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The mycobiont community above the alpine forest line may act as a barrier to seedling establishment of *Betula pubescens*.

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Abstract

Climate change is affecting ecosystems worldwide. The northern hemisphere has experienced significant warming over the last decades, particularly strong in arctic and alpine ecosystems. Forests are predicted to migrate into these ecosystems as temperatures increase, although the predicted migration falls short of what is actually observed. In this study, I test the hypothesis that the soil fungal community above the tree- and forest line may act as a barrier to seedling establishment of *Betula pubescens*. I predict that the soil fungal community may lack the symbionts necessary for the plants to thrive, even if the temperature is suitable. I tested this hypothesis by collecting soil from two alpine areas above the forest line and two areas of semi-natural grasslands with natural populations of *B. pubescens* and compare the growth of seedlings in a common garden experiment. The seedlings were exposed to two different temperatures. After eleven weeks of growth the fungal communities in both soil and roots were analyzed using a metabarcoding approach. I found that *B. pubescens* grown in alpine soils associated with typical alpine mycorrhizal fungi, normally found in the roots of Ericaceous plants. These plants showed impaired growth compared to the plants growing in lowland soil. I found support for the hypothesis that the alpine fungal community may act as a biotic barrier for establishment of *B. pubescens* seedlings above the forest line.

Introduction

The soil microbiome is of major importance to the aboveground biodiversity and ecosystem functions (Wagg et al. 2014). Nearly all plants associate with microorganisms, including fungi, through their roots. Most widespread of these important symbioses are mycorrhiza, a mutualistic plant-fungi association where the fungi provides nutrients to the plant in exchange for photosynthates (Smith and Read 2008). Most land plants depend on some form of mycorrhizal symbiosis. About 2% of all plants form ectomycorrhiza (ECM), being most widespread among trees (van der Heijden et al. 2015, Brundrett and Tedersoo 2018). Although associated with relatively few species, the ECM symbiosis is of high importance since ECM forming forest trees (e.g. in *Pinaceae*, *Betulaceae*, *Fagaceae*) cover a large part of the terrestrial surface (Smith and Read 2008, Brundrett and Tedersoo 2018). Root-associated fungi, and in particular mycorrhizal fungi, has been shown to be important in long-term carbon (C) sequestration and soil C cycling (Clemmensen et al. 2013, Averill et al. 2014, Averill and Hawkes 2016).

The northern hemisphere has experienced significant warming over the last decades (IPCC 2014). This may lead to a shift in geographical and elevational range limits for certain species (including several ECM host plants) and a shift in species composition (Pickles et al. 2012, Bryn and Pothoff 2018,

Song et al. 2018). Modelling based on satellite data show an increase in tree-canopy cover in the northern latitudes and a decrease in short vegetation cover in these same areas (Song et al. 2018). The current observed upper limit of mountain forests in southern Norway is at 1300 meters above sea level (m.a.s.l.), but there are local variability due to current and historical land use (e.g. seasonal farming, Bryn & Pothoff 2018). The changes in the tree and forest line (TFL) can therefore be attributed to both a change in land use (e.g. less intensive seasonal farming) and climate change (e.g. increased temperatures), and separating these effects are difficult (Bryn and Pothoff 2018, Song et al. 2018). Studies on TFL dynamics and vegetation change are often based on remote sensing (Bryn and Pothoff 2018, Song et al. 2018, Rannow 2013) although there are some field studies available (e.g. Dalen and Hofgaard 2005). Using remote sensing, Rannow (2013) documents an increase in elevation for the TFL in 30 out of 43 plots, but notes that the increase falls short of modelled responses based on increased temperature as the only driver. In another study, Dalen and Hofgaard (2005) show an overall stable TLF in south-central Norway, but with regional variability, and note grazing and insect outbreaks as important factors limiting establishment of new trees.

Climatic factors and population dynamics alone are not able to explain the time-lag in TFL elevation as temperatures increase. Studies of the soil microbiota show that there is a

substantial turnover in community composition of both soil biota and vegetation only a short distance above and below the TFL. The plant community above the TFL is dominated by shrubs and graminoids forming either ericoid (ERM) or arbuscular mycorrhiza (AM) (Tonjer et al. preprint). In Norway, the TFL is normally made up of *Betula pubescens* Ehrh. which is an ECM plant (Bryn and Pothoff 2018). *B. pubescens* is an early successional plant mostly established in low competition areas and dependent on its symbionts in order to thrive (Ruotsalainen et al. 2009). The presence of suitable symbionts might affect its ability to establish in areas above the TFL dominated by plants with different mycorrhizal associations. While there are many studies on soil biodiversity and its response to changing conditions (e.g. Singh et al. 2010, Wagg et al. 2014), the effect of a shift in soil microbial communities on the above-ground community, and vice versa, is less well studied (Hagedorn et al. 2019, Pickles et al. 2012). Interactions between vegetation and belowground biota has been proposed as important factors for predicting community response to a changing climate (Alexander et al. 2018, Hagedorn et al 2019). This makes it necessary to look at soil biotic factors that may affect the potential change in TFL, as the temperatures in the northern hemisphere has steadily been rising and increasing the potential range for trees (Pickles et al. 2012, Song et al. 2018). As the TFL expands, the microbial community will also shift along with their symbiotic hosts. These interactions are extremely complex and difficult to untangle (Dickie et al. 2017), but identifying key drivers will enable us to better predict and understand the process of forest expansion.

Interactions between vegetation and soil microorganisms are also important for nutrient cycling and C storage in soils (Clemmensen et al. 2021, Tonjer et al. preprint). The dominant type of mycorrhiza has been shown to be an important factor for long term C storage in soils (Averill et al. 2014, Clemmensen et al. 2015). Clemmensen et al (2021) show that ERM shrub dominated vegetation contain the greatest carbon stocks in a gradient from forest to tundra. Several other studies show similar effects of a high amount of recalcitrant carbon stock related to ERM vegetation types (e.g. Clemmensen et al. 2013, Clemmensen et al 2015, and Hagedorn et al 2019). An increase in temperature also increases the fungal biomass

and the amount of mycelia in alpine soil, and a potential change in mycorrhizal community might affect the turnover rates of mycelium (Smith and Read 2008, Hagenbo et al. 2017). Pickles et al. (2012) also highlight temperature change as a driver of a functional shift in ECM fungal communities. This will have an effect on both CO₂ sequestration and respiration, whether this may result in a net gain or loss of sequestered CO₂ is currently unknown (Pickles et al 2012).

To investigate the effect of fungal community and temperature on the establishment of *B. pubescens* seedlings, a common garden experiment was set up. In this study I used soils from semi-natural grasslands of ecosystems with or without *B. pubescens*. The main questions of this study is as follows:

1. Will the mycobiont community above the TFL act as a biotic barrier to the establishment of *B. pubescens*?
2. How will an increase in temperature affect the fungal community in terms of species composition and biomass?

Based on the research questions I formulated the following two hypothesis:

H1: The growth of *Betula pubescens* seedlings will be limited due to a lack of appropriate symbionts in the alpine soil regardless of temperature.

H2: Fungal biomass will increase in the warming treatment

Materials and methods

Sampling

Sampling was conducted in August 2019 in four semi-natural grasslands sites across south-central Norway (Fig. 1), ranging from a dry continental climate in the eastern parts, to wet coastal climate in the western part (see Meineri et al. 2013; table 1). The eastern sites, Fauske (Lowland Dry) and Ulvehaugen (Alpine Dry), are located in semi-natural grasslands at 589 m.a.s.l., and in the low-alpine zone at 1208 m.a.s.l. respectively. The western sites, Ovstedal (Lowland Wet) and Skjellingahaugen (Alpine Wet), are located in a semi-natural grasslands at 476 m.a.s.l. and in the low-alpine zone at 1133 m.a.s.l. respectively. The mean annual precipitation at each site is 600 mm and 696 mm for the two dry sites, and 2923 mm and 2725 mm for the two wet sites. Permanent temperature and precipitation loggers are installed at the sites. At each site, established plots for vegetation monitoring (Meineri et al.

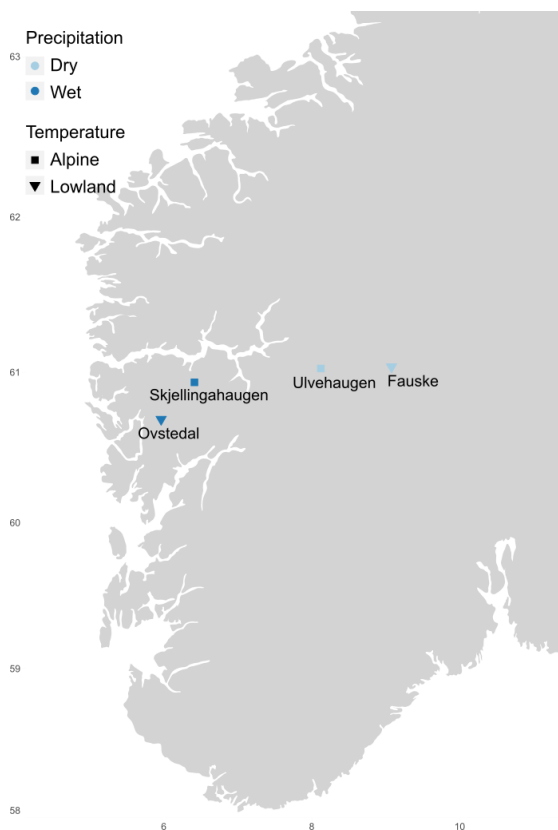


Figure 1: Location of sites where soil samples were taken in southern Norway. Two continental climate locations in light blue (Ulvehaugen and Fauske) and two coastal climate locations in dark blue (Ovstedal and Skjellingahaugen).

2013) were identified, and soil was sampled by removing the top layer of vegetation with a shovel and a small amount (~0.5 kg) of organic soil was collected from the root zone. In order to get a representative collection of the soil community, this was repeated at random spots in each of the sites for a total of about 5 kg soil from each site. The soil was then placed in zip-lock bags and stored in a cooler at 4 °C for up to five days while field work was conducted. The samples were brought back to the laboratory at the University of Oslo, and stored for up to a further seven days at 4 °C while awaiting processing.

Processing of soil and seeds

Soil from each site was homogenized through a 5 mm sieve under a laminar flow hood, removing large root fragments and rocks. Homogenized soil was again stored in zip-lock bags for up to seven days while preparing seeds.

Betula pubescens seeds were obtained from a lowland population in central Norway (Balestrand), through the firm Sagaplant AS. The surface structures of the seeds (wings) were removed by rubbing and the seeds were then surface sterilized for 6 minutes in 5% chlorine and rinsed in distilled water. The cleaned seeds were then distributed on petri-dishes covered with wet carbon-paper (Macherey & NagelCo., Düren, Germany) for germination. The dishes were checked and rewetted every day, removing any seeds that showed signs of fungal infections.

Pots of soil were prepared while the seeds germinated. Sixteen 100 ml plastic pots were filled with approximately 80 ml of homogenized soil from each site, totaling 64 pots. Another fourteen 100 ml pots of the same type were filled with mixed soil, where equal amounts from each of the four sites were mixed. Seedlings were placed in pots as they germinated and within a week all the seedlings were planted. One pot in each category (except the mixed soil pots) were left without a seedling as a negative control.

Experimental Design

A common garden design was chosen for the growth experiment. Fourteen seedlings were planted for each soil type leaving two pots without any seedlings as a control for how the fungal community would look devoid of plant

influence. The pots were split between two incubators (Termaks KB8400, Bergen, Norway), one to represent temperature conditions in the lowland and one to represent alpine temperatures. Both incubators had a day/night cycle of 16 h/8 h with light on during the day and darkness during the night. Temperatures were chosen based on data from the loggers on the sites (Meineri et al. 2013), using average temperatures for the growth seasons in the alpine and lowland sites, 14 °C/6 °C for the alpine incubator and 18 °C/10 °C for the lowland incubator. All pots were watered with approximately 20ml distilled water three days a week (Monday, Wednesday and Friday). Weeds were regularly pulled out in order to reduce competition effects from other plants in relation to root colonization. Due to issues with the incubators not cooling properly, all the plants experienced three periods (1-2 days) of higher temperatures (up to 30 °C) over the 11 weeks. I argue that this is within the normal fluctuations that the seedlings would experience in nature and thus not having a major negative impact on the execution of the growth experiment. The planned duration of the experiment was 12 weeks, but after 11 weeks some of the plants were showing signs of withering and the experiment was therefore ended one week early.

Processing of plants

The plants were harvested after 11 weeks of the planned 12 weeks of growth, to avoid the establishment of saprotrophic fungi and decomposition of dying roots. The plants, with the entire root system attached, were carefully extracted from the soil in a laminar flow hood. The roots were then further cleaned in water under a dissecting microscope to remove as much of the soil particles as possible. Once cleaned, the roots were weighed, photographed and stored in a CTAB buffer in 2 ml Eppendorf tubes at -20 °C to await further processing. The shoots were weighed and split into two 2 ml Eppendorf tubes. These were then freeze-dried using a Labconco FreeZone 2.5 freeze dryer (Labconco corporation, Kansas City, MO, USA) for at least 24 h and stored at -20 °C before C/N/P analysis (same as for soil, see below).

Processing and chemical analysis of soil

From each pot of soil, one 50 ml Falcon tube was filled and freeze dried for at least 36 h. With five ceramic beads added in each Falcon tube, the freeze-dried soil samples were homogenized and powdered using FastPrep-24 beadbeater (M.P. Biomedicals, CA, USA) at 4 M/S for 40 seconds (two times for each tube). From each sample, two grams of soil was transferred into a 15 ml Falcon tube with 10 ml CTAB buffer and mixed well. From this soil/CTAB sludge, 600 µl was transferred into a 2 ml Eppendorf tube for DNA extraction.

From each powdered soil sample, two grams was transferred into a 15 ml Falcon tube for later pH analysis, and a further two 2 ml Eppendorf tubes were filled with 0.5 grams of soil for C/N/P and ergosterol analysis. All samples were stored at -20 °C while awaiting further analysis.

For pH measurement, 0.5g of soil of freeze-dried soil was diluted with 5 ml of dH₂O for at least one hour. pH was then measured using a LAQUA-TWIN-11 pH Meter (Horiba Scientific, Kyoto, Japan) following the manufacturers protocol.

Soil C and N concentration was determined by a flash elemental analyzer (Thermo Finnigan Flash EA 1112, ThermoFisher Scientific, Waltham, USA). Soil P concentration was determined by a segmented flow analyzer (SEAL AA3 HR AutoAnalyse, SEAL Analytical Ltd, Southampton, UK), all C/N/P analyses done at UiO.

Total soil ergosterol concentrations (mg g⁻¹ DW) was measured using a modified protocol of Davey et al. (2009). Approximately 200 mg of each soil sample was mixed with 7 ml 3M KOH in MeOH, vortexed and sonicated in a 70 °C ultrasonic water bath in darkness for 90 min. The samples were then centrifuged at approximately 16.400 g for 15 min and the supernatants mixed with 2 ml purified water in new tubes. Then 5 ml hexane was added and vortexed. The hexane phase was collected after the two phases divided. The hexane step was repeated twice. Both extracts were collected in one vial and evaporated to dryness, before being dissolved in 500 µl MeOH. The extracts were analysed for total ergosterol content using HPLC (Agilent Series 1200, Agilent Technologies, Waldbronn, Germany). Ergosterol was separated using a reversed

phase ODS ultrasphere column (250 mm × 4.6 mm; particle size 5 µm), with MeOH as the mobile phase. Ergosterol absorption was detected at 280 nm and identified by co-chromatography at a commercial standard (Sigma, St. Louis, USA). Ergosterol measurements were done at NMBU (Norges miljø- og biovitenskapelige Universitet).

Molecular methods

Two 3 mm tungsten carbide beads were added to each 2 ml Eppendorf tube containing roots in 600 µl CTAB, or 600 µl soil/CTAB sludge (both roots and soil were processed using the same protocol) and these were then grinded using TissueLyser II (Qiagen, Hilden, Germany) for one min at 25 Hz, two times for each tube. After grinding the roots, the samples were incubated for 30 minutes at 65 °C. Once cooled to room temperature, 600 µl chloroform was added to each tube and the solution was mixed with a vortex. The tubes were then centrifuged at 13 200 rpm in order for the layers to separate. 400 µl of the upper layer was transferred over to tubes containing 400 µl isopropanol (taken straight out of a -20 °C freezer). These tubes were inverted several times and the mixture was allowed to sit for 1 hour or more for the DNA to precipitate. These tubes were then centrifuged at 13 000 g for 10 minutes in order to make a compact DNA pellet. The supernatant was discarded and the DNA was eluted in 200 µl EZNA elution buffer. Cleanup of the DNA pellet was done with E.Z.N.A.® Soil DNA Kit, following the manufacturer's protocol (Omega Bio-tek, Norcross, USA). Each session of extraction consisted of 23 samples plus one extraction negative.

Technical replicates and mock communities were introduced in the PCR step for quality control. Due to limited space, the extraction negatives were amplified separately and checked for DNA using 1% agarose gel. The ITS1 region of rDNA was targeted using ITS-1F (forward) and ITS1 (reverse) primers (White et al. 1990, Gardes and Bruns 1993). All primers were tagged with molecular identifiers for retrieval in downstream bioinformatics. Each PCR reaction consisted of 1 µl DNA template and 24 µl master mix: 15.7 µl milli-Q H₂O, 2.5 µl GoldBuffer, 2.5 µl GoldMgCl, 0.2 µl 25nmol dNTP, 1 µl 20 ng/ml BSA, 0.125 µl AmpliTaq Gold, 1 µl 10 µmol forward primer and 1 µl 10 µmol reverse primer. Ten samples amplified

poorly after two tries and were then amplified using the same mastermix but with 3 µl DNA template instead of 1 µl. PCR reactions for ITS1 were run with initial denaturation at 95 °C for 5 min, followed by 32 cycles of denaturation at 95 °C for 30 sec, primer annealing at 55 °C for 30 sec and elongation at 72 °C for 1 min. An elongation step was included after the cycles at 72 °C for 7 min, before cooling down to 4 °C. Two PCR negatives, one mock community and three technical replicates were done on each plate of 96 samples. Each PCR product was controlled for positive amplification with gel electrophoresis using a 1 % agarose gel, before individual clean-up and purification of the amplicons with ZR-96 DNA Clean & Concentrator-5 kit (Zymo Research, California, USA). DNA concentrations were measured using QUBIT and pooled to equimolar concentrations into two pools of 30 µl with at least 500 ng total DNA in each. Each pool was cleaned and concentrated with DNA Clean & Concentrator-5 (Zymo Research, California, USA). The two pools were sequenced using Illumina MiSeq paired-end sequencing at Fasteris (Geneva, Switzerland).

