

Managing with fire: effects of recurring prescribed fire on soil and root-associated fungal communities

By

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Abstract

Prescribed fire is a necessary management tool used to reduce fuel loads and to maintain fire-adapted ecosystems over time. Although the effects of fire on vegetation and soil properties are well understood, the long-term impacts of different fire regimes on soil fungi, root-inhabiting and ectomycorrhizal (ECM) fungi remain largely unknown. Previous studies show that high intensity wildfires reduce soil fungal biomass and alter fungal communities, however the effects of repeated low intensity prescribed fires are less understood. Studies described in this thesis took advantage of a long-term (>25 years) fire management regime in southern yellow pine stands in the southeastern United States to analyze the effects of repeated prescribed fires on soil fungi, root-associated and ECM fungal communities. The fire management regimes included five fire treatments varying in season (winter and summer) and interval length (two-year, three-year, six-year, and unburned control) allowing us to address effects of burn season and fire frequency on these fungal communities. We used 454-pyrosequencing to analyze ECM roots to specifically focus on the root-associate fungi and ECM. After a pilot study comparing the use of non-proofreading and proofreading polymerases to generate deep high throughput sequence data on soil fungal communities using Illumina MiSeq technology, proofreading polymerase was chosen to create amplicon libraries to minimize overestimation of community richness and underestimation of community evenness. We found that season had no or only minimal effect on diversity and community composition on any of these fungal communities. However, both soil and root-associated fungi responded compositionally to frequent fire intervals. In contrast, we observed no effects of recurring fire on ECM communities. Indicator taxon analyses identified many taxa in each dataset (soil, root-associated, and ECM fungi) that represent potentially fire suppressed or fire adapted taxa. These findings indicate that frequent recurring prescribed fires result in distinct fire adapted/tolerant soil and root-associated fungal communities that are correlated with the desired fire-adapted plant communities. However, the ECM symbionts colonizing these hosts remain largely unaffected.

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Dedication

I would like to dedicate this to the wonderful world of mycorrhiza.

Preface

All chapters for this thesis were written and formatted to specific journals as laid out in the footnotes for each chapter title page. Therefore, in-text citation and reference formats were followed for said journal and differ slightly for each chapter. Chapter 1 serves as an introduction and was not submitted for publication but follows the same formatting as Chapter 2 for consistency. Chapter 2 has citations and references formatted for *Fungal Ecology*. Chapter 3 is formatted for *Forest Ecology and Management*. Chapters 4 and 5 are formatted for *Mycorrhiza*. Chapter 5 serves as a conclusion and was not submitted for publication.

Chapter 1- Introduction

Managing fire-adapted forest ecosystems requires the implementation of prescribed fire to accomplish preservation of desired vegetation and reduce fuel load accumulation (Waldrop et al., 1992; Callaham et al., 2012). This practice is especially important for southern yellow pine fire-adapted ecosystems in the southeastern United States, as they provide necessary habitat for wildlife (Ligon et al., 1986; Kowal et al., 2013; Steen et al., 2013) and are economically valuable in silviculture (Talbert et al., 1985; Borders et al., 2001). Silviculture practices are continually refined to optimize stand production (Borders et al., 2001; Ramsey et al., 2003). As such, the effects of silviculture practices on beneficial microbes, specifically soil fungi and ectomycorrhizal (ECM) communities (van der Heijden et al., 1998; Jeffries et al., 2003), should be studied. These belowground communities contribute to ecosystem processes, are a key component in nutrient cycling, and promote plant health and productivity (Fogel and Hunt, 1982; Fogel, 2006; Ekblad et al., 2013; Luo et al., 2014). It has previously been determined that high intensity wildfires can have negative effects on soil fungi and ECM communities as they significantly reduce their biomass (Fritze et al., 1993; Pietikäinen et al., 1993; Dooley and Treseder, 2012) and can alter belowground fungal communities (Baar et al., 1999; Chen et al., 2002). However, the effects of low intensity prescribed fires are less understood, especially the long-term forest management practices that require repeated burning. As management practices vary in time of burning and frequency, it is also important to study how different prescribed fire regimes affect these beneficial organisms in the long-term.

The effects of fire on fungal communities depend on many factors, including fire intensity and duration, as well as pre-fire soil parameters (Visser 1994; Longo et al. 2011; Dooley and Treseder 2013; Holden et al. 2013). Previous studies have found that repeated frequent (two- and four-year) prescribed fires can alter soil fungal and ECM communities in Australian sclerophyll forests (Anderson et al., 2007; Bastias et al., 2006a). However, these results are difficult to compare with managed silviculture practices in the southeastern United States. Studies described here took advantage of a long-term experiment implementing different fire regimes in a southern yellow pine forest to address the effects of long-term repeated prescribed fire on soil fungi, root-associated fungi, and ECM. The overarching goal of the

management plan was to preserve the fire-adapted plant communities and to evaluate prescribed burning treatments varying in season and interval. The treatments included unburned plots that served as a reference to represent the undesirable outcome of fire suppression. The remaining treatments vary in season of burn (winter, summer) and interval (two-year, three-year, six-year). Using this long-term management plan we aimed to address 1) if recurring prescribed fires have a long-term effect on soil fungi, root-associated fungi, and ECM; 2) if these responses depend on fire interval; and 3) if these responses depend of seasonal timing of fires.

Next generation sequencing (NGS) has become the dominant method in studying fungal ecology for analyzing diversity, richness, and community composition (Hibbert et al. 2009). In recent years many studies have focused on data produced by different available sequencing technologies (Schuster 2007; Quail et al. 2012; Brown et al. 2013). However, the data produced using different materials, protocols, and reagents are less studied. In addition to the ecological questions previously discussed, we aimed to determine if the sequence data produced differed as a result of the choice of DNA polymerases. Using soil fungi DNA we compared community composition and diversity and evenness estimators produced by non-proofreading and proofreading polymerases.

With continual technological improvements, studies on fungal ecology move toward a more comprehensive query of the resident communities. The results from our studies further our understanding of the effects of prescribed fire on belowground fungal communities and how management practices impact them.

References

- Anderson, I.C., Bastias, B.A., Genney, D.R., Parkin, P.I., Cairney, J.W.G., 2007. Basidiomycete fungal communities in Australian sclerophyll forest soil are altered by repeated prescribed burning. *Mycological Research*, 111: 482-486.
- Baar, J., Horton, T.R., Kretzer, A.M., Bruns, T.D., 1999. Mycorrhizal Colonization of *Pinus muricata* from Resistant Propagules after a Stand-Replacing Wildfire. *New Phytologist*, 143: 409-418.

Bastias, B.A., Huang, Z.Q., Blumfields, T., Xu, Z., Cairney, J.W.G., 2006a. Influence of repeated prescribed burning on the soil fungal community in an eastern Australian wet sclerophyll forest. *Soil Biology and Biochemistry*, 38: 3492-3501.

Borders, B.E., Bailey, R.L., 2001. Loblolly pine-pushing the limits of growth. *Southern Journal of Applied Forestry* 25: 69-74.

Brown, S.P., Callaham, Jr. M.A., Oliver, A.K., Jumpponen, A., 2013. Deep Ion Torrent sequencing identifies soil fungal community shifts after frequent prescribed fires in a southeastern US forest ecosystem. *FEMS Microbiology Ecology* 86: 557-566.

Brown, S.P., Callaham, Jr. M.A., Oliver, A.K., Jumpponen, A., 2013. Deep Ion Torrent sequencing identifies soil fungal community shifts after frequent prescribed fires in a southeastern US forest ecosystem. *FEMS Microbiology Ecology*, 86: 557-566.

Callaham, M.A. Jr., Scott, D.A., O'Brien, J.J., Stanturf, J.A., 2012. Cumulative effects of fuel management on the soils of eastern U.S., in: LaFayette, R., Brooks, M.T., Potyondy, J.P., Audin, L., Krieger, S.L., Trettin, C.C. (Eds.), *Cumulative watershed effects of fuel management in the Eastern United States*. Gen. Tech. Rep. SRS-161. Asheville, NC: U.S. Department of Agriculture Forest Service, Southern Research Station, pp. 202-228.

Chen, D.M., Cairney, W.G.J., 2002. Investigation of the influence of prescribed burning on ITS profiles of ectomycorrhizal and other soil fungi at three Australian sclerophyll forest sites. *Mycological Research*, 106: 532-540.

Dooley, S.R., Treseder, K.K., 2012. The effect of fire microbial biomass: a meta-analysis of field studies. *Biogeochemistry*, 109: 49-61.

Ekblad, A., Wallander, H., Godbold, D.L., Cruz, C., Johnson, D., Baldrian, P., Björk, R.G., Epron, D., Keiliszewska-Rokicka, B., Kjoller, R., Kraigher, H., Matzner, E., Newmann, J.,

Plassard, C., 2013. The production and turnover of extramatrical mycelium of ectomycorrhizal fungi in forest soils: role in carbon cycling. *Plant Soil* 366: 1-27.

Fogel, R., Hunt, G., 1982. Contribution of mycorrhizae and soil fungi to nutrient cycling in a Douglas-fir ecosystem. *Canadian Journal of Forest Research* 13: 219- 232.

Fogel, R., 2006. Mycorrhizae and nutrient cycling in natural forest ecosystems. *New Phytologist* 86: 199-212.

Fritze, H., Pennanen, T., Pietikäinen, J., 1993. Recovery of soil microbial biomass and activity from prescribed burning. *Canadian Journal of Forest Research* 23: 1286-1290.

Hibbett, D.S., Ohman, A., Kirk, P.M., 2009. Fungal ecology catches fire. *New Phytologist* 184: 279-282.

Holden, S.R., Treseder, K.K., 2013. A meta-analysis of soil microbial biomass responses to forest disturbances. *Frontiers in Microbiology*, 4: article 163.

Jeffries, P., Gianinazzi, S., Perotto, S., Turnau, K., Barea, J., 2003. The contribution of arbuscular mycorrhizal fungi in sustainable maintenance of plant health and soil fertility. *Biology and Fertility of Soils*. 37: 1-16.

Kowal, V.A., Scholke, A., Kanagaraj, R., Bruggeman, D., 2013. Resource selection probability functions for gopher tortoise: providing a management tool application across the species' range. *Environmental Management* 53: 594-605.

Ligon, D.J., Stacey, P.B., Conner, R.N., Bock, C.E., Adkisson, C.S., 1986. Report of the American ornithologists' union committee for the conservation of the red-cockaded woodpecker. *The Auk* 103: 848-855.

Longo, M.S., Urcelay, C., Nouhra, E., 2011. Long term effects of fire on ectomycorrhizas and soil properties in *Nothofagus pumilio* forest in Argentina. *Forest Ecology and Management*, 262: 348-354.

Luo, Z., Wu, C., Zhang, C., Li, H., Lipka, U., Polle, A., 2014. The role of ectomycorrhizas in heavy metal stress tolerance of host plants. *Environmental and Experimental Botany* 108: 47-62.

Pietikäinen, J., Fritze, H., 1993. Microbial biomass and activity in the humus layer following burning: short-term effects of two different fires. *Canadian Journal of Forest Research* 23: 1275-1285.

Quail, M.A., Smith, M., Coupland, P., Otto, T.D., Harris, S.R., Connor, T.R, Bertoni, A., Swerdlow, H.P., Gu, Y., 2012. A tale of three next generation sequencing platforms: comparison of Ion Torrent, Pacific Biosciences and Illumina MiSeq sequencers. *BMC Genomics*. 13: 341

Ramsey, C.L, Jose, S., Brecke, B.J., Merritt, S., 2003. Growth response of longleaf pine (*Pinus palustris* Mill.) seedlings to fertilization and herbaceous weed control in an old field in southern USA. *Forest Ecology and Management*. 172: 281-289.

Schuster, S.C., 2007. Next-generation sequencing transforms today's biology. *Nature Methos*.15: 16- 18.

Steen, D.A., Smith, L.L., Morris, G., Conner, M., Litt, A.R., Pokswinski, S., Guyer, C., 2013. Response of six-lined racerunner (*Aspidoscelis sexlineata*) to habitat restoration in fire-suppressed longleaf pine (*Pinus palustris*) sandhills. *Restoration Ecology* 21: 457- 463.

Talbert, J.T., Weir, R.J., Arnold, R.D., 1985. Cost and benefits of a mature first-generation loblolly pine tree improvement program. *Journal of forestry* 83: 162-166.

van der Heijden, M.G.A., Klironomos, J.N., Ursic, M., Moutoglis, P., Streitwolf-Engle, R., Boller, T., Wiemken, A., Sanders, I.R., 1998. Mycorrhizal fungal diversity determines plant biodiversity, ecosystem variability and productivity. *Nature*. 396: 69-72.

Visser, S., 1994. Ectomycorrhizal fungal succession in jack pine stands following wildfire. *New Phytologist*, 129: 389-401.

Waldrop, T.A, White, D.L, Jones, S.M., 1992. Fire regimes for pine-grassland communities in the southeastern United States. *Forest Ecology and Management* 47: 195-210.

Chapter 2- Polymerase matters: non-proofreading enzymes inflate richness estimates by up to 20%¹

Abstract

Metabarcoding data generated using next-generation sequencing (NGS) are overwhelmed with rare taxa. Low frequency Operational Taxonomic Units (OTUs) may be artifacts primarily generated by PCR-amplification errors resulting from polymerase mis-pairing or slippage. We analyzed two Internal Transcribed Spacer 2 (ITS2) MiSeq libraries generated with proofreading (ThermoScientific Phusion®) and non-proofreading (ThermoScientific Phire®) polymerases from same MiSeq reaction, same samples, and using the same DNA tags to evaluate the effect of the polymerase choice on the estimates of the richness, diversity and community composition. Our data show that while the overall communities from the two libraries are comparable, richness estimators are exaggerated by the use of the non-proofreading polymerase – up to 20% depending on the threshold of low frequency OTUs to cull. The overestimation of richness also led to consequent underestimation of community evenness, a result of increase in the low frequency OTUs. Stringent thresholds of eliminating the rare reads partially remedy this issue, but exclusion of reads that occur ≤ 10 times still likely overestimated richness by 3.2% on average. As a result of our findings, we strongly recommend the use of proofreading polymerases to improve the data integrity and the reliability of richness estimators as well as the use of stringent culling thresholds for rare sequences.

Keywords: DNA polymerase, fungal communities, proofreading, richness, community composition

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The adoption of next generation sequencing (NGS) tools has enabled deep interrogation of hyper-diverse fungal communities (Hibbett et al., 2009). NGS data can be overwhelmed by rare Operational Taxonomic Units (OTUs) that may represent a ‘rare biosphere’ (Sogin et al., 2006), cryptic taxa, or simply PCR and sequencing artifacts (Tedersoo et al., 2010; Brown et al., 2014). While some rare OTUs likely represent true biological variability, the artifact OTUs may lead to inflation of richness estimators from NGS data (Huse et al., 2010; Kunin et al., 2010; Quince et al., 2011).

As most metabarcoding data are generated through polymerase chain reaction (PCR) carried out by DNA polymerases, we aimed to quantify the effects of polymerase choice. We aimed to answer the question ‘Do the data from proofreading and non-proofreading polymerases differ?’ To do this, we compared two thermostable hot start polymerases from the same manufacturer and examined whether the proofreading enzyme would minimize potentially erroneous sequences resulting from PCR errors in complex environmental templates. We used 24 experimental units from a long-term prescribed fire experiment that was designed to evaluate the effects of fires on ecosystem properties and attributes (see Brown et al., 2013). Samples from the two polymerase libraries originated from the same DNA extract and were amplified using a two-step PCR reaction (Berry et al., 2011). The primary PCR reaction used primers ITS1F (Gardes and Bruns, 1993) and ITS4 (White et al., 1990) (25 cycles) and subsequent secondary PCR reactions (5 cycles) used a nested primer (fITS7) (Ihrmark et al., 2012) and a sample identifying 12-bp DNA tag in the reverse primer (ITS4).

To generate PCR-amplicons, we used two hot start polymerases from one manufacturer: a proofreading Phusion® Green Hot Start II High-Fidelity DNA polymerase and non-proofreading Phire® Green Hot Start II DNA polymerase (Thermo Scientific®, Pittsburgh, PA,

USA). Three technical replicates per experimental unit were combined after secondary PCRs and the experimental units equimolarly pooled into two amplicon libraries (24 experimental units/library; one generated with Phire®, another with Phusion® polymerase). The two amplicon libraries were sequenced in one reaction using MiSeq paired-end sequencing (v.2, Illumina, San Diego, CA) at Integrated Genomics Facility at Kansas State University Manhattan, KS. Paired fastq files for Phusion® and Phire® generated libraries are accessions in the Sequence Read Archive at NCBI (www.ncbi.nlm.nih.gov) under the accessions SRR1508275 and SRR1508273 respectively. Each sample was amplified and sequenced with identical reaction conditions and DNA-tags; this permitted us to evaluate the performance of these polymerases side by side and to specifically test differences in the generation of potential PCR artifacts by the two enzymes. We acknowledge that we were unable to estimate generation of PCR artifacts by the proofreading enzyme and will thus focus solely on the differences between the polymerases.

We analyzed the sequence data with the MOTHR pipeline (v. 1.32.2; Schloss et al., 2009) following suggestions from (Schloss et al., 2011; Kozich et al., 2013). After contiging the paired end reads, the Phire® library contained 6,292,965 sequences and the Phusion® library contained 5,425,946 sequences. The libraries were screened to remove sequences with less than 100bp contig overlap, ambiguous bases, any disagreements with primer or DNA-tag sequences (Table A.1), sequences shorter than 250 bp, or homopolymers ≥ 8 bp. This resulted in 1,182,870 remaining sequences for Phire® and 1,113,584 for the Phusion® quality controlled datasets. Remaining sequences were truncated to 250bp and the two libraries merged. Near identical sequences ($\geq 99\%$ similar) were preclustered to minimize sequencing bias (Huse et al., 2010), screened for chimeras (UCHIME, Edgar et al., 2011). After chimera removal, the experimental units were rarefied to 15,000 sequences per experimental unit (from each of the Phire and

Phusion libraries) for a total of 720,000 sequences total. We calculated a pairwise distance matrix and clustered sequences into OTUs at 97% sequence similarity. From the subsampled data, we enumerated sequences assigned to OTUs that were comprised of 1 sequence, ≤ 2 sequences, ≤ 5 sequences, and ≤ 10 sequences to estimate the numbers of low frequency OTUs that may represent artifacts (Tedersoo et al., 2010, Brown et al., 2014). Coverage (Good's coverage), richness and diversity estimators (Richness – S_{Obs} , complement of Simpson's diversity – 1-D, Evenness – Simpson's E_D , extrapolative richness – Chao1; Table A.2) were calculated for both Phusion® and Phire® datasets.

We tested for differences in numbers of putatively chimeric sequences, rare OTUs, and richness and diversity estimators generated with Phire® or Phusion® polymerases using a non-parametric Wilcoxon signed-rank tests using JMP® (version 7.0.2). To visualize and infer compositional differences in the fungal communities generated from the two polymerases, we derived a Bray-Curtis distance matrix in MOTHUR. The differences between polymerases associated communities were tested using Analysis of MOlecular VAriance (AMOVA; PERMANOVA in Anderson, 2001) and visualized using Non-metric Multi-Dimensional Scaling (NMDS) after estimating axis loading scores for first four ordination axes representing 57.9% of the variance (stress ≤ 0.20).

While the proportion of potential chimeras did not differ between the ITS2 libraries the proportion of rare OTUs did (Table A.2). Although the proportion of rare OTUs was low (≤ 2.5 % of the sequences), the Phire®-generated libraries consistently yielded a greater proportion of low frequency OTUs than those generated with Phusion®. This resulted in a consistent inflation of richness (S_{Obs}): the Phire®-generated data had ~20% greater richness when singletons were included compared to the Phusion®-generated data (Fig. 2.1). While the richness inflation was

consistent, removal of rare sequences somewhat controlled for this: inclusion of doubletons resulted in 7% greater richness and inclusion of reads that occurred ≤ 5 times resulted in 5% greater richness with the non-proofreading enzyme compared to the proofreading enzyme (Fig. 2.1). Overall, the increase in the proportion of rare OTUs in the Phire® dataset resulted in a small (on average 3.2%) but significant inflation of richness and subsequent deflation (6.6%) of evenness (Table A.2), even after omission of OTUs that were represented by ≤ 10 sequences. However, neither the extrapolative richness (Chao1) nor the diversity (1-D) estimators were strongly affected by the choice of the polymerase (Table A.2). Similarly, community composition did not differ between the datasets generated with the two polymerases (AMOVA: $F_{1,47} = 0.445$; $P = 0.9890$): the paired Phire® and Phusion® samples were tightly coupled to each other in our NMDS community visualization (Supplementary Fig. A.1).

Our comparison of proofreading and non-proofreading polymerases strongly indicates that richness estimators, but not compositional distributions were consistently sensitive to polymerase choices in MiSeq amplicon libraries. The ~20% inflation of richness was alarming and highlights the importance of diligent removal of rare OTUs from NGS data (Tedersoo et al., 2010; Brown et al., 2014). As deep sequencing of an excess of 10^4 reads per experimental unit affords for even more stringent and cautious quality control, we suggest that omission of reads occurring in counts ≤ 10 should be removed when possible. While it was impossible to determine the proportion of artifact sequences in the dataset generated with the proofreading enzymes, the combination of higher rare OTU omission thresholds and the selection of polymerases was likely to increase the quality and reliability of the NGS data. Agreeably, the proofreading enzymes tend to be more costly, but the increase in the polymerase costs can be balanced by more aggressive multiplexing and decreasing costs of sequencing.

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References

- Anderson, M.J., 2001. A new method for non-parametric multivariate analysis of variance. *Austral Ecology* 26. 32-46.
- Berry, D., Mahfoudh, K.B., Wagner, M., Loy, A., 2011. Barcoded primers used in multiplex amplicon pyrosequencing bias amplification. *Applied and Environmental Microbiology* 77, 7846–7849.
- Brown, S.P., Callahan, M.A., Oliver, A.K., Jumpponen, A., 2013. Deep Ion Torrent sequencing identifies soil fungal community shifts after frequent prescribed fires in a southeastern US forest ecosystem. *FEMS Microbiology Ecology* 86, 557-566.

Brown, S.P., Veach, A.M., Rigdon-Huss, A.R., Grond, K., Lickteig, S.K., Lothamer, K., Oliver, A.K., Jumpponen, A., 2014. Scraping the bottom of the barrel: are rare high throughput sequences artifacts? *Fungal Ecology* 13, 221-225.

Edgar, R.C., Haas, B.J., Clemente, J.C., Quince, C., Knight, R., 2011. UCHIME improves sensitivity and speed of chimera detection. *Bioinformatics* 27, 2194-2200.

Gardes, M., Bruns, T.D., 1993. ITS primers with enhanced specificity for Basidiomycetes – Application to the identification of mycorrhizae and rusts. *Molecular Ecology* 2, 113–118.

Huse, S.M., Welch, D.M., Morrison, H.G., Sogin, M.L., 2010. Ironing out the wrinkles in the rare biosphere through improved OTU clustering. *Environmental Microbiology* 12, 1889-1898.

Ihrmark, K., Bödeker, I.T.M., Cruz-Martinez, K., Friberg, H., Kubartova, A., Schenck, J., Stenlid, J., Brandström-Durling, M., Clemmensen, K.E., Lindahl, B.D., 2012. New primers to amplify the fungal ITS2 region - evaluation by 454-sequencing of artificial and natural communities. *FEMS Microbiology Ecology* 82, 666-677.

Kozich, J.J., Westcott, S.L., Baxter, N.T., Highlander, S.K., Schloss, P.D., 2013. Development of a dual-index sequencing strategy and curation pipeline for analyzing amplicon sequence data on the MiSeq Illumina sequencing platform. *Applied and Environmental Microbiology* 79, 5112-5120.

Pietikäinen, J., Fritze H., 1993. Microbial biomass and activity in the humus layer following burning: short-term effects of two different fires. *Canadian Journal of Forest Research* 23,1275-1285.

Fritze H., Pennanen T., Pietikäinen J., 1993. Recovery of soil microbial biomass and activity from prescribed burning. *Canadian Journal of Forest Research* 23, 1286-1290.

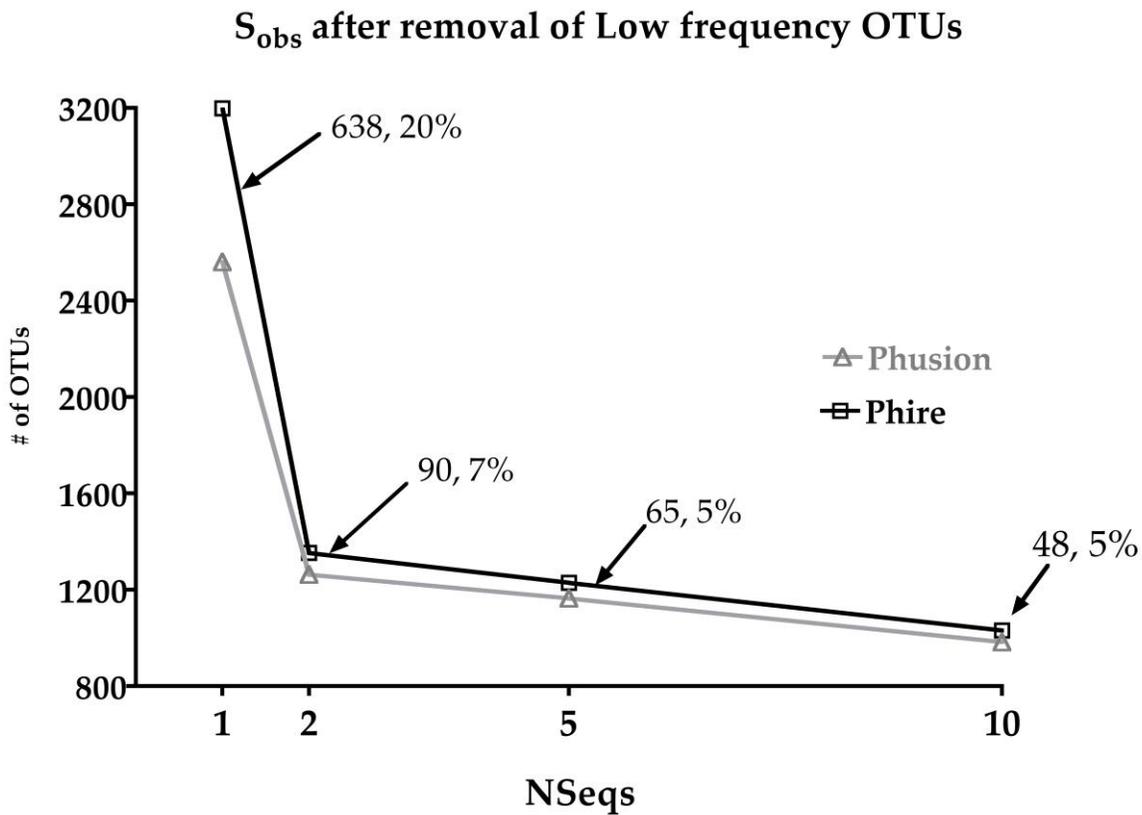
Tedersoo L., Nilsson R.H., Abarenkov K., Jairus T., Sadam A., Saar I., Bahram M., Bechem E., Chuyong G., Kõljalg U., 2010. 454 Pyrosequencing and Sanger sequencing of tropical mycorrhizal fungi provide similar results but reveal substantial methodological biases. *New Phytologist* 188, 291-301.

