobacter	uncultured_bacterium
OTU34	256	272	125	174	79	161	136	249	Bacteria	Actinobacteria	Actinobacteria	Frankiales	Geodermatophilaceae	Modestobacter	unidentified_marine_bacterioplankton
OTU35	0	0	1	1	0	0	6	1	Bacteria	Actinobacteria	Actinobacteria	Frankiales	Geodermatophilaceae	Modestobacter	
OTU36	0	0	2	9	29	1	0	0	Bacteria	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Micromonospora	
OTU37	0	0	10	3	4	21	2	3	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Micrococcus	
OTU38	0	0	11	45	3	14	0	0	Bacteria	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	Marmoricola	uncultured_bacterium
OTU39	28	16	0	0	32	19	27	11	Bacteria	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	Marmoricola	
OTU40	0	0	0	0	16	9	7	12	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Marisediminicola	
OTU41	0	0	0	0	9	8	23	5	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Leifsonia	
OTU42	239	138	72	182	398	475	565	349	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Kocuria	
OTU43	49	3	0	0	20	7	4	3	Bacteria	Acidobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Kocuria	
OTU44	9	4	3	13	18	22	18	19	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Kocuria	
OTU45	0	0	0	0	0	0	2	22	Bacteria	Actinobacteria	Actinobacteria	Kineosporiales	Kineosporiaceae	Kineococcus	
OTU46	0	0	0	0	1	1	0	0	Bacteria	Actinobacteria	Actinobacteria	Kineosporiales	Kineosporiaceae	Kineococcus	
OTU47	44	10	17	25	33	59	16	54	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Intrasporangiaceae	Janibacter	
OTU48	0	0	0	0	0	0	8	30	Bacteria	Actinobacteria	Acidimicrobiia	Microtrichales	Iamiaceae	Iamia	uncultured_bacterium
OTU49	0	0	22	29	13	6	10	30	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Herbiconiux	
OTU50	73	33	0	0	0	0	0	0	Bacteria	Actinobacteria	Actinobacteria	Frankiales	Geodermatophilaceae	Geodermatophilus	
OTU51	171	84	8	97	19	7	4	2	Bacteria	Actinobacteria	Actinobacteria	Frankiales	Geodermatophilaceae	Geodermatophilus	
OTU52	3	19	0	0	3	4	0	0	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Frigoribacterium	
OTU53	0	0	0	0	1	1	0	0	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Frigoribacterium	
OTU54	33	7	4	18	19	4	7	22	Bacteria	Actinobacteria	Actinobacteria	Propionibacteriales	Propionibacteriaceae	Friedmanniella	uncultured_bacterium
OTU55	0	0	0	0	10	2	0	0	Bacteria	Actinobacteria	Actinobacteria	Corynebacteriales	Dietziaceae	Dietzia	uncultured_bacterium
OTU56	11	4	6	13	0	0	0	0	Bacteria	Actinobacteria	Actinobacteria	Propionibacteriales	Propionibacteriaceae	Cutibacterium	uncultured_bacterium
OTU57	4	2	0	0	6	3	7	7	Bacteria	Actinobacteria	Actinobacteria	Corynebacteriales	Corynebacteriaceae	Corynebacterium_1	
OTU58	16	2	0	0	0	0	0	0	Bacteria	Actinobacteria	Actinobacteria	Corynebacteriales	Corynebacteriaceae	Corynebacterium_1	
OTU59	0	0	10	21	0	0	5	1	Bacteria	Actinobacteria	Actinobacteria	Corynebacteriales	Corynebacteriaceae	Corynebacterium_1	uncultured_bacterium
OTU60	0	0	8	10	2	5	9	8	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Citricoccus	
OTU61	0	0	0	0	8	3	0	0	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Cellulomonadaceae	Cellulomonas	
OTU62	0	0	0	0	5	87	14	45	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Cellulomonadaceae	Cellulomonas	
OTU63	0	0	1	10	0	0	0	0	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Cellulomonadaceae	Cellulomonas	
OTU64	118	41	10	40	15	30	35	72	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Cellulomonadaceae	Cellulomonas	Cellulomonas_cellasea
OTU65	0	0	0	0	0	0	11	1	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Cellulomonadaceae	Cellulomonas	uncultured_bacterium
OTU66	0	0	0	0	0	0	1	24	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Cellulomonadaceae	Cellulomonas	
OTU67	1	7	0	0	1	1	0	0	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Dermabacteraceae	Brachybacterium	
OTU68	0	0	0	0	50	26	0	0	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Dermabacteraceae	Brachybacterium	
OTU69	0	0	0	0	18	9	0	0	Bacteria	Actinobacteria	Actinobacteria	Frankiales	Geodermatophilaceae	Blastococcus	
OTU70	0	0	0	0	2	4	1	8	Bacteria	Actinobacteria	Actinobacteria	Frankiales	Geodermatophilaceae	Blastococcus	uncultured_bacterium
OTU71	99	161	103	240	129	121	75	100	Bacteria	Actinobacteria	Actinobacteria	Frankiales	Geodermatophilaceae	Blastococcus	
OTU72	0	0	8	1	15	15	29	15	Bacteria	Actinobacteria	Actinobacteria	Frankiales	Geodermatophilaceae	Blastococcus	
OTU73	29	63	1	30	44	53	77	147	Bacteria	Actinobacteria	Actinobacteria	Frankiales	Geodermatophilaceae	Blastococcus	
OTU74	1	20	0	0	3	1	5	1	Bacteria	Actinobacteria	Actinobacteria	Frankiales	Geodermatophilaceae	Blastococcus	uncultured_bacterium
OTU75	275	232	146	347	236	379	455	232	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Arthrobacter	
OTU76	0	0	0	0	8	2	0	0	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Arthrobacter	
OTU77	0	0	0	0	0	0	5	1	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Arthrobacter	
OTU78	0	0	0	0	0	0	29	11	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Arthrobacter	uncultured_bacterium
OTU79	3	2	2	3	3	6	3	1	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Arthrobacter	