Bioinformatics

All bioinformatics was performed on the SAGA computer cluster located at NTNU Trondheim. The paired-end forward and reverse sequences were demultiplexed with simultaneous primer removals using *CUTADAPT* (Martin, 2011), allowing no mismatch with primer tags and a minimum overlap between forward and reverse primer of 26bp. Minimum length of 100bp per sequence after matching was set and no indels permitted. Further processing was done using the *DADA2* pipeline (Callahan et al. 2016) in the R statistical environment (R Core Team (2020)) for dereplication and error correction. To account for length variability in ITS1 *BAND_SIZE* was set to 32 and *maxEE=c(2,2)* allowing two errors in the overlapping sequences for each direction. The forward and reverse sequences were then merged. Minimum 50 nucleotide overlap was set in order to merge sequences. This was used to construct an amplicon sequence variant (ASV) table of the ITS1 sequences that was checked for chimeras which were removed. The ASVs were further clustered into operational taxonomic units (OUTs) at 97% similarity using *VSEARCH* (Rognes et al. 2016) due to high interspecific variability in ITS1. Finally, *LULU*

post clustering curation (Frøslev et al. 2017) with default setting was performed on the ASV table to correct for over-splitting of OTUs.

Taxonomic annotation was performed by blasting the ITS1 sequences against UNITE (Nilsson et al 2018). In order to make sure each OTU had a meaningful taxonomy the search was set to return the top five hits for each OTU and a threshold for query coverage was set to 80%. Of the 813 OTUs, 679 were returned with a taxonomic annotation and the remaining 134 OTUs without any hits were removed from the data. These hits were then further curated in R (R Core Team (2020)). For two of the OTU's all the top five hits from UNITE were unidentified and the taxonomic assignment was kept as "Fungi_sp.". For the remaining 677 the best hit with a known taxonomic identity (i.e. the first hit that did not return "fungi_sp.") was chosen based on identity score unless there was ambiguity at a high taxonomic level. Nine OTUs had ambiguity at the Phylum level and these were curated manually.

Three samples were lost in the quality-filtering steps, two of these were PCR negatives and the third was a real sample (sample id: 6T3). A further seventeen samples were dropped during rarefying due to low number of reads (< 1000 total reads), where two of these were PCR negatives. Two samples containing mock communities were also removed before rarefying. The remaining samples were rarefied to the lowest sample read number (2807 reads) using the *rrarefy* function in the R package *vegan* (Oksanen et al. 2020). After this, a functional annotation was done by matching the taxonomic output against the FUNGuild database (Nguyen et al. 2016) using the python scripts provided on the FUNGuild github pages: <https://github.com/UMNFuN/FUNGuild>.

These functional annotations were further curated into categories as follows: "Ectomycorrhizal", "Root Associated Fungi", "Arbuscular Mycorrhizal", "Plant Pathogen", "Animal Pathogen", "Saprotroph", "Endophyte", "Lichen", "Chytrid", "Rozellomycota", "Yeast". OTUs where the taxonomic assignment was not of high enough certainty (e.g Helotiales_sp) or the taxon has an uncertain ecology (e.g Archaeorhizomycetes) were placed in "Undefined. The final rarefied and curated OTU table consisted of 138 samples with 562 OTUs

with taxonomic and functional assignment (Supplementary Table 1).

Statistical analysis

All statistical analysis were done in the R 4.0.3 environment (R Core Team (2020)). I used the packages used are *vegan* (Oksanen et al. 2020) for rarefaction, ordination and diversity measures, and *phyloseq* (McHurdie and Holmes 2013) for handling of taxonomy tables. I used *tidyverse* (Wickham et al. 2019) for graphical presentation. All variables used for statistical analysis were zero-skewness transformed and standardised.

Species composition was analysed with global non-metric multidimensional scaling using the untransformed rarefied read numbers (GNMDS) with settings recommended in Liu et al. (2008). Further visualization of the species composition was done using the *tax_glom* function in *phyloseq* to gather all the OTUs at the order and guild levels and then I used *aggregate()* to sum the number of reads for each order. These were ordered in a descending manner and the top 15 were kept while all the rest were collapsed into "Other" for easier visualization of bar graphs.

To analyse how the seedlings responded to the different soil-communities the content of limiting nutrients (N and P), partly supplied by root-symbionts, in the shoot, as well as the weight of seedling at the end of the experiment were used as response variables. The final list of response variables are: mgN in shoot, mgP in shoot and total fresh-weight of the seedling. In addition, change of C and ergosterol content in the soil was chosen as soil responses. These responses were modelled using forward model selection with a decrease in BIC ($k = \log(n)$) as a criterion for adding complexity to the model using the *addterm()* function from the package MASS (Venables and Ripley 2002). Models were then cross-validated with *caret* (Kuhn 2008) using the leave-one-out method to test for model accuracy. Tukey Honest Significant Difference (Tukey HSD) tests were used in addition to analysis of variance (ANOVA) to test for differences in response between soil types and temperature treatments.

Results

Fungal community in soil

The ordinations show clearly differentiated fungal communities between the soil types and no effect within groups of temperature treatments (Fig. 2A). The proportion of reads belonging to each order showed only small differences between the temperature treatments within the soil types (Fig. 3). Ascomycetes dominated the alpine soils, while the lowland soils were more heterogeneous (Fig. 3). The dominant group in the soil samples were Archaeorhizomycetales, 57% of the rarefied reads from the soil samples belonged to this group, represented with 41 OTUs (Table S2). In the alpine and mixed soils, Archaeorhizomycetales had a higher relative abundance than all the other groups combined. Moreover, in the alpine dry soils more than 90% of the reads belonged to this group (Fig. 3). Mortierellales was the second largest group, with 13% of the rarefied reads across all soil samples. This order in Mucoromycotina were present in a similar proportions in all pots except the lowland dry soil, where it was the second largest order. 7% of the rarefied reads belonged to an order of basidiomycete yeasts, Filobasidiales, represented with 3 OTUs. Neither of these groups had any notable presence in the roots. Only 3.5% and 2.8% of the rarefied reads belonged to Agaricales and Helotiales respectively, in contrast to these groups' dominance in the roots (Fig. 3). A full summary of all orders are presented in supplementary table S2.

Fungal community in roots

The ordinations show that the fungal community in the roots differ between soil types, but show no clear effect of temperature (Fig. 2B). Temperature had some effects on the relative proportion at the order level. In general, the basidiomycetes were most abundant in the warm treatments, although the lowland dry roots deviate from this. The most marked difference between temperature treatments was found in the roots from the mixed soil. Ascomycetes dominated in the mixed+cold roots while basidiomycetes, mainly Telephorales, dominated in the mixed+warm roots. The plants in the lowland soils and the mixed+warm treatment also had a higher abundance of ECM fungi than the plants from the alpine soils and mixed+cold (Fig. S1). The

plants in the alpine soils have fewer ECM fungi and a higher proportion of saprotrophs, endophytes and "Unidentified" (Fig. 3, Fig. S1). Root-associated-Helotiales (48% of the rarefied reads) were present in all the different soil types and were dominant in roots from alpine soils and in the mixed+cold treatment. The most abundant Helotiales OTUs in roots from the alpine soils were *Phialocephala sp.* (OTUs 200 and 436) and *Helotiales sp.*, represented with 13 OTUs, of which only 1 was shared between both alpine dry and wet soils (OTU444). Three

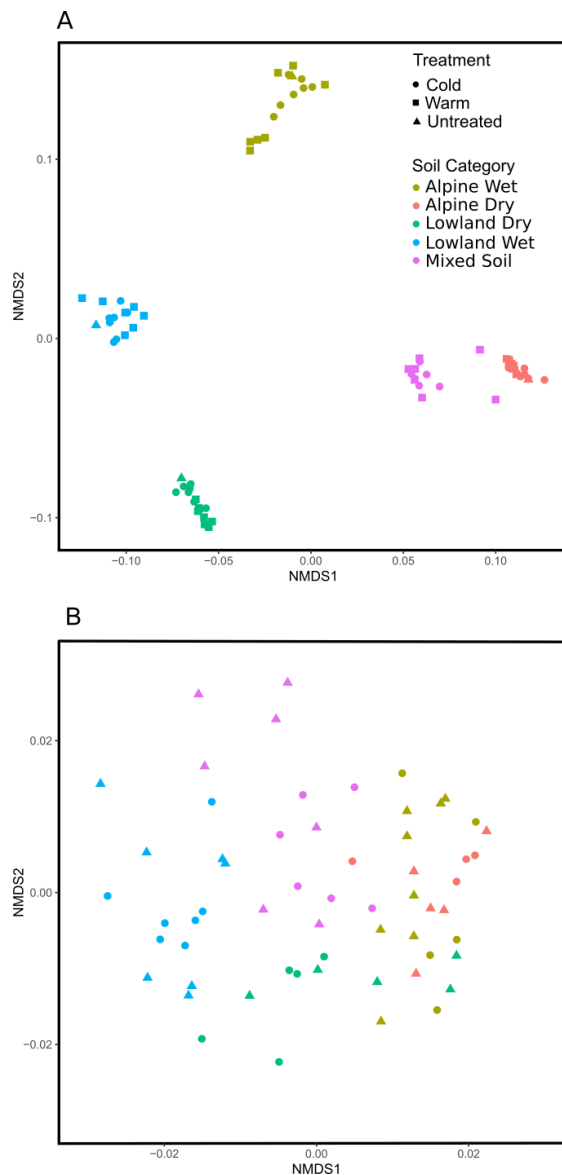


Figure 2: GNMDS ordination of the fungal community from soil in pots containing *Betula pubescens* (A) and seedling roots (B) after three months of temperature treatment. Soil categories are shown with separate colors and treatments are shown with separate symbols

OTUs with affinity towards *Pezoloma ericae* was represented in the alpine dry soil (OTUs 76, 67 and 19), and was absent from the roots in alpine wet soils. *Acephala sp.* was present in both dry and wet alpine soils with one OTU (OTU404). Some saprotrophic Helotiales were also present in the roots (e.g. *Hyaloschypha sp.*, OTUs 85, 79 and 27). Some important basidiomycete OTUs in the roots from alpine soils had affinity towards *Telephora terrestris* Ehrh. :Fr (OTU153, only in alpine wet), *Hymenogaster sp.* (OTU6), *Russula sp.* (OTU102, only in alpine dry), *Serendipita sp.* (OTU373) and *Sebacinales sp.* (OTU353). The two OTUs with affinity towards *Sebacinales* and *Serendipita* were most common in alpine wet soils. Pots with lowland soil contained more basidiomycetes in the roots (Fig 3). Agaricales was the largest basidiomycete order (26% of the rarefied reads) and 44% of the Agaricales reads belong to just one OTU (OTU29) with affinity to the ECM fungi *Naucoria bohemica* (synonym to *Alnicola bohemica* (Velen) Kühner). Other ECM fungi in the lowland roots include *Laccaria* (OTUs 182, 208), *T. terrestris* (OTU153), *Hymenogaster sp.* (OTUs 33, 141, 254, 380). Ascomycete genera in the lowland roots include *Phialocephala sp.* (OTU200),

Acephala sp. (OTU404), several *Helotiales sp.* and *Cenococcum geophilum* Fr. (OTU248).

Diversity

The observed fungal richness differed markedly between the soil and roots (Fig. 4). Highest richness was seen in the lowland wet and the mixed soils, with no marked difference between temperature treatments. The soil fungal richness was lowest in the alpine dry soils, and this was the only soil type to deviate significantly from every other soil type (Tukey HSD, $p < 0.05$, Table S1). Moreover, the lowland wet soils, being more intermediate in richness, differed significantly from the lowland dry and from the mixed soils ($p < 0.05$). All other pairwise comparisons were non-significant. For the root fungal richness, the only significant pairwise differences were between lowland wet and both alpine dry and alpine wet (TukeyHSD, $p < 0.05$, Table S3). There were no significant differences between temperature treatments on the richness, neither in the soil, nor in the roots (Table S3). The beta diversity within each category was higher in the roots (Fig. 4). In some cases (mixed soil plants) the beta diversity index was close to 1, meaning that

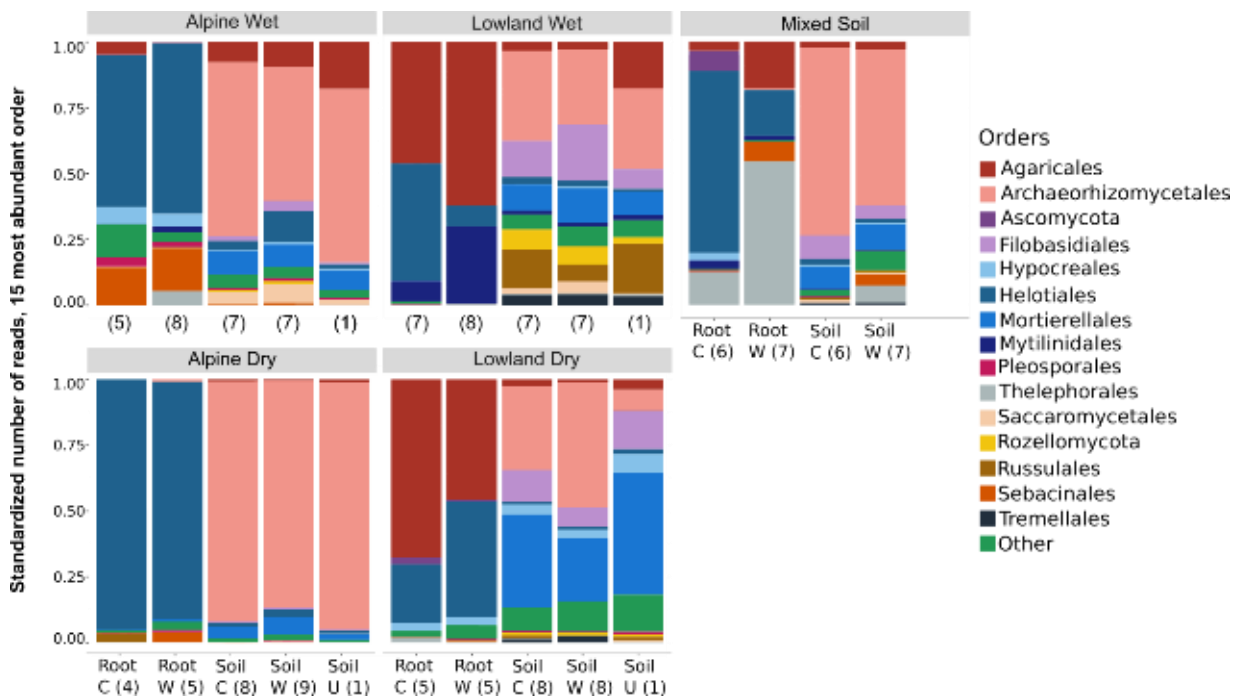


Figure 3: Bargraph of the relative abundance of the 15 most abundant fungal orders found in *Betula pubescens* roots and soil samples from their pots after three months of experimental temperature treatment. Roots and soil from the cold (C) and warm (W) treatment are placed next to each other within each soil category in addition to one untreated soil sample (U) taken from the homogenized soil from each location before the experiment started. Number of samples in parenthesis.

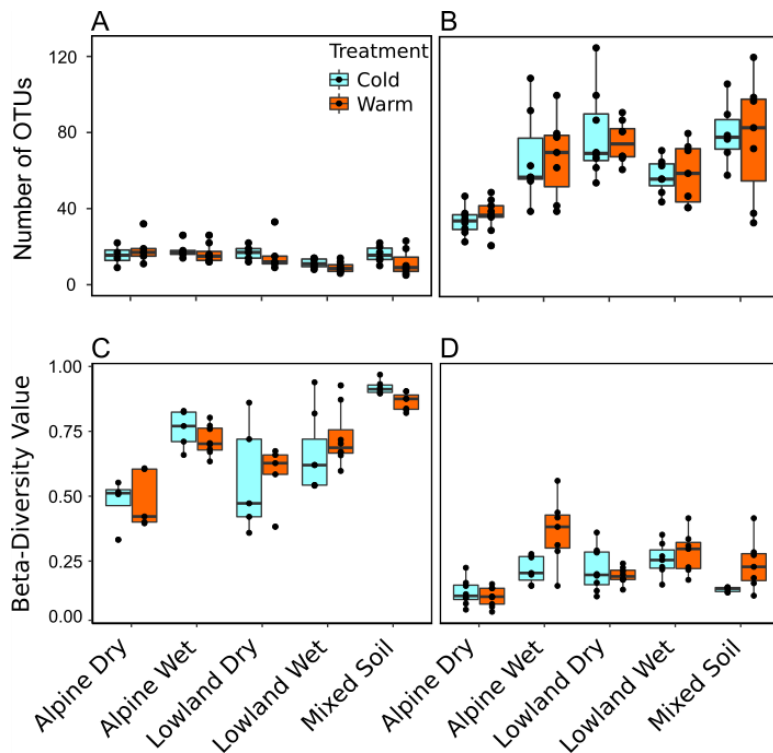


Figure 4: Boxplot of richness (number of OTUs) and diversity in an experimental set up using *Betula pubescens* seedlings under different temperature treatments. A) Observed richness in roots, B) Observed richness in soil, C) Beta-diversity values of roots, D) Beta-diversity values in soil. Different treatments are shown with different colors, blue for cold and orange for warm. Each individual sample is represented with a dot.

there are few OTUs common across the roots. The compositional heterogeneity in root-communities was also evident from the ordination where the roots have an extensive spread within soil types compared to the soil communities (Fig. 2).

Plant responses

Plant weight and content of growth limiting nutrients (N & P), partly supplied through the mycorrhizal network to the shoots was chosen to measure how the plants responded to the different soil communities. Temperature influenced plant growth, with plants from the warm treatment being several times larger than in the cold treatment (Fig. 5). There was also a clear effect of soil type. Both soil type, temperature treatment and an interaction effect between these two were significant for all three responses (ANOVA $p < 0.05$, Table S4). The weight of the seedlings was negatively related to the proportion of Helotiales in the roots ($b = -0.27$, $p < 0.001$) and Mortierellales in soil ($b = -0.39$, $p < 0.001$), and positively correlated with Agaricales in the roots ($b = 0.1$, $p = 0.051$)

(Adjusted $R^2 = 0.82$, Table 1). N and P content largely followed the weight of the plants, with some deviation in the N content of lowland wet+warm plants (Fig. 5). Linear regression models revealed some potential drivers for the difference in nutrient content. Both soil type and temperature significantly related to the N content, increasing in the lowland and mixed soil and in the warm temperature treatment. Higher proportion of Helotiales ($b = -0.20$, $p = 0.004$) in the roots, and Hypocreales ($b = -0.25$, $p = 0.013$) in the soil related negatively to N content, while increased proportion of Agaricales in the roots positively related to N content ($b = 0.20$, $p = 0.014$) (Adjusted $R^2 = 0.83$, Table 1).

Soil type and temperature treatment was significantly related to seedling P content (ANOVA $p < 0.05$, Table S4). The proportion of Helotiales in the roots had a negative relation to P content ($b = -0.13$, $p = 0.08$), and the proportion of Agaricales in the roots positively correlated with seedling P content ($b = 0.17$, $p = 0.09$). None of these were significant (at $p < 0.05$), but they were included in the best model using the BIC criterion for adding variables compared to a model with just soil and temperature as explanatory variables (Adjusted $R^2 = 0.58$, Table 1).