Wang Q., Garrity G.M., Tiedje J.M., Cole J.R., 2007. Naïve Bayesian Classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. *Applied and Environmental Microbiology* 73, 5261-5267.

White T.J., Bruns T., Lee S., Taylor J., 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics in: Innis, M.A.I, Gelfand, D.H., Sninsky, J.J., White, W.J. (Eds.), *PCR Protocols: A Guide to Methods and Applications*. Academic Press, San Diego, CA pp. 315–322.

Tables and Figures

Figure 2.1 Observed richness (S_{Obs}) in MiSeq ITS2 amplicon libraries generated with the non-proofreading Phire and proofreading Phusion polymerases. Inserted numbers indicate the difference in counts of OTUs comprised of rare sequences (singletons, doubletons, etc.) and their proportion relative to the Phire-generated amplicon library. Total number of rare OTUs comprised of ≤ 10 sequences was 2,168 (Phire) and 1,578 (Phusion) suggesting that non-proofreading polymerase generated 590 additional OTUs prior to the removal of rare OTUs – more than 20% inflation of richness estimators when rare OTUs were included.



Chapter 3- Soil fungal communities respond compositionally to frequent prescribed burning in a managed southeastern U.S. forest ecosystem²

Abstract

Prescribed fire is an important management tool to reduce fuel loads, to remove non-fire adapted species and to sustain fire-adapted taxa over time in many forested ecosystems of the southeastern USA. Yet, the long-term effects of recurring prescribed fires on soil fungi and their communities in these ecosystems remain unclear. We analyzed fungal Illumina MiSeq Internal Transcribed Spacer (ITS2) amplicons from a long-term prescribed burn experiment that has implemented different regimes for nearly a quarter century to evaluate the effects of differing prescribed fire intervals and the season of their implementation on soil-inhabiting fungal communities. Unburned plots were used as a reference to represent the compositional state resulting from no fire management. Our data showed that while recurring burning and the time of the prescribed burning do not affect richness and diversity of the fungal communities, the frequent (two and three year interval) fires maintain a fire-adapted community that is distinct from those in unburned reference plots. Subsequent indicator taxon analyses identified a total of 77 OTUs with differing degrees of fire adaptation: 37 OTUs that were more frequent in the frequently implemented burns and 26 OTUs that were more frequent in the fire suppressed treatment. We conclude that frequent prescribed burning maintains fire selected soil fungal

communities that may support plant communities that are composed of desired fire adapted or fire tolerant species that dominate the frequently burned areas.

Keywords: *fire management, prescribed fire, soil fungi, yellow pine*

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Introduction

Fire is a commonly implemented management tool used to reduce fuel loads in forested ecosystems of the southeastern USA (Waldrop et al., 1992; Callaham et al., 2012). Fire-regimes need to be continually refined to best fit the management goals (Stephens et al., 2005). In the southeastern USA, silviculture is a common practice of great economic importance (Borders et al., 2001; Talbert et al., 1985). To properly maintain forest stands for silviculture, fire must be implemented to retain the desired fire-adapted species and remove competing non-fire adapted species (Waldrop et al., 1992; Glitzenstein et al., 1995; Callaham et al., 2012). In many natural southern forest types, fire exclusion can lead to successional changes away from the diverse, fire-adapted ecosystems that developed there following Pleistocene glaciations (Abrahamson and Hartnett, 1990; Kirkman and Mitchell, 2006). Prescribed fire is viewed as a tool for restoration of these ecosystems, and frequent fires can result in overall improvement in terms of plant species richness, and animal food and habitat requirements (Ligon et al., 1986; Kowal et al., 2013; Steen et al., 2013). In determining optimal fire-regimes, a variety of ecosystem properties should be taken into account to ensure ecosystem stability and sustainability in the long-term. In non-fire adapted systems, or systems where fire has been long excluded, frequent fires can significantly reduce soil fungal biomass (Dooley and Treseder, 2012; Fritze et al., 1993; Pietikäinen et al., 1993), reduce the quantity and quality of soil carbon (Neff et al. 2005) as well as change nutrient availability (Harden et al., 2003; Wan et al. 2001; Certini, 2005) indicating that both the biotic and abiotic soil properties are sensitive to fire, at least in the short-term.

Forest fires affect soil microbial communities both in short- and long-term (Holden and Treseder, 2013) and may preferentially select for fire adapted soil-inhabiting microbes. The fire effects and their duration depend on the intensity and frequency of burns (Anderson et al., 2007; Bastias et al., 2006a; Baar et al., 1999; Chen et al., 2002; Dooley and Treseder, 2013; Hebel et al., 2009; Holden et al., 2013; Longo et al., 2011; Visser, 1994). Meta-analyses indicate that fires often reduce soil microbial biomass, at least in the short term (Dooley and Treseder, 2012; Holden and Treseder, 2013). Some microbial guilds are more sensitive to fire disturbance than others; Holden et al. (2013) concluded that ectomycorrhizal fungi exemplified such fire sensitive guilds. Others have pointed out specific taxa that are either resistant or adapted to fire disturbance. Examples of genera such include *Wilcoxina* (Fujimura et al., 2005; Baar et al., 1999; Kipfer et al., 2009), *Russula*, *Suillus* (Horton et al., 1998a), *Coltricia*, *Thelephora* (Visser, 1994), *Rhizopogon*, (Barr et al., 1999, Kipfer et al., 2009), *Tomentella* (Barr et al., 1999), and *Cenococcum* (Kipfer et al., 2009). While the fire effects to fungal biomass are often negative, some fungi respond positively to fire treatments (Baar et al., 1999; Fritze et al., 1993; Kipfer et al., 2009; Visser, 1994) and fruit abundantly soon after fire (Wicklow, 1973; 1975).

Although prescribed burning has become an increasingly important management tool, much of our current understanding of the fire effects on soil properties comes from wildfires. It is still uncertain whether the impacts of wildfires are comparable to those of a prescribed burning. Wildfires tend to be more severe than prescribed fires (Carter and Foster, 2004; Certini, 2005), burn hotter, consume more of the aboveground biomass and organic matter, and result in greater nutrient volatilization (Hatten and Zabowski, 2010). This is partly attributable to one of the basic principles of fire management: prescribed fires are usually conducted under conditions that result in lower fire intensity and severity, and generally outside of the high risk conditions

that are most conducive to the high intensity wildfires. Choromanska and DeLuca (2001) compared fire severity during a wildfire and prescribed burn in a temperate forest. They observed that prescribed fire consumed 42% of the fine fuel and resulted in no overstory tree mortality. In contrast, the wildfire consumed all fine fuel and led to complete stand mortality. Further, although both wildfires and prescribed fires tend to reduce soil fungal biomass (Dooley and Treseder, 2012), prescribed fires result in lesser loss of microbial biomass C than wildfires (Choromanska and DeLuca, 2001). Although prescribed fire effects may be less severe than those of wildfires, the long-term effects of recurring prescribed fires on soils and fungal communities therein have remained largely unknown, especially in the southeastern United States. This information is important to properly manage forests over time without compromising the composition and function of the soil fungal communities, which provide many crucial ecosystem services through nutrient cycling and facilitate plant productivity (Wardle et al., 2004).

Soil microbial communities may quickly return to the levels preceding the fire disturbance especially if undisturbed stands or undisturbed mineral soils serve as an inoculum source (Barker et al., 2013; Grogan et al., 2000). Yet, the recovery times of many ecosystem attributes tend to be long. Eddy covariance studies and vegetation surveys suggest that re-establishment of primary productivity may require up to more than a decade after fires in boreal forests (Amiro et al., 2010; Goulden et al., 2011; Mack et al., 2008). Following wildfires, fungal hyphal lengths in the organic horizon required more than two decades to return to pre-fire levels (Holden et al., 2013) and soil fungal successional changes can continue several decades after a wildfire disturbance (Visser, 1994). However, Fritze et al. (1993) estimated a 12-year recovery time to a pre-fire state after a prescribed fire event. Finally, post-fire effects on soil carbon and

organic matter may similarly persist a decade after forest fires in boreal systems (Johnson and Curtis, 2001; Treseder et al., 2004). These studies, as well as recent meta-analyses (Dooley and Treseder, 2012; Holden and Treseder, 2013), strongly suggest that post-fire community shifts back to an unburned state may require decades, not single years. However, the community and abiotic soil property recovery after low-intensity prescribed fires are unknown.

In this study, we took advantage of a long-term experiment that has implemented different burning regimes for nearly a quarter century, thus allowing a unique means to address questions about long-term effects of recurring fires on soils and communities therein. The objectives of the implemented fire-regime management plan were to promote the native fire-adapted plant community. Unburned plots were used as a reference to represent the undesirable compositional state resulting from no fire management. Since the experiments have controlled both fire frequencies and the season of the fire treatments, we aimed to address 1) if recurring prescribed fires have a long-term effect on soil fungus communities; 2) if these responses depend on fire interval (2-yr, 3-yr, 6-yr); and, 3) if these responses depend on timing (summer vs. winter) of the burn. Our data provide further evidence that the fire effects are distinctly visible in regimes that apply prescribed burning at frequent intervals. As the vegetation in the frequently burned plots is largely composed of desired species it may be inferred that the soil fungal communities residing in these plots are adapted to the recurring fires and thus better support such plant communities under frequent prescribed burning regimes.

Materials and Methods

Study site

The long-term prescribed burn experiment is located in the Hitchiti Experimental Forest (HEF) in Jones County, Georgia, U.S.A. located between the North and South Units of the Piedmont National Wildlife Refuge. HEF is in the Ocmulgee branch of the Altamaha River Basin approximately 18 km east of Gray, Georgia. Overstory is composed primarily of loblolly pine (*Pinus taeda* L.) stands that are typical and widely distributed throughout the Southern Piedmont region of the southeastern United States. Southern yellow pine stands are important both economically and ecologically: they are managed for timber harvest as well as to provide wildlife habitat. Before conversion to forest, large proportions of HEF, including the sites for the current experiment, were used for cotton production. After the severely eroded and degraded lands were converted to forest, the stands remained a mix of pines and hardwoods and had not been burned for at least 50 years before a fire regime was established in 1988. Upon conversion to forest from cotton plantation, the area was planted with loblolly pine (*Pinus taeda* L.), which has remained the dominant tree species at the site.

Soils

Common to the Georgia Piedmont, the study site contains highly eroded Alfisols and Ultisols. According to the United States Department of Agriculture Soil Conservation Service mapping (http://www.nrcs.usda.gov/Internet/FSE_DOCUMENTS/nrcs142p2_051233.pdf), the soils represent Wilkes and Davidson Series. Wilkes Series are shallow, well-drained soils with moderately slow to slow permeability. Davidson Series consists of very deep, well-drained, and moderately permeable soils. These soils formed on uplands in the Piedmont, and are classified as

loamy, mixed, active, thermic, shallow Typic Hapludalfs and are found on gently sloping to moderately steep uplands in the Piedmont.

Experimental design

The fire management experiment at HEF has been implemented since its establishment in 1988. The experiment contains 24 plots, each ~0.8 ha in size. All plots were burned upon establishment, excluding unburned control plots, with low intensity backfires during the winter of 1988/1989. The experiment includes five treatments: unburned control plots (4 replicates), 2 year winter (4 replicates), 3 year winter (8 replicates), 3 year summer (4 replicates), and 6 year summer burns (4 replicates). Thus, the experimental design permits assessing the effects of fire intervals as well as the effects of season of the prescribed fire (3 year fire intervals only). Since the establishment of the experiment, HEF has experienced damaging outbreaks of southern pine beetle the since 2004. These plots were sampled regardless of damage and our previous analyses indicated that the insect damage had no or only minor effects on the fungal communities at the time of sampling in 2011 (Brown et al., 2013).

Soil sampling and sample processing

To avoid any confounding effects resulting from time of sampling, a minimum of one plot representing each treatment was sampled every day of sampling within four days between

November 1 and 16, 2011. Fifteen dominant canopy trees (loblolly pine; *Pinus taeda* L.) were selected a minimum of 10 m from plot edge to avoid edge effects. At each target tree, one 10 cm deep 5 cm diameter soil core was collected 3 m directly south of the tree bole for a total of 15 soil cores per plot. The cores were composited into one sample per plot. Pine beetle outbreak caused extensive damage in one plot leaving few remaining overstory trees. From this plot, soil cores were sampled systemically using a grid with fifteen points spaced ~5 m apart.

The pooled samples were frozen at -20°C immediately on each sample date upon return to the laboratory, and then shipped frozen on dry ice to Kansas State University where stored at -80°C until processing. The samples were thawed at room temperature and sieved through 1 mm mesh (No. 18 American Society for Testing and Materials (ASTM) E-11 Specification, Fisher Scientific Inc. Waltham, Massachusetts) to remove leaf litter, rocks, large particles, and roots. Sieved samples were manually homogenized for ~5 minutes and four 50 ml aliquots stored for DNA extraction at -80°C. The remaining soil was dried at 50°C for 48 hours and analyzed for pH, total nitrogen, and total carbon at the Kansas State University Soil Testing Laboratory. Total genomic DNA was extracted from ~10g (9.07-10.7g fresh weight) subsample using UltraClean Mega Soil DNA Kit (MoBio, Carlsbad, California) following the manufacturer's instructions and stored at -80°C until aliquoting and PCR amplification.

PCR amplification and sequencing

The DNA was quantitated with ND1000 spectrometer (NanoDrop Technologies, Wilmington, Delaware) and standardized to 5.0ng/μl for PCR amplification of the Internal

Transcribed Spacer 2 (ITS2) region of the ribosomal RNA gene cluster. ITS2 was chosen as it has been proposed as the universal barcode for fungi (Schoch et al., 2012) as well as to target shorter reads available with the paired-end Illumina MiSeq and amplified with the forward primer fITS7 (5' - GTGARTCATCGAATCTTTG - 3T, Ihrmark et al., 2012) and reverse primer ITS4 (5'-TCCTCCGCTTATTGATATGC- 3', White et al., 1990). All PCR reactions were performed in 25µl reaction volumes in a two-step PCR process following protocol recommended by Berry et al. (2011) with three technical replicates of each of the 24 experimental units and a negative control (molecular biology grade water). The primary PCRs contained the following amounts/concentrations: 25 ng DNA template (5µl), 200 µM dNTPs, 1µM of both forward (fITS7) and reverse (ITS4) primers, 5µl 5x Phusion Green HF Buffer containing 1.5mM MgCl₂, 7.3µl molecular biology grade water, and 1/2 unit (0.25 µl) of the proof-reading Phusion Green Hot Start II High-Fidelity DNA polymerase (Thermo Scientific, Pittsburgh, USA). PCR cycling parameters included an initial denaturing at 98°C for 30 seconds, followed by 25 cycles of denaturing at 94°C for 30 seconds, annealing at 54°C for 1 minute and extension at 72°C for 2 min, and a final extension at 72°C for 8 min. A unique, sample-specific 12-base-pair sequence barcode was incorporated in a secondary PCR using an ITS4 fusion primer synthesized with sample specific DNA-tags (Table A.1). Secondary PCR conditions were identical to those for the primary PCR except that they included 5 µl of the primary PCR product as template, tagged reverse primers (ITS4), and the number of PCR cycles was reduced to five.

The secondary PCR amplicons were cleaned using Agencourt AmPure XP magnetic 96-well SPRIplate system (Beckman Coulter, Indianapolis, Indiana) following the manufacturer's protocol with 1:1 AmPure XP solution to amplicon ratio. The three technical replicates per experimental unit (24 in total) were combined and the experimental units equimolarly pooled

into one amplicon library. The libraries were AmPure cleaned again to remove any residual short DNA contaminants and submitted to the Integrated Genomics Facility at Kansas State University (Manhattan, KS, USA), where Illumina specific primers and adapters were ligated using a NEBNext® DNA MasterMix (Protocol E6040, New England Biolabs Inc., Ipswich, MA, USA) and sequenced using a MiSeq Reagent Kit v2 (Illumina, San Diego, CA, USA) with 500 cycles. Paired fastq files (SRR1508275) are available in the Sequence Read Archive at NCBI (www.ncbi.nlm.nih.gov).

Sequence Analysis

The sequence data were analyzed using the program mothur (v. 1.32.2; Schloss et al., 2009) following a modified standard operating protocol (Schloss et al., 2011). After initial contigging the paired-end read library contained 5,425,946 sequences. The data were screened to remove contigs with less than 100bp overlap, any ambiguous bases, any disagreements with primer or DNA-tag sequences, sequences shorter than 250 bp, or homopolymers longer than 8bp (1,113,584 remaining sequences). The sequences were truncated to 250bp, near identical sequences preclustered to reduce potential sequencing bias (Huse et al., 2008) and screened for chimeras (uchime; Edgar et al., 2011). After quality control and removal of chimeras experimental units were subsampled to an equal 15,000 sequences. A pairwise distance matrix was calculated and sequences clustered into Operational Taxonomic Units (OTUs) at 97% sequence similarity. Low frequency OTUs (representing ≤ 10 sequences) that may be PCR and/or sequencing artifacts were removed (Tedersoo et al., 2010) resulting in a total of 1,412 OTUs and 348,994 total sequences in the dataset. The 1,412 OTUs were assigned to taxa using

the Naïve Bayesian Classifier at 97% sequence similarity (Wang et al., 2007) and the UNITE taxonomy reference (<http://unite.ut.ee/repository.php>). Coverage {Good's coverage ($G = 1 - (n_1)/(N)$), where n_1 = the number of OTUs that have been sampled once and N = the total number of individuals in the sample}, observed (S_{Obs} : number of OTUs) and extrapolated [Chao1: $S_{\text{Chao1}} = S_{\text{Obs}} + \{n_1(n_1 - 1)/2(n_2 + 1)\}$, where n_1 = the number of OTUs with only 1 sequence and n_2 = the number of OTUs with only two sequences] richness, diversity (1-D or compliment of Simpson's diversity index: $1 - D = 1 - \sum p_i^2$, where D = Simpson's diversity index and p_i = proportional abundance of the i th species), and evenness {Simpson's equitability or E_D : $E_D = (1/\sum p_i^2)/S$, where p_i = proportional abundance of the i th species and S = richness} were calculated using mothur (v. 1.31.2; Schloss et al., 2009).

Statistical Analyses

We first tested for differences in soil properties including pH, total nitrogen, and total carbon across all treatments. Soil parameter means were tested using one-way ANOVA (ANOVA: $P > 0.05$) in JMP® (version 7.0.2).

We tested for differences in diversity and richness estimators across treatments to detect any effects of season or time-interval using both one way ANOVA and mixed models with season as an a random variable in JMP® (version 7.0.2). For these analyses data were transformed to meet the assumptions of variance homogeneity and/or normality: response variables ranging from $0 \leq 1$ (percentages) were arcsine square root transformed, whereas others were log₁₀-transformed. Both mixed model and one-way ANOVA analyses gave congruent

results. As a result, only one-way ANOVA results will be presented. We first analyzed the effects of summer and winter burns relative to the control using only the unburned control treatments and prescribed fires that occurred every three years, because this was the only fire interval that included fires scheduled for both burn seasons. These analyses indicated that season of the prescribed fire had no effect on communities; therefore, we resolved to compare all treatments to conclude on any effects of the fire interval.

To detect compositional differences in the fungal communities across treatments, we first derived a Bray-Curtis distance matrix and compared treatments by Multi-Response Permutation Procedure (MRPP) in PC-ORD (version 5; McCune and Mefford, 2006). To visualize these community data clouds, we estimated Non-metric Multidimensional Scaling (NMS) axis scores for first two ordination axes that represented 84.3% of the variation to obtain a stress of 0.15. In addition to evaluating the responses on the whole community level, we used Indicator Species Analysis in PC-ORD to identify OTUs that were present in one treatment more commonly than in others. To ensure true significance of indicator OTUs the results were run using false discovery rate (FDR) with the false detection rate (q-value) set to 0.20.

Results

Soil Parameters

We observed no strong evidence for responses to fire intervals when each soil parameter was analyzed separately for differences among the five prescribed fire treatments (ANOVA: $P > 0.05$; Table 3.1). However, soil pH tended to be higher in the most frequent fire treatments (Table 1).

General fungal community data description

The dataset initially contained 5,425,956 sequences. After quality control, subsampling, and removal of low frequency OTUs (≤ 10 sequences) we included a total of 1,412 OTUs and 348,994 sequences in the final analyses. A total of 15.4% (53,971 sequences; 244 OTUs, 17.2%) of sequences were only assigned to Kingdom fungi but remained unclassified at the phylum level. Communities overall were dominated by Basidiomycota (203,990 sequences, 58.5%; 801 OTUs, 56.7%), followed by basal lineages – mainly taxa formerly assigned to Zygomycota (53,729 sequences, 15.4%; 42 OTUs, 2.9%), and a smaller proportion to Ascomycota (36,806 sequences, 10.5%; 308 OTUs, 21.8%). On the order level, our data were dominated by sequences that remained unclassified (55,759 sequences, 15.9%; 396 OTUs, 28.0%), but included Russulales (52,729 sequences, 15.1%; 100 OTUs, 7.1%) with many taxa that form ectomycorrhizae (ECM), Agaricales (46,043 sequences, 13.2%; 260 OTUs, 18.4%) with diverse ecologies, and Mucorales (10,246 sequences, 11.5%; 22 OTUs, 1.6%) that likely represent soil-inhabiting, free-living fungi. On the family level, Russulaceae composed of mainly ECM members contributed 15.1% (52,729 sequences) with 100 OTUs (7.1%), followed by the largely soil-inhabiting family Umbelopsidaceae (11.4%, 39,873 sequences) with 17 OTUs (1.2%), and basidiomycetous Geminibasidiaceae (5.5%, 19,414) with 19 OTUs (1.3%). The most common

OTUs represented mainly soil-inhabiting fungi (OTU0001 with affinity to *Umbelopsis dimorpha* – 28,163 sequences, 8.1% and OTU0002 *Geminibasidium* 16,897 sequences, 4.8%), but included also unclassified, unknown taxa (OTU0003 unclassified, 8,635 sequences, 2.4%). In addition, the ten most common OTUs included common ECM taxa (OTU0005 *Russula sp.* – 7,297 sequences, 2.1%; OTU0007 *Suillus sp.* – 5,223, 1.5%; and, OTU0010 *Russula sp.* – 4,239, 1.2%). A complete list of OTUs with their taxon assignments and sequence counts is included in the Supplemental Table A.2.

Effect of prescribed fire season

We used 3-year summer and 3-year winter burn treatments to evaluate the effects of burn season. Overall, the season of the prescribed fire implementation had only minimal effects on the soil-inhabiting fungal communities, particularly when compared to the responses to short-term recurring fires. The richness and diversity estimators were unaffected by the choice of burning season: Good's coverage, observed (S_{Obs}) and extrapolative (Chao1) richness, diversity (1-D), or evenness (E_D) did not differ across treatments (Table 3.2).

Similarly, the season of prescribed burn implementation had no effect on the fungal community composition: whereas the communities in both winter and summer burns at three year intervals differed clearly from those in the unburned control (MRPP: $T_{2,7} = -4.25$, $A_{2,7} = 0.25$, $P = 0.001$; $T_{2,11} = -2.8$, $A_{2,11} = 0.18$, $P = 0.006$, respectively), the communities in the winter and summer fire regimes at three year intervals did not differ from each other (MRPP: $T_{2,11} = 1.05$, $A_{2,11} = -0.04$, $P = 0.862$). The observed community responses were thus mainly driven by

the short, 3-year fire intervals, consistently with the broader analyses of fire interval effects (see below).

Effect of prescribed fire intervals

In concluding that the fire implementation season had no effect, we decided to compare all fire treatments (2-yr winter, 3-yr winter, 3-yr summer, 6-yr summer, and control) to evaluate the effects of fire interval. None of the diversity and richness estimators (Good's coverage, S_{Obs} , E_D , Chao1, and 1-D) differed among the fire interval treatments (Table 3.2). Although diversity and richness estimators were minimally affected, burn treatments resulted in compositional shifts in soil fungal communities (Fig. 3.1; MRPP: $T_{5,23} = -2.19$, $A_{5,23} = 0.09$, $P = 0.021$). In pairwise comparisons, the short fire interval (2-yr winter, 3-yr winter, 3-year summer) treatments differed strongly and significantly from the unburned control (Figure 3.1.; MRPP: $T_{2,7} = -3.12$, $A_{2,7} = 0.18$, $P = 0.007$; $T_{2,7} = -4.26$, $A_{2,7} = 0.26$, $P = 0.001$; $T_{2,11} = -2.8$, $A_{2,11} = 0.17$, $P = 0.006$, respectively). In contrast to the frequent fire treatments, the 6-year fire interval treatments were only marginally significantly different from the control ($T_{2,7} = -1.62$, $A_{2,7} = 0.10$, $P = 0.05$). These community distinctions were most obvious along the first NMS axis: the unburned control plots were all located left of the second NMS axis and in the third quadrant, whereas the communities in the frequently burned 2- and 3-year fire interval treatments were mainly located right of the second NMS axis in first and fourth quadrants (Fig. 3.1). Long-interval 6-year fire treatments, which only marginally differed from the unburned control, were mainly located near the second NMS axis between control and short fire intervals. However, again, the treatments with different fire intervals did not differ from each other.