OTU80	16	20	8	13	16	14	30	16	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Arthrobacter	
OTU81	9	3	0	0	2	11	0	0	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Intrasporangiaceae	Aquipuribacter	uncultured_bacterium
OTU82	0	0	0	0	2	10	0	0	Bacteria	Actinobacteria	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Actinomycetospora	uncultured_bacterium
OTU83	0	0	0	0	95	7	0	0	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Dermatophilaceae		
OTU84	0	0	0	0	0	0	30	4	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Dermatophilaceae		
OTU85	15	41	0	0	0	0	0	0	Bacteria	Actinobacteria	Acidimicrobiia	IMCC26256	uncultured_bacterium		
OTU86	4	15	32	1	26	17	40	88	Bacteria	Actinobacteria	Actinobacteria	Frankiales	uncultured		
OTU87	0	0	28	5	0	0	0	0	Bacteria	Bacteroidetes	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	uncultured	uncultured_bacterium
OTU88	0	0	18	56	0	0	0	0	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prolixibacteraceae	uncultured	uncultured_bacterium
OTU89	0	0	0	0	11	6	0	0	Bacteria	Bacteroidetes	Bacteroidia	Cytophagales	Spirosomaceae	Persicitalea	uncultured_bacterium
OTU90	0	0	0	0	3	45	51	21	Bacteria	Bacteroidetes	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	
OTU91	0	0	0	0	26	3	0	0	Bacteria	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Nibribacter	uncultured_bacterium
OTU92	0	0	0	0	10	17	0	0	Bacteria	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Nibribacter	uncultured_bacterium
OTU93	0	0	0	0	11	1	0	0	Bacteria	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	uncultured_bacterium
OTU94	9	23	0	0	22	29	2	8	Bacteria	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	uncultured_bacterium
OTU95	4	7	0	0	0	0	0	0	Bacteria	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	
OTU96	0	0	0	0	8	8	15	19	Bacteria	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	
OTU97	0	0	0	0	3	11	0	0	Bacteria	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	uncultured_bacterium
OTU98	37	60	0	0	0	0	0	0	Bacteria	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	uncultured_bacterium
OTU99	0	0	0	0	0	0	28	1	Bacteria	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	uncultured_bacterium
OTU100	0	0	10	21	0	0	0	0	Bacteria	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	
OTU101	0	0	0	0	19	22	0	0	Bacteria	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	
OTU102	0	0	2	6	6	3	1	22	Bacteria	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	
OTU103	37	1	0	0	0	0	36	3	Bacteria	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	
OTU104	12	24	0	0	0	0	0	0	Bacteria	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	uncultured_bacterium
OTU105	0	0	0	0	16	3	0	0	Bacteria	Bacteroidetes	Bacteroidia	Cytophagales	Spirosomaceae	Dyadobacter	
OTU106	75	18	0	0	2	10	0	0	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	DMER64	uncultured_bacterium
OTU107	0	0	1	40	0	0	0	0	Bacteria	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	uncultured_bacterium	
OTU108	0	0	22	3	0	0	0	0	Bacteria	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	uncultured_bacterium	
OTU109	0	0	4	9	0	0	0	0	Bacteria	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	uncultured_bacterium	
OTU110	0	0	0	0	0	0	14	17	Bacteria	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45		
OTU111	0	0	0	0	6	15	0	0	Bacteria	Chloroflexi	KD4-96	uncultured_bacterium			
OTU112	1	20	0	0	0	0	0	0	Bacteria	Cyanobacteria	Oxyphotobacteria	Nostocales	Phormidiaceae	Tychonema_CCAP_1459-11B	uncultured_bacterium
OTU113	0	0	0	0	21	19	15	20	Bacteria	Cyanobacteria	Oxyphotobacteria	Leptolyngbyales	Leptolyngbyaceae	Chamaesiphon_PCC-7430	uncultured_cyanobacterium
OTU114	0	0	0	0	5	12	0	0	Bacteria	Cyanobacteria	Oxyphotobacteria	Nostocales	Chroococcidiopsaceae	Aliterella_CENA595	
OTU115	0	0	0	0	10	16	0	0	Bacteria	Deinococcus-Thermus	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	
OTU116	0	0	0	0	22	8	0	0	Bacteria	Deinococcus-Thermus	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	uncultured_bacterium
OTU117	0	0	0	0	13	5	8	2	Bacteria	Deinococcus-Thermus	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	
OTU118	0	0	0	0	10	17	7	20	Bacteria	Deinococcus-Thermus	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	uncultured_bacterium
OTU119	0	0	0	0	3	10	0	0	Bacteria	Deinococcus-Thermus	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	
OTU120	0	0	0	0	8	4	0	0	Bacteria	Deinococcus-Thermus	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Deinococcus_marmoris
OTU121	0	0	0	0	4	11	0	0	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Terribacillus	Terribacillus_aidingensis
OTU122	19	17	0	0	10	5	1	63	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus	uncultured_bacterium
OTU123	22	17	12	61	37	6	32	6	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus	
OTU124	0	0	0	0	89	54	0	0	Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planococcus	
OTU125	0	0	0	0	0	0	5	10	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Peptoclostridium	uncultured_bacterium
OTU126	0	0	9	10	0	0	0	0	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus	Lactobacillus_crispatus