Fungal and soil responses

The fungal response was measured as a change in soil ergosterol content (Fig. 6), used as an approximation for fungal biomass. Change in ergosterol content differed significantly between soil types and temperature treatments (ANOVA, Table S4). Significant differences in treatment combinations were shown for most pairs, except for the different temperature treatments in Alpine Wet, between Alpine Dry+Warm, Lowland Wet+Warm and between Lowland Wet and Mixed Soil at both treatments (Tukey HSD, Table S3). The best linear regression model for change in ergosterol content showed a positive relation with the proportion of

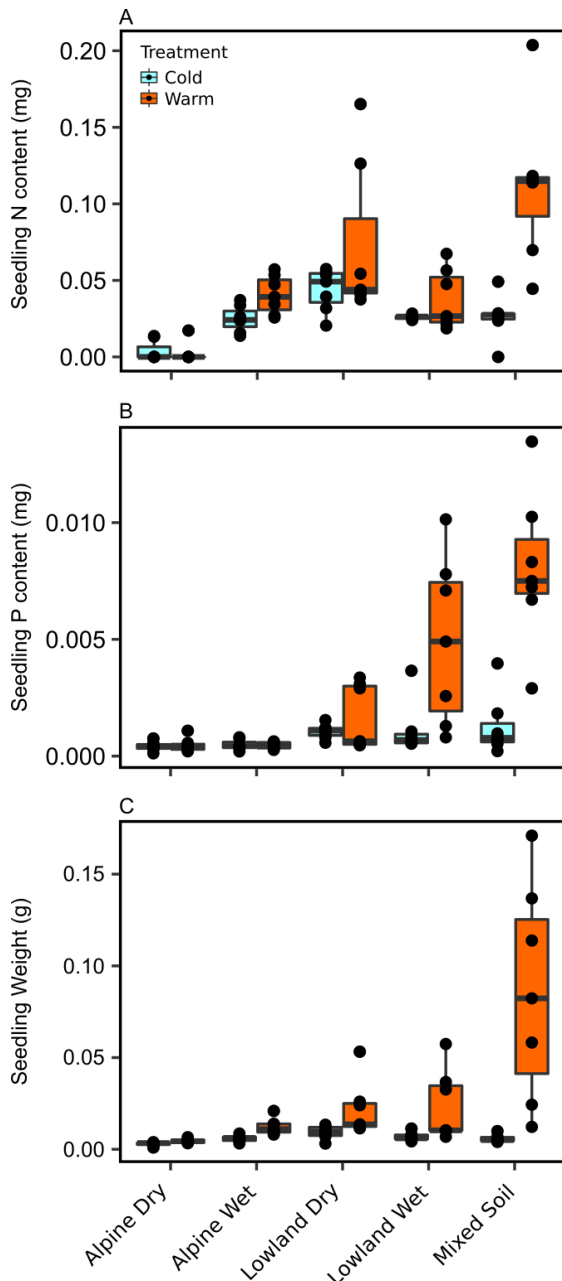


Figure 5: Plant responses of *Betula pubescens* seedlings after three months of experimental temperature treatment. A) Nitrogen content in seedlings measured in mg, B) Phosphorus content in seedlings measured in mg, C) Freshweight of seedlings measured in g. Different treatments are shown in different colors, blue for cold and orange for warm. Individual plants are represented by dots.

Archaeorhizomycetales ($b = 0.52$, $p < 0.001$) and Russulales ($b = 0.29$, $p = 0.061$), together with a non-significant increase in soil C content ($b = 0.14$, $p = 0.086$) (Adjusted $R^2 = 0.82$, Table 2). On the contrary, the proportion of Helotiales related negatively to the change in ergosterol content ($b = -0.42$, $p = 0.004$). Fungal richness

in the roots also negatively correlated with the soil ergosterol content ($b = -0.22$, $p = 0.02$).

Changes in soil C content was significantly different between both soil type and temperature treatment (Fig. 6, Table S3/S4). In the best model soil C change is positively correlated with N change ($b = 0.64$, $p < 0.001$), and the proportions of Helotiales in the roots ($b = 0.14$, $p = 0.005$) and Hypocreales in soil ($b = 0.24$, $p = 0.002$). Richness in soil ($b = -0.23$, $p = 0.003$) and pH ($b = -0.30$, $p = 0.003$) were negatively correlated with soil C change (Table S2). The best regression model also includes a non-significant negative effect of proportion of Telephorales in soil ($b = -0.12$, $p = 0.056$) (Adjusted $R^2 = 0.90$, Table 2).

Discussion

The aim of this study was to investigate if the soil fungal community in the low-alpine zone could be a barrier to the establishment of seedlings above the tree line. In order to do this, I planted seedlings of *B. pubescens* in soil from two different alpine environments and cultivated the seedlings under two different temperature treatments. Considering that *B. pubescens* is dependent on ECM fungi to survive (Ruotsalainen et al. 2009), the expectation was that the fungal community above the TFL would lack the appropriate symbionts for the seedlings to establish and thrive.

Effect of fungal community on seedlings

In the alpine soils, the seedlings were mostly colonized by ascomycetes of the order Helotiales. Helotiales is an ecologically diverse order commonly found in arctic and alpine environments, often forming ericoid mycorrhiza (*Pezoloma ericae* complex). They may also appear as root endophytes (*Phialocephala* sp.) or as ECM (*Acephala* sp.) (Smith and Read 2008, Tedersoo et al. 2009, Walker et al. 2011). Previous studies of alpine fungal diversity show that there are several other ECM genera normally occurring in alpine environments (Gardes and Dahlberg 1996, Thoen et al. 2019, Tonjer et al. preprint), but these were mostly absent from the roots in this study.

The seedlings in the alpine wet category grew better than seedlings in the alpine dry category. The main difference in fungal community between these two types of soil was the occurrence of Sebaciniales in the roots of the

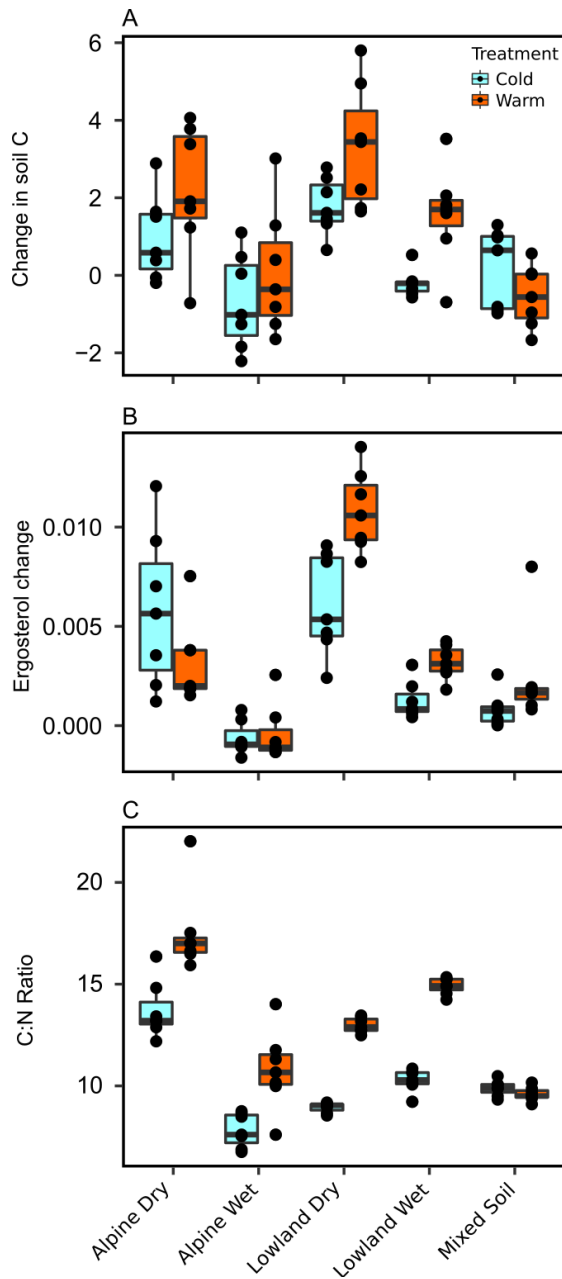


Figure 6: Soil responses after 3 months of experimental temperature treatment. A) Change in soil carbon, measured as change in %C content in soil, B) Ergosterol change measured as mg/g soil, C) C:N ratio. Different treatments are shown in different colors, blue for cold and orange for warm. Individual samples represented as dots.

alpine wet seedlings. Sebaciniales has been reported as a ubiquitous root symbiont, with species forming either ECM or ERM on a wide range of hosts (Selosse et al 2007, Weiss et al. 2016). Thus, the Sebaciniales might act as beneficial symbionts in the wet alpine soils, which could help explain the seedlings' better growth in these pots.

The fungal communities found in the roots of *B. pubescens* from the alpine soils in this study closely resembles the fungal communities found in ericaceous roots from studies of alpine ericoid plants (Kjøller et al. 2009, Walker et al. 2011). The plants that were investigated by Kjøller et al (2010) and Walker et al (2011) include *Empetrum nigrum* L. and *Vaccinium vitis-idea* L., and these were abundant at the alpine sites used in this study (personal observation). The typical ericoid-associated Helotiales found in alpine and tundra heathlands show little to no host specificity (Walker et al. 2011, Kjøller et al. 2010). It is therefore likely that these are opportunistic colonizers of roots and as such may infect the roots of *B. pubescens*. Walker et al (2011) suggest that different fungal strains from Helotiales may form either ERM or ECM depending on host. ERM fungi are efficient in taking up organically bound N in the nutrient poor alpine environments (Smith and Read 2008), but they may be less efficient in transferring this to an unfamiliar host. This may explain the trend shown in the models where abundance of Helotiales in roots showed a negative correlation with content of N and P in seedlings, as well as a negative impact on seedling size.

The effect of temperature on the root fungal community was strongest in the mixed soils. Fungi from Thelephorales dominate the roots in the warm treatment. This is faster growing fungi with more extensive mycelium than what is common in Helotiales (Smith and Read 2008). All the largest plants had *Thelephorales sp.* as the root symbiont with highest proportion of reads. It is possible that the increased plant productivity due to the higher temperatures has given the symbionts from Thelephorales a competitive advantage over the slower growing Helotiales. This may have allowed the faster growing Thelephorales to take over the root system, leading to a positive feedback on both plant and fungal growth. This can explain the extreme differences in plant size from the mixed+warm soil type. This is in line with what Pickles et al (2012) discuss, where they predict an increase in temperature could drive functional shifts in ECM community composition.

Table 1: Model coefficients and p-values for plant response regression models. . Standard errors in parenthesis next to coefficients.

| Variables | Coefficient: mgN | P-value: mgN | Coefficient: mgP | P-value: mgP | Coefficient: weight | P-value: weight |
|---------------------|---------------------|-----------------|---------------------|-----------------|------------------------|--------------------|
| Intercept | 0.154 (0.076) | 0.050 | 0.543 (0.090) | 0.000 | 0.850 (0.067) | 0.000 |
| SoilAlpine Wet | 0.469 (0.068) | 0.000 | 0.028 (0.063) | 0.660 | 0.136 (0.037) | 0.001 |
| SoilLowland Dry | 0.517 (0.110) | 0.000 | -0.013 (0.097) | 0.891 | 0.206 (0.069) | 0.005 |
| SoilLowland Wet | 0.201 (0.090) | 0.031 | 0.050 (0.100) | 0.617 | 0.028 (0.058) | 0.633 |
| SoilMixed Soil | 0.543 (0.072) | 0.000 | 0.244 (0.073) | 0.002 | 0.191 (0.043) | 0.000 |
| TempWarm | 0.142 (0.033) | 0.000 | 0.083 (0.038) | 0.032 | 0.141 (0.021) | 0.000 |
| Helotiales_root | -0.197 (0.064) | 0.004 | -0.134 (0.075) | 0.080 | -0.273 (0.043) | 0.000 |
| Agaricales_root | 0.202 (0.078) | 0.014 | 0.171 (0.092) | 0.071 | 0.106 (0.052) | 0.051 |
| Hypocreales_soil | -0.252 (0.097) | 0.013 | NA | NA | NA | NA |
| Mortierellales_soil | NA | NA | NA | NA | -0.397 (0.103) | 0.000 |

Fungal community and ergosterol content in soil

The order Archaeorhizomycetales dominate the alpine and in the mixed soils, with a slight increase in proportion of reads in the cold treatment. This group of fungi belong to the subphylum Taphrinomycotina in Ascomycota and often found associated with roots in soil samples from a wide range of habitats (Rosling et al. 2011). Archaeorhizomycetales are not considered symbiotic, but rather a part of the rhizosphere where they coexist with symbiotic fungi in the soil and even inside root tips (Rosling et al. 2011), although very little is known about their ecology. Their dominance in the soil may be connected to their seasonality, considering all the sampling was done in late summer. Archaeorhizomycetales are reported to be dominant during the summer and nearly absent at other times of the year in a tundra ecosystem (Schadt et al. 2003).

There were no major changes in the soil fungal community between the temperature treatments. There were, however, an effect of temperature on soil ergosterol content. The increase in ergosterol content is largest in the dry soils regardless of temperature. The only edaphic variable related to an increase in ergosterol is the amount of C in the soil, which was positively correlated, although not significant. The increased amount of C in the soils may be related to plant productivity, as the warm temperature treatments has a positive effect as well.

The proportion of Archaeorhizomycetales was the best explanatory variable for an increase in ergosterol, with a relatively high positive correlation. The proportion of Helotiales in the soil however, has a negative correlation to ergosterol change. It seems that Archaeorhizomycetales thrived in the pots and displaced other groups of soil inhabiting fungi. Rosling et al. (2011) describe Archaeorhizomycetales as being affiliated with root inhabiting fungi and partly dependent on root-derived C compounds, but also exhibiting decomposing abilities. It may be that in a short-term experimental set-up like this, Archaeorhizomycetales gains a competitive advantage over the root-associated fungi that may be more dependent on root-derived C. The alpine soils differ in the change in ergosterol content, with the alpine wet soils not changing and the alpine dry soils showing an increase in both cold and warm treatments. In the latter soil type, this change is unrelated to the plant growth, as the plants in this soil type barely increased in size throughout the experiment. The change was likely related to decomposition of organic material already present in the soil. Even in the lowland and mixed soils where the seedling grew better, there is only a slight change, if any, in the ergosterol content. However, there is not enough support in these results to discard the null hypothesis for H2, an increase in fungal biomass cannot be explained by increased temperatures alone.

Table 2: Model coefficients and p-values for the soil ergosterol and soil carbon change models. Standard errors in parenthesis next to coefficients.

| Variables | Coefficient: ErgosterolChange | P-value: ErgosterolChange | Coefficient: CarbonChange | P-value: CarbonChange |
|----------------------------|----------------------------------|------------------------------|------------------------------|--------------------------|
| Intercept | 0.222(0.166) | 0.188 | 0.133(0.074) | 0.079 |
| SoilAlpine Wet | -0.051(0.081) | 0.532 | -0.001(0.067) | 0.986 |
| SoilLowland Dry | 0.399(0.089) | 0.000 | 0.065(0.072) | 0.373 |
| SoilLowland Wet | 0.065(0.096) | 0.500 | 0.093(0.053) | 0.084 |
| SoilMixed Soil | -0.059(0.062) | 0.345 | -0.067(0.058) | 0.254 |
| TempWarm | 0.138(0.037) | 0.001 | 0.192(0.023) | 0.000 |
| percC_Soil | 0.194(0.110) | 0.086 | NA | NA |
| Helotiales_soil | -0.425(0.138) | 0.004 | NA | NA |
| Archaeorhizomycetales_soil | 0.521(0.129) | 0.000 | NA | NA |
| N_OTU_root | -0.219(0.090) | 0.020 | NA | NA |
| Russulales_soil | 0.209(0.109) | 0.061 | NA | NA |
| N_Change | NA | NA | 0.640(0.052) | 0.000 |
| Telephorales_soil | NA | NA | -0.116(0.059) | 0.056 |
| pH | NA | NA | -0.299(0.090) | 0.002 |
| Helotiales_root | NA | NA | 0.143(0.048) | 0.005 |
| Hypocreales_soil | NA | NA | 0.235(0.067) | 0.002 |
| N_OTU_Soil | NA | NA | -0.227(0.070) | 0.003 |

Soil carbon and nitrogen

Temperature did have an effect on soil C. In all the soil types, excluding the mixed soils, there was an increase in C content and a higher C:N ratio in the warm treatment. The model for C change showed a positive relationship between root-associated Helotiales and C content. These fungi are often characterized as important for C storage in alpine systems (Clemmensen et al. 2021). The positive relation of temperature on C:N ratio supports the idea that root-associated Helotiales, through symbiotic interactions with the plants, extract N from the soil and deposits C. The opposite trend was seen for the mixed soils, where Telephorales dominated the roots in the warm treatment and Helotiales in the cold treatment. Here the C:N ratio was much lower and there is less C deposited into the soil. Fungi in the order Telephorales may have a higher respiration since they form a more extensive mycelia than species from Helotiales (Smith and Read 2008). This may explain the trend in the model where proportion of Telephorales negatively relates to soil C.

Conclusions

The main goal of this study was to investigate if the fungal community above the TFL could act as a biotic barrier to the establishment of trees and as such slow the advance of trees, even if the temperature in alpine zones increase. While the second hypothesis (H2) was not supported, I suggest that data from this experiment supports the first hypothesis (H1), at least for the establishment of *B. pubescens*. The fungal community in the roots of seedlings from the alpine soils were very similar to communities found in ericaceous roots collected from alpine habitats. Even though the fungi manage to infect the roots of this ECM plant, they do not seem to exchange nutrients as effectively as the symbionts found where *B. pubescens* naturally occur. While there are indications of nitrogen exchange, the growth rate and both N and P uptake were negatively correlated with proportions of alpine fungal symbionts. The fungal community in the TFL gradient shifts into a dominance of mainly ERM fungal groups only a short distance above the TFL (Clemmensen et al. 2021, Tonjer et al. pre-print). The fungal community above the TFL may thus act as a biotic barrier to the establishment of *B. pubescens* above the TFL, regardless of temperature.