We used indicator taxon analyses as a conservative tool to identify OTUs that may be adapted to recurring prescribed fires. Across the five fire treatments, we identified a total of 77 indicator OTUs that occurred more frequently in one treatment compared to others (Supplemental Table C.3). All indicator OTUs remained significant after FDR correction for multiple comparisons. More than a third of the indicator taxa (26 OTUs) were enriched in the unburned control plots relative to other treatments and thus likely fire sensitive. The unburned control indicators included a large proportion of fungi that remained unclassified beyond a phylum (13 OTUs), but also a variety of basidiomycete OTUs that likely form ECM (3 OTUs in genus *Russula*, 1 in *Sistotrema*, 1 in family Atheliaceae, 1 in Thelephoraceae) as well as soil-inhabiting or saprotrophic fungi (1 in genus *Callistosporium*, 1 *Geminibasidium*). There were also four ascomycete OTUs that represented saprobic Eurotiomycetes (3 OTUs) and Xylaria (1 OTU). Short fire intervals (2 and 3 year burns, for a total of three treatment combinations and sixteen experimental units) included a total 37 indicator OTUs consisting of thirteen unclassified OTUs and one OTU assigned to a genus *Umbelopsis* representative of the soil-inhabiting basal lineages. The remaining OTUs included five ascomycetes largely dominated by lichen-forming Verrucariales (3 OTUs) and two possibly endophytic or pathogenic OTUs – Herpotrichiellaceae and Bionectria. There were an additional 19 basidiomycetes identified as indicators for the short-fire intervals. A large portion (12 OTUs) of these likely form ECM (1 Russulaceae, 4 Thelephoraceae, 3 *Suillus*, 1 *Amanita*, 1 *Tylospora*, 1 *Ramaria*, and 1 *Clavulina*). The remaining basidiomycete indicator OTUs represent taxa that include saprobes, parasites, and other soil-inhabiting taxa (2 Clavariaceae, 1 *Geastrum*, and 4 unclassified Agaricomycetes). The indicator taxon analyses identified no OTUs that were completely lost in the frequent fire treatments. As a

result, we conclude that the overall compositional community responses to recurring prescribed fires are largely driven by community member reordering rather than taxon replacement.

Discussion

Prescribed fire is an important management tool used to reduce fuel loads, remove non-fire adapted species and to maintain forest stands over time. However, the long-term effects of recurring prescribed fires on soil micro-organisms and their community composition have remained unclear (Holden and Treseder, 2013) despite their essential roles in nutrient cycling as well as in soil and plant health. In the short-term (directly following a fire), fire may decrease fungal biomass in soil (Fritze et al., 1993; Pietikäinen et al., 1993; Dooley and Treseder, 2012) and alter soil fungal communities (Baar et al., 1999; Chen et al., 2002). The legacy effects of repeated burning in the long-term remain largely unknown, especially in the southeastern United States. Although fire disturbance tends to decrease fungal biomass, it has remained unclear how fungal communities respond to such disturbances in the long term as these responses depend on how fire may affect soil properties and plant communities (Dooley and Treseder, 2013; Hebel et al., 2009). More intense wildfires tend to have greater impacts and longer lasting legacy effects than low intensity fires, such as the prescribed fires (Carter and Foster 2004; Certini, 2005). Fungal communities respond to fires and fire effects can be visible decades after a wildfire (Dooley and Treseder, 2013; Hebel et al., 2009; Holden et al., 2013; Longo et al., 2011; Visser, 1994). Similarly, more frequent fires often have greater effects on soil fungi (Cairney and Bastias, 2007).

Here we evaluated the effects of different fire regimes on soil fungal communities over time using an experimental design that has implemented prescribed burning for nearly a quarter century. As a result of the complexity of the experimental design, we separately addressed the effects of timing of the fire (summer vs. winter burn) and the interval (2-yr, 3-yr, 6-yr and control unburned) between the fire treatments on fungal richness and diversity as well as overall community composition. Our data show that while season of the burn has minimal effects, frequent burns will shift overall community structure and may select for fire adapted and/or fire tolerant fungi. In contrast to community compositional attributes, neither the fire season nor the interval had any detectable effects on species richness or diversity. As a result, our data suggest that frequent recurring fires likely lead to taxon re-ordering rather than loss of the common community constituents. Our analyses indicated that the fungal communities in shorter fire intervals (2 and 3 year burns) were most distinct from the unburned control treatments, whereas we detected no significant differences between communities in any of the treatments that had been burned during our experiment. Interestingly, the fungal communities residing in the treatments in which the fires implemented at six-year intervals were positioned intermediately between the unburned control treatments and the frequently burned treatments possibly indicating that the six-year intervals between prescribed fires may be inadequate to maintain the fire-adapted communities. Our studies were not designed to decouple mechanisms that result in the distinct fire adapted communities. Thus, our observed differences between frequently burned treatments and unburned treatments may reflect the difference in fire adapted and fire sensitive aboveground plant communities: unburned plots have shifted to include undesirable hardwood competitors and shrubs whereas the frequently burned plots are mainly composed of fire-adapted

pinus and grasses. These data suggest that short fire intervals that prevent the expansion of unwanted vegetation have similar effects in the associated below-ground fungal communities. Further, since frequent fires do not negatively affect diversity and richness of fungal communities the communities can still be perceived as stable and resilient.

Consistently with other reports and meta-analyses (Dooley and Treseder 2012; Holden et al., 2013; Holden and Treseder, 2013) our data suggest that ecosystems and communities shift gradually back to an unburned state and do so even after extended periods of prescribed fire. Despite the low intensity stripped head-fires used in our experimental implementation, our results are consistent with findings from other studies (Amiro et al., 2010; Dooley and Treseder, 2012; Goulden et al., 2011; Holden et al., 2013; Holden and Treseder, 2013; Johnson and Curtis, 2001; Mack et al., 2008; Treseder et al., 2004) and indicate that shifts back to an unburned state following fire disturbance require several years. Fritze et al. (1993) estimated a 12 year recovery time after prescribed fire in a boreal forest system. Similarly, meta-analyses (Dooley and Treseder, 2012) as well as fire chronosequence studies (Holden et al., 2013) arrive at similar conclusions and suggest that at least a decade, or even up to two and a half decades may be necessary for complete shift to the unburned state after a fire disturbance. Our results are in line with these: while the short interval fire treatments clearly differed in their community composition from the unburned plots, the long interval, 6-year burns differed neither from the fire treatments nor from the unburned controls. Based on this, we conclude that community shifts from even low-intensity fires take more than half a decade to reach a community state clearly distinguishable from the frequent fire implementation. With the management goals in mind, our

findings suggest that fire intervals exceeding six years may allow soil fungal communities to shift in the direction of states associated with unwanted vegetation.

Analyses of fungal community responses to fire are few (Holden and Treseder, 2013); our current studies aim to contribute towards deeper appreciation of soil fungi community responses to fire. Similarly to our study, previous research on Australian sclerophyll forests using Restriction Fragment Length Polymorphism (RFLP) and Denaturing Gradient Gel Electrophoresis (DGGE) analyses suggested that long-term short-interval regimes alter fungal communities (Anderson et al., 2007; Bastias et al., 2006a). Holden et al. (2013) utilized a chronosequence approach and concluded that recently burned sites were distinct from those with more distant fire history. ECM fungal communities may be particularly responsive to repeated fire disturbance: short-fire intervals often have greater effects on ECM fungal communities than long-interval fire regimes (Bastias et al., 2006b; Buscardo et al., 2010). Our indicator taxon analyses identified 17 OTUs representing a number of ECM fungi that were favored by either the unburned or frequently burned treatments indicating that, across the ECM fungal guild, taxa can have opposite responses to fires. These taxa potentially respond to fire or – alternatively – to the concomitant shifts in the plant communities (*i.e.*, from broadleaf hardwoods and shrubs to pines and grasses). While some ECM associations are host specific (Newton et al., 1998; Horton et al., 1998b), our data do not permit decoupling mechanisms underlying the observed community responses. It is perhaps tempting to speculate that ECM fungi respond most strongly to fire disturbance, particularly when considering stand replacing wildfires. However, this may not be the case for low intensity prescribed burning where soil physicochemical and biotic responses may be minimal (Callaham et al., 2012).

Inferences about changes in functional attributes of soil inhabiting communities are rare and our analyses permit them only cursorily by taxon assignment. In contrast to previous suggestions that ECM taxa may be most sensitive to fire disturbance (*e.g.*, Holden et al., 2013), our data suggest that many functional guilds may respond but mainly through a few disturbance sensitive and adapted taxa. More detailed functional assays targeting either soil enzyme activities directly or genes that code for those enzymes permit further functional inference. Artz et al. (2009) analyzed laccase genes of soil basidiomycetes in a clone library study of fire effects and observed a greater diversity and evenness of these carbon polymer-modifying genes following the fires than in the unburned control. Holden et al. (2013) assayed a number of enzyme systems that contribute to the cycling of macro-nutrients in soil (carbon, nitrogen, phosphorus). These studies suggest that metabolic activities as well as the metagenomic content permitting those activities shift in response to recent fires. This is likely a result of a combination of changes in substrate quality and quantity, (Certini, 2005; Harden et al., 2003; Neff et al., 2005; Wan et al., 2001), reductions in soil inhabiting microbial biomass (Dooley and Treseder, 2012; Fritze et al., 1993; Holden et al., 2013; Holden and Treseder, 2013; Pietikäinen et al., 1993), and shifts in the soil-inhabiting communities (Brown et al., 2013; Holden et al., 2013) in response to the fires.

To further elaborate on the community level responses, our indicator taxon analysis identified a total of 77 indicator taxa across our treatments. Previous studies have identified early-successional fungi that increase in abundance following a fire and include representatives of ECM genera such as *Coltricia*, *Thelephora* (Visser et al., 1994), *Russula*, *Suillus* (Horton et

al., 1998a), *Rhizopogon*, *Wilcoxina* (Barr et al., 1999; Kipfer et al., 2009; Horton et al., 1998a), *Tomentella* (Barr et al., 1999), and *Cenococcum* (Kipfer et al., 2009). Although our analyses included many of these taxa, they were not identified as indicators. However, it is important to bear in mind that many of the earlier studies have focused on recent fires within the first ninety days after the fire (Baar et al., 1999; Chen et al., 2002) or followed the effects of a single fire application over time (Fritze et al., 1993; Visser, 1994; Longo et al., 2011; Holden et al., 2013). In contrast, our study focused explicitly on the long-term effects of recurring fire regimes that had been implemented for nearly a quarter century. As a result, our study operates on a different time scale in terms of community responses and is therefore perhaps difficult to compare to earlier studies.

Burning litter layer and ground vegetation often leads to a short-term decrease in soil organic matter and loss of nitrogen and carbon as a result of combustion and volatilization (Certini, 2005; Hernández et al., 1997). Different forms of nitrogen may also respond differently to fire: while inorganic nitrogen may increase in the short term, organic nitrogen in soil may greatly decline (Prieto-Fernández et al., 2003). Most commonly in forest ecosystems, fires tend to reduce soil organic matter and nutrient availability in the short term, although the addition of burnt plant material can increase these parameters in the long-term (Certini, 2005; Prieto-Fernández et al., 2003). Toberman et al. (2014) and Williams et al. (2011) observed that a greater frequency in prescribed fires lead to greater loss in available soil nutrients in the long-term. We observed no or only minimal differences in the soil parameters (pH, total N, and total C) across the different burn treatments, even though our experimental manipulations have been in place for nearly a quarter century. Comparison across experiments is difficult because fires can have a

wide range of effects on soil parameters depending on fire intensity, duration, or the soil properties (*e.g.*, volumetric soil moisture) before the fire (Certini, 2005; Glass et al., 2008).

While we observed no shifts in the soil chemistry resulting from frequent burning, our results are congruent with Glass et al. (2008), who also found no effects of low-intensity fires in the short- or long-term. This demonstrates the range of variation in fire effects across fire intensities and soil parameters.

Our study identifies clear community shifts resulting from frequently implemented prescribed fires. In contrast to fire frequency, we found no effects of season as a variable. However, Smith et al. (2004) suggested that seasonal timing of burn regimes can have short-term (< 2 years) effects on fungal communities finding a greater richness in fall burns compared to summer burns. In our study, the longer (6 year) fire intervals were particularly interesting, as they provide clues to how soil fungal communities return to states preceding disturbance over time. While the long fire interval treatments did not clearly differ from any of the other treatments, they only marginally differed from the unburned treatments. Based on this, we speculated that return to community state preceding the fires takes half a decade or more. These estimates are congruent with those of others. While our data suggested clear compositional shifts as a result of the frequent fires, the richness or diversity of the communities remained unchanged suggesting likely taxon re-ordering rather than replacement. This re-ordering is likely driven by fire disturbance and the resulting vegetative communities present rather than by the altered soil properties. With the management goals in mind, we conclude that frequent burns maintain stable diversity and richness of fungal communities over time that are associated with the desirable

vegetation and that fire intervals should not surpass a decade to avoid communities returning to the unfavored unburned state.

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References

Abrahamson, W.G., Hartnett, D.C. 1990. Pine flatwoods and dry prairies. In: Myers, R.L. and Ewel, J.L. (eds.), *Ecosystems of Florida*. University of Central Florida Press, Orlando, USA. Pp. 103-149.

Amiro, B.D., Barr, A.G., Barr, J.G., Black, T.A., Bracho, R., Brown, M., Chen, J., Clark, K.L., Davis, K.J., Desai, A.R., Dore, S., Engel, V., Fuentes, J.D., Goldstein, A.H., Goulden, M.L., Kolb, T.E., Lavigne, M.B., Law, B.E., Margolis, H.A., Martin, T., McCaughney, J.H., Misson, L., Montes-Helu, M., Noormets, A., Randerson, J.T. 2010. Ecosystem carbon dioxide fluxes after disturbance in forests of North America. *Journal of Geophysical Research*, 115: G00K02.

Anderson, I.C., Bastias, B.A., Genney, D.R., Parkin, P.I., Cairney, J.W.G. 2007. Basidiomycete fungal communities in Australian sclerophyll forest soil are altered by repeated prescribed burning. *Mycological Research*, 111: 482-486.

Artz, R.R.E., Reid, E., Anderson, I.C., Campbell, C.D., Cairney, J.W.G. 2008. Long term repeated prescribed burning increases evenness in the basidiomycete laccase gene pool in forest soils. *FEMS Microbial Ecology*, 67: 397-410.

Bastias, B.A., Huang, Z.Q., Blumfields, T., Xu, Z., Cairney, J.W.G. 2006a. Influence of repeated prescribed burning on the soil fungal community in an eastern Australian wet sclerophyll forest. *Soil Biology and Biochemistry*, 38: 3492-3501.

Bastias, B.A., Xu, Z.H., Cairney, J.W.G. 2006b. Influence of long-term repeated prescribed burning on mycelial communities of ectomycorrhizal fungi. *New Phytologist*, 172: 149-158.

Baar, J., Horton, T.R., Kretzer, A.M., Bruns, T.D. 1999. Mycorrhizal Colonization of *Pinus muricata* from Resistant Propagules after a Stand-Replacing Wildfire. *New Phytologist*, 143: 409-418.

Barker, J.S., Simard, S.W., Jones, M.D., Durall, D.M. 2013. Ectomycorrhizal fungal community assembly on regenerating douglasfir after wildfire and clearcut harvesting. *Oecologia*, 172: 1179-1189.

Borders, B.E., Bailey, R.L. 2001. Loblolly pine-pushing the limits of growth. *Southern Journal of Applied Forestry*, 25: 69-74.

Brown, S.P., Callaham, Jr. M.A., Oliver, A.K., Jumpponen, A. 2013. Deep Ion Torrent sequencing identifies soil fungal community shifts after frequent prescribed fires in a southeastern US forest ecosystem. *FEMS Microbiology Ecology*, 86: 557-566.

Buscardo, E., Rodríguez-Echeverría, S., Martic, M.P., Angelis, P.D., Pereira, J.S., Freitas, H. 2010. Impact of wildfire return interval on the ectomycorrhizal resistant propagules communities of a Mediterranean open forest. *Fungal Biology*, 114: 628–636.

Cairney, J.W.G., Bastias, B.A. 2007. Influence of fire on forest soil fungal communities. *Canadian Journal of Forest Research*, 37: 207-215.

Callaham, M.A. Jr., Scott, D.A., O'Brien, J.J., Stanturf, J.A. 2012. Cumulative effects of fuel management on the soils of eastern U.S. In: LaFayette, R., Brooks, M.T., Potyondy, J.P., Audin, L., Krieger, S.L., Trettin, C.C. (eds.). *Cumulative watershed effects of fuel management in the Eastern United States*. Gen. Tech. Rep. SRS-161. Asheville, NC: U.S. Department of Agriculture Forest Service, Southern Research Station, pp. 202-228.

Carter, M.C., Foster, C.D. 2004. Prescribed burning and productivity in southern pine forests: a review. *Forest Ecology and Management*, 191: 93–109.

Certini, G. 2005. Effects of fire on properties of forest soils: a review. *Oecologia*, 143: 1-10.

Chen, D.M., Cairney, W.G.J. 2002. Investigation of the influence of prescribed burning on ITS profiles of ectomycorrhizal and other soil fungi at three Australian sclerophyll forest sites. *Mycological Research*, 106: 532-540.

Choromanska, U., DeLuca, T.H. 2001. Prescribed fire alters the impact of wildfire on soil biochemical properties in a ponderosa pine forest. *Soil Science Society of America Journal*, 65: 232–238.

Dooley, S.R., Treseder K.K. 2012. The effect of fire microbial biomass: a meta-analysis of field studies. *Biogeochemistry*, 109: 49-61.

Edgar, R.C., Haas, B.J., Clemente, J.C., Quince, C., Knight, R. 2011. UCHIME improves sensitivity and speed of chimera detection. *Bioinformatics*, 27: 2194-2200.

Fritze, H., Pennanen, T., Pietikäinen, J. 1993. Recovery of soil microbial biomass and activity from prescribed burning. *Canadian Journal of Forest Research*, 23: 1286-1290.

Fujimura, K.E., Smith, J.E., Horton, T.R., Weber, N.S., Spatafora, J.W. 2005 Pezizalean mycorrhizas and sporocarps in ponderosa pine (*Pinus ponderosa*) after prescribed fires in eastern Oregon, USA, *Mycorrhiza*, 15:79-86.

Glass, D.W., Johnson, D.W, Blank, R.R, Miller, W.W. 2008. Factors affecting mineral nitrogen

transformations by soil heating: a laboratory-simulated fire study. *Soil Science*, 173: 387-400.

Glitzenstein, J.F., Platt, W.J., Streng, D.R. 1995. Effects of fire regime and habitat on tree dynamics in north Florida longleaf pine savannas. *Ecological Monographs*, 65: 441-476.

Goulden, M.L., McMillan, A.M.S., Winston, G.C., Rocha, A.V., Manies, K.L., Harden, J.W., Bond-Lamberty, B.P. 2011. Patterns of NPP, GPP, respiration, and NEP during boreal forest succession. *Global Change Biology*, 17: 855–871.

Grogan, P., Baar, J., Bruns, T.D. 2000. Below-ground ectomycorrhizal community structure in a recently burned bishop pine forest. *Journal of Ecology*, 88: 1051–1062.

Harden, J.W., Mack, M.C., Veldhuis, H., Gower, S.T. 2003. Fire dynamics and implications for nitrogen cycling in boreal forests. *Journal of Geophysical Research*, 108: 8223–8230.

Hatten J.A., Zabowski, D. 2010. Fire severity effects on soil organic matter from a ponderosa pine forest: a laboratory study. *International Journal of Wildland Fire*, 19: 613–623.

Hebel, C.L., Smith, J.E., Cromack, K. Jr. 2009. Invasive plant species and soil microbial response to wildfire burn severity in Cascade Range of Oregon. *Applied Soil Ecology*, 42: 150-159.

Hernández, T., García, C., Reinhardt, I. 1997. Short-term effect of wildfire on chemical, biochemical and microbiological properties of Mediterranean pine forest soils. *Biology and Fertility of Soils*, 25: 109-116.

Holden, S.R., Gutierrez, A., Treseder, K.K. 2013. Changes in soil fungal communities, extracellular enzyme activities, and litter decomposition across a fire chronosequence in Alaskan boreal forests. *Ecosystems*, 16: 34-46.

Holden, S.R., Treseder, K.K. 2013. A meta-analysis of soil microbial biomass responses to forest disturbances. *Frontiers in Microbiology*, 4: article 163.

Horton, T.R., Cázares, E., Bruns, T.D. 1998a. Ectomycorrhizal, vesicular-arbuscular and dark septate fungal colonization of bishop pine (*Pinus muricata*) seedlings in the first 5 months of growth after wildfire. *Mycorrhiza*, 8:11-18.

Horton, T.R., Bruns, T.D. 1998b. Multiple-host fungi are the most frequent and abundant ectomycorrhizal types in a mixed stand of Douglas fir (*Pseudotsuga menziesii*) and bishop pine (*Pinus muricata*). *New Phytologist*, 139: 331-339.

Huse, S.M., Dethlefsen, L., Huber, J.A., Welch, M.D., Relman, D.A., Sogin, M.L. 2008. Exploring microbial diversity and taxonomy using SSU rRNA hypervariable tag sequencing. *PLoS Genetics*, 4: e1000255.

Ihrmark, K. B., Decker, I.T.M., Cruz-Martinez, K., Friberg, H., Kubartova, A., Schenck, J., Stenlid, J., Brandströmrandström, M., Clemmensen, K.E., Lindahl, B.D. 2012. New primers to amplify the fungal ITS2 region- evaluation by 454-sequencing of artificial and natural communities. *FEMS Microbiology Ecology*, 82: 666-677.

Johnson, D.W., Curtis, P. S. 2001. Effects of forest management on soil C and N storage: meta analysis. *Forest Ecology and Management*, 140: 227–238.

Kifer, T., Simon, E., Ghazoul, J., Moser, B., Wohlgemuth, T. 2010. Susceptibility of ectomycorrhizal fungi to soil heating. *Fungal Biology*, 114: 467-472.

Kirkman, L.K., Mitchell, R.J. 2006. Conservation management of *Pinus palustris* ecosystems from a landscape perspective. *Applied Vegetation Science* 9:67-74.

Kowal, V.A., Scholke, A., Kanagaraj, R., Bruggeman, D. 2013. Resource selection probability functions for gopher tortoise: providing a management tool application across the species' range. *Environmental Management*, 53: 594-605.

Ligon, D.J., Stacey, P.B., Conner, R.N., Bock, C.E., Adkisson, C.S. 1986. Report of the American ornithologists' union committee for the conservation of the red-cockaded woodpecker. *The Auk*, 103: 848-855.

Longo, M.S., Urcelay, C., Nouhra, E. 2011. Long term effects of fire on ectomycorrhizas and soil properties in *Nothofagus pumilio* forest in Argentina. *Forest Ecology and Management*, 262: 348-354.

Mack, M.C., Treseder, K.K., Manies, K.L., Harden, J.W., Schuur, E.A.G., Vogel, J.G., Randerson, J.T., Chapin, F.S. 2008. Recovery of aboveground plant biomass and productivity after fire in mesic and dry black spruce forests of interior Alaska. *Ecosystems*, 11: 209–225.

McCune, B., M. J. Mefford. 2006 PC-ORD. Multivariate analysis of ecological data. Version 5. MjM Software, Gleneden Beach, Oregon, U.S.A.

Neff, J.C., Harden, J.W., Gleixner, G. 2005. Fire effects on soil organic matter content, composition, and nutrients in boreal interior Alaska. *Canadian Journal of Forest Research*, 35: 2178–2187.

Newton, A.C., Haigh, J.M. 1998. Diversity of ectomycorrhizal fungi in Britain: a test of the species- area relationship, and the role of host specificity. *New Phytologist*, 138: 619-627.

Pietikäinen, J., Fritze, H. 1993. Microbial biomass and activity in the humus layer following burning: short-term effects of two different fires. *Canadian Journal of Forest Research*, 23: 1275-1285.

Prieto-Fernández, Á., Carballas M., Carballas, T. 2004. Inorganic and organic N pools in soils burned or heated: immediate alteration and evolution after forest wildfires. *Geoderma*, 121: 291-306.

Schoch, C.L., Seifert, K.A., Huhndorf, S., Robert, V., Spouge, J.L., Levesque, C.A., Chen, W., Fungal Barcoding Consortium. 2012. Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. *Proceedings of the National Academy of Science, USA*, 109: 6241-6246.

Smith, J.E., McKay, D. Niwa, C.G, Thies, W.G., Brenner, G., Spatafora J.W. 2004. Short-term effects of seasonal prescribed burning on the ectomycorrhizal fungal community and fine root biomass in ponderosa pine stands in the Blue Mountains of Oregon. *Canadian Journal of Forest Research*, 34: 2477-2491.

Steen, D.A., Smith, L.L., Morris, G., Conner, M., Litt, A.R., Pokswinski, S., Guyer, C. Response of six-lined racerunner (*Aspidoscelis sexlineata*) to habitat restoration in fire-suppressed longleaf pine (*Pinus palustris*) sandhills. *Restoration Ecology*, 21: 457- 463.

Stephens, S.L., Ruth, L.W. 2005. Federal forest-fire policy in the United States. *Ecological Applications*, 15: 532-542.

Talbert, J.T., Weir, R.J., Arnold, R.D. 1985. Cost and benefits of a mature first-generation loblolly pine tree improvement program. *Journal of forestry*, 83: 162-166.

Tedersoo, L., Nilsson, R.H., Abarenkov, K., Jairus, T., Sadam, A., Saar, I., Bahram, M., Bechem, E., Chuyong, G., Kõljalg, U. 2010. 454 Pyrosequencing and Sanger sequencing of tropical mycorrhizal fungi provide similar results but reveal substantial methodological biases. *New Phytologist*, 188: 291-301.

Toberman, H., Chen, C., Lewis, T., Elser, J.J. 2014. High-frequency fire alters C: N: P

stoichiometry in forest litter. *Global Change Biology*, 20: 2321-2331.

Treseder, K.K., Mack, M.C., Cross, A. 2004. Relationships among fires, fungi, and soil dynamics in Alaskan boreal forests. *Ecological Applications*, 14: 1826–1838.

Visser, S. 1994. Ectomycorrhizal fungal succession in jack pine stands following wildfire. *New Phytologist*, 129: 389-401.

Waldrop, T.A., White, D.L., Jones, S.M. 1992. Fire regimes for pine-grassland communities in the southeastern United States. *Forest Ecology and Management*, 47: 195-210.

Wan, S., Hui, D., Luo, Y. 2001. Fire effects on nitrogen pools and dynamics in terrestrial ecosystems: a meta-analysis. *Ecological Applications*, 11:1349–1365.

Wang, Q., Garrity, G.M., Tiedje, J.M., Cole, J.R. 2007. Naïve Bayesian Classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. *Applied and Environmental Microbiology*, 73:5261-5267.