OTU127	0	0	0	0	5	2	0	0	Bacteria	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Jeotgalibaca	uncultured_bacterium
OTU128	0	0	13	18	0	0	0	0	Bacteria	Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	Facklamia	
OTU129	0	0	0	0	15	7	0	0	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Xenophilus	uncultured_bacterium
OTU130	34	93	19	78	61	119	46	22	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Variovorax	uncultured_bacterium
OTU131	0	0	0	0	10	1	0	0	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Variovorax	
OTU132	1	5	1	2	7	10	1	1	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Variovorax	uncultured_bacterium
OTU133	3	5	1	1	5	9	0	0	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Variovorax	uncultured_bacterium
OTU134	72	13	16	57	0	0	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae	uncultured	uncultured_bacterium
OTU135	0	0	0	0	1	9	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	uncultured	uncultured_bacterium
OTU136	26	27	0	0	34	7	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	uncultured	
OTU137	0	0	13	2	6	9	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Devosiaceae	uncultured	
OTU138	0	0	0	0	0	0	42	1	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingorhabdus	
OTU139	0	0	0	0	38	33	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	uncultured_alpha_proteobacterium
OTU140	0	0	0	0	0	0	14	1	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	uncultured_bacterium
OTU141	0	0	0	0	0	0	27	32	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	
OTU142	0	0	0	0	0	0	9	5	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	uncultured_Sphingomonas_sp_
OTU143	38	17	49	79	40	23	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	
OTU144	0	0	0	0	10	13	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	uncultured_bacterium
OTU145	31	27	0	0	0	0	39	5	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	
OTU146	81	26	0	0	85	53	86	76	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	uncultured_bacterium
OTU147	171	67	0	0	22	7	97	109	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	uncultured_bacterium
OTU148	0	0	0	0	9	16	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	uncultured_bacterium
OTU149	0	0	0	0	0	0	29	4	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	
OTU150	39	7	0	0	13	3	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	uncultured_organism
OTU151	0	0	0	0	35	1	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	uncultured_bacterium
OTU152	0	0	0	0	0	0	6	36	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	uncultured_bacterium
OTU153	0	0	16	1	7	22	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	
OTU154	0	0	0	0	2	17	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	uncultured_bacterium
OTU155	0	0	0	0	20	13	31	37	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	uncultured_bacterium
OTU156	0	0	38	66	38	31	39	96	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	uncultured_bacterium
OTU157	0	0	1	11	1	3	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	uncultured_bacterium
OTU158	0	0	0	0	2	15	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	uncultured_bacterium
OTU159	0	0	0	0	10	7	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium	
OTU160	0	0	0	0	0	0	76	23	Bacteria	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Skermanella	uncultured_bacterium
OTU161	0	0	0	0	0	0	22	23	Bacteria	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Skermanella	uncultured_bacterium
OTU162	9	39	33	1	0	0	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Skermanella	
OTU163	43	260	72	94	168	162	162	48	Bacteria	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Skermanella	uncultured_bacterium
OTU164	0	0	0	0	7	11	5	1	Bacteria	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Skermanella	uncultured_bacterium
OTU165	2	4	1	4	0	0	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Skermanella	uncultured_bacterium
OTU166	0	0	0	0	3	5	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	uncultured_bacterium
OTU167	169	68	163	32	253	128	13	64	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	uncultured_bacterium
OTU168	0	0	0	0	11	5	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	uncultured_bacterium
OTU169	0	0	28	77	27	44	187	197	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	uncultured_bacterium
OTU170	0	0	0	0	1	15	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	uncultured_bacterium
OTU171	0	0	17	121	1	5	157	47	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Roseomonas	
OTU172	1	1	1	1	5	1	1	2	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Roseomonas	
OTU173	0	0	0	0	23	24	10	25	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Roseomonas	
OTU174	144	72	130	46	22	65	164	78	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Roseomonas	
OTU175	0	0	0	0	38	4	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Roseomonas	
OTU176	3	5	7	1	0	0	5	4	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Roseomonas	
OTU177	0	0	4	9	1	3	12	5	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Roseomonas	
OTU178	0	0	0	0	0	0	13	8	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Roseomonas	