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Supplementary

Supplementary table 1: OTU Table

| OTU_id | Accession_nr | Phylum | Order | Species | Guild | Reads |
|--------|--------------|-------------------|-----------------------|--------------------------|-----------------------------|-------|
| OTU24 | KF617964 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 56222 |
| OTU200 | MF948651 | Ascomycota | Helotiales | Phialocephala_sp | Endophyte | 31006 |
| OTU29 | UDB036669 | Basidiomycota | Agaricales | Naucoria_bohemica | Ectomycorrhizal | 22999 |
| OTU444 | KU516463 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 18817 |
| OTU322 | KC455352 | Ascomycota | Helotiales | Helotiaceae_sp | Undefined | 13574 |
| OTU58 | MG820047 | Basidiomycota | Filobasidiales | Solicocozyma_terricola | Yeast | 12359 |
| OTU15 | KF617332 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 12284 |
| OTU152 | KC686883 | Basidiomycota | Thelephorales | Thelephoraceae_sp | Ectomycorrhizal | 12225 |
| OTU248 | EF634067 | Ascomycota | Mylitridales | Cenococcum_geophilum | Ectomycorrhizal | 10151 |
| OTU333 | FJ552837 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 8592 |
| OTU537 | MN385502 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 8440 |
| OTU373 | JX630403 | Basidiomycota | Sebacinales | Serendipita_sp | Root Associated Fungi | 8135 |
| OTU48 | KF617305 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 7795 |
| OTU182 | KU685720 | Basidiomycota | Agaricales | Laccaria_ohiensis | Ectomycorrhizal | 7436 |
| OTU283 | KU176263 | Basidiomycota | Agaricales | Mallocybe_sp | Ectomycorrhizal | 5752 |
| OTU66 | KF617655 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 4911 |
| OTU464 | DQ182455 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 4849 |
| OTU118 | MK331819 | Ascomycota | Hypocreales | Ilyonectria_destructans | Plant Pathogen | 4739 |
| OTU183 | EF434108 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 4160 |
| OTU153 | MH310782 | Basidiomycota | Thelephorales | Thelephora_terrestris | Ectomycorrhizal | 3580 |
| OTU119 | KU924614 | Basidiomycota | Russulales | Russula_sp | Ectomycorrhizal | 3552 |
| OTU33 | JQ666552 | Basidiomycota | Agaricales | Hymenogaster_sp | Ectomycorrhizal | 3495 |
| OTU237 | KY102953 | Basidiomycota | Filobasidiales | Solicocozyma_terrea | Yeast | 3358 |
| OTU404 | KC480052 | Ascomycota | Helotiales | Acephala_sp | Ectomycorrhizal | 3354 |
| OTU374 | KP889951 | Mortierellomycota | Mortierellales | Mortierellales_sp | Saprotroph | 3259 |
| OTU295 | MK513845 | Mortierellomycota | Mortierellales | Mortierella_clonocystis | Saprotroph | 3184 |
| OTU27 | HQ850137 | Ascomycota | Helotiales | Hyaloscypha_sp | Saprotroph | 3156 |
| OTU545 | JQ347010 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 3122 |
| OTU473 | HM030614 | Ascomycota | Archaeorhizomycetes | Archaeorhizomycetes_sp | Undefined | 2883 |
| OTU495 | GU174280 | Ascomycota | Archaeorhizomycetes | Archaeorhizomycetes_sp | Undefined | 2784 |
| OTU270 | MG670440 | Basidiomycota | Tremellales | Trimorphomycetaceae_sp | Yeast | 2745 |
| OTU78 | KM504408 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 2464 |
| OTU5 | DQ420865 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 2422 |
| OTU185 | KY104307 | Ascomycota | Saccharomycetales | Nadsonia_commutata | Yeast | 2399 |
| OTU305 | JF908060 | Basidiomycota | Agaricales | Hygrocybe_conica | Root Associated Fungi | 2392 |
| OTU480 | KF617820 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 2293 |
| OTU500 | GU174327 | Ascomycota | Archaeorhizomycetes | Archaeorhizomycetes_sp | Undefined | 2074 |
| OTU497 | EU292600 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 2012 |
| OTU578 | KU516597 | Ascomycota | Pleosporales | Pleotrichocladium_opacum | Undefined | 1932 |

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|--------|------------|-------------------|-----------------------|----------------------------|-----------------------------|------|
| OTU498 | GU174419 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 1917 |
| OTU298 | MH790415 | Mortierellomycota | Mortierellales | Mortierella_alpina | Saprotroph | 1895 |
| OTU293 | AF504876 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 1830 |
| OTU579 | KY031654 | Ascomycota | Ascomycota | Pezizomycotina | Undefined | 1774 |
| OTU225 | MK272957 | Basidiomycota | Trichosporonales | Apiotrichum_porosum | Saprotroph | 1750 |
| OTU380 | UDB0778583 | Basidiomycota | Agaricales | Hymenogaster_sp | Ectomycorrhizal | 1672 |
| OTU46 | MG938353 | Ascomycota | Saccharomycetales | Nadsonia_starkeyi-henricii | Yeast | 1639 |
| OTU401 | LC206544 | Ascomycota | Helotiales | Varicosporium_elodeae | Saprotroph | 1616 |
| OTU79 | KF000612 | Ascomycota | Helotiales | Hyaloscypha_sp | Saprotroph | 1478 |
| OTU32 | HQ211704 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 1376 |
| OTU89 | UDB036836 | Basidiomycota | Agaricales | Hygrocybe_subpapillata | Root Associated Fungi | 1335 |
| OTU124 | KF617367 | Basidiomycota | Russulales | Russula_sp | Ectomycorrhizal | 1215 |
| OTU385 | FM999517 | Ascomycota | Helotiales | Meliniomyces_sp | Root Associated Fungi | 1186 |
| OTU235 | KP309847 | Ascomycota | Pezizales | Byssonectria_fusispora | Saprotroph | 1181 |
| OTU141 | UDB032933 | Basidiomycota | Agaricales | Hymenogaster_sp | Ectomycorrhizal | 1180 |
| OTU136 | MK793704 | Ascomycota | Capnodiales | Cladosporium_sp | Saprotroph | 1176 |
| OTU85 | KF617631 | Ascomycota | Helotiales | Hyaloscypha_sp | Saprotroph | 1173 |
| OTU303 | MK163719 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 1133 |
| OTU355 | MG670441 | Mortierellomycota | Mortierellales | Mortierellales_sp | Saprotroph | 1124 |
| OTU566 | DQ093782 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 1073 |
| OTU368 | KF617953 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 1004 |
| OTU246 | MF228807 | Ascomycota | Geoglossales | Trichoglossum_hirsutum | Undefined | 998 |
| OTU95 | KY687535 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 958 |
| OTU7 | KF617626 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 954 |
| OTU523 | AB520435 | Basidiomycota | Platyglloeales | Eocronartium_sp | Plant Pathogen | 908 |
| OTU381 | HM136654 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 899 |
| OTU465 | GU174346 | Ascomycota | Archaeorhizomycetes | Archaeorhizomycetes_sp | Undefined | 876 |
| OTU437 | GU366746 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 859 |
| OTU431 | FJ552837 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 838 |
| OTU281 | AF504874 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 835 |
| OTU143 | KF617964 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 823 |
| OTU574 | MG670434 | Basidiomycota | Basidiomycota | Basidiomycota_sp | Undefined | 817 |
| OTU460 | GU174419 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 749 |
| OTU176 | KC222850 | Rozellomycota | GS11 | GS11_sp | Rozellomycota | 745 |
| OTU254 | KT220262 | Basidiomycota | Agaricales | Hymenogaster_sp | Ectomycorrhizal | 724 |
| OTU63 | KF617495 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 707 |
| OTU359 | KP257105 | Basidiomycota | Agaricales | Camarophylloopsis_sp | Saprotroph | 700 |
| OTU302 | HQ021781 | Mortierellomycota | Mortierellales | Mortierellaceae_sp | Saprotroph | 699 |
| OTU3 | HQ211824 | Ascomycota | Helotiales | Neobulgaria_sp | Saprotroph | 653 |
| OTU6 | KT220262 | Basidiomycota | Agaricales | Hymenogaster_sp | Ectomycorrhizal | 651 |
| OTU474 | GU174327 | Ascomycota | Archaeorhizomycetes | Archaeorhizomycetes_sp | Undefined | 625 |
| OTU130 | MN385496 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 624 |

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|--------|----------|-------------------|-----------------------|------------------------|-----------------------|-----|
| OTU145 | FJ552837 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 598 |
| OTU353 | KJ482669 | Basidiomycota | Sebacinales | Sebacinales_sp | Root Associated Fungi | 597 |
| OTU30 | KT728231 | Basidiomycota | Trechisporales | Trechisporales_sp | Saprotroph | 593 |
| OTU86 | JQ666346 | Ascomycota | Helotiales | Hyaloscyphaceae_sp | Saprotroph | 592 |
| OTU26 | JQ666484 | Rozellomycota | GS11 | GS11_sp | Rozellomycota | 578 |
| OTU484 | GU174345 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 575 |
| OTU134 | KU176249 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 523 |
| OTU447 | GU174326 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 523 |
| OTU263 | KF291225 | Basidiomycota | Agaricales | Hygrocybe_ingrata | Root Associated Fungi | 512 |
| OTU102 | KU176242 | Basidiomycota | Russulales | Russula_sp | Ectomycorrhizal | 506 |
| OTU451 | GQ160018 | Ascomycota | Archaeorhizomycetes | Archaeorhizomyces_sp | Undefined | 500 |
| OTU41 | MK614832 | Ascomycota | Sordariales | Sordariales_sp | Undefined | 487 |
| OTU421 | KX611562 | Ascomycota | Helotiales | Leohumicola_sp | Undefined | 440 |
| OTU23 | GU174302 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 436 |
| OTU65 | KP889615 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 410 |
| OTU82 | JF908054 | Basidiomycota | Agaricales | Hygrocybe_ceracea | Root Associated Fungi | 377 |
| OTU585 | JQ666442 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 368 |
| OTU17 | HQ211778 | Ascomycota | Helotiales | Hyaloscyphaceae_sp | Saprotroph | 365 |
| OTU198 | KJ742400 | Basidiomycota | Russulales | Lactarius_flexuosus | Ectomycorrhizal | 350 |
| OTU4 | KP889411 | Basidiomycota | Leucosporidiales | Leucosporidiales_sp | Undefined | 347 |
| OTU8 | HM164562 | Ascomycota | Helotiales | Hyaloscypha_finlandica | Saprotroph | 339 |
| OTU178 | KF617342 | Ascomycota | Leotiomycetes | Leotiomycetes_sp | Undefined | 333 |
| OTU375 | JQ666648 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 331 |
| OTU343 | KF617277 | Mortierellomycota | Mortierellales | Mortierellales_sp | Saprotroph | 329 |
| OTU208 | MG076771 | Basidiomycota | Agaricales | Laccaria_tortilis | Ectomycorrhizal | 319 |
| OTU67 | KF660568 | Ascomycota | Helotiales | Pezoloma_ericae | Root Associated Fungi | 313 |
| OTU229 | KU176321 | Ascomycota | Helotiales | Tetracladium_sp | Undefined | 305 |
| OTU299 | MG076773 | Ascomycota | Helotiales | Cadophora_sp | Endophyte | 301 |
| OTU461 | KF800622 | Basidiomycota | Polyporales | Polyporales_sp | Undefined | 298 |
| OTU547 | FJ552797 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 286 |
| OTU76 | KM504506 | Ascomycota | Helotiales | Pezoloma_ericae | Root Associated Fungi | 285 |
| OTU22 | KY687581 | Rozellomycota | GS03 | GS03_sp | Rozellomycota | 278 |
| OTU274 | MF615035 | Ascomycota | Hypocreales | Nectriaceae_sp | Undefined | 257 |
| OTU576 | JF449733 | Basidiomycota | Auriculariales | Auriculariales_sp | Saprotroph | 253 |
| OTU197 | JF340267 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 253 |
| OTU80 | FN610999 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 253 |
| OTU301 | MH855304 | Ascomycota | Hypocreales | Metarhizium_carneum | Animal pathogen | 245 |
| OTU513 | KF617898 | Ascomycota | Helotiales | Neobulgaria_sp | Saprotroph | 242 |
| OTU179 | KY977601 | Ascomycota | Thelebolales | Pseudogymnoascus_sp | Undefined | 242 |

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|--------|-----------|-------------------|-----------------------|-----------------------------|-----------------------|-----|
| OTU103 | JX270369 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 240 |
| OTU470 | MF614983 | Ascomycota | Dothideomycetes | Dothideomycetes_sp | Undefined | 235 |
| OTU106 | DQ102685 | Basidiomycota | Agaricales | Cortinarius_sp | Ectomycorrhizal | 232 |
| OTU304 | KF617753 | Ascomycota | Helotiales | Hyaloscyphaceae_sp | Saprotroph | 226 |
| OTU472 | GU174280 | Ascomycota | Archaeorhizomycetes | Archaeorhizomycetes_sp | Undefined | 223 |
| OTU330 | KY031669 | Ascomycota | Helotiales | Halenospora_sp | Undefined | 214 |
| OTU2 | HQ212080 | Basidiomycota | Agaricales | Clavaria_sphagnicola | Undefined | 208 |
| OTU452 | JQ346944 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 206 |
| OTU548 | GU174280 | Ascomycota | Archaeorhizomycetes | Archaeorhizomycetes_sp | Undefined | 193 |
| OTU242 | JQ666691 | Ascomycota | Chaetothyriales | Exophiala_sp | Undefined | 190 |
| OTU331 | AY515360 | Ascomycota | Sordariales | Podospora_ellisiana | Saprotroph | 189 |
| OTU91 | KF617495 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 187 |
| OTU276 | MG670412 | Mortierellomycota | Mortierellales | Mortierellaceae_sp | Saprotroph | 185 |
| OTU407 | KF617857 | Ascomycota | Chaetothyriales | Chaetothyriales_sp | Undefined | 182 |
| OTU218 | JF519259 | Ascomycota | Helotiales | Alatospora_acuminata | Undefined | 182 |
| OTU582 | KF296841 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 182 |
| OTU550 | HM037687 | Basidiomycota | Trechisporales | Trechisporales_sp | Saprotroph | 178 |
| OTU430 | JF691019 | Ascomycota | Chaetothyriales | Herpotrichiellaceae_sp | Undefined | 176 |
| OTU586 | HQ211860 | Basidiomycota | Basidiomycota | Basidiomycota_sp | Undefined | 171 |
| OTU411 | KC222855 | Rozellomycota | GS11 | GS11_sp | Rozellomycota | 161 |
| OTU253 | KM359781 | Entorrhizomycota | Entorrhizales | Entorrhiza_aschersoniana | Plant Pathogen | 159 |
| OTU448 | MK285924 | Basidiomycota | Thelephorales | Thelephoraceae_sp | Ectomycorrhizal | 157 |
| OTU195 | MN082023 | Basidiomycota | Agaricales | Entoloma_conferendum | Root Associated Fungi | 152 |
| OTU350 | KP889973 | Ascomycota | Chaetothyriales | Cladophialophora_sp | Undefined | 152 |
| OTU81 | KC455351 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 152 |
| OTU213 | HG936871 | Ascomycota | Sordariales | Chaetomiaceae_sp | Undefined | 151 |
| OTU573 | AB520435 | Basidiomycota | Platyglloeales | Eocronartium_sp | Plant Pathogen | 139 |
| OTU13 | KP889862 | Basidiomycota | Russulales | Russula_sp | Ectomycorrhizal | 139 |
| OTU424 | KF617753 | Ascomycota | Helotiales | Hyaloscyphaceae_sp | Saprotroph | 138 |
| OTU205 | UDB036830 | Basidiomycota | Agaricales | Hygrocybe_salicis-herbaceae | Root Associated Fungi | 138 |
| OTU189 | LC133885 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 130 |
| OTU557 | JX270340 | Ascomycota | Thelebolales | Pseudeurotium_sp | Undefined | 129 |
| OTU268 | FJ475766 | Ascomycota | Chaetothyriales | Cladophialophora_sp | Undefined | 127 |
| OTU154 | AM292198 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 124 |
| OTU408 | KX611550 | Ascomycota | Helotiales | Helotiaceae_sp | Undefined | 123 |
| OTU38 | KF617416 | Basidiomycota | Trechisporales | Luellia_sp | Saprotroph | 119 |
| OTU204 | KC222855 | Rozellomycota | GS11 | GS11_sp | Rozellomycota | 116 |
| OTU409 | MK394102 | Ascomycota | Saccharomycetales | Candida_sake | Yeast | 115 |
| OTU478 | GU174419 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 114 |
| OTU172 | HF675488 | Basidiomycota | Thelephorales | Thelephoraceae_sp | Ectomycorrhizal | 114 |
| OTU100 | KP257112 | Basidiomycota | Agaricales | Clavaria_falcata | Undefined | 113 |
| OTU233 | KJ938775 | Basidiomycota | Agaricales | Inocybe_xanthomelas | Ectomycorrhizal | 113 |

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|--------|-----------|-------------------|-------------------|-------------------------------|-----------------------|-----|
| OTU216 | MN450634 | Ascomycota | Hypocreales | Fusicolla_merismoides | Undefined | 113 |
| OTU53 | KF212327 | Ascomycota | Hypocreales | Metapochonia_suchlasporia | Undefined | 111 |
| OTU165 | MK304328 | Ascomycota | Hypocreales | Tolypocladium_album | Animal pathogen | 110 |
| OTU151 | KY103483 | Basidiomycota | Filobasidiales | Goffeauzyma_gastrica | Yeast | 109 |
| OTU514 | KF359562 | Ascomycota | Helotiales | Helotiaceae_sp | Undefined | 107 |
| OTU393 | HQ212138 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 106 |
| OTU211 | JF300382 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 105 |
| OTU240 | KY977594 | Ascomycota | Helotiales | Pezicula_melanigena | Plant Pathogen | 104 |
| OTU180 | FJ553081 | Ascomycota | Leotiomycetes | Leotiomycetes_sp | Undefined | 103 |
| OTU94 | MK808781 | Ascomycota | Hypocreales | Trichoderma_sp | Undefined | 102 |
| OTU496 | FJ552802 | Basidiomycota | Agaricales | Hygrophoraceae_sp | Root Associated Fungi | 101 |
| OTU511 | AM113716 | Ascomycota | Lecanoromycetes | Lecanoromycetes_sp | Lichen | 101 |
| OTU25 | UDB037688 | Basidiomycota | Agaricales | Camarophylloopsis_schulzeri | Saprotroph | 99 |
| OTU257 | MK179256 | Ascomycota | Eurotiales | Penicillium_canescens | Saprotroph | 98 |
| OTU471 | GU174395 | Basidiomycota | Agaricales | Clavaria_sp | Undefined | 96 |
| OTU575 | KT728243 | Ascomycota | Ascomycota | Ascomycota_sp | Undefined | 95 |
| OTU68 | FJ553835 | Basidiomycota | Agaricales | Clavariaceae_sp | Undefined | 93 |
| OTU581 | AM260828 | Entorrhizomycota | Entorrhizomycota | Entorrhizomycota_sp | Plant Pathogen | 93 |
| OTU166 | GU931771 | Ascomycota | Saccharomycetales | Debaryomyces_sp | Yeast | 90 |
| OTU520 | FJ552797 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 85 |
| OTU569 | MF542269 | Glomeromycota | Glomerales | Glomeraceae_sp | Arbuscular Mycorrhiza | 84 |
| OTU107 | KF617605 | Ascomycota | Leotiomycetes | Leotiomycetes_sp | Undefined | 84 |
| OTU307 | KT768315 | Ascomycota | Sordariales | Chaetomiaceae_sp | Undefined | 83 |
| OTU125 | KF617364 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 81 |
| OTU485 | JX042929 | Ascomycota | Sordariomycetes | Sordariomycetes_sp | Undefined | 79 |
| OTU389 | MK958563 | Ascomycota | Hypocreales | Tolypocladium_cylindrosporium | Animal pathogen | 78 |
| OTU190 | KC965937 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 76 |
| OTU215 | KF206525 | Olpidiomycota | Olpidiales | Olpidiaceae_sp | Plant Pathogen | 75 |
| OTU61 | KM504464 | Ascomycota | Lecanoromycetes | Lecanoromycetes_sp | Lichen | 72 |
| OTU502 | FM997952 | Basidiomycota | Leucosporidiales | Leucosporidiales_sp | Undefined | 71 |
| OTU175 | HQ445992 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 71 |
| OTU568 | KT728347 | Ascomycota | Venturiales | Venturiaceae_sp | Undefined | 71 |
| OTU459 | KF618031 | Ascomycota | Annulatascales | Annulatasceae_sp | Saprotroph | 69 |
| OTU509 | FJ553093 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 69 |
| OTU117 | HQ212010 | Basidiomycota | Agaricales | Clavariaceae_sp | Undefined | 68 |
| OTU377 | HQ211504 | Basidiomycota | Agaricales | Clavulinopsis_sp | Undefined | 68 |
| OTU416 | HM230873 | Ascomycota | Chaetothyriales | Herpotrichiellaceae_sp | Undefined | 68 |
| OTU21 | GQ149464 | Ascomycota | Pezizales | Hydnotrya_bailii | Ectomycorrhizal | 66 |
| OTU450 | UDB031919 | Basidiomycota | Stereopsidales | Clavulicium_delectabile | Saprotroph | 64 |
| OTU392 | FM999525 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 63 |
| OTU243 | MK958538 | Ascomycota | Capnodiales | Cladosporium_sp | Saprotroph | 60 |
| OTU220 | KC966301 | Ascomycota | Chaetothyriales | Herpotrichiellaceae_sp | Undefined | 59 |