Warbale, D.A., Bardgett, R.D., Klironomos, J.N., Set, S.H., Van Der Putten, W.H., Wall, D.H. 2004. Ecological linkages between aboveground and belowground biota. *Science*, 304: 1629-1633.

White, T.J., Bruns, T., Lee, S., Taylor, J. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In Innis, M.A., Gelfand, D.H., Sninsky, J.J., White, T.J. (eds). *PCR Protocols: A Guide to Methods and Applications*, Academic Press, San Diego, CA, pp. 315–322.

Wicklow, D. 1973. Microfungal populations in surface soils of manipulated prairie stands.

Ecology, 54: 1302–1310.

Wicklow, D. 1975 Fire as an environmental cue initiating ascomycete development in a tallgrass prairie. *Mycologia*, 67: 852–862.

Williams, R.J., Hallgren, S.W., Wilson, G.W.T. 2011. Frequency of prescribed burning in an upland oak forest determines soil and litter properties and alters soil microbial community. *Forest Ecology and Management*, 265: 241-247.

“Maps: Dominant Soil Orders in the United States”

http://www.nrcs.usda.gov/Internet/FSE_DOCUMENTS/nrcs142p2_051233.pdf . Natural Resources Conservation Service. USDA, Web. 13 August 2014.

Figures and Tables

Figure 3.1 Non-metric Multidimensional Scaling (NMS) ordination of long-term prescribed fire treatments. The NMS ordination was optimally resolved on two axes (stress = 0.15) that represented 48.0% and 36.2% of the variability for a total of 84.2%. Multiple Response Permutation Procedure (MRPP) indicated significantly different communities ($T_{5,23} = -2.19$, $A_{5,23} = 0.09$, $P = 0.021$). Subsequent pairwise comparisons among the treatments indicated that communities in the short fire interval treatments (2-yr and 3-yr) differed from the unburned control and are mainly located right of NMS Axis 2 (MRPP: $P < 0.05$), whereas the long fire interval treatment (6-yr) marginally differed from control (MRPP: $P = 0.05$) but did not differ from other fire treatments (MRPP: $P \geq 0.05$). Small filled circles exemplify dominant indicator taxa for control and short fire intervals. OTU 0018 (*Trechispora sp.*), OTU 0218 (*Russula sp.*), and OTU0112 (*Sistorema sp.*) are indicators for the unburned control treatment, OTU0090 (*Amanita sp.*), OTU0213 (*Clavulina sp.*), and OTU0400 (*Suillus sp.*) indicators for the short fire intervals.

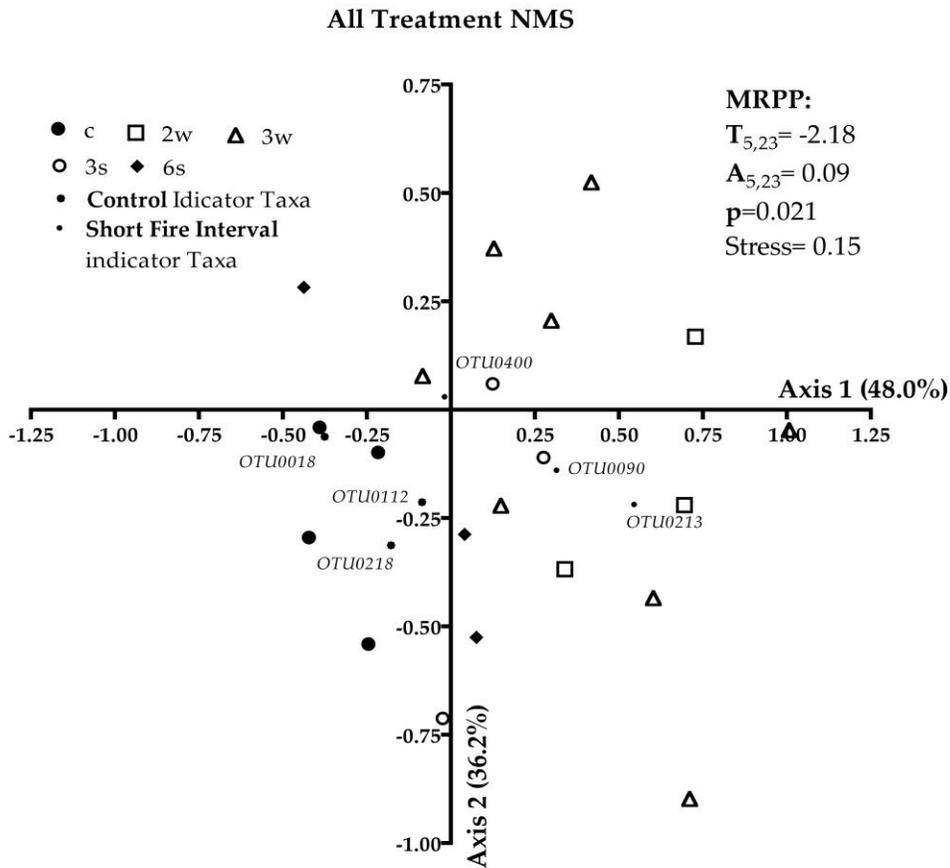


Table 3.1 Means and standard deviations of soil parameters from 5 cm across different prescribed fire treatments. Comparison of treatments across all measured soil parameters indicates no significant differences between the treatments. F-statistics refer to one-way ANOVA that compares means of all five treatments. Note that while no pairwise differences were observed (ANOVA: $P > 0.05$), the ANOVA suggests a nearly significant difference among the fire treatments in the soil pH.

Soil Parameter	Control	2-yr Winter	3-yr Winter	3-yr Summer	6-yr Summer	$F_{4,23}$; Prob> F
pH	4.68 ± 0.096	5.15 ± 0.238	4.95 ± 0.256	4.95 ± 0.125	4.88 ± 0.171	2.57; 0.07
Total N (%)	0.08 ± 0.0001	0.09 ± 0.0009	0.09 ± 0.0002	0.09 ± 0.0009	0.13 ± 0.0007	1.22; 0.33
Total C (%)	2.00 ± 0.000	2.75 ± 0.027	2.25 ± 0.005	2.62 ± 0.005	2.75 ± 0.009	1.12; 0.38

Table 3.2 Means and standard deviations of community diversity and richness estimators across different prescribed fire treatments. F-statistics refer to one-way ANOVA that compares means of all five treatments. One-way ANOVAs ($F_{4,23}$, Prob > F) comparing all treatments indicate no significant differences across treatments.

Parameter	Control	2-yr Winter	3-yr Winter	3-yr Summer	6-year Summer	$F_{4,23}$; Prob> F
Coverage	$0.99 \pm 0.2 \%$	$0.99 \pm 0.1 \%$	$0.99 \pm 0.1\%$	$0.99 \pm 0.2\%$	$0.99 \pm 0.04\%$	0.44; 0.78
Richness (S_{Obs})	668.00 ± 77.42	656.5 ± 59.80	680.5 ± 41.92	659.75 ± 7.9	687.5 ± 43.02	0.34; 0.85
Richness (Chao1)	902.71 ± 142.05	899.16 ± 71.57	934.87 ± 51.22	883.90 ± 72.21	915.31 ± 35.17	0.41; 0.81
Diversity (1-D)	0.98 ± 0.001	0.97 ± 0.007	0.98 ± 0.003	0.97 ± 0.009	0.98 ± 0.009	0.68; 0.61

Evenness (E_D)	0.07 ± 0.003	0.06 ± 0.01	0.06 ± 0.01	0.06 ± 0.02	0.07 ± 0.02	1.23; 0.33
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Chapter 4 - Recurring prescribed fire minimally affects ectomycorrhizal communities while root-associated fungal communities respond to frequent burning

Abstract

Prescribed fire is a management tool to reduce fuel loads and to maintain fire-adapted ecosystems over time. Although the fire effects on vegetation and soil properties are well understood, the long-term impacts of different fire regimes on root-inhabiting and ectomycorrhizal (ECM) fungi remain largely unknown. Previous studies show that high intensity wildfires reduce soil fungal biomass and alter fungal communities. However, the effects of repeated low intensity prescribed fires are less well understood. This study took advantage of a long-term (~25 years) fire management regime in a southern yellow pine stand in the southeastern United States to analyze the effects of repeated prescribed fires on root-associated and ECM fungus communities. The fire management regimes included five fire treatments varying in season (winter and summer) and interval length (two-year winter, three-year winter, three-year summer, six-year summer, and unburned control) allowing us to address effects of burn season and fire frequency on root-inhabiting fungi. We used 454-pyrosequencing of ECM roots to specifically focus on the root-associated and ECM fungi that have been proposed most sensitive to fire disturbance. Our sequence data included a large number of off-target, non-ECM sequences. As a result, we analyzed all root-associated fungi as well as those representing only ECM taxa. We found that season had no or only minimal effects on diversity and community

composition of either all root-associated or ECM fungi. Similarly, prescribed burn interval had no effect on diversity or richness of either all root-inhabiting or ECM fungi. However, the communities in our shortest interval treatment (two-year winter) had root-associated communities that differed compositionally from those in unburned plots. Subsequent indicator taxon analyses identified nine indicators that represent potentially fire suppressed (*Coltricia* sp., *Tuber* sp., *Phialophora* sp., Ceratobasidiaceae sp, *Glomus* sp.) or fire adapted taxa (*Bionectria* sp. , *Powellomyces* sp., *Hypocrea* sp., *Rhizopogon* sp.). These results indicate that frequent, recurring prescribed fires result in distinct fire adapted/tolerant root-associated fungal communities that are correlated with the desired fire-adapted plant communities, whereas the ECM symbionts of these plant communities remain largely unaffected.

Introduction

Prescribed fire is a commonly used tool in fire-adapted ecosystems to control vegetation and prevent potentially destructive high-intensity fires (Waldrop et al. 1992; Callaham et al. 2012). Fire-adapted forest ecosystems in the southeastern United States are valuable for silviculture (Talbert et al. 1985; Borders et al. 2001) and provide necessary wildlife habitat (Ligon et al. 1986; Kowal et al. 2013; Steen et al. 2013). Fire must be implemented to maintain these forest stands over time, to reduce fuel loads, and to remove competing non-fire adapted hardwood and shrub species (Waldrop et al. 1992; Glitzenstein et al. 1995; Callaham et al. 2012). Although it is widely acknowledged that fire is a necessary tool to maintain forest stands (Waldrop et al. 1992; Glitzenstein et al. 1995; Callaham et al. 2012), it remains poorly understood how repeated low-intensity prescribed fires affect the below-ground fungal communities in the long-term. These

below-ground communities – especially ectomycorrhizal (ECM) and other root-associated fungi – contribute to ecosystem processes, are a key component in nutrient cycling, and promote plant health and productivity (Fogel and Hunt 1982; Fogel 2006; Smith et al. 2008; Ekblad et al. 2013; Luo et al. 2014).

Previous studies have focused on short-term (<2 years) effects of fire or secondary successional trends following single, isolated fire events on belowground fungal communities (Fritze et al. 1993; Pietikäinen et al. 1993; Visser 1994; Baar et al. 1999; Chen et al. 2002; Longo et al. 2011; Holden et al. 2013). These studies have generally observed lower fungal biomass following a fire (Fritze et al. 1993; Pietikäinen et al. 1993; Dooley and Treseder 2012) and shifts in fungal communities (Visser 1994; Horton et al. 1998; Holden et al. 2013; Longo et al. 2011). The effects of fire on fungal communities depend on many factors, including fire intensity and duration, as well as pre-fire soil parameters or conditions (Visser 1994; Longo et al. 2011; Dooley and Treseder 2013; Holden et al. 2013). The ECM taxa may be particularly sensitive to fire (Visser 1994; Chen et al. 2002; Bastias et al. 2006b; Buscardo et al. 2010; Holden et al. 2013) because they may directly respond to changes in soil physicochemical properties and indirectly through fire effects on the hosts that they depend on. Alternatively, some ECM taxa may respond positively to fire, fruiting soon after a fire (Wicklow, 1973; 1975; Fujimura et al. 2005) or quickly colonizing host roots and becoming dominant following a fire (Fritze et al. 1993; Visser 1994; Horton et al. 1998; Barr et al. 1999; Kipfer et al. 2009).

This study took advantage of a long-term fire management regime in the southeastern United States to analyze the effects of repeated prescribed fires on root-associated and ECM fungal communities that may be sensitive to recurring fires. Our goal was to fill a critical research gap identified in Holden et al. (2013): while many studies have estimated fungal biomass responses to fire, few have broadly assessed fungal community responses. Our study specifically addressed the effects of recurring and frequent prescribed burning after extended period of time (~ 25 years). The management plan in our study system has been implemented since 1988 and includes different interval and seasonal fire regimes allowing us to address the effects of both season (winter, summer) and fire interval (2-yr, 3-yr, 6-yr). Comparisons among our treatments allowed us to identify optimal fire intervals to maintain fire-adapted fungal communities below-ground. Our data show that the root-associated fungal communities respond to recurring low-intensity fires when applied at frequent intervals (two-year), whereas – contrary to our expectations – the ECM communities do not. Further, our data pinpoint few fire-sensitive or fire-adapted root-inhabiting taxa that are distributed among many life history strategies.

Materials and Methods

Study site

Our study stands were located within the Hitchiti Experimental Forest (HEF) in Jones County, Georgia, U.S.A. (32°58'N, 90°44'W). HEF is a sub-unit of the larger Oconee National Forest between the North and South Units of the Piedmont National Wildlife Refuge, falling within the Altamaha River Basin approximately 18 km east of Gray, Georgia. The stand was

historically used for cotton production before converted to forest. Prior to current management, the forest stands were 70+ year-old natural mixes of pine and hardwoods and had not been burned for at least 50 years before a fire regime was established. Upon conversion to forest from cotton plantation the area was planted with loblolly pine (*Pinus taeda* L.), which has remained the dominant tree species in the experimental stands.

The stands reside on highly eroded Alfisols and Ultisols soils that represent those occurring commonly in the Georgia Piedmont area. Soils have been classified as Wilkes and Davidson Series by the United States Department of Agriculture Soil Conservation Service mapping. Wilkes Series soils tend to be shallow and well-drained with moderately slow to slow permeability, indicating moderate soil moisture. These soils formed in residuum weathered from intermediate and mafic crystalline rocks on uplands in the Piedmont, and are classified as loamy, mixed, active, thermic, shallow Typic Hapludalfs. Davidson Series soils consist of very deep, well-drained, moderately permeable soils that formed in materials weathered from dark colored rocks high in ferromagnesian minerals. These soils reside mainly on gently sloping to moderately steep uplands in the Piedmont, and are classified as fine, kaolinitic, thermic Rhodic Kandiudults.

Experimental design

The fire management plan for HEF was established in 1988 with prescribed burns. The management plan includes five treatments across 24 plots, each ~0.8 ha in size. Upon establishment, all plots - excluding unburned control plots - were burned with low intensity backfires during the winter of 1988/1989. The five treatments include: unburned control plots (4

replicates), 2 year winter (4 replicates), 3 year winter (8 replicates), 3 year summer (4 replicates), and 6 year summer burns (4 replicates). Since implementation of this management plan, HEF has experienced an outbreak of southern yellow pine beetle in the past 7-10 years, causing damage to several plots. Sampling in these plots was completed as planned, regardless of damage, because of the question of long-term (~ 25 years) recurring fire effects on root-associated fungal communities.

Soil sampling and ECM root tip collection

To reduce any temporal effects causing variation between sampling times, plots for the different treatments were separated into four sampling blocks so that a representative of each treatment could be sampled in a single day. Samples were collected during four days between November 1 and 16, 2011. Soil cores (10 cm deep, 5 cm diameter) were sampled near fifteen representative dominant canopy trees (loblolly pine; *P. taeda*). For each tree, a soil core was collected 3 m directly south of the tree; all cores were at least 10 m away from the plot edge to minimize the edge effects. The soil cores for each plot were combined into one composite sample. One plot (plot 25, three-year summer burn) suffered from a recent southern pine beetle outbreak and had few remaining overstory trees. This plot was sampled using a mapped grid covering fifteen points spaced approximately 5 m apart. Our previous analyses (Brown et al., 2013) focusing on soil communities in general and using a lightless Ion Torrent sequencing platform did not find any evidence that this plot would represent an outlier. As a result this experimental unit was included in the analyses here.

Soil samples were kept on ice until frozen at -20°C . Samples were shipped to Kansas State University on dry ice and stored at -80°C until further processing. To sample the ECM and root-associated communities, the samples were thawed at room temperature and sieved through a 1 mm mesh (No. 18 American Society for Testing and Materials (ASTM) E-11 Specification, Fisher Scientific Inc. Waltham, Massachusetts) to collect roots. All roots were rinsed with tap water and ECM root tips collected under a Nikon SMZ800 model C-DS dissecting microscope (Nikon Instruments, Melville, New York). A total of 9,600 root tips were collected – four hundred (400) random tips from each of the 24 experimental units – and stored frozen in Bead Solution Tubes (Ultra Clean Soil DNA Isolation Kit, MoBio Laboratories, Carlsbad, California) in -20°C until DNA extraction. Genomic DNA was extracted following manufacturer's instructions and eluted in 50 μl of kit solution S5. DNA yields and concentrations were quantitated with ND1000 spectrometer (NanoDrop Technologies, Wilmington, Delaware) and standardized to a final $5.0\text{ng } \mu\text{l}^{-1}$ concentration for PCR amplification.

Sequence Analysis

A region of the Large SubUnit (LSU) of the ribosomal RNA gene was amplified the forward primer LR0R ($5^{\prime}\text{-CCGCTGAACTTAAGCATATCAATA-3}^{\prime}$; Amend et al. 2010) and reverse primer LR3 ($5^{\prime}\text{-CCGTGTTTCAAGACGGG-3}^{\prime}$; Vilgalys and Hester 1990). We chose LSU for these analyses to take advantage of its alignability against a reference and the availability of the Naïve Bayesian Classifier (Wang et al. 2007) that can utilize the fungal training set consisting of 8506 high-quality public Sanger sequences spanning the first 1400 bp of the LSU gene (Liu et al. 2012) available through the ribosomal database project (RDP; Cole et al. 2009). To reduce 3'

end primer biases resulting from DNA-tagged-primers, we adopted a two-step PCR protocol as recommended by Berry et al. (2011). In the primary PCR, the samples and a negative control (molecular biology grade water) were PCR-amplified in triplicate 25 μ l reactions with following amounts or concentrations: 25 ng μ l⁻¹ DNA template (5 μ l), 200 μ M dNTPs, 1 μ M of both forward (LR0R) and reverse (LR3) primers, 5 μ l of 5x Green GoTaq Flexi Buffer (Promega, Madison, Wisconsin), 2.5mM MgCl₂, 4.8 μ l of molecular biology grade water, and one unit (0.2 μ l) GoTaq Hot Start Polymerase (Promega, Madison, Wisconsin). The reaction conditions included an initial denaturing at 94°C for 4 min, followed by 29 cycles of denaturing at 94°C for 1 min, annealing at 53°C for 45 sec and extension at 72°C for 2 min, and a final extension at 72°C for 8 min. In the secondary PCR, unique 10-base-pair, sample-specific sequence tags (Table B.1) and 454-FLX Titanium (Roche Applied Science, Indianapolis, Indiana, USA) specific A- and B-adaptors were incorporated in a PCR reaction similar to the primary PCR but with number of cycles reduced to five. Similarly to the primary PCR, 25 μ l secondary PCR included following amounts or concentrations: 5 μ l of primary PCR template, 200 μ M dNTPs, 1.25 μ M of DNA-tagged forward (A-tag-LR0R) and reverse primers (B-LR3), 5 μ l of 5x Green GoTaq Flexi Buffer, 2.5 mM MgCl₂, 7.3 μ l of molecular biology grade water, and 0.2 μ l GoTaq Hot Start Polymerase. All PCR reactions were carried out in 96-well plates with 3 technical replicates per sample in a MasterCycler (Eppendorf, Hamburg, Germany). To confirm expected primary and secondary LSU-amplicons, the samples were visualized on a 1.5% agarose gel. The PCR reactions were contamination-free: negative controls had no visible amplicons. The final amplicons in three technical replicates were cleaned using Agencourt AmPure XP magnetic 96-well SPRIplate system (AgenCourt Bioscience, Beverly, Massachusetts) following the manufacturer's protocol with 1:1 AmPure XP solution to amplicon ratio. After AmPure cleaning,

technical replicates were pooled to one per experimental unit and quantified with ND1000 spectrometer. Amplicons were combined equimolarly and the pooled product AmPure-cleaned again to remove residual non-target DNA. The clean amplicons were assessed for size and DNA concentration using a Bioanalyzer 2100 (Agilent Technologies, Santa Clara, California) and 454-pyrosequenced (GS FLX Titanium, Roche Applied Science) at the Integrated Genomics Facility at Kansas State University (Manhattan, KS).

The sequence data were analyzed using the program MOTHUR (v. 1.25.0; Schloss et al. 2009) following a modified standard operating protocol (Schloss et al. 2011). A total of 362,694 sequences were generated. After extracting fasta, qual, and flow files from the .sff file, the sequences were checked to ensure an exact match to the primer (LROR-A; Table C.1) and sample-specific DNA-tags. Sequences that did not match the primer or the DNA-tag, or did not meet any of the following criteria were removed: ambiguous bases (count=0), maximum homopolymer (length \leq 8), minimum length (length \geq 250bp). All sequences were trimmed to lengths equal 250bp length to omit terminal ends of the reads that tend to be of questionable quality. Non-redundant, unique sequences were identified and aligned against mafft-aligned (Kato et al. 2005) LSU training dataset from the Ribosomal Database Project (RDP) comprised of 8,506 high-quality public Sanger sequences spanning the first 1,400 bp of the LSU gene (Liu et al. 2012). Less than 1% dissimilar sequences were pre-clustered to reduce sequencing noise (Huse et al. 2008) and potentially chimeric sequences identified by mothur-embedded uchime (Edgar et al. 2011) removed. The non-chimeric sequences were classified against RDP's taxonomy reference at a 50% bootstrap threshold and non-fungal sequences removed. The remaining unisequences (57,299) were clustered to Operational Taxonomic Units (OTUs) at 97%

similarity using the nearest-neighbor algorithm and OTUs assigned to taxon affinities using a Bayesian Classifier with the RDP-taxonomy reference (Liu et al. 2012) resulting in 669 OTUs. The sequence yields varied from 233 to 4507 sequences per sample. As a result, the data were subsampled to 1,200 to minimize the effects of unequal sequence yields (Gihring et al. 2011); one experimental unit (a replicate of three-year winter burn) with the lowest sequence yield was omitted. Any remaining singletons were removed as they may represent PCR or sequencing artifacts (Tedersoo et al. 2010; Brown et al. 2014). The remaining 499 non-singleton OTUs were annotated to ecological groups: unclassified, unknown, saprobic, pathogenic/parasitic, entomopathogenic, arbuscular mycorrhizal, and ECM. A complete list of taxonomies present with their ecological annotations is available in supplemental Table C.2. We analyzed the sequence data in two sets: one that included all root-associated fungi, and another that included only ECM fungi with all non-ECM taxa removed. The removal of non-ECM taxa resulted in a shallow sequence yields in many samples and varied from 68 to 1511 sequences per sample indicating the great diversity and abundance of fungi that occupy ECM root tips. The diversity and richness metrics were iteratively estimated for both the comprehensive (subsampled to 1,180 sequences per experimental unit) and ECM data sets (subsampled to 235 sequences per experimental unit, resulting in a loss of two experimental units - two-year winter plot and three-year winter plot - from these analyses). The richness and diversity metrics for each of the two datasets were estimated using MOTHUR (v. 1.25.0; Schloss *et al.*, 2009): rarefaction (Maura, 1988), observed (S_{Obs} : number of OTUs) and extrapolated OTU richness (Chao1: $S_{\text{Chao1}} = S_{\text{Obs}} + \{n_1(n_1-1)/2(n_2+1)\}$, where n_1 =the number of OTUs with only 1 sequence and n_2 = the number of OTUs with only two sequences), diversity (1-D or compliment of Simpson's diversity index: $1-D = 1 - \sum p_i^2$, where D = Simpson's diversity index and p_i = proportional abundance of

the i th species), evenness (Simpson's equitability or E_D : $E_D = (1/\sum p_i^2)/S$), where p_i = proportional abundance of the i th species and S = richness), and Good's coverage (Good's coverage ($G = 1 - (n_1)/(N)$), where n_1 = the number of OTUs that have been sampled once and N = the total number of individuals in the sample).

Statistical Analyses

Differences in diversity and richness across the treatments were tested using one-way ANOVA in JMP® (version 7.0.2). Data for these analyses were transformed to meet assumptions of variance homogeneity and/or normal distribution. Response variables ranging from zero to one (percentages) were arcsine square root transformed, whereas others were \log_{10} -transformed. To analyze community compositional differences among treatments we first derived a Bray-Curtis distance matrix for each dataset (all root fungi and ECM only) and pairwise compared treatments with Multi-Response Permutation Procedure (MRPP) in PC-ORD (version 5; McCune and Mefford 2006). To visualize data clouds for our two datasets we estimated Non-metric Multidimensional Scaling (NMS) axis scores. The dataset incorporating all root fungi was optimally resolved in three ordination axes ($k=3$) representing 79.5% of the variation and with a final stress of 0.29. In contrast to the all root-associated fungi, no NMS solution significantly better than those derived at random ($P > 0.05$) could be found for the ECM. This is likely a result of numerous high/low abundance OTUs having a disproportionate weight on the ordination since removal of potential outliers (plots with Bray-Curtis distances more than two standard deviations from the mean) yielded similarly weak ordinations. In addition to these community-wide

descriptors, we performed permutational Indicator Species Analyses for each dataset in PC-ORD to detect any taxa that may have frequencies higher in one treatment than in others.