OTU179	1	21	0	0	0	0	1	1	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Ralstonia	
OTU180	0	0	0	0	0	0	10	11	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Psychrobacter	Psychrobacter_faecalis
OTU181	0	0	0	0	0	0	7	7	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	
OTU182	28	61	0	0	16	9	0	0	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas_lutea
OTU183	84	8	0	0	0	0	0	0	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas_pseudoalcaligenes
OTU184	1	9	1	3	5	9	11	1	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Polaromonas	
OTU185	18	2	0	0	10	2	2	1	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Paracoccus	
OTU186	58	37	1	64	146	102	248	64	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Paracoccus	uncultured_bacterium
OTU187	82	94	128	41	107	193	120	117	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Paracoccus	
OTU188	0	0	0	0	27	63	38	77	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Paracoccus	unidentified
OTU189	14	40	0	0	0	0	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Paracoccus	uncultured_bacterium
OTU190	1	5	0	0	0	0	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Paracoccus	uncultured_bacterium
OTU191	0	0	0	0	6	3	0	0	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Pantoea	Pantoea_agglomerans
OTU192	0	0	0	0	6	5	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium	
OTU193	17	44	0	0	19	87	78	74	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Noviherbaspirillum	
OTU194	21	11	0	0	0	0	0	0	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Noviherbaspirillum	
OTU195	10	32	0	0	0	0	0	0	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Noviherbaspirillum	uncultured_bacterium
OTU196	0	0	0	0	5	11	0	0	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Nitrosomonadaceae	Nitrosospira	
OTU197	31	37	0	0	0	0	25	12	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Microvirga	
OTU198	1	4	0	0	5	1	3	1	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylobacterium	
OTU199	0	0	27	46	7	6	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylobacterium	
OTU200	49	72	0	0	17	22	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylobacterium	
OTU201	325	269	95	24	131	97	106	73	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylobacterium	
OTU202	323	102	68	39	133	285	111	39	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Massilia	uncultured_bacterium
OTU203	21	63	13	10	48	71	16	18	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Massilia	uncultured_bacterium
OTU204	3	5	0	0	0	0	0	0	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Massilia	uncultured_bacterium
OTU205	0	0	0	0	8	48	0	0	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Massilia	Massilia_dura
OTU206	5	48	0	0	11	35	0	0	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Massilia	uncultured_bacterium
OTU207	1	18	0	0	15	39	0	0	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Massilia	
OTU208	0	0	0	0	17	1	0	0	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Limnobacter	uncultured_bacterium
OTU209	0	0	2	7	3	3	5	5	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	
OTU210	34	20	3	36	19	6	41	20	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Enterobacter	
OTU211	0	0	0	0	16	1	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Devosiaceae	Devosia	uncultured_bacterium
OTU212	0	0	0	0	16	8	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Devosiaceae	Devosia	uncultured_bacterium
OTU213	0	0	35	44	27	6	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Devosiaceae	Devosia	
OTU214	0	0	0	0	0	0	7	28	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Devosiaceae	Devosia	uncultured_bacterium
OTU215	25	8	15	4	0	0	0	0	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Cupriavidus	
OTU216	0	0	11	1	0	0	0	0	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Cupriavidus	
OTU217	39	33	133	36	173	223	352	167	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Craurococcus	uncultured_bacterium
OTU218	9	15	35	52	11	5	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Craurococcus	
OTU219	0	0	2	12	0	0	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Craurococcus	
OTU220	2	1	0	0	4	9	7	4	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Craurococcus	uncultured_bacterium
OTU221	0	0	57	1	11	14	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Caulobacter	
OTU222	0	0	31	27	0	0	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Brucella	
OTU223	0	0	0	0	8	14	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	
OTU224	21	23	0	0	0	0	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Blastomonas	
OTU225	0	0	0	0	60	34	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Belnapia	Belnapia_rosea
OTU226	0	0	0	0	0	0	52	32	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Altererythrobacter	
OTU227	1	8	0	0	0	0	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	
OTU228	23	24	0	0	0	0	0	0	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	
OTU229	28	15	0	0	0	0	0	0	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Acidiphilium	

OTU_ID	Ground_1	Ground_2	m_1	m_2	m_1	m_2	m_1	m_2	Kingdom	Phylum	Class	Order	Family	Genus	Species