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|--------|-----------|---------------|-----------------------|-------------------------------|-----------------------------|----|
| OTU534 | KU550110 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 59 |
| OTU445 | EF434059 | Ascomycota | Helotiales | Hyaloscyphaceae_sp | Saprotroph | 59 |
| OTU349 | HQ211604 | Ascomycota | Helotiales | Leptodontidium_sp | Endophyte | 59 |
| OTU546 | KC966235 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 59 |
| OTU318 | FJ528732 | Basidiomycota | Sporidiobolales | Sporidiobolales_sp | Yeast | 59 |
| OTU395 | KF617859 | Basidiomycota | Agaricales | Clavariaceae_sp | Undefined | 57 |
| OTU170 | AY157489 | Ascomycota | Eurotiales | Penicillium_citreonigrum | Saprotroph | 57 |
| OTU18 | KF617536 | Ascomycota | Lecanoromycetes | Lecanoromycetes_sp | Lichen | 55 |
| OTU370 | GU187836 | Ascomycota | Coniochaetales | Coniochaetales_sp | Undefined | 54 |
| OTU554 | KP889516 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 53 |
| OTU114 | MN413151 | Ascomycota | Eurotiales | Penicillium_brunneoconidiatum | Saprotroph | 53 |
| OTU149 | JQ256430 | Ascomycota | Geoglossales | Trichoglossum_walteri | Undefined | 53 |
| OTU126 | FN610922 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 53 |
| OTU518 | KX464131 | Ascomycota | Botryosphaerales | Tiarospora_sp | Endophyte | 52 |
| OTU223 | MH374550 | Ascomycota | Eurotiales | Penicillium_virgatum | Saprotroph | 52 |
| OTU112 | KT268963 | Ascomycota | Pleosporales | Paraphaeosphaeria_sp | Undefined | 52 |
| OTU55 | MH930171 | Basidiomycota | Agaricales | Entoloma_vernum | Root Associated Fungi | 51 |
| OTU441 | JQ256426 | Ascomycota | Geoglossales | Sabuloglossum_arenarium | Undefined | 51 |
| OTU436 | JN995643 | Ascomycota | Helotiales | Phialocephala_sp | Endophyte | 51 |
| OTU376 | MK808050 | Ascomycota | Helotiales | Lachnum_sp | Saprotroph | 50 |
| OTU148 | UDB037022 | Basidiomycota | Agaricales | Clavaria_sphagnicola | Undefined | 49 |
| OTU19 | KF617598 | Ascomycota | Helotiales | Pezoloma_ericae | Root Associated Fungi | 49 |
| OTU232 | KP889780 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 48 |
| OTU558 | MK102701 | Ascomycota | Helotiales | Cadophora_sp | Endophyte | 47 |
| OTU400 | AY969887 | Basidiomycota | Agaricales | Agaricales_sp | Undefined | 46 |
| OTU290 | KF617737 | Basidiomycota | Cantharellales | Ceratobasidiaceae_sp | Undefined | 46 |
| OTU515 | KY031654 | Ascomycota | Ascomycota | Pezizomycotina | Undefined | 44 |
| OTU10 | MN265972 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 43 |
| OTU358 | GU054164 | Ascomycota | Sordariomycetes | Sordariomycetes_sp | Undefined | 42 |
| OTU191 | FJ553008 | Ascomycota | Geoglossales | Sabuloglossum_sp | Undefined | 41 |
| OTU258 | AY634118 | Basidiomycota | Sebacinales | Serendipitaceae_sp | Root Associated Fungi | 41 |
| OTU188 | DQ273344 | Ascomycota | Myrmecridiales | Myrmecridiales_sp | Undefined | 40 |
| OTU487 | GU174420 | Ascomycota | Archaeorhizomycetes | Archaeorhizomycetes_sp | Undefined | 38 |
| OTU31 | KR935838 | Ascomycota | Coniochaetales | Coniochaeta_ligniaria | Plant Pathogen | 38 |
| OTU271 | JQ346833 | Basidiomycota | Cantharellales | Ceratobasidiaceae_sp | Undefined | 35 |
| OTU239 | KY687808 | Ascomycota | GS35 | GS35_sp | Undefined | 35 |
| OTU342 | KT728257 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 35 |
| OTU425 | HG937083 | Basidiomycota | Leucosporidiales | Leucosporidiales_sp | Undefined | 35 |
| OTU361 | MG230329 | Ascomycota | Helotiales | Rhizoscyphus_sp | Root Associated Fungi | 34 |
| OTU250 | JF519062 | Ascomycota | Sordariales | Sordariales_sp | Undefined | 33 |

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|--------|-----------|-------------------|-----------------------|---------------------------|-----------------------|----|
| OTU291 | GQ154488 | Ascomycota | Helotiales | Hyaloscypha_bicolor | Saprotroph | 32 |
| OTU162 | JX546606 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 32 |
| OTU504 | AB214657 | Ascomycota | Glomerellales | Verticillium_leptobactrum | Undefined | 31 |
| OTU384 | KF617422 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 30 |
| OTU121 | HM230883 | Ascomycota | Chaetothyriales | Herpotrichiellaceae_sp | Undefined | 30 |
| OTU512 | KC966301 | Ascomycota | Chaetothyriales | Herpotrichiellaceae_sp | Undefined | 29 |
| OTU99 | KP714632 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 29 |
| OTU561 | AY336133 | Ascomycota | Pleosporales | Drechslera_sp | Plant Pathogen | 29 |
| OTU64 | KP257114 | Basidiomycota | Agaricales | Clavaria_falcata | Undefined | 28 |
| OTU551 | KF617587 | Ascomycota | GS34 | GS34_sp | Undefined | 28 |
| OTU138 | KF493951 | Olpidiomycota | Olpidiales | Olpidium_sp | Plant Pathogen | 28 |
| OTU217 | MK671625 | Ascomycota | Thelebolales | Pseudeurotium_hygrophilum | Undefined | 28 |
| OTU93 | JQ346993 | Basidiomycota | Atheliales | Athelopsis_lembospora | Saprotroph | 27 |
| OTU98 | MK514443 | Ascomycota | Orbiliales | Orbiliaceae_sp | Saprotroph | 27 |
| OTU35 | HQ154277 | Basidiomycota | Sebacinales | Serendipita_sp | Root Associated Fungi | 26 |
| OTU300 | FJ553220 | Ascomycota | Chaetothyriales | Herpotrichiellaceae_sp | Undefined | 26 |
| OTU214 | DQ420720 | Ascomycota | Chaetothyriales | Herpotrichiellaceae_sp | Undefined | 26 |
| OTU84 | EU645626 | Basidiomycota | Sebacinales | Sebacina_sp | Root Associated Fungi | 26 |
| OTU326 | AM260794 | Basidiomycota | GS29 | GS29_sp | Undefined | 25 |
| OTU499 | AM260798 | Basidiomycota | GS29 | GS29_sp | Undefined | 25 |
| OTU108 | AY706329 | Ascomycota | Helotiales | Leohumicola_minima | Undefined | 25 |
| OTU269 | MH465656 | Basidiomycota | Agaricales | Mycena_sp | Saprotroph | 24 |
| OTU412 | KC222128 | Ascomycota | Geoglossales | Glutinoglossum_glutinosum | Undefined | 24 |
| OTU50 | UDB028535 | Basidiomycota | Cantharellales | Ceratobasidiaceae_sp | Undefined | 23 |
| OTU364 | KF617962 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 23 |
| OTU171 | HM164556 | Ascomycota | Helotiales | Hyaloscypha_finlandica | Saprotroph | 23 |
| OTU115 | HQ446004 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 23 |
| OTU323 | KT728336 | Basidiomycota | Trechisporales | Trechisporales_sp | Saprotroph | 23 |
| OTU542 | HQ445987 | Ascomycota | Ascomycota | Ascomycota_sp | Undefined | 22 |
| OTU236 | MH859123 | Ascomycota | Eurotiales | Penicillium_sacculum | Saprotroph | 22 |
| OTU360 | HG937106 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 22 |
| OTU540 | KP889469 | Ascomycota | Leotiomycetes | Leotiomycetes_sp | Undefined | 22 |
| OTU285 | JX545195 | Ascomycota | Pezizales | Scutellinia_sp | Saprotroph | 22 |
| OTU426 | UDB014586 | Ascomycota | Saccharomycetales | Saccharomycetales_sp | Yeast | 22 |
| OTU503 | AY969881 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 21 |
| OTU101 | KY322548 | Ascomycota | Helotiales | Phialocephala_fortinii | Endophyte | 21 |
| OTU196 | KC869724 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 21 |
| OTU328 | UDB014586 | Ascomycota | Saccharomycetales | Saccharomycetales_sp | Yeast | 21 |
| OTU163 | KY105380 | Ascomycota | Saccharomycetales | Schwanniomyces_capriottii | Yeast | 21 |
| OTU563 | KP889332 | Chytridiomycota | Chytridiomycota | Chytridiomycota_sp | Chytrid | 20 |
| OTU494 | JQ666638 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 20 |
| OTU438 | KP714556 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 20 |

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|--------|-----------|-------------------|-----------------------|------------------------------|-----------------------------|----|
| OTU468 | JQ666741 | Ascomycota | Orbiliales | Orbiliales_sp | Undefined | 20 |
| OTU56 | DQ485681 | Chytridiomycota | Rhizophydiales | Terramyces_sp | Chytrid | 20 |
| OTU532 | KU534738 | Basidiomycota | Basidiomycota | Basidiomycota_sp | Undefined | 19 |
| OTU339 | HM136675 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 19 |
| OTU410 | GU256966 | Basidiomycota | Trechisporales | Hydnodontaceae_sp | Saprotroph | 19 |
| OTU439 | AB925920 | Ascomycota | Hypocreales | Polycephalomycetes_formosus | Undefined | 18 |
| OTU44 | FJ553081 | Ascomycota | Leotiomycetes | Leotiomycetes_sp | Undefined | 18 |
| OTU206 | MH979277 | Basidiomycota | Agaricales | Laccaria_proxima | Ectomycorrhizal | 16 |
| OTU564 | KT160726 | Ascomycota | Ascomycota | Ascomycota_sp | Undefined | 16 |
| OTU282 | MK614851 | Chytridiomycota | Chytridiomycota | Chytridiomycota_sp | Chytrid | 16 |
| OTU142 | MH862665 | Ascomycota | Helotiales | Spirosphaera_carici-graminis | Saprotroph | 16 |
| OTU357 | MH859820 | Ascomycota | Sordariales | Apodus_deciduus | Saprotroph | 16 |
| OTU280 | JQ666627 | Ascomycota | Thelebolales | Gymnostellatospora_sp | Saprotroph | 16 |
| OTU486 | JQ347162 | Basidiomycota | Tremellales | Cryptococcus_sp | Yeast | 16 |
| OTU156 | UDB031325 | Basidiomycota | Agaricales | Mycena_flavoalba | Saprotroph | 15 |
| OTU354 | KP889430 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 15 |
| OTU20 | EF016385 | Ascomycota | Chaetothyriales | Cladophialophora_minutissima | Undefined | 15 |
| OTU77 | JX318034 | Fungi | Fungi | Fungi_sp | Undefined | 15 |
| OTU311 | KF296819 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 15 |
| OTU418 | UDB026013 | Ascomycota | Helotiales | Lachnellula_sp | Saprotroph | 15 |
| OTU227 | JQ666464 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 15 |
| OTU297 | HM240145 | Basidiomycota | Agaricales | Clavaria_sp | Undefined | 14 |
| OTU463 | HM030614 | Ascomycota | Archaeorhizomycetes | Archaeorhizomycetes_sp | Undefined | 14 |
| OTU488 | KX765316 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 14 |
| OTU51 | HQ211612 | Ascomycota | Helotiales | Hyaloscypha_sp | Saprotroph | 14 |
| OTU109 | GU934571 | Kickxellomycota | Kickxellales | Ramicandelaber_sp | Undefined | 14 |
| OTU549 | MN385505 | Mortierellomycota | Mortierellomycota | Mortierellomycotina | Saprotroph | 14 |
| OTU562 | GU174378 | Ascomycota | Sordariales | Cephalotheca_sp | Saprotroph | 14 |
| OTU228 | UDB023735 | Basidiomycota | Agaricales | Entoloma_glaucobasis | Root Associated Fungi | 13 |
| OTU467 | FJ553837 | Basidiomycota | Agaricomycetes | Agaricomycetes_sp | Undefined | 13 |
| OTU45 | JF300546 | Ascomycota | Chaetothyriales | Chaetothyriales_sp | Undefined | 13 |
| OTU477 | KP889807 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 13 |
| OTU210 | MH864072 | Ascomycota | Hypocreales | Trichoderma_hamatum | Undefined | 13 |
| OTU347 | KT991667 | Ascomycota | Myrmecridiales | Atractospora_decumbens | Undefined | 13 |
| OTU34 | AB986396 | Ascomycota | Pleosporales | Pleosporales_sp | Undefined | 13 |
| OTU334 | JX042929 | Ascomycota | Sordariomycetes | Sordariomycetes_sp | Undefined | 13 |
| OTU417 | KF617859 | Basidiomycota | Agaricales | Clavariaceae_sp | Undefined | 12 |
| OTU168 | UDB036532 | Basidiomycota | Agaricales | Hygrocybe_phaeococcinea | Root Associated Fungi | 12 |
| OTU335 | KP889516 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 12 |
| OTU541 | KP889925 | Rozellomycota | GS05 | GS05_sp | Rozellomycota | 12 |
| OTU517 | FJ553681 | Ascomycota | Helotiales | Alatospora_sp | Undefined | 12 |
| OTU337 | KP889824 | Ascomycota | Leotiomycetes | Leotiomycetes_sp | Undefined | 12 |

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|--------|-----------|-----------------|-----------------------|------------------------------|-----------------------|----|
| OTU479 | MN275853 | Basidiomycota | Tremellomycetes | Tremellomycetes_sp | Undefined | 12 |
| OTU420 | KT728224 | Glomeromycota | Diversisporales | Acaulosporaceae_sp | Arbuscular Mycorrhiza | 11 |
| OTU572 | EU474843 | Glomeromycota | Glomeromycota | Glomeromycota_sp | Arbuscular Mycorrhiza | 11 |
| OTU42 | HG936815 | Ascomycota | Pleosporales | Preussia_sp | Saprotroph | 11 |
| OTU429 | KC965205 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 11 |
| OTU458 | KP889733 | Ascomycota | Saccharomycetales | Saccharomycetales_sp | Yeast | 11 |
| OTU267 | MH858965 | Ascomycota | Sordariales | Triangularia_verruculosa | Undefined | 11 |
| OTU489 | KT160912 | Basidiomycota | Tremellales | Tremellales_sp | Undefined | 11 |
| OTU481 | KP889944 | Ascomycota | Archaeorhizomycetes | Archaeorhizomycetes_sp | Undefined | 10 |
| OTU519 | HM239685 | Ascomycota | Ascomycota | Ascomycota_sp | Undefined | 10 |
| OTU140 | GU054314 | Basidiomycota | Cystofilobasidiales | Itersonilia_annonica | Yeast | 10 |
| OTU12 | JQ666443 | Fungi | Fungi | Fungi_sp | Undefined | 10 |
| OTU588 | JX317978 | Glomeromycota | Glomeromycetes | Glomeromycetes_sp | Arbuscular Mycorrhiza | 10 |
| OTU365 | HG937124 | Ascomycota | Hypocreales | Hypocreales_sp | Undefined | 10 |
| OTU209 | JN572910 | Basidiomycota | Polyporales | Hyphoderma_obtusiforme | Undefined | 10 |
| OTU567 | HM240125 | Chytridiomycota | Rhizophydiales | Rhizophydiales_sp | Chytrid | 10 |
| OTU288 | JX898594 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 10 |
| OTU135 | MK290701 | Basidiomycota | Thelephorales | Pseudotomentella_sp | Ectomycorrhizal | 10 |
| OTU272 | MH862538 | Ascomycota | Venturiales | Scolecobasidium_excentricum | Undefined | 10 |
| OTU394 | KY548838 | Basidiomycota | Classicales | Classicaleae_sp | Undefined | 9 |
| OTU1 | KT957783 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 9 |
| OTU415 | KF617533 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 9 |
| OTU184 | KP889497 | Ascomycota | Chaetothyriales | Herpotrichiellaceae_sp | Undefined | 9 |
| OTU71 | FN555282 | Glomeromycota | Paraglomerales | Paraglomerales_sp | Arbuscular Mycorrhiza | 9 |
| OTU199 | KU534730 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 9 |
| OTU49 | LT548267 | Basidiomycota | Tremellales | Filobasidiella_sp | Yeast | 9 |
| OTU157 | KP889479 | Basidiomycota | Agaricales | Clavariaceae_sp | Undefined | 8 |
| OTU321 | KF617859 | Basidiomycota | Agaricales | Clavariaceae_sp | Undefined | 8 |
| OTU16 | KC965833 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 8 |
| OTU164 | HM141044 | Basidiomycota | Cantharellales | Ceratobasidiaceae_sp | Undefined | 8 |
| OTU402 | EU669387 | Ascomycota | Pezizales | Pseudaleuria_quinaultiana | Saprotroph | 8 |
| OTU571 | KP889727 | Chytridiomycota | Rhizophydiales | Terramycetaceae_sp | Undefined | 8 |
| OTU363 | AM260915 | Ascomycota | Sordariales | Sordariales_sp | Undefined | 8 |
| OTU428 | MN128860 | Basidiomycota | Tremellales | Vishniacozyma_victoriae | Yeast | 8 |
| OTU341 | KP133511 | Chytridiomycota | Chytridiomycota | Chytridiomycota_sp | Chytrid | 7 |
| OTU310 | HQ871874 | Ascomycota | Chaetothyriales | Cladophialophora_chaetospira | Undefined | 7 |
| OTU14 | UDB036614 | Basidiomycota | Agaricales | Clavaria_flavipes | Undefined | 7 |
| OTU433 | FN397402 | Basidiomycota | Agaricales | Clavariaceae_sp | Undefined | 7 |
| OTU158 | JQ272382 | Basidiomycota | Agaricales | Galerina_sp | Saprotroph | 7 |
| OTU507 | KU975066 | Ascomycota | Annulatascales | Ascitendus_austriacus | Undefined | 7 |
| OTU526 | FJ827743 | Chytridiomycota | Chytridiales | Phlyctochytrium_californicum | Plant Pathogen | 7 |
| OTU74 | AM260932 | Fungi | Fungi | Fungi_sp | Undefined | 7 |