Results

General data description

We acquired a total of 362,694 sequences. After quality control, removal of singleton OTUs, and subsampling, dataset contained 274 OTUs and 27,140 sequences – one experimental unit (three-year winter burn) was lost as a result of low yield that did not meet our minimum threshold. All OTUs in the dataset were classified at least to the phylum level but many lacked taxon assignments on less inclusive levels. Our data were dominated by the phylum Ascomycota (15,830 sequences, 58.3%; 103 OTUs, 37.6%), followed by Basidiomycota (10,592 sequences, 39.0%; 128 OTUs, 46.7%). The remaining sequences belonged to Glomeromycota (516 sequences, 1.9%; 15 OTUs, 5.4%) and basal fungal lineages (202 sequences, 0.66%; 28 OTUs, 10.2%). The most abundant orders included potentially pathogenic Magnaporthales (5,017 sequences, 18.4%; 12 OTUs, 4.3%) and endophytic Helotiales (3,607 sequences, 13.3%; 8 OTUs, 2.9%) followed by mainly ECM and/or free-living taxa Russulales (3,412 sequences, 12.6%; 11 OTUs, 4.0%) and Agaricales (2,994 sequences, 11.0%; 49 OTUs, 17.9%). On a family level, potentially pathogenic Magnaporthaceae was the most abundant (5,017 sequences, 18.4%; 12 OTUs, 4.3%) followed by the ECM family Russulaceae (3,410 sequences, 12.6%; 10 OTUs, 3.6%). The most abundant OTUs included the potentially pathogenic or endophytic OTU001 representing *Phialophora* sp. (5,017 sequences, 18.4%), followed by the likely saprobic

OTU002 representing *Vibrissea* sp. (2,391 sequences, 8.8%), and the likely ECM forming OTU003 *Russula* sp. (2,119 sequences, 7.8%). A complete list of OTUs with their taxon assignments and sequence counts is available in Supplemental Table C.3.

All root-associated fungi

To assess our sampling effort we used rarefaction curves (Fig. 4.1) and Good's coverage (Table 4.1). The two metrics provided contrasting results. After removal of rare sequences and subsampling, the rarefaction curves still continue in an upward trajectory indicating more OTUs could be captured with greater sequencing. However, Good's coverage was relatively high ($98.5\% \pm 0.36\%$) suggesting adequate sampling.

Diversity and richness estimators [observed (S_{Obs}) and extrapolative (Chao1) richness, diversity (1-D), evenness (E_D)] for root-associated fungal communities were not affected by season or interval length, as no differences were observed across any treatments (Table 1). Again, we observed no effects of season between root-associated communities of three-year winter and three-year summer treatments (MRPP: $T_{2,10} = -0.63$, $A_{2,10} = 0.03$, $P = 0.239$). Taken together, these results indicate that the season of the prescribed burn implementation had no effect on root-associated fungal communities – their richness or composition. However, pairwise MRPP analyses of all treatments suggest that root-associated communities do respond compositionally to prescribed burn interval. The shortest, two-year fire interval significantly differed compositionally from the unburned plots (MRPP: $T_{2,8} = -2.19$, $A_{2,8} = 0.17$, $P = 0.018$) but only marginally from six-year interval treatments (MRPP: $T_{2,8} = -1.68$, $A_{2,8} = 0.14$, $P =$

0.058). Three-year winter treatments were also marginally different from six-year interval and unburned plots (MRPP: $T_{2,10} = -1.78$, $A_{2,10} = 0.09$, $P = 0.051$; MRPP: $T_{2,10} = -1.43$, $A_{2,10} = 0.06$, $P = 0.085$, respectively). In contrast to the three-year winter treatment, the three-year summer burns did not differ from any other treatment (MRPP: $T_{2,7(10)} \leq 1.27$, $A_{2,7(10)} \leq 0.03$, $P \geq 0.239$). The root-associated fungal communities in the longest fire interval, six-year summer, treatments did not differ from those in unburned treatments (MRPP: $T_{2,8} = 0.37$, $A_{2,8} = -0.03$, $P = 0.565$). These results suggest that the shortest fire interval resulted in a community clearly distinct from those in the unburned treatments. However, the longest burn intervals had communities similar to unburned control treatments indicating that the six-year burn interval length allowed communities to return to states similar to those in the unburned reference plots.

Root-associated fungal community data clouds were visualized using NMS (Fig. 4.2). Our MRPP results showed that only two-year interval treatments significantly differed from unburned treatments. Yet, the majority of the short fire interval lengths (two- and three-year burns) plots fall above the x-axis while the longer six-year intervals and unburned reference plots fall mainly below the x-axis (Fig. 2).

To identify OTUs that represent likely fire-sensitive or fire-adapted taxa, we utilized indicator taxon analyses. We detected a total of eight indicator OTUs, a relatively small proportion (3.2%) of the 247 OTUs in the dataset. The short fire interval treatments (2- and 3-year burns) included a total of three potentially fire-adapted taxa: saprobic or pathogenic ascomycete *Bionectria* sp. (OTU098), soil-inhabiting chytridiomycete *Powellomyces* sp. (OTU132), and saprobic *Hypocrea* sp. (OTU176). The unburned reference treatment included

two potentially fire-sensitive taxa: *Coltricia* sp. (OTU047) and *Tuber* sp. (OTU028). It is of note that both these fire-sensitive OTUs form ECM. The long, six-year burn intervals included another three indicator OTUs: potentially parasitic, saprobic, or endophytic *Phialophora* sp. (OTU263); potentially parasitic or saprobic Ceratobasidiaceae sp. (OTU062); and, arbuscular mycorrhizal *Glomus* sp. (OTU203) (Fig 4.3).

ECM fungi

Only a proportion of fungi present in our root tips represented ECM taxa: 18.2% of sequences and 7.7% of OTUs. As a result, we opted to conduct additional analyses with all non-ECM OTUs removed. After removal of all non-ECM taxa and subsequent removal of singletons, we omitted two additional experimental units with low remaining sequence yields (one two-year winter plot and one three-year winter plot) to permit a reasonable subsampling of sequences (235 sequences per experimental unit). This dataset included 4,935 sequences and 45 ECM OTUs. Two ECM forming phyla were present in the dataset, dominated by Basidiomycota (4,785 sequences, 96.9%; 44 OTUs, 97.8%) and followed by Ascomycota (150 sequences, 3.0%; 1 OTU, 2.2%). The most dominant orders were Russulales (2,151 sequences, 43.6%; 8 OTUs, 17.8%) and Thelephorales (1,129 sequences, 22.9%; 5 OTUs, 11.1%). The remaining orders included Agaricales (581 sequences, 11.8%; 9 OTUs, 20.0%), Boletales (523 sequences, 10.6%; 13 OTUs, 28.9%), Cantharellales (278 sequences, 5.6%; 2 OTUs, 4.4%), Pezizales (150 sequences, 3.0%; 1 OTU, 2.2%), Hymenochaetales (79 sequences, 1.6%; 1 OTU, 2.2%), Atheliales (25 sequences, 0.5%; 2 OTUs, 4.4%), and Sebacinales (10 sequences, 0.4%; 4 OTUs, 8.9%). On the genus level, *Russula* (1,624 sequences, 32.9%; 4 OTUs, 8.8%) was the most common encompassing almost a third of dataset, followed by *Tomentella* (888 sequences,

17.9%; 2 OTUs, 4.4%) and *Lactarius* (527 sequences, 10.6%; 4 OTUs, 8.8%). Genus *Rhizopogon* was the most species rich (6 OTUs, 13.3%). OTU003 (*Russula* sp.- 1,465 sequences, 29.7%) was the most abundant, followed by OTU004 (*Tomentella* sp.- 802 sequences, 16.3%). A complete list of all ECM OTUs with their associated taxonomic affinities can be found in Supplemental Table C.4.

We used Good's coverage (Table 4.2) and rarefaction (Fig. 4.4) analyses to estimate and visualize sampling effort. The majority of the 21 experimental units that remained after excluding non-ECM taxa and subsampling have rarefaction curves that continue on an upward trajectory indicating greater sequencing efforts would result in more OTUs. In contrast, Good's coverage was high and suggested adequate sampling effort ($99.1\% \pm 0.59\%$).

Similar to our analyses that included all root-associated fungi, we observed no effect of season or fire interval on richness or diversity of the ECM communities (Table 4.2). Similarly, our pairwise comparison of three-year winter and three-year summer treatments showed no evidence for compositional responses in the ECM communities to season of fire implementation (MRPP: $T_{2,10} = -0.03$, $A_{2,10} = 0.002$, $P = 0.446$). The remaining pairwise comparisons across all treatments similarly showed no evidence for differences in ECM community compositions, indicating no significant effects of fire interval on ECM communities (MRPP: $T_{2,7(10)} \leq 0.52$, $A_{2,7(10)} \leq 0.06$, $P \geq 0.119$). We were unable to find an NMS ordination solution superior to those derived at random – even after removal of outliers. Such results typically suggest lacking

structure in the dataset – in our case, a likely result of a small dataset and overlap of many taxa across treatments.

Our indicator taxon analyses identified three ECM OTUs, two of which were associated with the unburned control treatments. Consistent with the analyses that included all root-associated fungi, the likely fire-sensitive indicators were ECM taxa *Tuber* sp. (OTU028) and *Coltricia* sp. (OTU047). In addition to these fire-suppressed taxa, our indicator taxon analyses identified one potentially fire-adapted ECM OTU in the two-year fire interval treatments: *Rhizopogon* sp. (OTU177) had elevated numbers in this treatment (Fig. 4.3).

Discussion

We aimed to determine the long-term effects of repeated prescribed fire treatments on root-associated fungal communities. As usual for high throughput sequencing studies that analyze mixed ECM communities (e.g, Jumpponen et al. 2010; Counce et al. 2013; Lothamer et al. 2014), our fungal communities in the root tips included a large proportion of non-target saprobes and plant antagonists. As a result, we analyzed our communities including all observed OTUs as well as those including only the ECM taxa. Our prescribed burning experiment has been in place for a quarter century and provided us with a unique opportunity to explicitly evaluate how recurring frequent low-intensity prescribed fires may affect these fungal communities in the long-term. Prescribed fire has become an increasingly important tool used to reduce fuel loads, whose accumulation may result in stand-replacing and hazardous high-intensity wildfires (Fernandes

and Botelho 2003; Ryan et al. 2013). In fire-adapted ecosystems, prescribed fire is also necessary to suppress non-fire adapted communities and to preserve and maintain native fire adapted species over time (Waldrop et al. 1992; Mitchell et al. 2006; Callaham et al. 2012). This is especially important for southern yellow pine stands in the southeastern United States as they are of great economic importance in silviculture (Talbert et al. 1985; Borders et al. 2001; Mitchell et al. 2006). Previous experiments have shown that fires, particularly high-intensity wildfires, reduce fungal biomass in soil (Fritze et al. 1993; Pietikäinen et al. 1993; Dooley and Treseder 2012) and can alter soil and ECM fungus communities (Baar et al. 1999; Chen et al. 2002) directly following a fire. The ECM communities may be particularly sensitive (Chen et al. 2002; Bastias et al. 2006b; Buscardo et al. 2010; Holden et al. 2013) or responsive to fire (Fritze et al. 1993; Visser 1994; Horton et al. 1998; Barr et al. 1999; Fujimura et al. 2005; Kipfer et al. 2009). Because of the importance of root-associated fungal communities on plant performance and health, we focused specifically on these fungal communities.

Fires – particularly high-intensity wildfires – can change soil chemistry and alter nutrient availability (Hernández et al. 1997; Prieto-Fernández et al. 2003; Certini 2005; Williams et al. 2011; Toberman et al. 2014) through combustion and volatilization of carbon and nitrogen (Hernández et al. 1997; Certini 2005). Similarly, even low-intensity prescribed fires have been observed to result in a loss of soil nutrients (Williams et al. 2011; Toberman et al. 2014). The fire effects on soil properties tend to be influenced by the pre-existing soil properties such as soil moisture (Certini 2005; Glass et al. 2008). Previous results indicate that after long-term repeated burns soil pH, total N, or total C may remain relatively unaffected in the plots used in this study (Callaham et al. 2012). While those findings are in line with Glass et al. (2008), they contrast

those of Williams et al. (2011) and Toberman et al. (2014). Changes in soil properties (soil moisture and nutrients) that can result from a fire disturbance have been previously linked to changes in ECM communities (Moeller et al. 2013; Holden and Treseder 2013; Holden et al. 2013; Toljander et al. 2006; van der Heijden et al. 2000). Our data suggest that the ECM communities are mainly resilient to low-intensity prescribed burning, findings that parallel the lack of fire-induced changes in soil chemistry.

Season of prescribed fire can influence fire intensity and the resulting effects on the ecosystem (Swezy and Agee 1991; Waldrop et al. 1992; Sparks et al. 2002; Knapp et al. 2007). Winter season burns have been historically preferred as they are easier to manage, although are not as efficient in the removal of non-fire adapted species (Sparks et al. 2002; Waldrop et al. 1992). Previous studies indicate that both summer and fall burns significantly reduce plant species richness (Knapp et al. 2007) and early growing season burns lead to greater tree mortality (Swezy and Agee 1991). While spring/summer burns may have greater success in maintaining the desired fire-adapted communities (Waldrop et al. 1992; Sparks et al. 2002) from the management perspective, little is known about their effects of seasonal burning on below-ground fungal communities. Smith et al. (2004) observed greater richness of ECM communities in areas burned during the fall compared to those burned during the spring. However, our data suggest that the season of fire implementation had no discernible effect on fungal community composition or diversity.

In contrast to no evidence of response to season of fire implementation, our most frequent two-year fire intervals resulted in root-associated communities distinct from those observed in unburned plots. Two-year winter burn treatments were also marginally distinct from six-year summer burns. Similarly, three-year winter burns were marginally distinct from the unburned reference treatments and six-year summer burn treatments, although no differences in communities were observed between six-year and unburned plots. These findings suggest that repeated low-intensity prescribed fires in short intervals, particularly as frequent as every two years, may facilitate fire-adapted fungal communities in the rhizosphere. Our findings are comparable to other studies that analyzed effects of repeated prescribed fires. For example, studies focusing on soil fungi in Australian sclerophyll forests found that short fire intervals (two-year and four-year) led to shifts in soil-inhabiting fungal communities and their composition. However, greater fire intensities result in greater effects on soil inhabiting fungal communities (Fritze et al. 1993; Pietikäinen et al. 1993; Dooley and Treseder 2012), whereas low-intensity backfires used in our study may only marginally affect on them.

In contrast to compositional shifts in the root-associated fungal communities resulting from recurring and frequent prescribed fires, our results suggest that fire interval had no impact on diversity and richness. This is in contrast with some studies that have observed lower diversity following repeated burns (e.g., Tuininga and Dighton 2004), although others (e.g., Anderson et al. 2007) have reported no effect of repeated burns on soil fungal community diversity. Based on the responses in community richness or diversity and the associated changes in community composition, we conclude that community responses to recurring fire are primarily driven by taxon reordering and replacement. In other words, the root-inhabiting

community changes can be mainly explained by changes in the community constituent frequencies rather than taxon losses.

Our analyses that specifically focused on the ECM communities suggest that ECM may not respond strongly to low-intensity prescribed fire management. Consistently with the general root-inhabiting communities, our data provide no evidence for changes in community richness or diversity as a result of prescribed fire management. Further, the ECM communities seem compositionally less sensitive than the general root-inhabiting communities: we observed no changes in community composition in response to fire regimes regardless of season or interval length. Our results are in contrast with many previous studies. Community shifts in plant symbiotic fungal communities are common following single fire occurrences (Horton et al. 1998; Visser 1994; Longo et al. 1994). Previous studies suggest that ECM communities may be particularly sensitive to fire (Holden et al. 2013), as they typically reside closer to the soil surface (Buchholz and Motto 1981; Dickie et al. 2002) and may respond fires both directly and indirectly via through physiological responses of their hosts. Results of Stendell et al. (1999) support these conclusions, observing a greater ECM biomass loss in the organic soil layers than in deeper mineral soil layers one year after a prescribed fire event. In addition, shorter fire intervals in particular tend to have visible impacts on ECM fungal communities that result in assemblies that differ from those inhabiting the unburned areas (Anderson et al. 2007; Bastias et al. 2006a).

Whilst many studies highlight the negative impacts of high-intensity wildfires (Dooley et al. 2012; Holden et al. 2013; Holden and Treseder 2013), controlled prescribed burning may

favor fire-adapted fungi (Fritze et al. 1993; Visser 1994; Horton et al. 1998; Barr et al. 1999; Fujimura et al. 2005; Kipfer et al. 2009). Some taxa respond quickly to a fire disturbance and dominate fungal communities after a fire: *Rhizopogon*, *Wilcoxina* (Horton et al. 1998; Barr et al. 1999; Kipfer et al. 2009); *Tomentella* (Barr et al. 1999); *Cenococcum* (Kipfer et al. 2009); *Russula*, *Suillus* (Horton et al. 1998); and, *Coltricia*, *Thelephora* (Visser 1994). Fujimura et al. (2005) observed several genera in the order Pezizales (*Anthracobia*, *Morchella*, *Peziza*, *Scutellinia*, and *Tricharina*) producing fruiting bodies after prescribed fires in a ponderosa pine forest. These phoenicoid, post-fire (Carpenter and Trappe, 1985) taxa have fire resistant propagules that allow them to persist and respond quickly after a fire (Taylor and Bruns 2002; Izzo et al. 2005; Peay et al 2009). To identify potentially fire-sensitive or fire-resistant taxa, we conducted indicator taxon analyses and identified a total of eight indicator OTUs among the root-associated fungi plus an additional one in the analyses focusing exclusively on ECM fungi. Three of these indicators occurred in the short fire interval treatments (two-year and three-year burns), representing fire-adapted saprobic or pathogenic ascomycete *Bionectria* sp., soil-inhabiting chytridiomycete *Powellomyces* sp., and saprobic *Hypocrea* sp. We identified two indicator taxa (*Coltricia* sp. and *Tuber* sp.) in the fire-suppressed, unburned treatments. These potentially fire-sensitive taxa likely form ECM associations, corroborating thus earlier conclusions that it is these mutualists that are among those suppressed by fire (Holden et al. 2013). The indicator taxon analyses were largely congruent between the two datasets that we analyzed and identified same two fire-sensitive ECM taxa (*Tuber* sp. and *Coltricia* sp.). However, our analyses on ECM communities identified an additional ECM indicator taxon (*Rhizopogon* sp.) that occurred more frequently in the shortest, two-year fire interval treatments suggesting it as fire-resistant. These indicator analyses are in line with several other studies

(Horton et al. 1998; Barr et al. 1999; Kipfer et al. 2009) that have observed *Rhizopogon* spp. abundantly after fires. Unfortunately, our high throughput sequencing approach did not permit us to assign many OTUs into species. This may underlay some incongruences between our study and those of others. For example, *Coltricia* sp. was among the potentially fire sensitive taxa in our indicator taxon analyses, whereas Visser (1994) observed *Coltricia perennis* to dominate in communities following a wildfire in a Jack pine forest. Furthermore, many previous studies have focused on short-term response (Baar et al. 1999; Fujimura et al. 2005) or follow one-time fire events (Visser, 1994; Horton et al. 1998; Kipfer et al. 2009), whereas we focused on the long-term effects of repeated prescribed fire.

Although the broad root-associated communities responded to prescribed fire in our study, the analyses that concentrated exclusively on the ECM communities were less conclusive. These analyses suggested that neither the richness and diversity or the composition of ECM communities responded strongly to fire management. However, the fire management resulted in shifts in the broader root-associated fungal communities when implemented repeatedly in the shortest fire intervals (two-year), whilst their diversity and richness remained stable. These results were consistent across all seasonal, winter and summer, treatments as well as across burn interval treatments indicating no noticeable effects of season or fire interval on the richness or diversity of these fungal root communities. Our conservative indicator taxon analyses pinpointed few strongly responding fire-adapted and fire-sensitive taxa, some of which represent genera proposed to show similar fire responses in other studies. We identified ECM taxa that likely benefit from either fire suppression (*Coltricia*, *Tuber*) or frequent prescribed fire implementation (*Rhizopogon*) as well as others that represent non-ECM functional guilds. In conclusion,

prescribed burning is an important tool used to facilitate fire-adapted vegetation and repeated fire may select for fire-adapted and/or fire-tolerant fungi – ECM or other rhizosphere inhabitants. Overall, we conclude that fire management implemented through low-intensity prescribed fires alter root-associated communities under short fire interval conditions but have minimal overall effects on ECM fungal communities, even when recurring in the long term.

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References

Amend AS, Seifert KA, Samson R, Bruns TD (2010) Indoor fungal composition is geographically pattered and more diverse in temperate zones than in the tropics. *Proceedings of the National Academy of Sciences* 107: 13748-13753.

Anderson IC, Bastias BA, Genney DR, Parkin PI, Cairney JWG (2007) Basidiomycete fungal communities in Australian sclerophyll forest soil are altered by repeated prescribed burning. *Mycological Research* 111: 482-486.

Artz RRE, Reid E, Anderson IC, Campbell CD, Cairney JWG (2008) Long term repeated prescribed burning increases evenness in the basidiomycete laccase gene pool in forest soils. *FEMS Microbial Ecology* 67: 397-410.

Bastias BA, Huang ZQ, Blumfields T, Xu Z, Cairney JWG (2006a) Influence of repeated prescribed burning on the soil fungal community in an eastern Australian wet sclerophyll forest. *Soil Biology and Biochemistry* 38: 3492-3501.

Bastias BA, Xu ZH, Cairney JWG (2006b) Influence of long-term repeated prescribed burning on mycelial communities of ectomycorrhizal fungi. *New Phytologist* 172: 149-158.

Barr J, Horton TR, Kretzer AM, Bruns TD (1999) Mycorrhizal colonization of *Pinus muricata* from resistant propagules after a stand-replacing wildfire. *New Phytologist* 143: 409-418.

Berry D, Mahfoudh KB, Wagner M, Loy A (2011) Barcoded primers used in multiplex amplicon pyrosequencing bias amplification. *Applied and Environmental Microbiology* 77: 7846-7849.

Borders BE, Bailey RL (2001) Loblolly pine-pushing the limits of growth. *Southern Journal of Applied Forestry* 25: 69-74. Brown SP, Callahan Jr. MA, Oliver AK and Jumpponen A (2013), Deep Ion Torrent sequencing identifies soil fungal community shifts after frequent prescribed fires in a southeastern US forest ecosystem. *FEMS Microbiology Ecology* 86: 557-566.

Brown SP, Jumpponen A (2014) Contrasting primary successional trajectories of fungi and bacteria in retreating glacier soils. *Molecular Ecology* 23: 481-497.

Bucholz K, Motto H (1981) Abundances and vertical distributions of mycorrhizae in Plains and Barrens forest soils from the New Jersey Pine Barrens. *Bulletin of the Torrey Botanical Club* 108: 268-271.

Buscardo E, Rodríguez-Echeverría S, Martic MP, Angelis PD, Pereira JS, Freitas H (2010) Impact of wildfire return interval on the ectomycorrhizal resistant propagules communities of a Mediterranean open forest. *Fungal Biology* 114: 628–636.

Callaham MA. Jr., Scott DA, O'Brien JJ, Stanturf JA (2012) Cumulative effects of fuel management on the soils of eastern U.S., in: LaFayette, R., Brooks, M.T., Potyondy, J.P., Audin, L., Krieger, S.L., Trettin, C.C. (Eds.), *Cumulative watershed effects of fuel management in the Eastern United States*. Gen. Tech. Rep. SRS-161. Asheville, NC: U.S. Department of Agriculture Forest Service, Southern Research Station, pp. 202-228.

Carpenter SE, Trappe JM (1985) Phoenicoid fungi – a proposed term for fungi that fruit after heat-treatment of substrates. *Mycotaxon* 23: 203-206.

Certini G (2005) Effects of fire on properties of forest soils: a review. *Oecologia* 143: 1-10.

Chen DM, Cairney WGJ (2002) Investigation of the influence of prescribed burning on ITS profiles of ectomycorrhizal and other soil fungi at three Australian sclerophyll forest sites. *Mycological Research* 106: 532-540.

Coince A, Caël, O, Bach C, Lengelle J, Cruaud C, Gavory F, Morin E, Murat C, Marcais B, Buée M (2013) Below-ground fine-scale distribution and soil *versus* fine root detection of fungal and soil oomycete communities in a French beech forest. *Fungal Ecology* 6: 223-235.

Cole JR, Wang Q, Cardenas E, Fish J, Chai B, Farris RJ, Kulam-Syed-Mohideen AS, McGarrell DM, Marsh T, Garrity GM, Tiedje JM (2009) The Ribosomal Database Project: improved alignments and new tools for rRNA analysis. *Nucleic Acids Res* 37: 141-145.

Dickie IA, Xu B, Koide RT (2002) Vertical niche differentiation of ectomycorrhizal hyphae in soil as shown by T-RFLP analysis. *New Phytologist* 156: 527–535.

Dooley SR, Treseder KK (2012) The effect of fire microbial biomass: a meta-analysis of field studies. *Biogeochemistry* 109: 49-61.

Edgar RC, Haas BJ, Clemente JC, Quince C, Knight R (2011) UCHIME improves sensitivity and speed of chimera detection. *Bioinformatics* 27: 2194-2200.

Ekblad A, Wallander H, Godbold DL, Cruz C, Johnson D, Baldrian P, Björk RG, Epron D, Keiliszewska-Rokicka B, Kjoller R, Kraigher H, Matzner E, Newmann J, Plassard C (2013) The production and turnover of extramatrical mycelium of ectomycorrhizal fungi in forest soils: role in carbon cycling. *Plant Soil* 366: 1-27.

Fernandes PM, Botelho HS (2003) A review of prescribed burning effectiveness in fire hazard reduction. *International Journal of Wildland Fire* 12: 117-128.

Fogel R, Hunt G (1982) Contribution of mycorrhizae and soil fungi to nutrient cycling in a Douglas-fir ecosystem. *Canadian Journal of Forest Research* 13: 219- 232.

Fogel R (2006) Mycorrhizae and nutrient cycling in natural forest ecosystems. *New Phytologist* 86: 199-212.

Fritze H, Pennanen T, Pietikäinen J (1993) Recovery of soil microbial biomass and activity from prescribed burning. *Canadian Journal of Forest Research* 23: 1286-1290.

Fujimura KE, Smith JE, Horton TR, Weber NS, Spatafora JW (2005) Pezizalean mycorrhizas and sporocarps in ponderosa pine (*Pinus ponderosa*) after prescribed fires in eastern Oregon, USA. *Mycorrhiza* 15:79-86.

Gihring TM, Green SJ, Schadt CW (2011) Massively parallel rRNA gene sequencing exacerbates the potential for biased community diversity comparisons due to variable library sizes. *Environmental Microbiology* 14: 285-290.

Glass DW, Johnson DW, Blank RR, Miller WW (2008) Factors affecting mineral nitrogen transformations by soil heating: a laboratory-simulated fire study. *Soil Science* 173: 387-400.

Glitzenstein JF, Platt WJ, Streng DR (1995) Effects of fire regime and habitat on tree dynamics in north Florida longleaf pine savannas. *Ecological Monographs* 65: 441-476.