OTU1	12	30	0	0	8	16	2	10	Fungi	Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Podosphaera	
OTU2	18	10	0	0	0	0	0	0	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	Penicillium roseopurpureum
OTU3	121	1	0	0	0	0	32	150	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Epicoccum	Epicoccum nigrum
OTU4	198	349	268	241	199	151	262	101	Fungi	Ascomycota	Leotiomycetes	Helotiales	Sclerotiniaceae	Botrytinia	
OTU5	6032	3879	3843	6	2	5	2	3	7241	6	2	2	1	8	6	4	Fungi	Ascomycota	Dothideomycetes	Capnodiales	Davidiellaceae	Davidiella	Davidiella tassiana
OTU6	0	0	0	0	24	12	8	23	Fungi	Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Chaetomium	
OTU7	2028	1955	155	39	198	443	218	123	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria	Alternaria tenuissima
OTU8	84	435	150	72	320	558	158	508	Fungi	Ascomycota	Dothideomycetes	Dothideales	Dothioraceae	Aureobasidium	Aureobasidium pullulans
OTU9	0	0	0	0	0	0	0	9	23	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Aspergillus	Aspergillus miniscleротigenes
OTU10	0	0	13	14	19	10	1	10	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Aspergillus	Aspergillus niger
OTU11	0	0	0	0	1	7	0	0	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	Penicillium digitatum
OTU12	94	51	1	24	0	0	0	0	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria	Alternaria malorum
OTU13	8	3	0	0	0	0	0	0	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria	Alternaria tenuissima
OTU14	10	6	16	4	31	37	48	48	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	Penicillium chrysogenum
OTU15	0	0	10	6	12	14	24	22	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Aspergillus	Aspergillus fumigatus
OTU16	8	17	10	20	5	5	2	2	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	Talaromyces rugulosus
OTU17	0	0	0	0	14	6	3	4	Fungi	Ascomycota	Eurotiomycetes	Chaetothyriales			
OTU18	18	4	0	0	0	0	0	0	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Incertae sedis	Periconia	
OTU19	0	0	0	0	3	7	0	0	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	Penicillium raistrickii
OTU20	8	10	5	2	2	3	1	2	Fungi	Ascomycota	Dothideomycetes	Capnodiales	Davidiellaceae	Cladosporium	Cladosporium sp TMS_2011
OTU21	21	1	16	23	17	11	8	9	Fungi	Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		
OTU22	8	4	3	9	6	6	2	5	Fungi	Ascomycota	Dothideomycetes	Capnodiales	Davidiellaceae	Davidiella	Davidiella tassiana
OTU23	7	74	0	0	0	0	0	0	Fungi	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae		
OTU24	7	7	0	0	0	0	0	0	Fungi	Ascomycota	Dothideomycetes	Incertae sedis	Myxotrichaceae	Oidiodendron	
OTU25	5	2	6	3	1	1	0	0	Fungi	Ascomycota	Dothideomycetes	Capnodiales	Davidiellaceae		
OTU26	0	0	0	0	3	1	0	0	Fungi	Ascomycota	Dothideomycetes	unidentified_Dothideomycetes	unidentified_Dothideomycetes	unidentified_Dothideomycetes	Dothideomycetes sp LS_2013g
OTU27	0	0	0	0	32	1	0	0	Fungi	Ascomycota	Eurotiomycetes	Chaetothyriales	unidentified_Chaetothyriales	unidentified_Chaetothyriales	Chaetothyriales sp
OTU28	80	22	0	0	0	0	0	0	Fungi	Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Hypomyces	
OTU29	5	2	0	0	0	0	0	11	3	Fungi	Ascomycota	Dothideomycetes	unidentified_Dothideomycetes	unidentified_Dothideomycetes	Dothideomycetes sp
OTU30	0	0	0	0	3	6	0	0	Fungi	Ascomycota	Dothideomycetes	Pleosporales	unidentified_Pleosporales	unidentified_Pleosporales	Pleosporales sp
OTU31	0	0	10	12	4	5	0	0	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Paecilomyces	Paecilomyces penicillatus
OTU32	0	0	0	0	6	1	0	0	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Venturiaceae	Venturia	
OTU33	0	0	0	0	0	0	15	13	Fungi	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Capronia	Capronia sp
OTU34	1	3	3	6	0	0	1	2	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Incertae sedis	Phoma	
OTU35	0	0	0	0	9	5	0	0	Fungi	Ascomycota	Eurotiomycetes	Verrucariales	Verrucariaceae	Verrucaria	Verrucaria viridula
OTU36	346	55	0	0	0	0	0	0	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Pyrenophora	
OTU37	14	7	0	0	0	0	0	0	Fungi	Ascomycota	Dothideomycetes	Pleosporales			
OTU38	0	0	1	6	0	0	0	0	Fungi	Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Blumeria	Blumeria graminis
OTU39	33	23	8	21	0	0	4	7	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	
OTU40	8	25	0	0	0	0	0	0	Fungi	Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Hypocrea	
OTU41	3916	2815	1752	2234	898	1427	1124	584	Fungi	Ascomycota	Dothideomycetes	Capnodiales	Davidiellaceae	Cladosporium	Cladosporium oxysporum
OTU42	0	0	113	6	0	0	0	0	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Pyrenophora	
OTU43	0	0	1	23	14	5	1	55	Fungi	Ascomycota	Dothideomycetes	Dothideales	Dothioraceae	unidentified_Dothioraceae	
OTU44	1	6	0	0	3	3	0	0	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria	Alternaria alternata
OTU45	0	0	0	0	19	8	7	8	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	Penicillium commune
OTU46	0	0	0	0	1	51	0	0	Fungi	Ascomycota	Eurotiomycetes	Chaetothyriales	Incertae sedis	Coniosporium	
OTU47	0	0	0	0	6	6	0	0	Fungi	Ascomycota	Dothideomycetes	Pleosporales			