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|--------|-----------|-------------------|-----------------------|------------------------|-----------------------|---|
| OTU92 | KT334710 | Ascomycota | Helotiales | Hyaloscyphaceae_sp | Saprotroph | 7 |
| OTU403 | KF617245 | Ascomycota | Helotiales | Meliniomyces_sp | Root Associated Fungi | 7 |
| OTU150 | MK163720 | Ascomycota | Helotiales | Oidiodendron_sp | Root Associated Fungi | 7 |
| OTU219 | KU556539 | Ascomycota | Hypocreales | Tolypocladium_sp | Animal pathogen | 7 |
| OTU386 | HQ446066 | Basidiomycota | Leucosporidiales | Mastigobasidium_sp | Undefined | 7 |
| OTU37 | DQ400287 | Glomeromycota | Paraglomerales | Paraglomerales_sp | Arbuscular Mycorrhiza | 7 |
| OTU351 | UDB014586 | Ascomycota | Saccharomycetales | Saccharomycetales_sp | Yeast | 7 |
| OTU396 | UDB014586 | Ascomycota | Saccharomycetales | Saccharomycetales_sp | Yeast | 7 |
| OTU308 | HQ446091 | Basidiomycota | Agaricales | Clavulinopsis_sp | Undefined | 6 |
| OTU57 | AB669645 | Basidiomycota | Agaricales | Laccaria_sp | Ectomycorrhizal | 6 |
| OTU505 | JX042812 | Ascomycota | Archaeorhizomycetales | Archaeorhizomyces_sp | Undefined | 6 |
| OTU155 | MH858348 | Basidiobolomycota | Basidiobolales | Basidiobolus_ranarum | Saprotroph | 6 |
| OTU278 | GU366669 | Ascomycota | Chaetothyriales | Herpotrichiellaceae_sp | Undefined | 6 |
| OTU378 | KJ735003 | Ascomycota | Coniochaetales | Coniochaeta_sp | Plant Pathogen | 6 |
| OTU414 | KY687581 | Rozellomycota | GS03 | GS03_sp | Rozellomycota | 6 |
| OTU544 | UDB035038 | Ascomycota | Helotiales | Chalara_vaccinii | Undefined | 6 |
| OTU493 | FJ554184 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 6 |
| OTU127 | MK801344 | Basidiomycota | Hymenochaetales | Trichaptum_abietinum | Saprotroph | 6 |
| OTU422 | MG813208 | Ascomycota | Microascales | Microasceae_sp | Saprotroph | 6 |
| OTU230 | HQ211696 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 6 |
| OTU181 | DQ421233 | Chytridiomycota | Rhizophlyctidales | Sonraphlyctis_sp | Chytrid | 6 |
| OTU336 | UDB014586 | Ascomycota | Saccharomycetales | Saccharomycetales_sp | Yeast | 6 |
| OTU131 | JX630611 | Basidiomycota | Sebacinales | Sebacina_sp | Root Associated Fungi | 6 |
| OTU469 | HG937127 | Basidiomycota | Tremellomycetes | Tremellomycetes_sp | Undefined | 6 |
| OTU120 | KP636858 | Basidiomycota | Agaricales | Inocybe_sp | Ectomycorrhizal | 5 |
| OTU320 | KP889364 | Ascomycota | Chaetothyriales | Herpotrichiellaceae_sp | Undefined | 5 |
| OTU521 | EU517014 | Chytridiomycota | Chytridiales | Chytridiales_sp | Chytrid | 5 |
| OTU371 | KC965268 | Ascomycota | Coniochaetales | Coniochaetales_sp | Undefined | 5 |
| OTU75 | KF206526 | Glomeromycota | Glomerales | Glomeraceae_sp | Arbuscular Mycorrhiza | 5 |
| OTU132 | GU256953 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 5 |
| OTU193 | JX371601 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 5 |
| OTU529 | KF617730 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 5 |
| OTU482 | KC965117 | Basidiomycota | Microbotryomycetes | Microbotryomycetes_sp | Undefined | 5 |
| OTU212 | FN565322 | Basidiomycota | Russulales | Russula_sp | Ectomycorrhizal | 5 |
| OTU455 | MF782833 | Ascomycota | Sordariales | Phialemonium_sp | Saprotroph | 5 |
| OTU39 | KF617459 | Basidiomycota | Thelephorales | Tomentellopsis_sp | Ectomycorrhizal | 5 |
| OTU287 | KF206543 | Glomeromycota | Archaeosporales | Ambisporaceae_sp | Undefined | 4 |
| OTU113 | HM239740 | Ascomycota | Ascomycota | Ascomycota_sp | Undefined | 4 |
| OTU344 | KC965268 | Ascomycota | Coniochaetales | Coniochaetales_sp | Undefined | 4 |
| OTU59 | LS398095 | Glomeromycota | Glomerales | Glomeraceae_sp | Arbuscular Mycorrhiza | 4 |

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|--------|-----------|-------------------|---------------------|------------------------------|-----------------|---|
| OTU449 | KF296993 | Rozellomycota | GS08 | GS08_sp | Rozellomycota | 4 |
| OTU530 | KY687753 | Mucoromycota | GS21 | GS21_sp | Undefined | 4 |
| OTU234 | EF434137 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 4 |
| OTU413 | KC965186 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 4 |
| OTU535 | KF617730 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 4 |
| OTU332 | GU174331 | Ascomycota | Helotiales | Lachnum_sp | Saprotroph | 4 |
| OTU565 | MH492941 | Ascomycota | Helotiales | Ombrophila_sp | Saprotroph | 4 |
| OTU177 | KF359557 | Ascomycota | Hypocreales | Tolypocladium_album | Animal pathogen | 4 |
| OTU249 | KP889676 | Ascomycota | Leotiomyces | Leotiomyces_sp | Undefined | 4 |
| OTU457 | DQ182459 | Ascomycota | Pleosporales | Petrakia_sp | Plant Pathogen | 4 |
| OTU338 | KC480046 | Ascomycota | Rhytismatales | Coccomyces_sp | Plant Pathogen | 4 |
| OTU348 | UDB014586 | Ascomycota | Saccharomycetales | Saccharomycetales_sp | Yeast | 4 |
| OTU261 | AF504837 | Ascomycota | Sordariales | Podospira_sp | Saprotroph | 4 |
| OTU264 | MK050409 | Basidiomycota | Sporidiobolales | Sporobolomyces_sp | Yeast | 4 |
| OTU244 | DQ421216 | Chytridiomycota | Chytridiomycota | Chytridiomycota_sp | Chytrid | 3 |
| OTU289 | KP889488 | Basidiomycota | Agaricales | Clavariaceae_sp | Undefined | 3 |
| OTU266 | HQ445570 | Basidiomycota | Agaricales | Ramariopsis_sp | Undefined | 3 |
| OTU434 | MF767285 | Basidiomycota | Agaricales | Ripartites_sp | Undefined | 3 |
| OTU528 | KJ735012 | Ascomycota | Ascomycota | Ascomycota_sp | Undefined | 3 |
| OTU97 | KT965071 | Basidiobolomycota | Basidiobolales | Basidiobolus_sp | Saprotroph | 3 |
| OTU286 | HQ871875 | Ascomycota | Chaetothyriales | Cladophialophora_chaetospora | Undefined | 3 |
| OTU137 | GU187836 | Ascomycota | Coniochaetales | Coniochaetales_sp | Undefined | 3 |
| OTU587 | KJ180739 | Basidiomycota | Cystofilobasidiales | Tausonia_sp | Yeast | 3 |
| OTU577 | KY687649 | Kickxellomycota | GS19 | GS19_sp | Undefined | 3 |
| OTU36 | HQ211636 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 3 |
| OTU552 | KF617618 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 3 |
| OTU560 | FJ554184 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 3 |
| OTU104 | MG250388 | Ascomycota | Hypocreales | Acremonium_furcatum | Saprotroph | 3 |
| OTU524 | KT728304 | Ascomycota | Lecanoromycetes | Lecanoromycetes_sp | Lichen | 3 |
| OTU432 | KP889469 | Ascomycota | Leotiomyces | Leotiomyces_sp | Undefined | 3 |
| OTU262 | FM997952 | Basidiomycota | Leucosporidiales | Leucosporidiales_sp | Undefined | 3 |
| OTU345 | GU559079 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 3 |
| OTU174 | GQ219900 | Mortierellomycota | Mortierellales | Mortierellales_sp | Saprotroph | 3 |
| OTU167 | JX319678 | Mucoromycota | Mucoromycota | Mucoromycota_sp | Undefined | 3 |
| OTU423 | MH107892 | Ascomycota | Pleosporales | Fusicnidium_lycopodiellae | Plant Pathogen | 3 |
| OTU398 | KP698722 | Ascomycota | Pleosporales | Phragmocephala_garethjonesii | Undefined | 3 |
| OTU203 | DQ485617 | Chytridiomycota | Rhizophydiales | Operculomyces_laminatus | Undefined | 3 |
| OTU159 | KF617532 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 3 |
| OTU476 | HM069375 | Ascomycota | Saccharomycetales | Saccharomycetales_sp | Yeast | 3 |
| OTU466 | FJ552766 | Ascomycota | Sordariomycetes | Sordariomycetes_sp | Undefined | 3 |
| OTU443 | KM504471 | Ascomycota | Venturiales | Venturiales_sp | Undefined | 3 |
| OTU543 | HQ022223 | Ascomycota | Acarosporales | Acarosporales_sp | Lichen | 2 |
| OTU556 | DQ421142 | Basidiomycota | Agaricales | Clavaria_sp | Undefined | 2 |
| OTU277 | HM488464 | Basidiomycota | Agaricales | Clavariaceae_sp | Undefined | 2 |

| | | | | | | |
|--------|-----------|-------------------|-------------------|----------------------------|-----------------------|---|
| OTU306 | UDB023694 | Basidiomycota | Agaricales | Entoloma_korhonenii | Root Associated Fungi | 2 |
| OTU128 | HQ604368 | Basidiomycota | Agaricales | Inocybe_sindonia | Ectomycorrhizal | 2 |
| OTU245 | AF193351 | Basidiomycota | Agaricales | Typhula_ishikariensis | Plant Pathogen | 2 |
| OTU525 | KT728219 | Ascomycota | Ascomycota | Ascomycota_sp | Undefined | 2 |
| OTU372 | JX984762 | Ascomycota | Capnodiales | Arthrocatena_sp | Undefined | 2 |
| OTU273 | GU187823 | Ascomycota | Chaetosphaeriales | Chloridium_sp | Undefined | 2 |
| OTU52 | HM230883 | Ascomycota | Chaetothyriales | Herpotrichiellaceae_sp | Undefined | 2 |
| OTU435 | MK614851 | Chytridiomycota | Chytridiomycota | Chytridiomycota_sp | Chytrid | 2 |
| OTU110 | FJ552932 | Ascomycota | Coniochaetales | Coniochaeta_sp | Plant Pathogen | 2 |
| OTU406 | KC965141 | Ascomycota | Coniochaetales | Coniochaetales_sp | Undefined | 2 |
| OTU90 | JX042781 | Glomeromycota | Glomerales | Glomeraceae_sp | Arbuscular Mycorrhiza | 2 |
| OTU501 | MH864644 | Ascomycota | Glomerellales | Verticillium_sp | Undefined | 2 |
| OTU252 | HM190114 | Ascomycota | Helotiales | Helotiaceae_sp | Undefined | 2 |
| OTU391 | MN518405 | Ascomycota | Helotiales | Helotiaceae_sp | Undefined | 2 |
| OTU440 | KP889812 | Ascomycota | Helotiales | Hyaloscyphaceae_sp | Saprotroph | 2 |
| OTU390 | KU516576 | Ascomycota | Helotiales | Pycnopeziza_symptodialis | Plant Pathogen | 2 |
| OTU570 | KP889825 | Ascomycota | Leotiomycetes | Leotiomycetes_sp | Undefined | 2 |
| OTU555 | JQ666439 | Ascomycota | Leotiomycetes | Leotiomycetes_sp | Undefined | 2 |
| OTU192 | MH860124 | Mortierellomycota | Mortierellales | Mortierella_echinula | Saprotroph | 2 |
| OTU9 | KF617678 | Mortierellomycota | Mortierellales | Mortierellales_sp | Saprotroph | 2 |
| OTU73 | KF296907 | Olpidiomycota | Olpidiales | Olpidium_brassicae | Plant Pathogen | 2 |
| OTU313 | MK720105 | Ascomycota | Pezizales | Pseudaleuria_fibrillosa | Saprotroph | 2 |
| OTU388 | KF617768 | Ascomycota | Phacidiales | Phacidiales_sp | Undefined | 2 |
| OTU539 | KY687565 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 2 |
| OTU133 | JQ666464 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 2 |
| OTU366 | KF617532 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 2 |
| OTU399 | KF297116 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 2 |
| OTU315 | UDB014586 | Ascomycota | Saccharomycetales | Saccharomycetales_sp | Yeast | 2 |
| OTU327 | UDB014586 | Ascomycota | Saccharomycetales | Saccharomycetales_sp | Yeast | 2 |
| OTU531 | FJ440938 | Ascomycota | Sordariales | Chaetomiaceae_sp | Undefined | 2 |
| OTU292 | MH859325 | Ascomycota | Sordariales | Schizothecium_vesticola | Saprotroph | 2 |
| OTU40 | KF617297 | Ascomycota | Sordariomycetes | Sordariomycetes_sp | Undefined | 2 |
| OTU475 | JF300531 | Ascomycota | Sordariomycetes | Sordariomycetes_sp | Undefined | 2 |
| OTU69 | FJ876182 | Basidiomycota | Thelephorales | Thelephoraceae_sp | Ectomycorrhizal | 2 |
| OTU454 | KP714547 | Basidiomycota | Tremellales | Cryptococcus_sp | Yeast | 2 |
| OTU492 | HG937127 | Basidiomycota | Tremellomycetes | Tremellomycetes_sp | Undefined | 2 |
| OTU483 | KX776448 | Basidiomycota | Trichosporonales | Tetragoniomyces_uliginosus | Undefined | 2 |
| OTU580 | MH861900 | Ascomycota | Xylariales | Basifimbria_sp | Saprotroph | 2 |
| OTU186 | KP889479 | Basidiomycota | Agaricales | Clavariaceae_sp | Undefined | 1 |
| OTU275 | GU328580 | Basidiomycota | Agaricales | Clavariaceae_sp | Undefined | 1 |
| OTU284 | FJ553613 | Basidiomycota | Agaricales | Clavariaceae_sp | Undefined | 1 |
| OTU317 | FN397402 | Basidiomycota | Agaricales | Clavariaceae_sp | Undefined | 1 |

| | | | | | | |
|--------|-----------|-------------------|---------------------------------------|------------------------------|-----------------------|---|
| OTU256 | UDB034225 | Basidiomycota | Agaricales | Cuphophyllus_virgineus | Root Associated Fungi | 1 |
| OTU161 | JQ801386 | Basidiomycota | Agaricales | Inocybe_calamistrata | Ectomycorrhizal | 1 |
| OTU122 | UDB027250 | Basidiomycota | Agaricales | Inocybe_sp | Ectomycorrhizal | 1 |
| OTU146 | AF476965 | Basidiomycota | Agaricales | Mycena_sp | Saprotroph | 1 |
| OTU224 | LC198700 | Basidiomycota | Agaricales | Pholiota_alnicola | Saprotroph | 1 |
| OTU194 | MK045710 | Basidiomycota | Agaricales | Psathyrella_tenuicula | Undefined | 1 |
| OTU506 | GU174346 | Ascomycota | Archaeorhizomycetes | Archaeorhizomycetes_sp | Undefined | 1 |
| OTU324 | AM902016 | Basidiomycota | Atheliales | Athelia_sp | Saprotroph | 1 |
| OTU231 | UDB037249 | Basidiomycota | Cantharellales | Clavulina_cinerea | Undefined | 1 |
| OTU241 | KP889506 | Basidiomycota | Cantharellales | Sistotrema_sp | Saprotroph | 1 |
| OTU144 | GU174433 | Ascomycota | Chaetosphaeriales | Chloridium_sp | Undefined | 1 |
| OTU279 | MH858340 | Ascomycota | Chaetothyriales | Cladophialophora_chaetospira | Undefined | 1 |
| OTU296 | EU754973 | Ascomycota | Chaetothyriales | Herpotrichiellaceae_sp | Undefined | 1 |
| OTU533 | KF297079 | Chytridiomycota | Chytridiomycota | Chytridiomycota_sp | Chytrid | 1 |
| OTU340 | JX338184 | Chytridiomycota | Chytridiomycota | Chytridiomycota_sp | Chytrid | 1 |
| OTU397 | KP889332 | Chytridiomycota | Chytridiomycota | Chytridiomycota_sp | Chytrid | 1 |
| OTU238 | HG936855 | Ascomycota | Coniochaetales | Lecythophora_sp | Endophyte | 1 |
| OTU116 | HM240100 | Mucoromycota | Endogonales | Endogonales_sp | Undefined | 1 |
| OTU123 | HM240100 | Mucoromycota | Endogonales | Endogonales_sp | Undefined | 1 |
| OTU329 | HM240100 | Mucoromycota | Endogonales | Endogonales_sp | Undefined | 1 |
| OTU346 | HM240100 | Mucoromycota | Endogonales | Endogonales_sp | Undefined | 1 |
| OTU584 | KY687656 | Fungi | Fungi | Fungi_sp | Undefined | 1 |
| OTU247 | GU174427 | Ascomycota | Geoglossales | Hemileucoglossum_sp | Saprotroph | 1 |
| OTU28 | HE795123 | Glomeromycota | Glomerales | Glomeraceae_sp | Arbuscular Mycorrhiza | 1 |
| OTU516 | KY687557 | Rozellomycota | GS04 | GS04_sp | Rozellomycota | 1 |
| OTU419 | AM260926 | Mucoromycota | GS22 | GS22_sp | Undefined | 1 |
| OTU442 | AM260794 | Basidiomycota | GS29 | GS29_sp | Undefined | 1 |
| OTU427 | KT160991 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 1 |
| OTU490 | AY781244 | Ascomycota | Helotiales | Helotiales_sp | Undefined | 1 |
| OTU362 | KC965121 | Ascomycota | Helotiales | Mycosymbiocytes_sp | Undefined | 1 |
| OTU379 | AB481286 | Ascomycota | Helotiales | Trichopeziza_mollissima | Saprotroph | 1 |
| OTU536 | MH864097 | Ascomycota | Hypocreales | Acremonium_felinum | Saprotroph | 1 |
| OTU60 | HQ021888 | Ascomycota | Lecanorales | Lecanorales_sp | Lichen | 1 |
| OTU312 | KP889469 | Ascomycota | Leotiomycetes | Leotiomycetes_sp | Undefined | 1 |
| OTU508 | KF617580 | Ascomycota | Leotiomycetes | Leotiomycetes_sp | Undefined | 1 |
| OTU387 | EF621933 | Basidiomycota | Microbotryales | Microbotryum_bistortarum | Plant Pathogen | 1 |
| OTU453 | HG937071 | Basidiomycota | Microbotryomycetes_ord_Incertae_sedis | Chrysozymaceae_sp | Yeast | 1 |
| OTU222 | KY105427 | Basidiomycota | Microbotryomycetes_ord_Incertae_sedis | Slooffia_cresolica | Yeast | 1 |
| OTU129 | JF926967 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 1 |
| OTU226 | KM504451 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 1 |
| OTU251 | GU366727 | Mortierellomycota | Mortierellales | Mortierella_sp | Saprotroph | 1 |
| OTU383 | KU668954 | Mortierellomycota | Mortierellales | Mortierellales_sp | Saprotroph | 1 |