Hernández T, García C, Reinhardt I (1997) Short-term effect of wildfire on chemical, biochemical and microbiological properties of Mediterranean pine forest soils. *Biology and Fertility of Soils* 25: 109-116.

Holden SR, Gutierrez A, Treseder KK (2013) Changes in soil fungal communities, extracellular enzyme activities, and litter decomposition across a fire chronosequence in Alaskan boreal forests. *Ecosystems* 16: 34-46.

Holden SR, Treseder KK (2013) A meta-analysis of soil microbial biomass responses to forest disturbances. *Frontiers in Microbiology* 4: article 163.

Horton TR, Cázares E, Bruns TD (1998). Ectomycorrhizal, vesicular-arbuscular and dark septate fungal colonization of bishop pine (*Pinus muricata*) seedlings in the first 5 months of growth after wildfire. *Mycorrhiza* 8:11-18.

Huse SM, Dethlefsen L, Huber JA, Welch MD, Relman DA, Sogin ML (2008) Exploring microbial diversity and taxonomy using SSU rRNA hypervariable tag sequencing. *PLoS Genetics* 4: e1000255.

Izzo A, Canright M, Bruns TD (2005) The effects of heat treatments on ectomycorrhizal resistant propagules and their ability to colonize bioassay seedlings. *Mycological Research* 110: 196-202.

Jumpponen A, Jones KL, Mattox JD, Yeage C (2010) Massively parallel 454-sequencing of fungal communities in *Quercus* spp. ectomycorrhizas indicates seasonal dynamics in urban and rural sites. *Molecular Ecology* 19: 41-53.

Katoh K, Kuma K, Toh H, Miyata T (2005) MAFFT version 5: improvement in accuracy of multiple sequence alignment. *Nucleic Acids Research* 33: 511-518.

Kifper T, Simon E, Ghazoul J, Moser B, Wohlgemuth T (2010) Susceptibility of ectomycorrhizal fungi to soil heating. *Fungal Biology* 114: 467-472.

Knapp EE, Schwilk DW, Kane JM, Keeley JE (2007) Role of burning season on initial understory vegetation response to prescribed fire in a mixed conifer forest. *Canadian Journal of Forest Research* 37: 11-22.

Kowal VA, Scholke A, Kanagaraj R, Bruggeman D (2013) Resource selection probability functions for gopher tortoise: providing a management tool application across the species' range. *Environmental Management* 53: 594-605.

Ligon DJ, Stacey PB, Conner RN, Bock CE, Adkisson CS (1986) Report of the American ornithologists' union committee for the conservation of the red-cockaded woodpecker. *The Auk* 103: 848-855.

Liu KL, Kuske CR, Porras-Alfaro A, Eichorst S, Xie G (2012) Accurate, rapid taxonomic classification of fungal large subunit rRNA genes. *Applied and Environmental Microbiology* 78: 1523-1533.

Longo MS, Urcelay C, Nouhra E (2011) Long term effects of fire on ectomycorrhizas and soil properties in *Nothofagus pumilio* forest in Argentina. *Forest Ecology and Management* 262: 348-354.

Lothamer K, Brown SP, Mattox JD, Jumpponen A (2014) Comparison of root-associated communities of native and non-native ectomycorrhizal hosts in an urban landscape. *Mycorrhiza* 24: 267-280.

Luo Z, Wu C, Zhang C, Li H, Lipka U, Polle A (2014) The role of ectomycorrhizas in heavy metal stress tolerance of host plants. *Environmental and Experimental Botany* 108: 47-62.

Mitchell RJ, Hiers JK, O'Brien, Jack SB, Engstrom RT (2006) Silviculture that sustains: the nexus between silviculture, frequent prescribed fire, and conservation of biodiversity in longleaf pine forests of the southeastern United States. *Canadian Journal of Forest Research* 36: 2724-2736.

Moeller HV, Peay KG, Fukami T (2013) Ectomycorrhizal fungal traits reflect environmental conditions along a coastal California edaphic gradient. *FEMS Microbiology Ecology* 87: 797-806.

Peay GP, Garbelotta M, Bruns TD (2009) Spore heat resistance plays an important role in disturbance-mediated assemblage shift of ectomycorrhizal fungi colonizing *Pinus muricata* seedlings. *Journal of Ecology* 97: 537-547.

Pietikäinen J, Fritze H (1993) Microbial biomass and activity in the humus layer following burning: short-term effects of two different fires. *Canadian Journal of Forest Research* 23: 1275-1285.

Prieto-Fernández Á, Carballas M, Carballas T (2004) Inorganic and organic N pools in soils burned or heated: immediate alteration and evolution after forest wildfires. *Geoderma* 121: 291-306.

Ryan KC, Knapp EE, Varner JM (2013) Prescribed fire in North American forests and woodlands: history, current practice, and challenges. *Frontiers in Ecology and the Environment* 11: e15-e24.

Schloss PD, Westcott SL, Ryabin T, Hall JR, Hartmann M, Hollister EB, Lesniewski RA, Oakley BB, Parks DH, Robinson CJ, Sahl JW, Stres B, Thallinger GG, Van Horn DJ, Weber CF (2009) Introducing mothur: open-source, platform-independent, community-supported software for describing and comparing microbial communities. *Applied and Environmental Microbiology* 75: 7537-7541.

Schloss PD, Gevers D, Westcott SL (2011) Reducing the effects of PCR amplification and sequencing artifacts on 16S rRNA-based studies. PLOS ONE 6:e27310.

Smith JE, McKay D, Niwa CG, Thies WG, Brenner G, Spatafora JW (2004) Short-term effects of seasonal prescribed burning on the ectomycorrhizal fungal community and fine root biomass in ponderosa pine stands in the Blue Mountains of Oregon. Canadian Journal of Forest Research 34: 2477-2491.

Smith SE, Smith FAA, Read DJ (2008). Mycorrhizal symbiosis. 3rd ed. Elsevier, London. 787 pp.

Sparks JC, Masters RE, Engle DM, Bukenhofer GA (2002) Season of burn influences fire behavior and fuel consumption in restored shortleaf pine-grassland communities. Restoration Ecology 10: 714-722.

Steen DA, Smith LL, Morris G, Conner M, Litt AR, Pokswinski S, Guyer C (2013) Response of six-lined racerunner (*Aspidoscelis sexlineata*) to habitat restoration in fire-suppressed longleaf pine (*Pinus palustris*) sandhills. Restoration Ecology 21: 457- 463.

Stendell ER, Horton TR, Bruns TD (1999) Early effects of prescribed fire on the structure of the ectomycorrhizal fungus community in Sierra Nevada ponderosa pine forest. Mycological Research 103: 1353-1359.

Swezy DM, Agee JK (1990) Prescribed fire effects on fine-root and tree mortality in old-growth ponderosa pine. Canadian Journal of Forest Research 21: 626-634.

Talbert JT, Weir RJ, Arnold RD (1985) Cost and benefits of a mature first-generation loblolly pine tree improvement program. Journal of forestry 83: 162-166.

Taylor DL, Bruns TD (2002) Community structure of ectomycorrhizal fungi in a *Pinus muricata* forest: minimal overlap between the mature forest and resistant propagule communities. *Molecular Ecology* 8: 1837-1850.

Tedersoo L, Nilsson RH, Abarenkov K et al. (2010) 454 pyrosequencing and Sanger sequencing of tropical mycorrhizal fungi provide similar results but reveal substantial methodological biases. *New Phytologist* 188: 291–301.

Toberman H, Chen C, Lewis T, Elser JJ (2014) High-frequency fire alters C: N: P stoichiometry in forest litter. *Global Change Biology* 20: 2321-2331.

Töljander JF, Eberhardt U, Toljander YK, Paul LR, Taylor AFS (2006) Species composition of an ectomycorrhizal fungal community along a local nutrient gradient in a boreal forest. *New Phytologist* 170: 873-884.

Tuininga AR, Dighton J (2004) Changes in ectomycorrhizal communities and nutrient availability following prescribed burns in two upland pine-oak forests in the New Jersey pine barrens. *Canadian Journal of Forest Research* 34: 1755-1765.

van der Heijden EW, de Vries FW, Kuyper TW (2000) Mycorrhizal associations of *Salix repens* L. communities in succession of dune ecosystems. I. Above-ground and below-ground views of ectomycorrhizal fungi in relation to soil chemistry. *Canadian Journal of Botany* 77: 1821-1832.

Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology* 172(8): 4238-4246.

Visser S. (1994) Ectomycorrhizal fungal succession in jack pine stands following wildfire. *New Phytologist* 129: 389-401.

Waldrop TA, White DL, Jones SM (1992) Fire regimes for pine-grassland communities in the southeastern United States. *Forest Ecology and Management* 47: 195-210.

Wang Q, Garrity GM, Tiedje JM, Cole RJ (2007) Naïve Bayesian Classifier for Rapid Assignment of rRNA Sequences into the New Bacterial Taxonomy. *Appl Environ Microbiol* 73:5261-7

Wicklow D (1973) Microfungal populations in surface soils of manipulated prairie stands. *Ecology* 54: 1302–1310.

Wicklow D (1975) Fire as an environmental cue initiating ascomycete development in a tallgrass prairie. *Mycologia* 67: 852–862.

Williams RJ, Hallgren SW, Wilson GWT (2011) Frequency of prescribed burning in an upland oak forest determines soil and litter properties and alters soil microbial community. *Forest Ecology and Management* 265: 241-247.

Figures and Tables

Figure 4.1 Rarefaction analyses of the OTUs representing for root-associated fungi in the dataset – a total of 1,180 sequences per experimental unit after strict quality control and subsampling. Experimental units are shown individually and are distinguished by treatment. Although Good's coverage indicates adequate sampling ($98.5\% \pm 0.36\%$) rarefaction curves do not hit a plateau indicating more OTUs could be captured with greater sequencing.

All Root Fungi Rarefaction

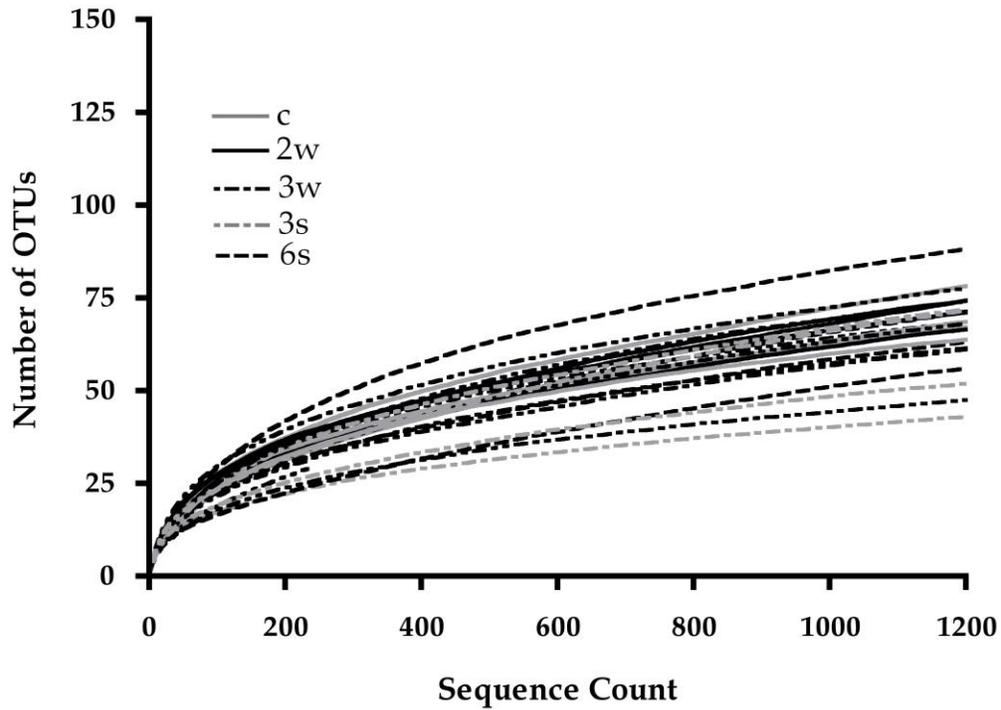


Figure 4.2 Non-metric Multidimensional Scaling (NMS) ordination of long-term prescribed fire treatments for root-associated fungi. Although MRPP results showed that only communities two-year interval treatments significantly differ from unburned treatments in pairwise comparisons (MRPP: $T_{2,8} = -2.19$, $A_{2,8} = 0.17$, $P = 0.018$), the majority of the short fire intervals (two- and three-year burns) plots fall above the x-axis while the longer six-year intervals and unburned

plots fall mainly below the x-axis.

NMS- Root-Associated Fungi

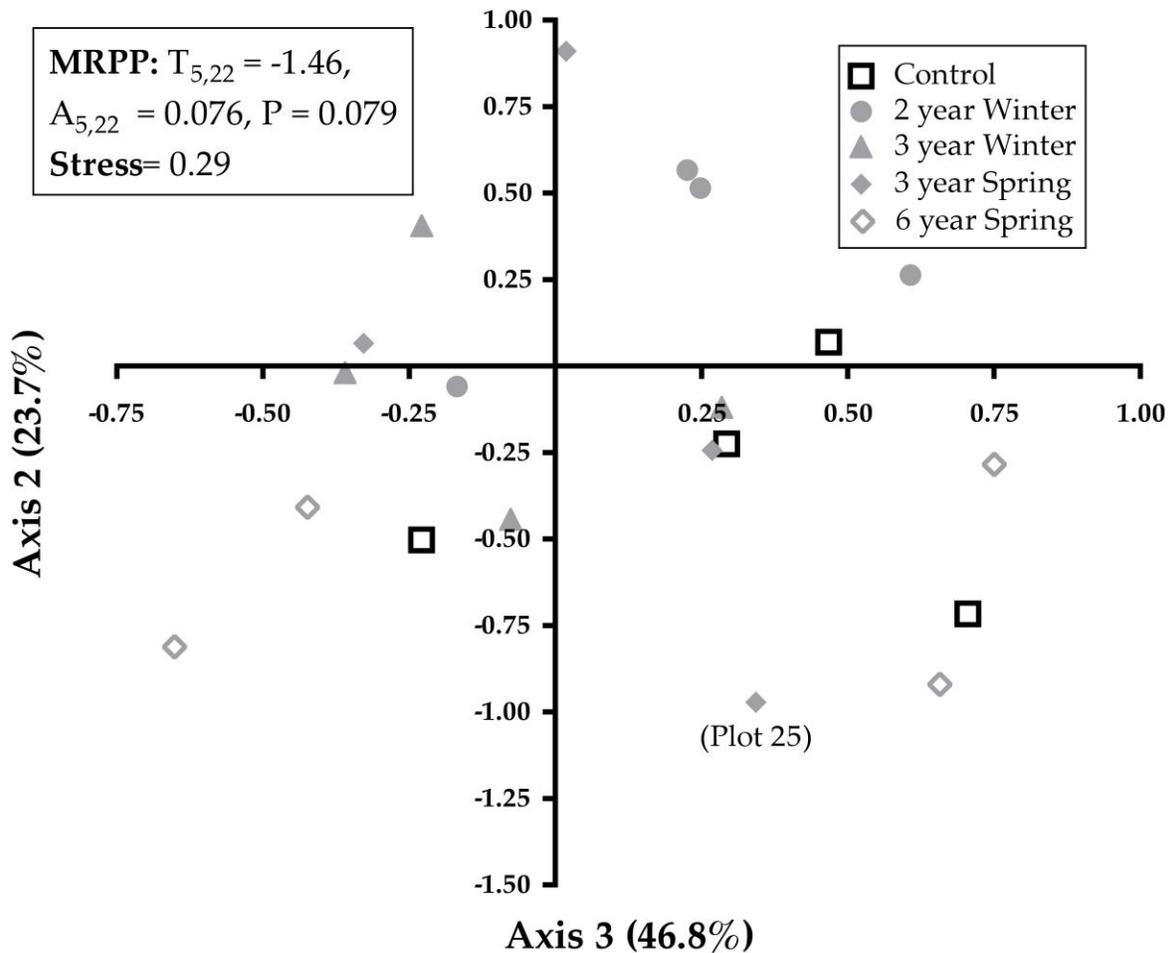


Figure 4.3 Indicator taxon analysis found nine total indicator OTUs that were seen to have significantly higher numbers associated with a given treatment. Of these two OTUs were associated with unburned control plots (A, B) representing potentially fire suppressed ECM taxa. Four OTUs were determined to have elevated numbers associated with the short fire intervals (C, D, E, F) representing potentially fire-adapted taxa.

Indicator OTUs

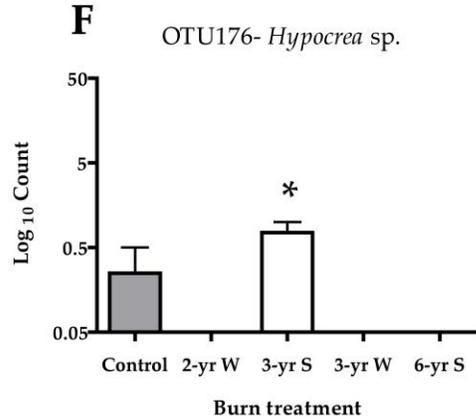
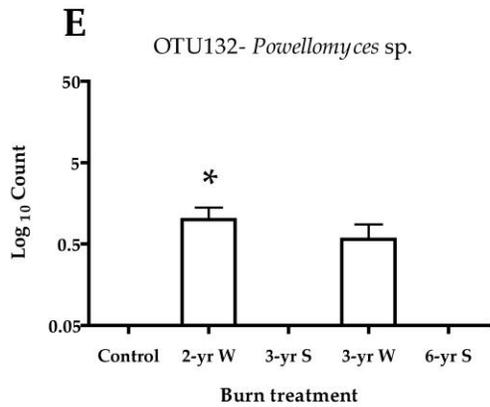
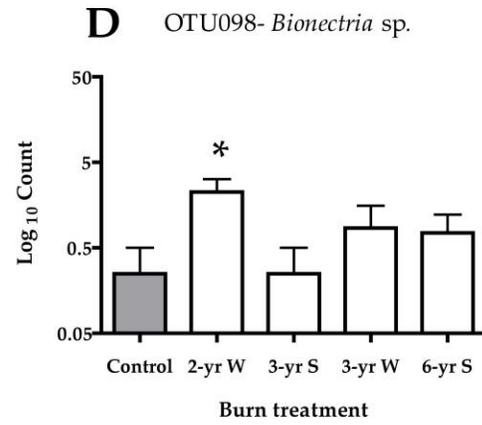
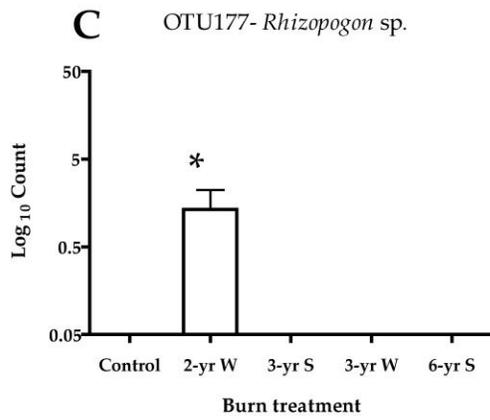
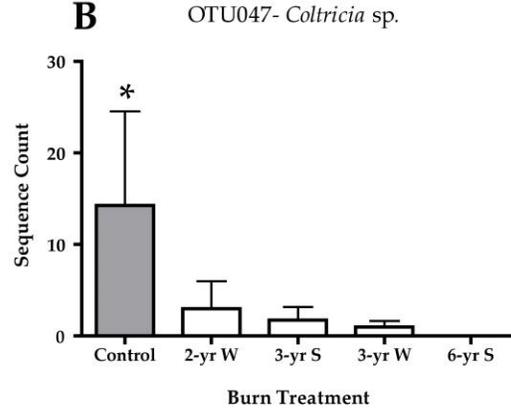
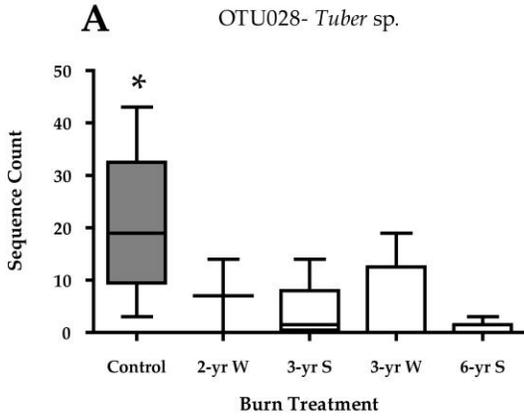


Figure 4.4 Rarefaction analyses of the ECM OTUs in the dataset after strict quality control and subsampling to 235 sequences per experimental unit. Experimental units are shown individually and are distinguished by treatment. Experimental units are mostly on an upward trajectory indicating sampling did not capture all OTUs.

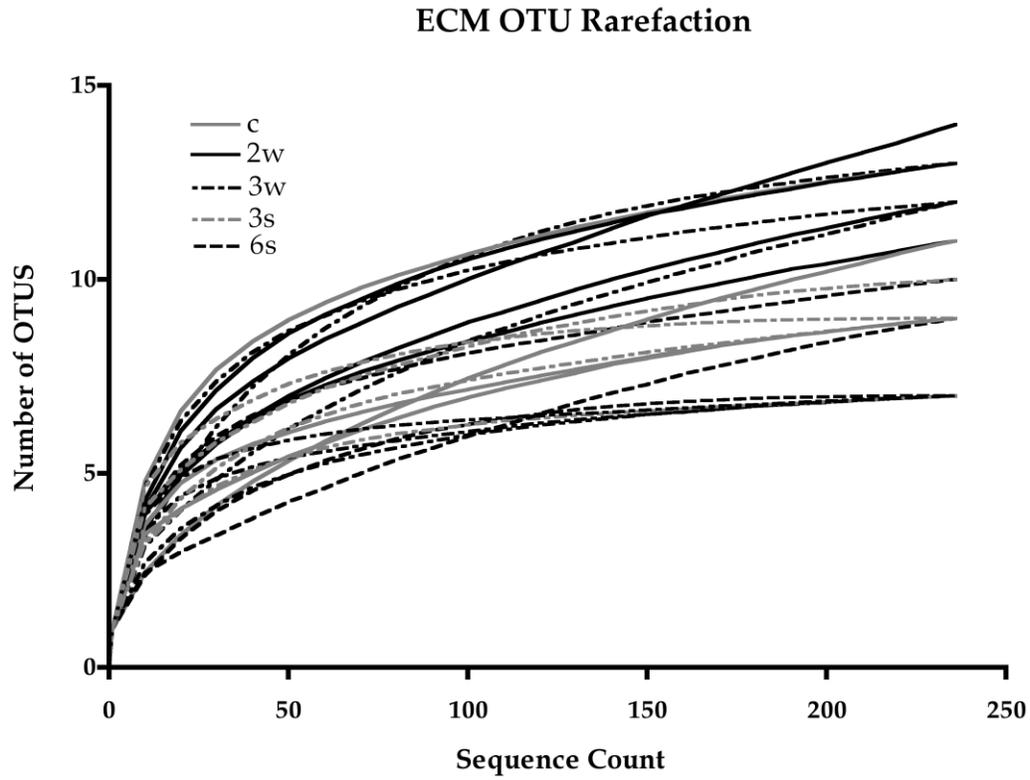


Table 4.1 All root –associated fungi mean and standard deviation of community diversity and richness estimators across different prescribed fire treatments. One-way ANOVA ($F_{4,23}$, Prob > F) comparing all treatments indicates no significant differences across treatments. F-statistics refer to one-way ANOVA that compares means of all five treatments.

ANOVA results	Control	2-yr Winter	3-yr Winter	3-yr Summer	6-year Summer	$F_{4,22}$; Prob> F
Coverage	0.98 ± 0.002	0.99 ± 0.003	0.99 ± 0.003	0.98 ± 0.005	0.98 ± 0.004	1.65; 0.21
Richness (S_{Obs})	60.5 ± 3.11	58.0 ± 2.83	56.29 ± 8.52	52.5 ± 11.21	60.25 ± 9.18	0.84; 0.51
Richness (Chao1)	74.78 ± 7.03	74.92 ± 10.7	69.76 ± 16.14	75.19 ± 18.19	85.14 ± 4.82	0.75; 0.57
Diversity (1-D)	0.88 ± 0.02	0.92 ± 0.01	0.87 ± 0.04	0.87 ± 0.05	0.86 ± 0.04	1.64; 0.21
Evenness (E_D)	0.14 ± 0.03	0.21 ± 0.03	0.15 ± 0.04	0.17 ± 0.05	0.13 ± 0.04	2.39; 0.09

Table 4.2 Mean and standard deviation of ECM community diversity and richness estimators across different prescribed fire treatments. One-way ANOVA ($F_{4,20}$, Prob > F) comparing all treatments indicates no significant differences across treatments. F-statistics refer to one-way ANOVA that compares means of all five treatments.

ANOVA results	Control	2-yr Winter	3-yr Winter	3-yr Summer	6-year Summer	$F_{4,20}$; Prob> F
Coverage	0.99 ± 0.005	0.99 ± 0.005	0.99 ± 0.001	0.99 ± 0.003	0.99 ± 0.007	1.31; 0.31
Richness (S_{Obs})	10.0 ± 2.2	12.0 ± 1.0	9.5 ± 2.8	8.75 ± 1.3	9.0 ± 1.4	1.20; 0.35
Richness (Chao1)	11.21 ± 3.05	14.17 ± 3.33	10.14 ± 3.47	8.87 ± 1.31	11.0 ± 2.83	1.29; 0.31
Diversity (1-D)	0.59 ± 0.19	0.68 ± 0.04	0.59 ± 0.14	0.65 ± 0.13	0.49 ± 0.16	0.96; 0.45
Evenness (E_D)	0.28 ± 0.09	0.26 ± 0.05	0.31 ± 0.12	0.37 ± 0.12	0.23 ± 0.05	0.99; 0.44

Chapter 5 - Conclusions

To better understand the effects of fire management practices on belowground fungal communities, this study took advantage of a long-term fire management experiment in the southeastern United States. Treatments varied in season (winter and summer) and interval (two-year, three-year, six-year) and thus allowed us to address questions on timing and frequency of fire on belowground fungal communities. Fungal communities were analyzed as all soil fungi, root-associated fungi, and ECM fungi.

After comparing data produced by non-proofreading and proofreading polymerases, amplicon libraries were produced using proofreading polymerases to avoid overestimating fungal community richness. The comparison of sequence data produced by the different polymerases strongly indicate that a non-proofreading polymerase can produce significantly more OTUs represented by rare (ten or less) sequences. These low frequency OTUs can be PCR and/or sequencing artifacts (Tedersoo et al. 2010; Brown et al. 2014) and should be either removed or carefully examined to prevent erroneous inflation of richness estimators (Brown et al. 2014).