OTU48	3	42	19	70	0	0	26	115	Fungi	Ascomycota	Dothideomycetes	Dothideales	unidentified_ Dothideales	unidentified_ Dothideales	
OTU49	0	0	0	0	0	0	6	3	Fungi	Ascomycota	Dothideomycetes	Incertae sedis	Pseudeurotiaceae	Pseudogymnoascus	Pseudogymnoascus pannorum
OTU50	0	0	0	0	0	0	39	8	Fungi	Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Blumeria	Blumeria graminis
OTU51	0	0	0	0	0	0	24	7	Fungi	Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Neoerysiphe	Neoerysiphe galii
OTU52	0	0	34	44	0	0	0	0	Fungi	Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Neoerysiphe	Neoerysiphe galeopsidis
OTU53	0	0	0	0	1	72	0	0	Fungi	Ascomycota	Dothideomycetes	Pleosporales	unidentified_Pleosporales	unidentified_Pleosporales	Pleosporales sp
OTU54	12	14	13	14	30	11	9	1	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	Penicillium brevicompactum
OTU55	98	44	54	58	124	117	72	64	Fungi	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Cladophialophora	Cladophialophora bantiana
OTU56	0	0	5	31	0	0	13	5	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Incertae sedis	Thermomyces	
OTU57	0	0	19	5	0	0	0	0	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria	Alternaria rosae
OTU58	48	20	56	48	52	35	18	29	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Eurotium	
OTU59	1	1	1	1	0	0	2	9	Fungi	Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Blumeria	Blumeria graminis
OTU60	0	0	0	0	7	7	0	0	Fungi	Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Articulospora	Articulospora sp
OTU61	6	6	0	0	9	15	14	29	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	Penicillium expansum
OTU62	26	14	0	0	0	0	0	0	Fungi	Ascomycota	Dothideomycetes	Pleosporales			
OTU63	26	20	0	0	5	43	0	0	Fungi	Ascomycota	Dothideomycetes	Botryosphaeriales	Botryosphaeriaceae	Dothiorella	Dothiorella sarmentorum
OTU64	31	9	3	13	0	0	3	2	Fungi	Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Blumeria	Blumeria graminis
OTU65	0	0	1	1	2	1	0	0	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	
OTU66	17	13	10	2	0	0	5	5	Fungi	Ascomycota	Dothideomycetes	Capnodiales	Davidiellaceae	Cladosporium	
OTU67	2	6	2	2	0	0	1	1	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae		
OTU68	0	0	0	0	0	0	11	2	Fungi	Ascomycota	Dothideomycetes	Dothideales	Dothioraceae	unidentified_Dothioraceae	Dothioraceae sp
OTU69	23	7	44	18	26	42	0	0	Fungi	Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Blumeria	Blumeria graminis
OTU70	3	4	0	0	0	0	0	0	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Incertae sedis	Phoma	
OTU71	12	28	0	0	8	24	0	0	Fungi	Ascomycota	Dothideomycetes	Pleosporales			
OTU72	0	0	15	1	0	0	0	0	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae		
OTU73	30	17	0	0	0	0	0	0	Fungi	Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Neoerysiphe	Neoerysiphe joerstadii
OTU74	11	4	0	0	0	0	0	0	Fungi	Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae	Hirsutella	
OTU75	0	0	0	0	8	10	0	0	Fungi	Ascomycota	Incertae sedis	Incertae sedis	Incertae sedis	Chalara	Chalara holubovae
OTU76	12	25	32	66	4	32	32	44	Fungi	Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Blumeria	Blumeria graminis
OTU77	1	14	13	39	25	9	0	0	Fungi	Ascomycota	Sordariomycetes	Microascales	Microascaceae	Scopulariopsis	Scopulariopsis fusca
OTU78	0	0	0	0	6	5	0	0	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	Talaromyces variabilis
OTU79	2	16	18	9	1	4	2	1	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	
OTU80	7	8	0	0	0	0	0	0	Fungi	Ascomycota	Dothideomycetes	Pleosporales			
OTU81	18	7	9	23	0	0	0	0	Fungi	Ascomycota	Sordariomycetes	Incertae sedis	Apiosporaceae	unidentified_Apiosporaceae	
OTU82	303	249	303	549	51	216	402	281	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Epicoccum	Epicoccum nigrum
OTU83	0	0	0	0	0	0	0	2	13	Fungi	Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Podosphaera	Podosphaera spiraeae
OTU84	22	90	0	0	0	0	0	0	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Lewia	Lewia infectoria
OTU85	177	283	219	95	41	255	88	21	Fungi	Ascomycota	Dothideomycetes	unidentified_Dothideomycetes	unidentified_Dothideomycetes	unidentified_Dothideomycetes	
OTU86	63	15	7	6	33	17	0	0	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria	
OTU87	73	61	64	66	0	0	52	146	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria	
OTU88	0	0	0	0	9	9	0	0	Fungi	Ascomycota	Incertae sedis	Incertae sedis	Incertae sedis		
OTU89	0	0	8	3	0	0	0	0	Fungi	Ascomycota	Sordariomycetes	Xylariales			
OTU90	0	0	0	0	4	6	0	0	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	Penicillium steckii
OTU91	25	36	24	13	9	10	8	7	Fungi	Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae	Beauveria	
OTU92	151	42	20	84	0	0	12	4	Fungi	Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Blumeria	Blumeria graminis
OTU93	0	0	0	0	0	0	4	7	Fungi	Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetaceae	Saccharomyces	Saccharomyces cerevisiae
OTU94	178	326	60	164	79	26	28	52	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria	
OTU95	0	0	10	15	1	16	0	0	Fungi	Ascomycota	Leotiomycetes	Helotiales	Sclerotiniaceae	Monilinia	Monilinia laxa
OTU96	17	8	5	4	4	4	8	5	Fungi	Ascomycota	Dothideomycetes	Capnodiales	Davidiellaceae	Cladosporium	