| | | | | | | |
|--------|-----------|-------------------|------------------------------------|--------------------------------|-----------------------|---|
| OTU553 | KF296953 | Mortierellomycota | Mortierellales | Mortierellales_sp | Saprotroph | 1 |
| OTU72 | KC965895 | Ascomycota | Orbiliales | Orbiliales_sp | Undefined | 1 |
| OTU316 | EU669387 | Ascomycota | Pezizales | Pseudaleuria_quinaultiana | Saprotroph | 1 |
| OTU207 | KU924647 | Ascomycota | Pezizales | Tarzetta_sp | Ectomycorrhizal | 1 |
| OTU352 | MH861760 | Ascomycota | Pleosporales | Phaeosphaeria_lutea | Plant Pathogen | 1 |
| OTU405 | KC965316 | Ascomycota | Pleosporales | Pleosporales_sp | Undefined | 1 |
| OTU369 | JQ666536 | Chytridiomycota | Rhizophydiales | Rhizophydiales_sp | Chytrid | 1 |
| OTU139 | KU534693 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 1 |
| OTU314 | KF297116 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 1 |
| OTU527 | KF617532 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 1 |
| OTU583 | KF617666 | Rozellomycota | Rozellomycota | Rozellomycota_sp | Rozellomycota | 1 |
| OTU538 | JQ796369 | Rozellomycota | Rozellomycotina_ord_Incertae_sedis | Paramicrosporidium_saccamoebae | Rozellomycota | 1 |
| OTU367 | UDB014586 | Ascomycota | Saccharomycetales | Saccharomycetales_sp | Yeast | 1 |
| OTU325 | HQ211732 | Basidiomycota | Sebacinales | Sebacinaceae_sp | Root Associated Fungi | 1 |
| OTU83 | EF433989 | Basidiomycota | Sebacinales | Serendipita_sp | Root Associated Fungi | 1 |
| OTU88 | KJ188548 | Basidiomycota | Sebacinales | Serendipitaceae_sp | Root Associated Fungi | 1 |
| OTU491 | HQ212042 | Ascomycota | Sordariomycetes | Sordariomycetes_sp | Undefined | 1 |
| OTU173 | JQ724070 | Basidiomycota | Thelephorales | Thelephoraceae_sp | Ectomycorrhizal | 1 |
| OTU265 | JQ791170 | Basidiomycota | Thelephorales | Thelephoraceae_sp | Ectomycorrhizal | 1 |
| OTU187 | KF617230 | Basidiomycota | Trechisporales | Trechisporales_sp | Saprotroph | 1 |
| OTU105 | DQ421269 | Basidiomycota | Tremellodendropsidales | Tremellodendropsidales_sp | Undefined | 1 |
| OTU96 | MN077485 | Ascomycota | Xylariales | Microdochium_phragmitis | Plant Pathogen | 1 |
| OTU11 | KT601327 | Zoopagomycota | Zoopagales | Syncephalis_sp | Animal pathogen | 1 |
| OTU62 | KU534817 | Zoopagomycota | Zoopagales | Syncephalis_sp | Animal pathogen | 1 |

Supplementary Table 2: Summary of number of reads in Phyla and Orders

| Phylum summary, roots | | |
|------------------------------|--------------------|-------------|
| <u>Phylum</u> | <u>Total reads</u> | <u>OTUs</u> |
| Ascomycota | 100362 | 124 |
| Basidiomycota | 67734 | 53 |
| Mortierellomycota | 215 | 11 |
| Chytridiomycota | 39 | 8 |
| Olpidiomycota | 28 | 1 |
| Rozellomycota | 20 | 4 |
| Glomeromycota | 17 | 2 |
| Entorrhizomycota | 4 | 1 |
| Mucoromycota | 1 | 1 |

| Order summary, roots | | |
|-----------------------------|--------------------|-------------|
| <u>Order</u> | <u>Total reads</u> | <u>OTUs</u> |
| Helotiales | 80810 | 55 |
| Agaricales | 43696 | 17 |
| Thelephorales | 14441 | 6 |
| Mytilinidales | 9442 | 1 |
| Sebacinales | 7774 | 6 |
| Hypocreales | 3341 | 4 |
| Ascomycota | 1891 | 4 |
| Pleosporales | 1234 | 4 |
| Capnodiales | 1225 | 2 |
| Trechisporales | 765 | 5 |
| Sordariales | 683 | 5 |
| Russulales | 603 | 4 |
| Leotiomycetes | 529 | 10 |
| Archaeorhizomycetales | 281 | 8 |
| Auriculariales | 252 | 1 |
| Dothideomycetes | 235 | 1 |
| Chaetothyriales | 227 | 9 |
| Mortierellales | 215 | 11 |
| Saccharomycetales | 121 | 3 |
| Cantharellales | 108 | 4 |
| Sordariomycetes | 89 | 2 |
| Lecanoromycetes | 75 | 3 |
| Pezizales | 68 | 3 |
| Botryosphaeriales | 52 | 1 |

| | | |
|---------------------|----|---|
| Platyglloeales | 36 | 1 |
| Olpidiales | 28 | 1 |
| Chytridiomycota | 26 | 6 |
| Tremellales | 18 | 2 |
| GS11 | 15 | 1 |
| GS34 | 14 | 1 |
| Myrmecridiales | 14 | 2 |
| Atheliales | 12 | 1 |
| Venturiales | 11 | 2 |
| Glomeromycetes | 10 | 1 |
| Classicales | 9 | 1 |
| Annulatascales | 8 | 1 |
| Rhizophydiales | 8 | 1 |
| Archaeorhizomycetes | 7 | 1 |
| Glomerales | 7 | 1 |
| Filobasidiales | 6 | 1 |
| Chytridiales | 5 | 1 |
| Rozellomycota | 5 | 3 |
| Entorrhizales | 4 | 1 |
| Hymenochaetales | 4 | 1 |
| Rhizismatales | 4 | 1 |
| Sporidiobolales | 4 | 1 |
| Cystofilobasidiales | 3 | 1 |
| Polyporales | 3 | 1 |
| Geoglossales | 1 | 1 |
| GS22 | 1 | 1 |

Phylum summary, soil

| <u>Phylum</u> | <u>Total reads</u> | <u>OTUs</u> |
|-------------------|--------------------|-------------|
| Ascomycota | 144300 | 260 |
| Basidiomycota | 39177 | 128 |
| Mortierellomycota | 29088 | 36 |
| Rozellomycota | 5781 | 34 |
| Entorrhizomycota | 248 | 2 |
| Glomeromycota | 131 | 10 |
| Olpidiomycota | 77 | 2 |
| Chytridiomycota | 72 | 10 |
| Fungi | 33 | 4 |
| Kickxellomycota | 17 | 2 |

| | | |
|----------------------------|--------------------|-------------|
| Mucoromycota | 11 | 6 |
| Basidiobolomycota | 9 | 2 |
| Zoopagomycota | 2 | 2 |
| Order summary, soil | | |
| <u>Order</u> | <u>Total reads</u> | <u>OTUs</u> |
| Archaeorhizomycetales | 124632 | 41 |
| Mortierellales | 29074 | 35 |
| Filobasidiales | 15820 | 3 |
| Agaricales | 7749 | 57 |
| Helotiales | 6347 | 74 |
| Russulales | 5164 | 6 |
| Saccharomycetales | 4229 | 15 |
| Rozellomycota | 3894 | 24 |
| Tremellales | 2773 | 5 |
| Hypocreales | 2470 | 15 |
| Trichosporonales | 1752 | 2 |
| Thelephorales | 1654 | 9 |
| GS11 | 1585 | 4 |
| Pezizales | 1213 | 6 |
| Geoglossales | 1167 | 6 |
| Sebacinales | 1060 | 6 |
| Platyglloeales | 1011 | 2 |
| Basidiomycota | 1007 | 3 |
| Chaetothyriales | 900 | 18 |
| Pleosporales | 815 | 8 |
| Mytilinidales | 709 | 1 |
| Leucosporidiales | 463 | 5 |
| Thelebolales | 415 | 4 |
| Sordariales | 322 | 11 |
| Polyporales | 305 | 2 |
| GS03 | 284 | 2 |
| Eurotiales | 282 | 5 |
| Trechisporales | 168 | 6 |
| Lecanoromycetes | 156 | 3 |
| Entorrhizales | 155 | 1 |
| Coniochaetales | 115 | 9 |
| Entorrhizomycota | 93 | 1 |
| Glomerales | 89 | 5 |

| | | |
|---------------------|----|---|
| Ascomycota | 79 | 7 |
| Olpidiales | 77 | 2 |
| Venturiales | 73 | 2 |
| Annulatascales | 68 | 2 |
| Stereopsidales | 64 | 1 |
| Sporidiobolales | 59 | 1 |
| Leotiomyces | 56 | 7 |
| Sordariomyces | 53 | 7 |
| GS29 | 51 | 3 |
| Orbiliales | 48 | 3 |
| Myrmecridiales | 39 | 2 |
| GS35 | 35 | 1 |
| Rhizophydiales | 34 | 4 |
| Fungi | 33 | 4 |
| Glomerellales | 33 | 2 |
| Chytridiomycota | 25 | 4 |
| Tremellomyces | 20 | 3 |
| Atheliales | 16 | 2 |
| Paraglomerales | 16 | 2 |
| GS34 | 14 | 1 |
| Kickellales | 14 | 1 |
| Mortierellomycota | 14 | 1 |
| Agaricomycetes | 13 | 1 |
| Capnodiales | 13 | 2 |
| GS05 | 12 | 1 |
| Diversisporales | 11 | 1 |
| Glomeromycota | 11 | 1 |
| Cystofilobasidiales | 10 | 1 |
| Basidiobolales | 9 | 2 |
| Chytridiales | 7 | 1 |
| Cantharellales | 6 | 3 |
| Microascales | 6 | 1 |
| Rhizophlyctidales | 6 | 1 |
| Microbotryomycetes | 5 | 1 |
| Archaeosporales | 4 | 1 |
| Endogonales | 4 | 4 |
| GS08 | 4 | 1 |
| GS21 | 4 | 1 |
| Chaetosphaeriales | 3 | 2 |

| | | |
|------------------------|---|---|
| GS19 | 3 | 1 |
| Mucoromycota | 3 | 1 |
| Xylariales | 3 | 2 |
| Acarosporales | 2 | 1 |
| Hymenochaetales | 2 | 1 |
| Microbotryomycetes | 2 | 2 |
| Phacidiales | 2 | 1 |
| Zoopagales | 2 | 2 |
| Auriculariales | 1 | 1 |
| GS04 | 1 | 1 |
| Lecanorales | 1 | 1 |
| Microbotryales | 1 | 1 |
| Rozellomycotina | 1 | 1 |
| Tremellodendropsidales | 1 | 1 |

Supplementary table 3: Tukey Honest Significant Difference Tests – Only significant differences are shown

| Tukey HSD - Observed richness in soil | | Tukey HSD - Observed richness in roots | |
|----------------------------------------------|----------------|-----------------------------------------------|----------------|
| <u>Category and Treatment</u> | <u>p-value</u> | <u>Category and Treatment</u> | <u>p-value</u> |
| Alpine Wet-Alpine Dry | 0.0000069 | Lowland Wet-Alpine Dry | 0.0110611 |
| Lowland Dry-Alpine Dry | 0.0000000 | Lowland Wet-Alpine Wet | 0.0026934 |
| Lowland Wet-Alpine Dry | 0.0006291 | Lowland Wet-Lowland Dry | 0.0266741 |
| Mixed Soil-Alpine Dry | 0.0000000 | Lowland Wet:Warm-Alpine Wet:Cold | 0.0338286 |
| Alpine Wet:Cold-Alpine Dry:Cold | 0.0044613 | Lowland Wet:Warm-Alpine Dry:Warm | 0.0367607 |
| Lowland Dry:Cold-Alpine Dry:Cold | 0.0000281 | | |
| Mixed Soil:Cold-Alpine Dry:Cold | 0.0000732 | | |
| Alpine Wet:Warm-Alpine Dry:Cold | 0.0042925 | | |
| Lowland Dry:Warm-Alpine Dry:Cold | 0.0000666 | | |
| Mixed Soil:Warm-Alpine Dry:Cold | 0.0002700 | | |
| Alpine Dry:Warm-Alpine Wet:Cold | 0.0154946 | | |
| Alpine Dry:Warm-Lowland Dry:Cold | 0.0001126 | | |
| Alpine Dry:Warm-Mixed Soil:Cold | 0.0002734 | | |
| Alpine Wet:Warm-Alpine Dry:Warm | 0.0149395 | | |
| Lowland Dry:Warm-Alpine Dry:Warm | 0.0002662 | | |
| Mixed Soil:Warm-Alpine Dry:Warm | 0.0010304 | | |
| Tukey HSD - Carbon change in soil | | Tukey HSD - Seedling total weight | |
| <u>Category and Treatment</u> | <u>p-value</u> | <u>Category and Treatment</u> | <u>p-value</u> |
| Alpine Wet-Alpine Dry | 0.0029470 | Alpine Wet-Alpine Dry | 0.0007062 |
| Mixed Soil-Alpine Dry | 0.0013363 | Lowland Dry-Alpine Dry | 0.0000025 |
| Lowland Dry-Alpine Wet | 0.0002193 | Lowland Wet-Alpine Dry | 0.0000477 |
| Lowland Wet-Lowland Dry | 0.0255047 | Mixed Soil-Alpine Dry | 0.0000000 |
| Mixed Soil-Lowland Dry | 0.0000797 | Mixed Soil-Alpine Wet | 0.0053583 |
| Warm-Cold | 0.0099380 | Mixed Soil-Lowland Wet | 0.0230093 |
| Alpine Dry:Warm-Alpine Wet:Cold | 0.0076051 | Warm-Cold | 0.0000000 |
| Lowland Dry:Warm-Alpine Wet:Cold | 0.0015247 | Lowland Dry:Cold-Alpine Dry:Cold | 0.0112789 |
| Alpine Dry:Warm-Lowland Wet:Cold | 0.0130834 | Alpine Wet:Warm-Alpine Dry:Cold | 0.0031230 |
| Lowland Dry:Warm-Lowland Wet:Cold | 0.0022909 | Lowland Dry:Warm-Alpine Dry:Cold | 0.0000927 |
| Lowland Dry:Warm-Mixed Soil:Cold | 0.0157770 | Lowland Wet:Warm-Alpine Dry:Cold | 0.0000579 |
| Alpine Wet:Warm-Alpine Dry:Warm | 0.0285899 | Mixed Soil:Warm-Alpine Dry:Cold | 0.0000000 |
| Mixed Soil:Warm-Alpine Dry:Warm | 0.0013660 | Mixed Soil:Warm-Alpine Wet:Cold | 0.0000035 |
| Lowland Dry:Warm-Alpine Wet:Warm | 0.0054143 | Mixed Soil:Warm-Lowland Dry:Cold | 0.0001867 |
| Mixed Soil:Warm-Lowland Dry:Warm | 0.0001945 | Lowland Wet:Warm-Lowland Wet:Cold | 0.0408854 |

| | | |
|--|----------------------------------|-----------|
| | Mixed Soil:Warm-Lowland Wet:Cold | 0.0000002 |
| | Lowland Dry:Warm-Mixed Soil:Cold | 0.0335682 |
| | Lowland Wet:Warm-Mixed Soil:Cold | 0.0271402 |
| | Mixed Soil:Warm-Mixed Soil:Cold | 0.0000003 |
| | Alpine Wet:Warm-Alpine Dry:Warm | 0.0220956 |
| | Lowland Dry:Warm-Alpine Dry:Warm | 0.0006337 |
| | Lowland Wet:Warm-Alpine Dry:Warm | 0.0004046 |
| | Mixed Soil:Warm-Alpine Dry:Warm | 0.0000000 |
| | Mixed Soil:Warm-Alpine Wet:Warm | 0.0002258 |
| | Mixed Soil:Warm-Lowland Dry:Warm | 0.0372262 |
| | Mixed Soil:Warm-Lowland Wet:Warm | 0.0186108 |

| Tukey HSD - Ergosterol Change | | Tukey HSD - C:N ratio | |
|-----------------------------------|-----------|----------------------------------|-----------|
| Category and Treatment | p-value | Category and Treatment | p-value |
| Alpine Wet-Alpine Dry | 0.0000001 | Alpine Wet-Alpine Dry | 0.0000000 |
| Lowland Dry-Alpine Dry | 0.0072683 | Lowland Dry-Alpine Dry | 0.0000000 |
| Mixed Soil-Alpine Dry | 0.0498418 | Lowland Wet-Alpine Dry | 0.0000258 |
| Lowland Dry-Alpine Wet | 0.0000000 | Mixed Soil-Alpine Dry | 0.0000000 |
| Lowland Wet-Alpine Wet | 0.0000478 | Lowland Dry-Alpine Wet | 0.0089497 |
| Mixed Soil-Alpine Wet | 0.0002562 | Lowland Wet-Alpine Wet | 0.0000002 |
| Lowland Wet-Lowland Dry | 0.0000015 | Lowland Wet-Lowland Dry | 0.0187900 |
| Mixed Soil-Lowland Dry | 0.0000003 | Mixed Soil-Lowland Wet | 0.0000047 |
| Warm-Cold | 0.0128274 | Warm - Cold | 0.0000000 |
| Alpine Wet:Cold-Alpine Dry:Cold | 0.0001159 | Alpine Wet:Cold-Alpine Dry:Cold | 0.0000000 |
| Alpine Wet:Warm-Alpine Dry:Cold | 0.0000543 | Lowland Dry:Cold-Alpine Dry:Cold | 0.0000005 |
| Lowland Dry:Cold-Alpine Wet:Cold | 0.0000067 | Lowland Wet:Cold-Alpine Dry:Cold | 0.0007857 |
| Alpine Dry:Warm-Alpine Wet:Cold | 0.0018029 | Mixed Soil:Cold-Alpine Dry:Cold | 0.0002325 |
| Lowland Dry:Warm-Alpine Wet:Cold | 0.0000000 | Alpine Wet:Warm-Alpine Dry:Cold | 0.0017527 |
| Lowland Wet:Warm-Alpine Wet:Cold | 0.0011383 | Mixed Soil:Warm-Alpine Dry:Cold | 0.0000042 |
| Mixed Soil:Warm-Alpine Wet:Cold | 0.0094633 | Lowland Wet:Cold-Alpine Wet:Cold | 0.0002363 |
| Lowland Wet:Cold-Lowland Dry:Cold | 0.0052200 | Mixed Soil:Cold-Alpine Wet:Cold | 0.0025404 |
| Mixed Soil:Cold-Lowland Dry:Cold | 0.0066785 | Alpine Dry:Warm-Alpine Wet:Cold | 0.0000000 |
| Alpine Wet:Warm-Lowland Dry:Cold | 0.0000019 | Alpine Wet:Warm-Alpine Wet:Cold | 0.0001024 |
| Lowland Dry:Warm-Lowland Wet:Cold | 0.0000008 | Lowland Dry:Warm-Alpine Wet:Cold | 0.0000000 |
| Lowland Dry:Warm-Mixed Soil:Cold | 0.0000015 | Lowland Wet:Warm-Alpine Wet:Cold | 0.0000000 |
| Alpine Wet:Warm-Alpine Dry:Warm | 0.0010113 | Mixed Soil:Warm-Alpine Wet:Cold | 0.0126390 |
| Lowland Dry:Warm-Alpine Dry:Warm | 0.0021198 | Alpine Dry:Warm-Lowland Dry:Cold | 0.0000000 |