Analyses of all soil fungi revealed that these communities respond to repeated prescribed burning. Season as a variable had no effect on community composition but burn interval influenced communities compositionally: short fire intervals (two- and three-year) had soil fungal communities that were distinct from unburned reference plots. Although community composition responded to fire frequency, diversity and richness were not affected by any burn treatment. Similarly to the soil fungal communities, our analyses of root-associated fungi also found communities to respond compositionally when fire treatments were implemented at the most frequent fire interval (two-year), although the community richness and diversity were unaffected. Again, season of burning had no effect on composition of these communities or their diversity and richness estimators. Our most exclusive dataset targeted ECM communities colonizing the roots. Neither fire interval nor season affected communities, compositionally or their diversity and richness. For each dataset, the six-year burn interval treatments had communities similar to the unburned reference plots indicating that after six years these fungal communities return to or migrate towards an unburned state.

The results from these studies strongly indicate that soil fungi and root-associated fungal communities respond compositionally to frequent fire intervals but retain stable diversity and

richness. However, we observed no compositional responses to fire treatments when targeting the less inclusive ECM communities. Our results on soil and root-associated fungi are similar to prior studies that focus on the long-term effects of repeated burning: soil fungi and basidiomycete communities shift compositionally in response to frequent fires in an Australian sclerophyll forests (Anderson et al., 2007; Bastias et al., 2006a). However, our ECM community results are in contrast with Bastias et al. (2006b) who found that ECM communities shifted in response to repeated prescribed fire. In addition our results counter prior conclusions on ECM communities, which suggest these communities are particularly sensitive to fire (Holden et al., 2013).

As diversity and richness estimators remained stable, while composition of the fungal communities tended to shift, we conclude that community changes are driven by taxon reordering and replacement instead of taxon losses. The frequent fire interval treatments favor fire adapted or fire tolerant fungal communities. Our longest fire interval, six-years, had communities similar to control unburned plots, which represent the undesirable outcome of fire suppression or lack of fire management. Our results and conclusions are important for management of southern yellow pine ecosystems as fire regimes should include frequent fire and should not reach six-year intervals to prevent these beneficial fungal communities shifting away from those that support a fire adapted ecosystem.

References

Anderson IC, Bastias BA, Genney DR, Parkin PI, Cairney JWG. 2007. Basidiomycete fungal communities in Australian sclerophyll forest soil are altered by repeated prescribed burning. *Mycological Research*, 111: 482-486.

Baar J, Horton TR, Kretzer AM, Bruns TD. 1999. Mycorrhizal Colonization of *Pinus muricata* from Resistant Propagules after a Stand-Replacing Wildfire. *New Phytologist*, 143: 409-418.

Bastias BA, Huang ZQ, Blumfields T, Xu Z, Cairney JWG. 2006a. Influence of repeated prescribed burning on the soil fungal community in an eastern Australian wet sclerophyll forest. *Soil Biology and Biochemistry*, 38: 3492-3501.

Bastias BA, Xu ZH, Cairney JWG. 2006b. Influence of long-term repeated prescribed burning on mycelial communities of ectomycorrhizal fungi. *New Phytologist*, 172: 149-158.

Brown SP, Veach AM, Rigdon-Huss AR, Grond K, Lickteig SK, Lothamer K, Oliver AK, Jumpponen A. 2014. Scraping the bottom of the barrel: are rare high throughput sequences artifacts? *Fungal Ecology* (revised and in review).

Holden SR, Treseder KK. 2013. A meta-analysis of soil microbial biomass responses to forest disturbances. *Frontiers in Microbiology*, 4: article 163

Tedersoo L., Nilsson R.H., Abarenkov K., Jairus T., Sadam A., Saar I., Bahram M., Bechem E., Chuyong G., Kõljalg U., 2010. 454 Pyrosequencing and Sanger sequencing of tropical mycorrhizal fungi provide similar results but reveal substantial methodological biases. *New Phytologist* 188, 291-301.

References

Chapter 1

- Anderson IC, Bastias BA, Genney DR, Parkin PI, Cairney JWG. 2007. Basidiomycete fungal communities in Australian sclerophyll forest soil are altered by repeated prescribed burning. *Mycological Research*, 111: 482-486.
- Baar J, Horton TR, Kretzer AM, Bruns TD. 1999. Mycorrhizal Colonization of *Pinus muricata* from Resistant Propagules after a Stand-Replacing Wildfire. *New Phytologist*, 143: 409-418.
- Bastias BA, Huang ZQ, Blumfields T, Xu Z, Cairney JWG. 2006a. Influence of repeated prescribed burning on the soil fungal community in an eastern Australian wet sclerophyll forest. *Soil Biology and Biochemistry*, 38: 3492-3501.
- Borders BE, Bailey RL. 2001. Loblolly pine-pushing the limits of growth. *Southern Journal of Applied Forestry* 25: 69-74.
- Brown SP, Callaham Jr. MA, Oliver AK and Jumpponen A. 2013. Deep Ion Torrent sequencing identifies soil fungal community shifts after frequent prescribed fires in a southeastern US forest ecosystem. *FEMS Microbiology Ecology* 86: 557-566.
- Brown SP, Callaham Jr. MA, Oliver AK, Jumpponen A. 2013. Deep Ion Torrent sequencing identifies soil fungal community shifts after frequent prescribed fires in a southeastern US forest ecosystem. *FEMS Microbiology Ecology*, 86: 557-566.
- Callaham MA. Jr., Scott DA, O'Brien JJ, Stanturf JA. 2012. Cumulative effects of fuel management on the soils of eastern U.S., in: LaFayette, R., Brooks, M.T., Potyondy, J.P., Audin, L., Krieger, S.L., Trettin, C.C. (Eds.), *Cumulative watershed effects of fuel management in the Eastern United States*. Gen. Tech. Rep. SRS-161. Asheville, NC: U.S. Department of Agriculture Forest Service, Southern Research Station, pp. 202-228.
- Chen DM, Cairney WJG. 2002. Investigation of the influence of prescribed burning on ITS profiles of ectomycorrhizal and other soil fungi at three Australian sclerophyll forest sites. *Mycological Research*, 106: 532-540.
- Dooley SR, Treseder KK. 2012. The effect of fire microbial biomass: a meta-analysis of field studies. *Biogeochemistry*, 109: 49-61.
- Ekblad A, Wallander H, Godbold DL, Cruz C, Johnson D, Baldrian P, Björk RG, Epron D, Keiliszewska-Rokicka B, Kjoller R, Kraigher H, Matzner E, Newmann J, Plassard C.

2013. The production and turnover of extramatrical mycelium of ectomycorrhizal fungi in forest soils: role in carbon cycling. *Plant Soil* 366: 1-27.
- Fogel R, Hunt G. 1982. Contribution of mycorrhizae and soil fungi to nutrient cycling in a Douglas-fir ecosystem. *Canadian Journal of Forest Research* 13: 219- 232.
- Fogel R. 2006. Mycorrhizae and nutrient cycling in natural forest ecosystems. *New Phytologist* 86: 199-212.
- Fritze H, Pennanen T, Pietikäinen J. 1993. Recovery of soil microbial biomass and activity from prescribed burning. *Canadian Journal of Forest Research* 23: 1286-1290.
- Hibbett DS, Ohman A, Kirk PM. 2009. Fungal ecology catches fire. *New Phytologist* 184: 279-282.
- Holden SR, Treseder KK. 2013. A meta-analysis of soil microbial biomass responses to forest disturbances. *Frontiers in Microbiology*, 4: article 163.
- Jeffries P, Gianinazzi S, Perotto S, Turnau K, Barea J. 2003. The contribution of arbuscular mycorrhizal fungi in sustainable maintenance of plant health and soil fertility. *Biology and Fertility of Soils*. 37: 1-16.
- Kowal VA, Scholke A, Kanagaraj R, Bruggeman D. 2013. Resource selection probability functions for gopher tortoise: providing a management tool application across the species' range. *Environmental Management* 53: 594-605.
- Ligon DJ, Stacey PB, Conner RN, Bock CE, Adkisson CS. 1986. Report of the American ornithologists' union committee for the conservation of the red-cockaded woodpecker. *The Auk* 103: 848-855.
- Longo MS, Urcelay C, Nouhra E. 2011. Long term effects of fire on ectomycorrhizas and soil properties in *Nothofagus pumilio* forest in Argentina. *Forest Ecology and Management*, 262: 348-354.
- Luo Z, Wu C, Zhang C, Li H, Lipka U, Polle A. 2014. The role of ectomycorrhizas in heavy metal stress tolerance of host plants. *Environmental and Experimental Botany* 108: 47-62.
- Pietikäinen J, Fritze H. 1993..Microbial biomass and activity in the humus layer following burning: short-term effects of two different fires. *Canadian Journal of Forest Research* 23: 1275-1285.
- Quail MA, Smith M, Coupland P, Otto TD, Harris SR, Connor TR, Bertoni A, Swerdlow HP, Gu Y. 2012. A tale of three next generation sequencing platforms: comparison of Ion Torrent, Pacific Biosciences and Illumina MiSeq sequencers. *BMC Genomics*. 13: 341

- Ramsey CL, Jose S, Brecke BJ, Merritt S. 2003. Growth response of longleaf pine (*Pinus palustris* Mill.) seedlings to fertilization and herbaceous weed control in an old field in southern USA. *Forest Ecology and Management*. 172: 281-289.
- Schuster SC. 2007. Next-generation sequencing transforms today's biology. *Nature Methods*. 15: 16- 18.
- Steen DA, Smith LL, Morris G, Conner M, Litt AR, Pokswinski S, Guyer C. 2013. Response of six-lined racerunner (*Aspidoscelis sexlineata*) to habitat restoration in fire-suppressed longleaf pine (*Pinus palustris*) sandhills. *Restoration Ecology* 21: 457- 463.
- Talbert JT, Weir RJ, Arnold RD. 1985. Cost and benefits of a mature first-generation loblolly pine tree improvement program. *Journal of forestry* 83: 162-166.
- van der Heijden MGA, Klironomos JN, Ursic M, Moutoglis P, Streitwolf-Engle R, Boller T, Wiemken A, Sanders IR. 1998. Mycorrhizal fungal diversity determines plant biodiversity, ecosystem variability and productivity. *Nature*. 396: 69-72.
- Visser S. 1994. Ectomycorrhizal fungal succession in jack pine stands following wildfire. *New Phytologist*, 129: 389-401.
- Waldrop TA, White DL, Jones SM. 1992. Fire regimes for pine-grassland communities in the southeastern United States. *Forest Ecology and Management* 47: 195-210.

Chapter 2

- Anderson, M.J., 2001. A new method for non-parametric multivariate analysis of variance. *Austral Ecology* 26. 32-46.
- Berry, D., Mahfoudh, K.B., Wagner, M., Loy, A., 2011. Barcoded primers used in multiplex amplicon pyrosequencing bias amplification. *Applied and Environmental Microbiology* 77, 7846–7849.
- Brown, S.P., Callahan, M.A., Oliver, A.K., Jumpponen, A., 2013. Deep Ion Torrent sequencing identifies soil fungal community shifts after frequent prescribed fires in a southeastern US forest ecosystem. *FEMS Microbiology Ecology* 86, 557-566.
- Brown, S.P., Veach, A.M., Rigdon-Huss, A.R., Grond, K., Lickteig, S.K., Lothamer, K., Oliver, A.K., Jumpponen, A., 2014. Scraping the bottom of the barrel: are rare high throughput sequences artifacts? *Fungal Ecology* (revised and in review).
- Edgar, R.C., Haas, B.J., Clemente, J.C., Quince, C., Knight, R., 2011. UCHIME improves sensitivity and speed of chimera detection. *Bioinformatics* 27, 2194-2200.
- Gardes, M., Bruns, T.D., 1993. ITS primers with enhanced specificity for Basidiomycetes – Application to the identification of mycorrhizae and rusts. *Molecular Ecology* 2, 113–118.

- Huse, S.M., Welch, D.M., Morrison, H.G., Sogin, M.L., 2010. Ironing out the wrinkles in the rare biosphere through improved OTU clustering. *Environmental Microbiology* 12, 1889-1898.
- Ihrmark, K., Bödeker, I.T.M., Cruz-Martinez, K., Friberg, H., Kubartova, A., Schenck, J., Stenlid, J., Brandström-Durling, M., Clemmensen, K.E., Lindahl, B.D., 2012. New primers to amplify the fungal ITS2 region - evaluation by 454-sequencing of artificial and natural communities. *FEMS Microbiology Ecology* 82, 666-677.
- Kozich, J.J., Westcott, S.L., Baxter, N.T., Highlander, S.K., Schloss, P.D., 2013. Development of a dual-index sequencing strategy and curation pipeline for analyzing amplicon sequence data on the MiSeq Illumina sequencing platform. *Applied and Environmental Microbiology* 79, 5112-5120.
- Pietikäinen, J., Fritze H., 1993. Microbial biomass and activity in the humus layer following burning: short-term effects of two different fires. *Canadian Journal of Forest Research* 23,1275-1285.
- Fritze H., Pennanen T., Pietikäinen J., 1993. Recovery of soil microbial biomass and activity from prescribed burning. *Canadian Journal of Forest Research* 23, 1286-1290.
- Tedersoo L., Nilsson R.H., Abarenkov K., Jairus T., Sadam A., Saar I., Bahram M., Bechem E., Chuyong G., Kõljalg U., 2010. 454 Pyrosequencing and Sanger sequencing of tropical mycorrhizal fungi provide similar results but reveal substantial methodological biases. *New Phytologist* 188, 291-301.
- Wang Q., Garrity G.M., Tiedje J.M., Cole J.R., 2007. Naïve Bayesian Classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. *Applied and Environmental Microbiology* 73, 5261-5267.
- White T.J., Bruns T., Lee S., Taylor J., 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics in: Innis, M.A.I, Gelfand, D.H., Sninsky, J.J., White, W.J. (Eds.), *PCR Protocols: A Guide to Methods and Applications*. Academic Press, San Diego, CA pp. 315–322.

Chapter 3

- Abrahamson, W.G., Hartnett, D.C. 1990. Pine flatwoods and dry prairies. In: Myers, R.L. and Ewel, J.L. (eds.), *Ecosystems of Florida*. University of Central Florida Press, Orlando, USA. Pp. 103-149.
- Amiro, B.D., Barr, A.G., Barr, J.G., Black, T.A., Bracho, R., Brown, M., Chen, J., Clark, K.L., Davis, K.J., Desai, A.R., Dore, S., Engel, V., Fuentes, J.D., Goldstein, A.H., Goulden, M.L., Kolb, T.E., Lavigne, M.B., Law, B.E., Margolis, H.A., Martin, T., McCaughney,

- J.H., Misson, L., Montes-Helu, M., Noormets, A., Randerson, J.T. 2010. Ecosystem carbon dioxide fluxes after disturbance in forests of North America. *Journal of Geophysical Research*, 115: G00K02.
- Anderson, I.C., Bastias, B.A., Genney, D.R., Parkin, P.I., Cairney, J.W.G. 2007. Basidiomycete fungal communities in Australian sclerophyll forest soil are altered by repeated prescribed burning. *Mycological Research*, 111: 482-486.
- Artz, R.R.E., Reid, E., Anderson, I.C., Campbell, C.D., Cairney, J.W.G. 2008. Long term repeated prescribed burning increases evenness in the basidiomycete laccase gene pool in forest soils. *FEMS Microbial Ecology*, 67: 397-410.
- Bastias, B.A., Huang, Z.Q., Blumfields, T., Xu, Z., Cairney, J.W.G. 2006a. Influence of repeated prescribed burning on the soil fungal community in an eastern Australian wet sclerophyll forest. *Soil Biology and Biochemistry*, 38: 3492-3501.
- Bastias, B.A., Xu, Z.H., Cairney, J.W.G. 2006b. Influence of long-term repeated prescribed burning on mycelial communities of ectomycorrhizal fungi. *New Phytologist*, 172: 149-158.
- Baar, J., Horton, T.R., Kretzer, A.M., Bruns, T.D. 1999. Mycorrhizal Colonization of *Pinus muricata* from Resistant Propagules after a Stand-Replacing Wildfire. *New Phytologist*, 143: 409-418.
- Barker, J.S., Simard, S.W., Jones, M.D., Durall, D.M. 2013. Ectomycorrhizal fungal community assembly on regenerating Douglas fir after wildfire and clearcut harvesting. *Oecologia*, 172: 1179-1189.
- Borders, B.E., Bailey, R.L. 2001. Loblolly pine-pushing the limits of growth. *Southern Journal of Applied Forestry*, 25: 69-74.
- Brown, S.P., Callaham, Jr. M.A., Oliver, A.K., Jumpponen, A. 2013. Deep Ion Torrent sequencing identifies soil fungal community shifts after frequent prescribed fires in a southeastern US forest ecosystem. *FEMS Microbiology Ecology*, 86: 557-566.
- Buscardo, E., Rodríguez-Echeverría, S., Martic, M.P., Angelis, P.D., Pereira, J.S., Freitas, H. 2010. Impact of wildfire return interval on the ectomycorrhizal resistant propagules communities of a Mediterranean open forest. *Fungal Biology*, 114: 628-636.
- Cairney, J.W.G., Bastias, B.A. 2007. Influence of fire on forest soil fungal communities. *Canadian Journal of Forest Research*, 37: 207-215.
- Callaham, M.A. Jr., Scott, D.A., O'Brien, J.J., Stanturf, J.A. 2012. Cumulative effects of fuel management on the soils of eastern U.S. In: LaFayette, R., Brooks, M.T., Potyondy, J.P.,

- Audin, L., Krieger, S.L., Trettin, C.C. (eds.). Cumulative watershed effects of fuel management in the Eastern United States. Gen. Tech. Rep. SRS-161. Asheville, NC: U.S. Department of Agriculture Forest Service, Southern Research Station, pp. 202-228.
- Carter, M.C., Foster, C.D. 2004. Prescribed burning and productivity in southern pine forests: a review. *Forest Ecology and Management*, 191: 93–109.
- Certini, G. 2005. Effects of fire on properties of forest soils: a review. *Oecologia*, 143: 1-10.
- Chen, D.M., Cairney, W.G.J. 2002. Investigation of the influence of prescribed burning on ITS profiles of ectomycorrhizal and other soil fungi at three Australian sclerophyll forest sites. *Mycological Research*, 106: 532-540.
- Choromanska, U., DeLuca, T.H. 2001. Prescribed fire alters the impact of wildfire on soil biochemical properties in a ponderosa pine forest. *Soil Science Society of America Journal*, 65: 232–238.
- Dooley, S.R., Treseder K.K. 2012. The effect of fire microbial biomass: a meta-analysis of field studies. *Biogeochemistry*, 109: 49-61.
- Edgar, R.C., Haas, B.J., Clemente, J.C., Quince, C., Knight, R. 2011. UCHIME improves sensitivity and speed of chimera detection. *Bioinformatics*, 27: 2194-2200.
- Fritze, H., Pennanen, T., Pietikäinen, J. 1993. Recovery of soil microbial biomass and activity from prescribed burning. *Canadian Journal of Forest Research*, 23: 1286-1290.
- Fujimura, K.E., Smith, J.E., Horton, T.R., Weber, N.S., Spatafora, J.W. 2005. Pezizalean mycorrhizas and sporocarps in ponderosa pine (*Pinus ponderosa*) after prescribed fires in eastern Oregon, USA, *Mycorrhiza*, 15:79-86.
- Glass, D.W., Johnson, D.W., Blank, R.R., Miller, W.W. 2008. Factors affecting mineral nitrogen transformations by soil heating: a laboratory-simulated fire study. *Soil Science*, 173: 387-400.
- Glitzenstein, J.F., Platt, W.J., Streng, D.R. 1995. Effects of fire regime and habitat on tree dynamics in north Florida longleaf pine savannas. *Ecological Monographs*, 65: 441-476.
- Goulden, M.L., McMillan, A.M.S., Winston, G.C., Rocha, A.V., Manies, K.L., Harden, J.W., Bond-Lamberty, B.P. 2011. Patterns of NPP, GPP, respiration, and NEP during boreal forest succession. *Global Change Biology*, 17: 855–871.
- Grogan, P., Baar, J., Bruns, T.D. 2000. Below-ground ectomycorrhizal community structure in a recently burned bishop pine forest. *Journal of Ecology*, 88: 1051–1062.

- Harden, J.W., Mack, M.C., Veldhuis, H., Gower, S.T. 2003. Fire dynamics and implications for nitrogen cycling in boreal forests. *Journal of Geophysical Research*, 108: 8223–8230.
- Hatten J.A., Zabowski, D. 2010. Fire severity effects on soil organic matter from a ponderosa pine forest: a laboratory study. *International Journal of Wildland Fire*, 19: 613–623.
- Hebel, C.L., Smith, J.E., Cromack, K. Jr. 2009. Invasive plant species and soil microbial response to wildfire burn severity in Cascade Range of Oregon. *Applied Soil Ecology*, 42: 150-159.
- Hernández, T., García, C., Reinhardt, I. 1997. Short-term effect of wildfire on chemical, biochemical and microbiological properties of Mediterranean pine forest soils. *Biology and Fertility of Soils*, 25: 109-116.
- Holden, S.R., Gutierrez, A., Treseder, K.K. 2013. Changes in soil fungal communities, extracellular enzyme activities, and litter decomposition across a fire chronosequence in Alaskan boreal forests. *Ecosystems*, 16: 34-46.
- Holden, S.R., Treseder, K.K. 2013. A meta-analysis of soil microbial biomass responses to forest disturbances. *Frontiers in Microbiology*, 4: article 163.
- Horton, T.R., Cázares, E., Bruns, T.D. 1998a. Ectomycorrhizal, vesicular-arbuscular and dark septate fungal colonization of bishop pine (*Pinus muricata*) seedlings in the first 5 months of growth after wildfire. *Mycorrhiza*, 8:11-18.
- Horton, T.R., Bruns, T.D. 1998b. Multiple-host fungi are the most frequent and abundant ectomycorrhizal types in a mixed stand of Douglas fir (*Pseudotsuga menziesii*) and bishop pine (*Pinus muricata*). *New Phytologist*, 139: 331-339.
- Huse, S.M., Dethlefsen, L., Huber, J.A., Welch, M.D., Relman, D.A., Sogin, M.L. 2008 Exploring microbial diversity and taxonomy using SSU rRNA hypervariable tag sequencing. *PLoS Genetics*, 4: e1000255.
- Ihrmark, K. B., Decker, I.T.M., Cruz-Martinez, K., Friberg, H., Kubartova, A., Schenck, J., Stenlid, J., Brandström-Andersson, M., Clemmensen, K.E., Lindahl, B.D. 2012. New primers to amplify the fungal ITS2 region- evaluation by 454-sequencing of artificial and natural communities. *FEMS Microbiology Ecology*, 82: 666-677.
- Johnson, D.W., Curtis, P. S. 2001. Effects of forest management on soil C and N storage: meta analysis. *Forest Ecology and Management*, 140: 227–238.
- Kifper, T., Simon, E., Ghazoul, J., Moser, B., Wohlgemuth, T. 2010. Susceptibility of ectomycorrhizal fungi to soil heating. *Fungal Biology*, 114: 467-472.

- Kirkman, L.K., Mitchell, R.J. 2006. Conservation management of *Pinus palustris* ecosystems from a landscape perspective. *Applied Vegetation Science* 9:67-74.
- Kowal, V.A., Scholke, A., Kanagaraj, R., Bruggeman, D. 2013. Resource selection probability functions for gopher tortoise: providing a management tool application across the species' range. *Environmental Management*, 53: 594-605.
- Ligon, D.J., Stacey, P.B., Conner, R.N., Bock, C.E., Adkisson, C.S. 1986. Report of the American ornithologists' union committee for the conservation of the red-cockaded woodpecker. *The Auk*, 103: 848-855.
- Longo, M.S., Urcelay, C., Nouhra, E. 2011. Long term effects of fire on ectomycorrhizas and soil properties in *Nothofagus pumilio* forest in Argentina. *Forest Ecology and Management*, 262: 348-354.
- Mack, M.C., Treseder, K.K., Manies, K.L., Harden, J.W., Schuur, E.A.G., Vogel, J.G., Randerson, J.T., Chapin, F.S. 2008. Recovery of aboveground plant biomass and productivity after fire in mesic and dry black spruce forests of interior Alaska. *Ecosystems*, 11: 209–225.
- McCune, B., M. J. Mefford. 2006 PC-ORD. Multivariate analysis of ecological data. Version 5. MjM Software, Gleneden Beach, Oregon, U.S.A.
- Neff, J.C., Harden, J.W., Gleixner, G. 2005. Fire effects on soil organic matter content, composition, and nutrients in boreal interior Alaska. *Canadian Journal of Forest Research*, 35: 2178–2187.
- Newton, A.C., Haigh, J.M. 1998. Diversity of ectomycorrhizal fungi in Britain: a test of the species- area relationship, and the role of host specificity. *New Phytologist*, 138: 619-627.
- Pietikäinen, J., Fritze, H. 1993. Microbial biomass and activity in the humus layer following burning: short-term effects of two different fires. *Canadian Journal of Forest Research*, 23: 1275-1285.
- Prieto-Fernández, Á., Carballas M., Carballas, T. 2004. Inorganic and organic N pools in soils burned or heated: immediate alteration and evolution after forest wildfires. *Geoderma*, 121: 291-306.
- Schoch, C.L., Seifert, K.A., Huhndorf, S., Robert, V., Spouge, J.L., Levesque, C.A., Chen, W., Fungal Barcoding Consortium. 2012. Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. *Proceedings of the National Academy of Science, USA*, 109: 6241-6246.
- Smith, J.E., McKay, D. Niwa, C.G, Thies, W.G., Brenner, G., Spatafora J.W. 2004. Short-term

- effects of seasonal prescribed burning on the ectomycorrhizal fungal community and fine root biomass in ponderosa pine stands in the Blue Mountains of Oregon. *Canadian Journal of Forest Research*, 34: 2477-2491.
- Steen, D.A., Smith, L.L., Morris, G., Conner, M., Litt, A.R., Pokswinski, S., Guyer, C. Response of six-lined racerunner (*Aspidoscelis sexlineata*) to habitat restoration in fire-suppressed longleaf pine (*Pinus palustris*) sandhills. *Restoration Ecology*, 21: 457- 463.
- Stephens, S.L., Ruth, L.W. 2005. Federal forest-fire policy in the United States. *Ecological Applications*, 15: 532-542.
- Talbert, J.T., Weir, R.J., Arnold, R.D. 1985. Cost and benefits of a mature first-generation loblolly pine tree improvement program. *Journal of forestry*, 83: 162-166.
- Tedersoo, L., Nilsson, R.H., Abarenkov, K., Jairus, T., Sadam, A., Saar, I., Bahram, M., Bechem, E., Chuyong, G., Kõljalg, U. 2010. 454 Pyrosequencing and Sanger sequencing of tropical mycorrhizal fungi provide similar results but reveal substantial methodological biases. *New Phytologist*, 188: 291-301.
- Toberman, H., Chen, C., Lewis, T., Elser, J.J. 2014. High-frequency fire alters C: N: P stoichiometry in forest litter. *Global Change Biology*, 20: 2321-2331.
- Treseder, K.K., Mack, M.C., Cross, A. 2004. Relationships among fires, fungi, and soil dynamics in Alaskan boreal forests. *Ecological Applications*, 14: 1826–1838.
- Visser, S. 1994. Ectomycorrhizal fungal succession in jack pine stands following wildfire. *New Phytologist*, 129: 389-401.
- Waldrop, T.A., White, D.L., Jones, S.M. 1992. Fire regimes for pine-grassland communities in the southeastern United States. *Forest Ecology and Management*, 47: 195-210.
- Wan, S., Hui, D., Luo, Y. 2001. Fire effects on nitrogen pools and dynamics in terrestrial ecosystems: a meta-analysis. *Ecological Applications*, 11:1349–1365.
- Wang, Q., Garrity, G.M., Tiedje, J.M., Cole, J.R. 2007. Naïve Bayesian Classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. *Applied and Environmental Microbiology*, 73:5261-5267.
- Warbale, D.A., Bardgett, R.D., Klironomos, J.N., Set, S.H., Van Der Putten, W.H., Wall, D.H. 2004. Ecological linkages between aboveground and belowground biota. *Science*, 304: 1629-1633.
- White, T.J., Bruns, T., Lee, S., Taylor, J. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In Innis, M.A., Gelfand, D.H., Sninsky, J.J.,

- White, T.J. (eds). PCR Protocols: A Guide to Methods and Applications, Academic Press, San Diego, CA, pp. 315–322.
- Wicklow, D. 1973. Microfungal populations in surface soils of manipulated prairie stands. *Ecology*, 54: 1302–1310.
- Wicklow, D. 1975 Fire as an environmental cue initiating ascomycete development in a tallgrass prairie. *Mycologia*, 67: 852–862.
- Williams, R.J., Hallgren, S.W., Wilson, G.W.T. 2011. Frequency of prescribed burning in an upland oak forest determines soil and litter properties and alters soil microbial community. *Forest Ecology and Management*, 265: 241-247.
- “Maps: Dominant Soil Orders in the United States”
http://www.nrcs.usda.gov/Internet/FSE_DOCUMENTS/nrcs142p2_051233.pdf . Natural Resources Conservation Service. USDA, Web. 13 August 2014.