OTU97	11	21	3	1	1	7	4	9	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Aspergillus	Aspergillus unguis
OTU98	0	0	0	0	0	0	244	40	Fungi	Ascomycota	Dothideomycetes	Dothideales	Dothioraceae	Aureobasidium	Aureobasidium pullulans
OTU99	8	14	0	0	0	0	0	0	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	unidentified_Phaeosphaeriaceae	Phaeosphaeriaceae sp
OTU100	0	0	0	0	6	9	0	0	Fungi	Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Chaetomium	Chaetomium nigricolor
OTU101	0	0	0	0	37	14	24	5	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Crivellia	Crivellia papaveracea
OTU102	20	19	0	0	0	0	0	0	Fungi	Basidiomycota	Tremellomycetes	Cystofiobasidiales	Cystofiobasidiaceae	Udeniomyces	Udeniomyces pannonicus
OTU103	0	0	0	0	0	0	58	16	Fungi	Basidiomycota	Incertae sedis	Malasseziales	Incertae sedis	Malassezia	Malassezia restricta
OTU104	0	0	0	0	0	0	0	9	Fungi	Basidiomycota	Cystobasidiomycetes	Erythrobasidiales	Incertae sedis	Erythrobasidium	Erythrobasidium sp
OTU105	0	0	9	27	176	34	33	23	Fungi	Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Cryptococcus	Cryptococcus uzbekistanensis
OTU106	810	803	108	113	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Physalacriaceae	Strobilurus	Strobilurus stephanocystis
OTU107	29	13	0	0	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	Cortinarius sp
OTU108	0	0	0	0	33	9	0	0	Fungi	Basidiomycota	Pucciniomycetes	Pucciniales	Phragmidiaceae	Phragmidium	
OTU109	77	52	31	34	31	30	13	46	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Coprinopsis	Coprinopsis radiata
OTU110	10	2	4	2	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Coprinopsis	Coprinopsis radiata
OTU111	53	59	0	0	0	0	0	0	Fungi	Basidiomycota	Tremellomycetes	Cystofiobasidiales	Cystofiobasidiaceae	Udeniomyces	
OTU112	39	1	0	0	0	0	0	0	Fungi	Basidiomycota	Tremellomycetes	Tremellales	Incertae sedis	Cryptococcus	Cryptococcus magnus
OTU113	0	0	0	0	0	0	14	22	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Coprinopsis	Coprinopsis sp
OTU114	0	0	10	2	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Polyporales	Fomitopsidaceae	Antrodia	Antrodia minuta
OTU115	0	0	0	0	14	8	0	0	Fungi	Basidiomycota	Microbotryomycetes	Sporidiobolales	Incertae sedis	Sporobolomyces	Sporobolomyces foliicola
OTU116	16	32	0	0	0	0	0	0	Fungi	Basidiomycota	Agaricostilbomycetes	Agaricostilbales	Kondoaceae	Kondoa	Kondoa aeria
OTU117	0	0	2	21	0	0	0	0	Fungi	Basidiomycota	Tremellomycetes	Tremellales unidentified_	Incertae sedis unidentified_	Cryptococcus uncultured	Cryptococcus neoformans
OTU118	0	0	0	0	2	30	0	0	Fungi	Basidiomycota	Tremellomycetes	Tremellomycetes	Tremellomycetes	unidentified_ Tremellomycetes	Filobasidiales
OTU119	0	0	0	0	0	0	0	9	44	Fungi	Basidiomycota	Microbotryomycetes	Sporidiobolales	Incertae sedis	Sporobolomyces	Sporobolomyces coprosmae
OTU120	11	21	0	0	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Boletales	Amylocorticiaceae	Amylocorticium	Amylocorticium cebennense
OTU121	2	2	8	16	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Coprinellus	Coprinellus heterosetulosus
OTU122	4	15	0	0	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	Trechispora sp
OTU123	18	8	0	0	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	unidentified_Psathyrellaceae	Psathyrellaceae sp
OTU124	54	21	0	0	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Coprinopsis	Coprinopsis sp
OTU125	16	7	0	0	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	unidentified_Agaricomycetes	unidentified_Agaricomycetes	unidentified_Agaricomycetes	Agaricomycetes sp
OTU126	55	62	7	7	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Physalacriaceae	Strobilurus	Strobilurus stephanocystis
OTU127	12	127	90	57	10	12	0	0	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Lycoperdon	Lycoperdon atropurpureum
OTU128	470	482	80	68	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Physalacriaceae	Strobilurus	Strobilurus stephanocystis
OTU129	2274	2758	416	398	0	0	0	1	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Physalacriaceae	Strobilurus	Strobilurus stephanocystis
OTU130	54	47	0	0	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Clitocybe	Clitocybe vermicularis
OTU131	0	0	30	13	0	0	10	8	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Incertae sedis	Panaeolus	
OTU132	37	7	0	0	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Coprinopsis	Coprinopsis sp
OTU133	151	126	0	0	0	0	0	0	Fungi	Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Cryptococcus	Cryptococcus peirensis
OTU134	357	426	24	25	0	0	0	0	Fungi	Basidiomycota	Tremellomycetes	Cystofiobasidiales	Cystofiobasidiaceae	Udeniomyces	Udeniomyces puniceus
OTU135	28	2	0	0	0	0	0	0	Fungi	Basidiomycota	Microbotryomycetes	Sporidiobolales	Incertae sedis	Sporobolomyces	Sporobolomyces salicinus
OTU136	0	0	0	0	0	0	22	81	Fungi	Basidiomycota	Microbotryomycetes	Sporidiobolales	Incertae sedis	Rhodotorula	Rhodotorula sp
OTU137	44	9	0	0	38	10	0	0	Fungi	Basidiomycota	Microbotryomycetes	Sporidiobolales	Incertae sedis	Sporobolomyces	Sporobolomyces coprosmae
OTU138	6	9	0	0	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Hymenochaetales	Hymenochaetaceae	Phellinus	Phellinus igniarius