| | | | |
|-----------------------------------|-----------|-----------------------------------|-----------|
| Lowland Dry:Warm-Alpine Wet:Warm | 0.0000000 | Lowland Dry:Warm-Lowland Dry:Cold | 0.0000080 |
| Lowland Wet:Warm-Alpine Wet:Warm | 0.0005428 | Lowland Wet:Warm-Lowland Dry:Cold | 0.0000000 |
| Mixed Soil:Warm-Alpine Wet:Warm | 0.0057166 | Alpine Dry:Warm-Lowland Wet:Cold | 0.0000000 |
| Lowland Wet:Warm-Lowland Dry:Warm | 0.0010491 | Lowland Dry:Warm-Lowland Wet:Cold | 0.0150023 |
| Mixed Soil:Warm-Lowland Dry:Warm | 0.0000338 | Lowland Wet:Warm-Lowland Wet:Cold | 0.0000169 |
| | | Alpine Dry:Warm-Mixed Soil:Cold | 0.0000000 |
| | | Lowland Dry:Warm-Mixed Soil:Cold | 0.0042858 |
| | | Lowland Wet:Warm-Mixed Soil:Cold | 0.0000054 |
| | | Alpine Wet:Warm-Alpine Dry:Warm | 0.0000000 |
| | | Lowland Dry:Warm-Alpine Dry:Warm | 0.0054673 |
| | | Mixed Soil:Warm-Alpine Dry:Warm | 0.0000000 |
| | | Lowland Dry:Warm-Alpine Wet:Warm | 0.0314998 |
| | | Lowland Wet:Warm-Alpine Wet:Warm | 0.0000439 |
| | | Mixed Soil:Warm-Lowland Dry:Warm | 0.0000825 |
| | | Mixed Soil:Warm-Lowland Wet:Warm | 0.0000000 |

| Tukey HSD - Seedling phosphorus content | | Tukey HSD - Seedling nitrogen content | |
|-----------------------------------------|-----------|---------------------------------------|-----------|
| Category and Treatment | p-value | Category and Treatment | p-value |
| Lowland Dry-Alpine Dry | 0.0103937 | Alpine Wet-Alpine Dry | 0.0000000 |
| Lowland Wet-Alpine Dry | 0.0000910 | Lowland Dry-Alpine Dry | 0.0000000 |
| Mixed Soil-Alpine Dry | 0.0000002 | Lowland Wet-Alpine Dry | 0.0000000 |
| Lowland Wet-Alpine Wet | 0.0069034 | Mixed Soil-Alpine Dry | 0.0000000 |
| Mixed Soil-Alpine Wet | 0.0000193 | Mixed Soil-Alpine Wet | 0.0207702 |
| Mixed Soil-Lowland Dry | 0.0141477 | Lowland Wet-Lowland Dry | 0.0094223 |
| Warm-Cold | 0.0039177 | Mixed Soil-Lowland Wet | 0.0007040 |
| Lowland Wet:Warm-Alpine Dry:Cold | 0.0002500 | Warm-Cold | 0.0000370 |
| Mixed Soil:Warm-Alpine Dry:Cold | 0.0000029 | Alpine Wet:Cold-Alpine Dry:Cold | 0.0003320 |
| Lowland Wet:Warm-Alpine Wet:Cold | 0.0326030 | Lowland Dry:Cold-Alpine Dry:Cold | 0.0000009 |
| Mixed Soil:Warm-Alpine Wet:Cold | 0.0007144 | Lowland Wet:Cold-Alpine Dry:Cold | 0.0003289 |
| Mixed Soil:Warm-Lowland Dry:Cold | 0.0165015 | Mixed Soil:Cold-Alpine Dry:Cold | 0.0001143 |
| Mixed Soil:Warm-Lowland Wet:Cold | 0.0021383 | Alpine Wet:Warm-Alpine Dry:Cold | 0.0000014 |
| Lowland Wet:Warm-Alpine Dry:Warm | 0.0008691 | Lowland Dry:Warm-Alpine Dry:Cold | 0.0000000 |
| Mixed Soil:Warm-Alpine Dry:Warm | 0.0000077 | Lowland Wet:Warm-Alpine Dry:Cold | 0.0000089 |
| Lowland Wet:Warm-Alpine Wet:Warm | 0.0031439 | Mixed Soil:Warm-Alpine Dry:Cold | 0.0000000 |
| Mixed Soil:Warm-Alpine Wet:Warm | 0.0000246 | Alpine Dry:Warm-Alpine Wet:Cold | 0.0014576 |
| Mixed Soil:Warm-Lowland Dry:Warm | 0.0110606 | Mixed Soil:Warm-Alpine Wet:Cold | 0.0004447 |
| | | Alpine Dry:Warm-Lowland Dry:Cold | 0.0000032 |

| | | |
|--|-----------------------------------|-----------|
| | Mixed Soil:Warm-Lowland Dry:Cold | 0.0269334 |
| | Alpine Dry:Warm-Lowland Wet:Cold | 0.0015354 |
| | Lowland Dry:Warm-Lowland Wet:Cold | 0.0104101 |
| | Mixed Soil:Warm-Lowland Wet:Cold | 0.0000093 |
| | Alpine Dry:Warm-Mixed Soil:Cold | 0.0005050 |
| | Mixed Soil:Warm-Mixed Soil:Cold | 0.0001790 |
| | Alpine Wet:Warm-Alpine Dry:Warm | 0.0000048 |
| | Lowland Dry:Warm-Alpine Dry:Warm | 0.0000000 |
| | Lowland Wet:Warm-Alpine Dry:Warm | 0.0000355 |
| | Mixed Soil:Warm-Alpine Dry:Warm | 0.0000000 |
| | Mixed Soil:Warm-Alpine Wet:Warm | 0.0045332 |
| | Mixed Soil:Warm-Lowland Wet:Warm | 0.0006011 |

Supplementary Table 4: ANOVA tests

| AOV - Shoot nitrogen content | | | | | |
|-------------------------------------|-----------|---------------|----------------|----------------|------------------|
| | <u>Df</u> | <u>Sum Sq</u> | <u>Mean Sq</u> | <u>F value</u> | <u>Pr(>F)</u> |
| Soil | 4 | 2.4879 | 0.6220 | 40.209 | 5.30e-14 |
| Temp | 1 | 0.3298 | 0.3298 | 21.320 | 3.51e-05 |
| Soil:Temp | 4 | 0.1927 | 0.0482 | 3.114 | 0.0246 |
| Residuals | 43 | 0.6652 | 0.0155 | | |

| AOV - Shoot phosphorus content | | | | | |
|---------------------------------------|-----------|---------------|----------------|----------------|------------------|
| | <u>Df</u> | <u>Sum Sq</u> | <u>Mean Sq</u> | <u>F value</u> | <u>Pr(>F)</u> |
| Soil | 4 | 0.9939 | 0.24847 | 15.087 | 8.79e-08 |
| Temp | 1 | 0.1542 | 0.15421 | 9.364 | 0.0038 |
| Soil:Temp | 4 | 0.1844 | 0.04611 | 2.800 | 0.0375 |
| Residuals | 43 | 0.7081 | 0.01647 | | |

| AOV - Shoot total weight | | | | | |
|---------------------------------|-----------|---------------|----------------|----------------|------------------|
| | <u>Df</u> | <u>Sum Sq</u> | <u>Mean Sq</u> | <u>F value</u> | <u>Pr(>F)</u> |
| Soil | 4 | 0.5911 | 0.1478 | 17.693 | 1.18e-08 |
| Temp | 1 | 0.3986 | 0.3986 | 47.728 | 1.75e-08 |
| Soil:Temp | 4 | 0.1905 | 0.0476 | 5.703 | 0.000897 |
| Residuals | 43 | 0.3591 | 0.0084 | | |

| AOV - Carbon change | | | | | |
|----------------------------|-----------|---------------|----------------|----------------|------------------|
| | <u>Df</u> | <u>Sum Sq</u> | <u>Mean Sq</u> | <u>F value</u> | <u>Pr(>F)</u> |
| Soil | 4 | 1.0437 | 0.26093 | 10.237 | 6.51e-06 |
| Temp | 1 | 0.1868 | 0.18679 | 7.329 | 0.0097 |
| Soil:Temp | 4 | 0.2250 | 0.05624 | 2.207 | 0.0842 |
| Residuals | 43 | 1.0960 | 0.02549 | | |

| AOV - C:N Ratio | | | | | |
|------------------------|-----------|---------------|----------------|----------------|------------------|
| | <u>Df</u> | <u>Sum Sq</u> | <u>Mean Sq</u> | <u>F value</u> | <u>Pr(>F)</u> |
| Soil | 4 | 1.1913 | 0.2978 | 44.640 | 9.01e-15 |
| Temp | 1 | 0.4924 | 0.4924 | 73.813 | 7.00e-11 |
| Soil:Temp | 4 | 0.2524 | 0.0631 | 9.456 | 1.42e-05 |
| Residuals | 43 | 0.2869 | 0.0067 | | |

AOV - Ergosterol change

| | <u>Df</u> | <u>Sum Sq</u> | <u>Mean Sq</u> | <u>F value</u> | <u>Pr(>F)</u> |
|-----------|-----------|---------------|----------------|----------------|------------------|
| Soil | 4 | 2.0350 | 0.5087 | 32.377 | 1.83e-12 |
| Temp | 1 | 0.1067 | 0.1067 | 6.792 | 0.0125 |
| Soil:Temp | 4 | 0.1430 | 0.0357 | 2.275 | 0.0767 |
| Residuals | 43 | 0.6757 | 0.0157 | | |

AOV - Richness, soil (number of OTUs)

| | <u>Df</u> | <u>Sum Sq</u> | <u>Mean Sq</u> | <u>F value</u> | <u>Pr(>F)</u> |
|-----------|-----------|---------------|----------------|----------------|------------------|
| Soil | 4 | 2.5791 | 0.6448 | 17.951 | 6.28e-10 |
| Temp | 1 | 0.0001 | 0.0001 | 0.003 | 0.954 |
| Soil:Temp | 4 | 0.0225 | 0.0056 | 0.156 | 0.959 |
| Residuals | 64 | 2.2987 | 0.0359 | | |

AOV - Richness, roots (number of OTUs)

| | <u>Df</u> | <u>Sum Sq</u> | <u>Mean Sq</u> | <u>F value</u> | <u>Pr(>F)</u> |
|-----------|-----------|---------------|----------------|----------------|------------------|
| Soil | 4 | 0.7647 | 0.19119 | 5.296 | 0.00123 |
| Temp | 1 | 0.1240 | 0.12405 | 3.436 | 0.06970 |
| Soil:Temp | 4 | 0.1477 | 0.03691 | 1.022 | 0.40485 |
| Residuals | 50 | 1.8052 | 0.03610 | | |

AOV - Beta diversity, roots

| | <u>Df</u> | <u>Sum Sq</u> | <u>Mean Sq</u> | <u>F value</u> | <u>Pr(>F)</u> |
|-----------|-----------|---------------|----------------|----------------|------------------|
| Soil | 4 | 1.0613 | 0.26533 | 21.753 | 1.92e-10 |
| Temp | 1 | 0.0000 | 0.00000 | 0.000 | 0.996 |
| Soil:Temp | 4 | 0.0330 | 0.00826 | 0.677 | 0.611 |
| Residuals | 50 | 0.6099 | 0.01220 | | |

AOV - Beta diversity, soil

| | <u>Df</u> | <u>Sum Sq</u> | <u>Mean Sq</u> | <u>F value</u> | <u>Pr(>F)</u> |
|-----------|-----------|---------------|----------------|----------------|------------------|
| Soil | 4 | 0.2837 | 0.07093 | 13.974 | 3e-08 |
| Temp | 1 | 0.0304 | 0.03037 | 5.984 | 0.01720 |
| Soil:Temp | 4 | 0.0815 | 0.02037 | 4.012 | 0.00576 |
| Residuals | 64 | 0.3249 | 0.00508 | | |

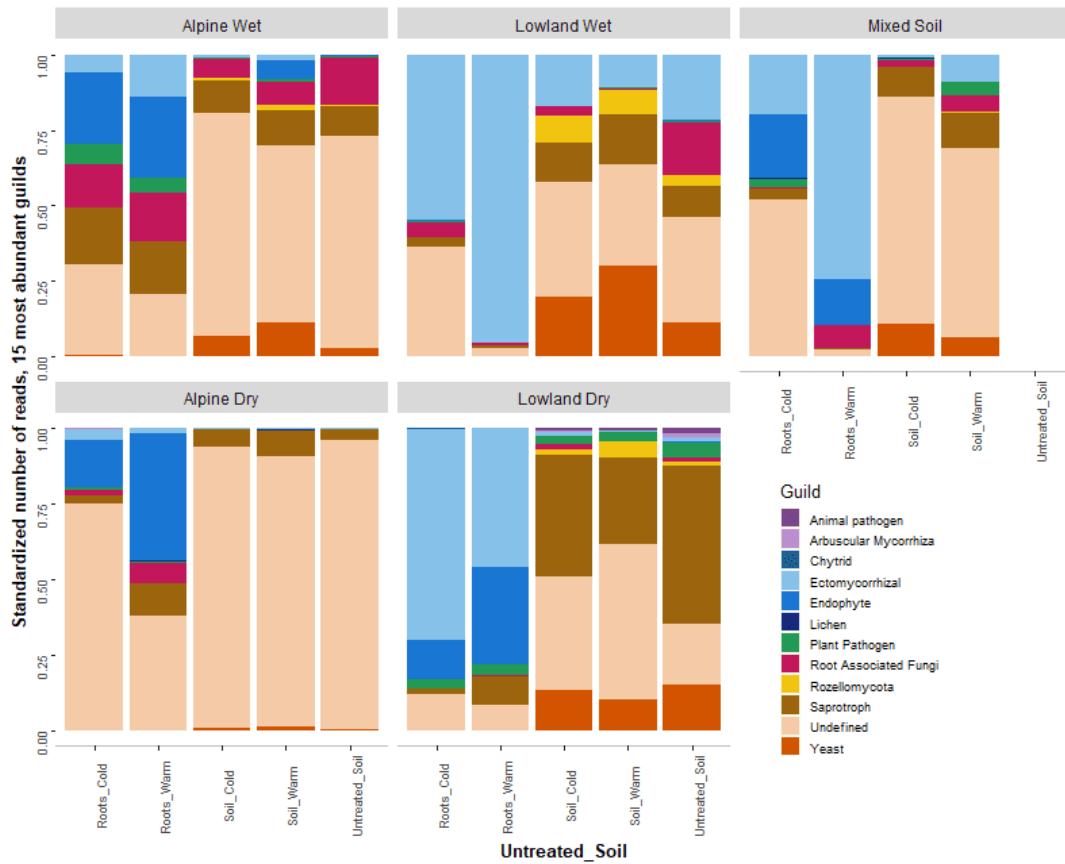


Figure S1: Relative abundance of functional guilds across root and soil samples. Roots and soil from cold and warm treatment are compared next to each other within soil categories in addition to one untreated soil sample taken from the homogenized soil from each location before the start of the experiment.

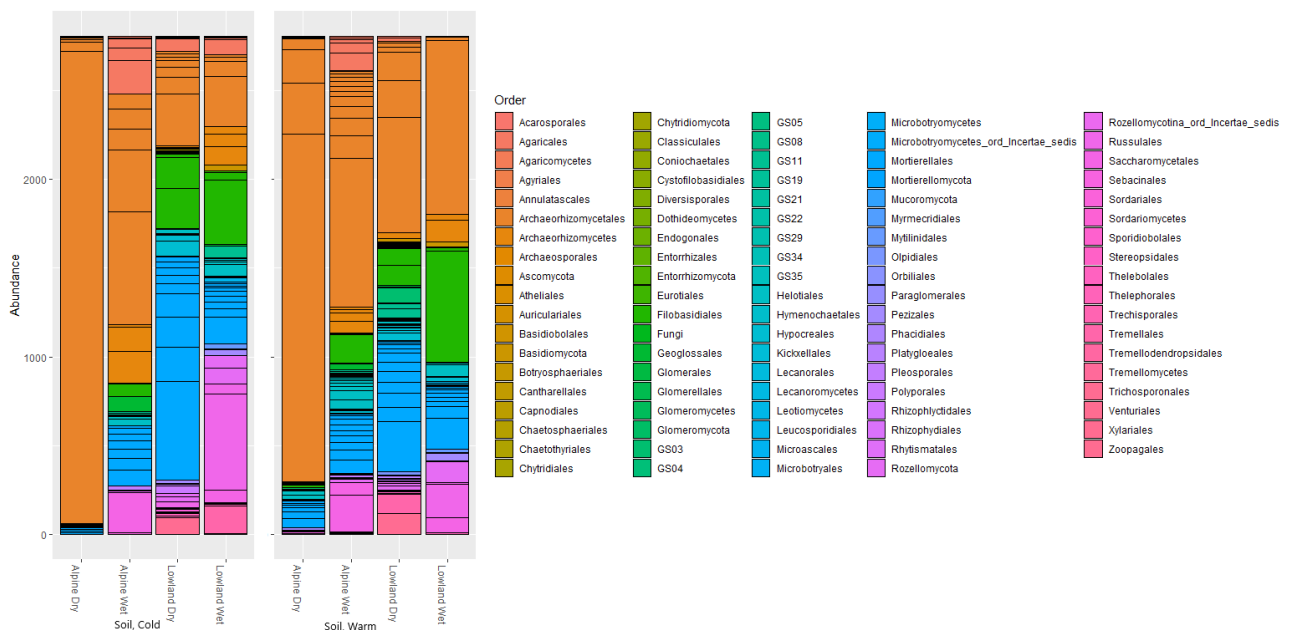


Figure S2: Relative abundance of fungal orders in control pots.