OTU139	2	2	3	1	3	7	0	0	Fungi	Basidiomycota	Ustilaginomycetes	Ustilaginales			
OTU140	35	87	0	0	0	0	0	0	Fungi	Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae	Sporidiobolus	
OTU141	0	0	0	0	9	5	0	0	Fungi	Basidiomycota	Pucciniomycetes	Pucciniales	Phragmidiaceae	Phragmidium	
OTU142	71	108	97	44	27	22	23	36	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Bovista	Bovista plumbea
OTU143	65	175	9	20	110	11	26	45	Fungi	Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Cryptococcus	Cryptococcus wieringae
OTU144	13	11	0	0	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Polyporales	Fomitopsidaceae	Antrodia	Antrodia sp OM_2012a
OTU145	0	0	11	11	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Agaricales			
OTU146	0	0	26	34	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	unidentified_ Psathyrellaceae	Psathyrellaceae sp
OTU147	58	49	0	0	0	0	0	0	Fungi	Basidiomycota	Tremellomycetes	Tremellales	Incertae sedis	Dioszegia	Dioszegia sp
OTU148	0	0	11	4	0	0	0	0	Fungi	Basidiomycota	Incertae sedis	Malasseziales	Incertae sedis	Malassezia	Malassezia globosa
OTU149	23	20	20	1	0	0	0	0	Fungi	Basidiomycota	Tremellomycetes	Tremellales	unidentified_Tremellales	unidentified_Tremellales	Tremellales sp
OTU150	0	0	62	22	10	48	0	0	Fungi	Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Cryptococcus	Cryptococcus saitoi Cryptococcus
OTU151	94	123	22	20	51	7	70	167	Fungi	Basidiomycota	Tremellomycetes	Tremellales	Incertae sedis	Cryptococcus	Cryptococcus magnus
OTU152	11	14	0	0	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Polyporales	Polyporaceae	Polyporus	Polyporus ciliatus
OTU153	207	160	140	156	91	54	44	124	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Coprinellus	Strobilurus tenacellus
OTU154	646	825	52	130	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Physalacriaceae	Strobilurus	Baeospora myosura
OTU155	27	78	0	0	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Marasmiaceae	Baeospora	
OTU156	30	30	5	23	7	18	0	0	Fungi	Basidiomycota	Agaricomycetes	Russulales	Bondarzewiaceae	Heterobasidion	
OTU157	67	93	6	21	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Russulales	Bondarzewiaceae	Heterobasidion	
OTU158	72	55	86	47	5	33	0	0	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Lycoperdaceae	unidentified_Lycoperdaceae	Lycoperdaceae sp
OTU159	5	13	0	0	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Polyporales	Phanerochaetaceae	Phlebiopsis	Phlebiopsis gigantea
OTU160	25	10	0	0	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Cantharellales	Botryobasidiaceae	Botryobasidium	Botryobasidium sp
OTU161	0	0	21	1	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Coprinellus	Coprinellus callinus
OTU162	27	69	0	0	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Entolomataceae	Entoloma	
OTU163	29	18	0	0	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Tylospora	Tylospora sp
OTU164	18	21	0	0	0	0	0	0	Fungi	Basidiomycota	Agaricomycetes	Polyporales	Meruliaceae	Bjerkandera	Bjerkandera adusta
OTU165	0	0	0	0	42	8	28	25	Fungi	Zygomycota	Incertae sedis	Mucorales	Mucoraceae	Mucor	

Table S2. Spearman's correlation coefficients between the abundances of the organisms across the vertical section.

Organism	Genus	Correlation with	Genus	*rho* value
Plants	*Cupressus*	Plants	*Juniperus*	0.762
		Bacteria	*Friedmanniella*	0.762
			Geodermatophilus	0.786
	Festuca	Plants	*Lolium*	0.952*
		Fungi	*Alternaria*	0.762
			Coprinopsis	0.786
	Fraxinus	Fungi	*Alternaria*	0.810
			Cladosporium	0.714
		Bacteria	*Massilia*	0.929*
	Juniperus	Fungi	*Cladosporium*	0.762
		Bacteria	*Geodermatophilus*	0.857
			Methylobacterium	0.857
	Lolium	Fungi	*Alternaria*	0.762
	Populus	Plants	*Ulmus*	0.714
		Fungi	*Aureobasidium*	0.833
		Bacteria	*Kocuria*	0.762
			Paracoccus	0.857
	Taxus	Plants	*Ulmus*	0.881*
		Fungi	*Aspergillus*	0.786
			Aureobasidium	0.762
			Cladophialophora	0.714
			Penicillium	0.762
		Bacteria	*Kocuria*	0.810
			Paracoccus	0.857
	Ulmus	Fungi	*Aspergillus*	0.857*
			Aureobasidium	0.786
			Cladophialophora	0.738
			Penicillium	0.738
		Bacteria	*Kocuria*	0.738
			Paracoccus	0.833
Fungi	*Alternaria*	Bacteria	*Massilia*	0.786
	Aspergillus	Fungi	*Aureobasidium*	0.857
			Cladophialophora	0.738
			Penicillium	0.857
		Bacteria	*Paracoccus*	0.762
	Aureobasidium	Fungi	*Penicillium*	0.881
		Bacteria	*Paracoccus*	0.786
	Beauveria	Fungi	*Bovista*	0.738
		Bacteria	*Methylobacterium*	0.786
	Blumeria	Fungi	*Epicoccum*	0.833
	Botryotinia	Bacteria	*Craurococcus*	0.714
			Paracoccus	0.714
			Skermanella	0.810
	Cladophialophora	Fungi	*Eurotium*	0.738
			Penicillium	0.857
		Bacteria	*Kocuria*	0.714
			Paracoccus	0.762
	Cladosporium	Bacteria	*Massilia*	0.786
			Methylobacterium	0.762
	Coprinopsis	Fungi	*Cryptococcus*	0.714
	Eurotium	Bacteria	*Rubellimicrobium*	0.810
	Penicillium	Bacteria	*Paracoccus*	0.762
	Talaromyces	Bacteria	*Variovorax*	0.762
Bacteria	*Cellulomonas*	Bacteria	*Janibacter*	0.786
	Friedmanniella	Bacteria	*Streptococcus*	0.833
	Geodermatophilus	Bacteria	*Methylobacterium*	0.810
	Kocuria	Bacteria	*Paracoccus*	0.762
	Polaromonas	Bacteria	*Skermanella*	0.833

* $p \leq 0.05$