Chapter 4

- Amend AS, Seifert KA, Samson R, Bruns TD (2010) Indoor fungal composition is geographically pattered and more diverse in temperate zones than in the tropics. *Proceedings of the National Academy of Sciences* 107: 13748-13753.
- Anderson IC, Bastias BA, Genney DR, Parkin PI, Cairney JWG (2007) Basidiomycete fungal communities in Australian sclerophyll forest soil are altered by repeated prescribed burning. *Mycological Research* 111: 482-486.
- Artz RRE, Reid E, Anderson IC, Campbell CD, Cairney JWG (2008) Long term repeated prescribed burning increases evenness in the basidiomycete laccase gene pool in forest soils. *FEMS Microbial Ecology* 67: 397-410.
- Bastias BA, Huang ZQ, Blumfields T, Xu Z, Cairney JWG (2006a) Influence of repeated prescribed burning on the soil fungal community in an eastern Australian wet sclerophyll forest. *Soil Biology and Biochemistry* 38: 3492-3501.
- Bastias BA, Xu ZH, Cairney JWG (2006b) Influence of long-term repeated prescribed burning on mycelial communities of ectomycorrhizal fungi. *New Phytologist* 172: 149-158.
- Barr J, Horton TR, Kretzer AM, Bruns TD (1999) Mycorrhizal colonization of *Pinus muricata* from resistant propagules after a stand-replacing wildfire. *New Phytologist* 143: 409-418.
- Berry D, Mahfoudh KB, Wagner M, Loy A (2011) Barcoded primers used in multiplex amplicon pyrosequencing bias amplification. *Applied and Environmental Microbiology* 77: 7846-7849.

- Borders BE, Bailey RL (2001) Loblolly pine-pushing the limits of growth. *Southern Journal of Applied Forestry* 25: 69-74.
- Brown SP, Callaham Jr. MA, Oliver AK and Jumpponen A (2013), Deep Ion Torrent sequencing identifies soil fungal community shifts after frequent prescribed fires in a southeastern US forest ecosystem. *FEMS Microbiology Ecology* 86: 557-566.
- Brown SP, Jumpponen A (2014) Contrasting primary successional trajectories of fungi and bacteria in retreating glacier soils. *Molecular Ecology* 23: 481-497.
- Bucholz K, Motto H (1981) Abundances and vertical distributions of mycorrhizae in Plains and Barrens forest soils from the New Jersey Pine Barrens. *Bulletin of the Torrey Botanical Club* 108: 268-271.
- Buscardo E, Rodríguez-Echeverría S, Martic MP, Angelis PD, Pereira JS, Freitas H (2010) Impact of wildfire return interval on the ectomycorrhizal resistant propagules communities of a Mediterranean open forest. *Fungal Biology* 114: 628–636.
- Callaham MA. Jr., Scott DA, O'Brien JJ, Stanturf JA (2012) Cumulative effects of fuel management on the soils of eastern U.S., in: LaFayette, R., Brooks, M.T., Potyondy, J.P., Audin, L., Krieger, S.L., Trettin, C.C. (Eds.), *Cumulative watershed effects of fuel management in the Eastern United States*. Gen. Tech. Rep. SRS-161. Asheville, NC: U.S. Department of Agriculture Forest Service, Southern Research Station, pp. 202-228.
- Carpenter SE, Trappe JM (1985) Phoenicoid fungi – a proposed term for fungi that fruit after heat-treatment of substrates. *Mycotaxon* 23: 203-206.
- Certini G (2005) Effects of fire on properties of forest soils: a review. *Oecologia* 143: 1-10.
- Chen DM, Cairney WGJ (2002) Investigation of the influence of prescribed burning on ITS profiles of ectomycorrhizal and other soil fungi at three Australian sclerophyll forest sites. *Mycological Research* 106: 532-540.
- Coince A, Caël, O, Bach C, Lengelle J, Cruaud C, Gavory F, Morin E, Murat C, Marcais B, Buée M (2013) Below-ground fine-scale distribution and soil *versus* fine root detection of fungal and soil oomycete communities in a French beech forest. *Fungal Ecology* 6: 223-235.
- Cole JR, Wang Q, Cardenas E, Fish J, Chai B, Farris RJ, Kulam-Syed-Mohideen AS, McGarrell DM, Marsh T, Garrity GM, Tiedje JM (2009) The Ribosomal Database Project: improved alignments and new tools for rRNA analysis. *Nucleic Acids Res* 37: 141-145.
- Dickie IA, Xu B, Koide RT (2002) Vertical niche differentiation of ectomycorrhizal hyphae in soil as shown by T-RFLP analysis. *New Phytologist* 156: 527–535.
- Dooley SR, Treseder KK (2012) The effect of fire microbial biomass: a meta-analysis of field studies. *Biogeochemistry* 109: 49-61.

- Edgar RC, Haas BJ, Clemente JC, Quince C, Knight R (2011) UCHIME improves sensitivity and speed of chimera detection. *Bioinformatics* 27: 2194-2200.
- Ekblad A, Wallander H, Godbold DL, Cruz C, Johnson D, Baldrian P, Björk RG, Epron D, Keiliszewska-Rokicka B, Kjølner R, Kraigher H, Matzner E, Newmann J, Plassard C (2013) The production and turnover of extramatrical mycelium of ectomycorrhizal fungi in forest soils: role in carbon cycling. *Plant Soil* 366: 1-27.
- Fernandes PM, Botelho HS (2003) A review of prescribed burning effectiveness in fire hazard reduction. *International Journal of Wildland Fire* 12: 117-128.
- Fogel R, Hunt G (1982) Contribution of mycorrhizae and soil fungi to nutrient cycling in a Douglas-fir ecosystem. *Canadian Journal of Forest Research* 13: 219- 232.
- Fogel R (2006) Mycorrhizae and nutrient cycling in natural forest ecosystems. *New Phytologist* 86: 199-212.
- Fritze H, Pennanen T, Pietikäinen J (1993) Recovery of soil microbial biomass and activity from prescribed burning. *Canadian Journal of Forest Research* 23: 1286-1290.
- Fujimura KE, Smith JE, Horton TR, Weber NS, Spatafora JW (2005) Pezizalean mycorrhizas and sporocarps in ponderosa pine (*Pinus ponderosa*) after prescribed fires in eastern Oregon, USA. *Mycorrhiza* 15:79-86.
- Gihring TM, Green SJ, Schadt CW (2011) Massively parallel rRNA gene sequencing exacerbates the potential for biased community diversity comparisons due to variable library sizes. *Environmental Microbiology* 14: 285-290.
- Glass DW, Johnson DW, Blank RR, Miller WW (2008) Factors affecting mineral nitrogen transformations by soil heating: a laboratory-simulated fire study. *Soil Science* 173: 387-400.
- Glitzenstein JF, Platt WJ, Streng DR (1995) Effects of fire regime and habitat on tree dynamics in north Florida longleaf pine savannas. *Ecological Monographs* 65: 441-476.
- Hernández T, García C, Reinhardt I (1997) Short-term effect of wildfire on chemical, biochemical and microbiological properties of Mediterranean pine forest soils. *Biology and Fertility of Soils* 25: 109-116.
- Holden SR, Gutierrez A, Treseder KK (2013) Changes in soil fungal communities, extracellular enzyme activities, and litter decomposition across a fire chronosequence in Alaskan boreal forests. *Ecosystems* 16: 34-46.
- Holden SR, Treseder KK (2013) A meta-analysis of soil microbial biomass responses to forest disturbances. *Frontiers in Microbiology* 4: article 163.

- Horton TR, Cázares E, Bruns TD (1998). Ectomycorrhizal, vesicular-arbuscular and dark septate fungal colonization of bishop pine (*Pinus muricata*) seedlings in the first 5 months of growth after wildfire. *Mycorrhiza* 8:11-18.
- Huse SM, Dethlefsen L, Huber JA, Welch MD, Relman DA, Sogin ML (2008) Exploring microbial diversity and taxonomy using SSU rRNA hypervariable tag sequencing. *PLoS Genetics* 4: e1000255.
- Izzo A, Canright M, Bruns TD (2005) The effects of heat treatments on ectomycorrhizal resistant propagules and their ability to colonize bioassay seedlings. *Mycological Research* 110: 196-202.
- Jumpponen A, Jones KL, Mattox JD, Yeage C (2010) Massively parallel 454-sequencing of fungal communities in *Quercus* spp. ectomycorrhizas indicates seasonal dynamics in urban and rural sites. *Molecular Ecology* 19: 41-53.
- Katoh K, Kuma K, Toh H, Miyata T (2005) MAFFT version 5: improvement in accuracy of multiple sequence alignment. *Nucleic Acids Research* 33: 511-518.
- Kifer T, Simon E, Ghazoul J, Moser B, Wohlgemuth T (2010) Susceptibility of ectomycorrhizal fungi to soil heating. *Fungal Biology* 114: 467-472.
- Knapp EE, Schwilk DW, Kane JM, Keeley JE (2007) Role of burning season on initial understory vegetation response to prescribed fire in a mixed conifer forest. *Canadian Journal of Forest Research* 37: 11-22.
- Kowal VA, Scholke A, Kanagaraj R, Bruggeman D (2013) Resource selection probability functions for gopher tortoise: providing a management tool application across the species' range. *Environmental Management* 53: 594-605.
- Ligon DJ, Stacey PB, Conner RN, Bock CE, Adkisson CS (1986) Report of the American ornithologists' union committee for the conservation of the red-cockaded woodpecker. *The Auk* 103: 848-855.
- Liu KL, Kuske CR, Porrás-Alfaro A, Eichorst S, Xie G (2012) Accurate, rapid taxonomic classification of fungal large subunit rRNA genes. *Applied and Environmental Microbiology* 78: 1523-1533.
- Longo MS, Urcelay C, Nouhra E (2011) Long term effects of fire on ectomycorrhizas and soil properties in *Nothofagus pumilio* forest in Argentina. *Forest Ecology and Management* 262: 348-354.
- Lothamer K, Brown SP, Mattox JD, Jumpponen A (2014) Comparison of root-associated communities of native and non-native ectomycorrhizal hosts in an urban landscape. *Mycorrhiza* 24: 267-280.

- Luo Z, Wu C, Zhang C, Li H, Lipka U, Polle A (2014) The role of ectomycorrhizas in heavy metal stress tolerance of host plants. *Environmental and Experimental Botany* 108: 47-62.
- Mitchell RJ, Hiers JK, O'Brien, Jack SB, Engstrom RT (2006) Silviculture that sustains: the nexus between silviculture, frequent prescribed fire, and conservation of biodiversity in longleaf pine forests of the southeastern United States. *Canadian Journal of Forest Research* 36: 2724-2736.
- Moeller HV, Peay KG, Fukami T (2013) Ectomycorrhizal fungal traits reflect environmental conditions along a coastal California edaphic gradient. *FEMS Microbiology Ecology* 87: 797-806.
- Peay GP, Garbelotta M, Bruns TD (2009) Spore heat resistance plays an important role in disturbance-mediated assemblage shift of ectomycorrhizal fungi colonizing *Pinus muricata* seedlings. *Journal of Ecology* 97: 537-547.
- Pietikäinen J, Fritze H (1993) Microbial biomass and activity in the humus layer following burning: short-term effects of two different fires. *Canadian Journal of Forest Research* 23: 1275-1285.
- Prieto-Fernández Á, Carballas M, Carballas T (2004) Inorganic and organic N pools in soils burned or heated: immediate alteration and evolution after forest wildfires. *Geoderma* 121: 291-306.
- Ryan KC, Knapp EE, Varner JM (2013) Prescribed fire in North American forests and woodlands: history, current practice, and challenges. *Frontiers in Ecology and the Environment* 11: e15-e24.
- Schloss PD, Westcott SL, Ryabin T, Hall JR, Hartmann M, Hollister EB, Lesniewski RA, Oakley BB, Parks DH, Robinson CJ, Sahl JW, Stres B, Thallinger GG, Van Horn DJ, Weber CF (2009) Introducing mothur: open-source, platform-independent, community-supported software for describing and comparing microbial communities. *Applied and Environmental Microbiology* 75: 7537-7541.
- Schloss PD, Gevers D, Westcott SL (2011) Reducing the effects of PCR amplification and sequencing artifacts on 16S rRNA-based studies. *PLOS ONE* 6:e27310.
- Smith JE, McKay D, Niwa CG, Thies WG, Brenner G, Spatafora JW (2004) Short-term effects of seasonal prescribed burning on the ectomycorrhizal fungal community and fine root biomass in ponderosa pine stands in the Blue Mountains of Oregon. *Canadian Journal of Forest Research* 34: 2477-2491.
- Smith SE, Smith FAA, Read DJ (2008). *Mycorrhizal symbiosis*. 3rd ed. Elsevier, London. 787 pp.

- Sparks JC, Masters RE, Engle DM, Bukenhofer GA (2002) Season of burn influences fire behavior and fuel consumption in restored shortleaf pine-grassland communities. *Restoration Ecology* 10: 714-722.
- Steen DA, Smith LL, Morris G, Conner M, Litt AR, Pokswinski S, Guyer C (2013) Response of six-lined racerunner (*Aspidoscelis sexlineata*) to habitat restoration in fire-suppressed longleaf pine (*Pinus palustris*) sandhills. *Restoration Ecology* 21: 457- 463.
- Stendell ER, Horton TR, Bruns TD (1999) Early effects of prescribed fire on the structure of the ectomycorrhizal fungus community in Sierra Nevada ponderosa pine forest. *Mycological Research* 103: 1353-1359.
- Swezy DM, Agee JK (1990) Prescribed fire effects on fine-root and tree mortality in old-growth ponderosa pine. *Canadian Journal of Forest Research* 21: 626-634.
- Talbert JT, Weir RJ, Arnold RD (1985) Cost and benefits of a mature first-generation loblolly pine tree improvement program. *Journal of forestry* 83: 162-166.
- Taylor DL, Bruns TD (2002) Community structure of ectomycorrhizal fungi in a *Pinus muricata* forest: minimal overlap between the mature forest and resistant propagule communities. *Molecular Ecology* 8: 1837-1850.
- Tedersoo L, Nilsson RH, Abarenkov K et al. (2010) 454 pyrosequencing and Sanger sequencing of tropical mycorrhizal fungi provide similar results but reveal substantial methodological biases. *New Phytologist* 188: 291–301.
- Toberman H, Chen C, Lewis T, Elser JJ (2014) High-frequency fire alters C: N: P stoichiometry in forest litter. *Global Change Biology* 20: 2321-2331.
- Töljander JF, Eberhardt U, Toljander YK, Paul LR, Taylor AFS (2006) Species composition of an ectomycorrhizal fungal community along a local nutrient gradient in a boreal forest. *New Phytologist* 170: 873-884.
- Tuininga AR, Dighton J (2004) Changes in ectomycorrhizal communities and nutrient availability following prescribed burns in two upland pine-oak forests in the New Jersey pine barrens. *Canadian Journal of Forest Research* 34: 1755-1765.
- van der Heijden EW, de Vries FW, Kuyper TW (2000) Mycorrhizal associations of *Salix repens* L. communities in succession of dune ecosystems. I. Above-ground and below-ground views of ectomycorrhizal fungi in relation to soil chemistry. *Canadian Journal of Botany* 77: 1821-1832.
- Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology* 172(8): 4238-4246.

- Visser S. (1994) Ectomycorrhizal fungal succession in jack pine stands following wildfire. *New Phytologist* 129: 389-401.
- Waldrop TA, White DL, Jones SM (1992) Fire regimes for pine-grassland communities in the southeastern United States. *Forest Ecology and Management* 47: 195-210.
- Wang Q, Garrity GM, Tiedje JM, Cole RJ (2007) Naïve Bayesian Classifier for Rapid Assignment of rRNA Sequences into the New Bacterial Taxonomy. *Appl Environ Microbiol* 73:5261-7
- Wicklow D (1973) Microfungal populations in surface soils of manipulated prairie stands. *Ecology* 54: 1302–1310.
- Wicklow D (1975) Fire as an environmental cue initiating ascomycete development in a tallgrass prairie. *Mycologia* 67: 852–862.
- Williams RJ, Hallgren SW, Wilson GWT (2011) Frequency of prescribed burning in an upland oak forest determines soil and litter properties and alters soil microbial community. *Forest Ecology and Management* 265: 241-247.

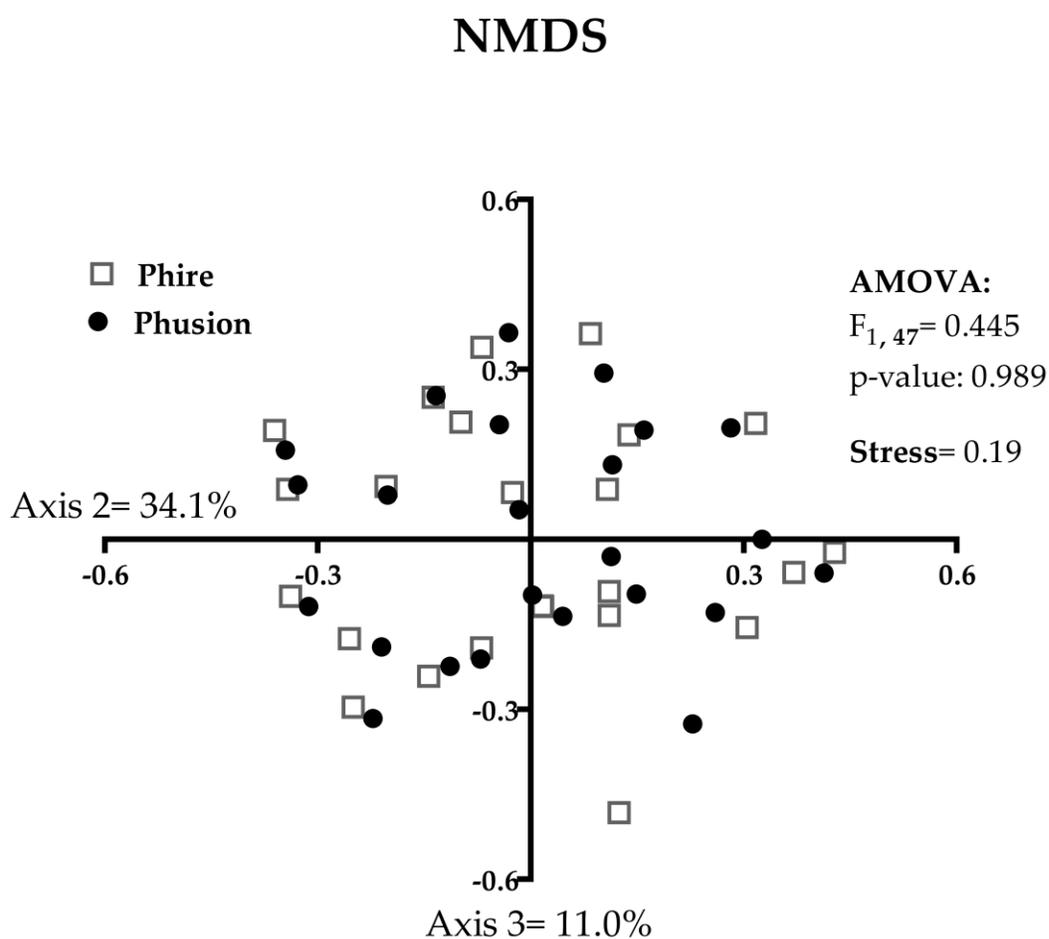
Chapter 5

- Anderson IC, Bastias BA, Genney DR, Parkin PI, Cairney JWG. 2007. Basidiomycete fungal communities in Australian sclerophyll forest soil are altered by repeated prescribed burning. *Mycological Research*, 111: 482-486.
- Bastias BA, Huang ZQ, Blumfields T, Xu Z, Cairney JWG. 2006. Influence of repeated prescribed burning on the soil fungal community in an eastern Australian wet sclerophyll forest. *Soil Biology and Biochemistry*, 38: 3492-3501.
- Tedersoo L., Nilsson R.H., Abarenkov K., Jairus T., Sadam A., Saar I., Bahram M., Bechem E., Chuyong G., Kõljalg U., 2010. 454 Pyrosequencing and Sanger sequencing of tropical mycorrhizal fungi provide similar results but reveal substantial methodological biases. *New Phytologist* 188, 291-301.
- Brown SP, Veach AM, Rigdon-Huss AR, Grond K, Lickteig SK, Lothamer K, Oliver AK, Jumpponen A. 2014. Scraping the bottom of the barrel: are rare high throughput sequences artifacts? *Fungal Ecology* (revised and in review).

Appendix A - Supplemental Information for Chapter 2

Figures

Figure A.1 Non-metric Multidimensional scaling (NMDS) ordination across Axis 2 (34.1% variance) and Axis 3 (11.0% variance) of the two MiSeg libraries generated with the non-proofreading Phire and proofreading Phusion polymerases. Although the data clouds from the two libraries are subtly shifted, the overall communities do not differ (AMOVA: $F_{1,47} = 0.445$; $P = 0.9890$).



Tables

Table A.1 Primer and DNA-tag (Multiplexing IDentifiers; MID) sequences used for sample specific PCR and sample identification in MiSeq ITS2 amplicon libraries generated with the non-proofreading Phire and proofreading Phusion polymerases. Note that both Phire and Phusion generated libraries shared the same MID's avoiding thus biases potentially resulting from MID selection. The two datasets were later merged in the pipeline to permit side-by-side comparisons.

Forward primer	fITS7	TCCTCCGCTTATTGATA TGC
Reverse primer	ITS4	GTGARTCATCGAATCT TTG
MID	Phire Sample	Phusion Sample
TCCCTTGCTCTCC	Phire_1_2w_1	Phusion_1_2w_1
ACGAGACTGATT	Phire_2_3w_2	Phusion_2_3w_2
TACCGCTTCTTC	Phire_3_c_3	Phusion_3_c_3
ATCACCAGGTGT	Phire_4_6s_4	Phusion_4_6s_4
TGGTCAACGATA	Phire_6_c_5	Phusion_6_c_5
ATCGCACAGTAA	Phire_7_6s_6	Phusion_7_6s_6
GTCGTGTAGCCT	Phire_8_3w_7	Phusion_8_3w_7
GATTATCGACGA	Phire_9_3w_8	Phusion_9_3w_8
ATCCTTTGGTTC	Phire_10_6s_9	Phusion_10_6s_9
GCCTAGCCCAAT	Phire_11_2w_10	Phusion_11_2w_10
ACCGGTATGTAC	Phire_12_3w_11	Phusion_12_3w_11
GATGTATGTGGT	Phire_13_3w_12	Phusion_13_3w_12
TGCATACACTGG	Phire_14_3s_13	Phusion_14_3s_13
AGTCGAACGAGG	Phire_15_c_14	Phusion_15_c_14
ACCAGTGACTCA	Phire_16_2w_15	Phusion_16_2w_15
GAATACCAAGTC	Phire_17_3s_16	Phusion_17_3s_16
GTAGATCGTGTA	Phire_18_3w_17	Phusion_18_3w_17
TAACGTGTGTGC	Phire_19_6s_18	Phusion_19_6s_18
ACTCCTTGTTGTT	Phire_21_c_19	Phusion_21_c_19
CCAATACGCCTG	Phire_22_2w_20	Phusion_22_2w_20
ACTTGGTGTAAG	Phire_23_3w_21	Phusion_23_3w_21
TCACCTCCTTGT	Phire_24_3w_22	Phusion_24_3w_22
CAAACAACAGCT	Phire_25_3s_23	Phusion_25_3s_23
GCAACACCATCC	Phire_26_3s_24	Phusion_26_3s_24

Figure A.2 Yields of chimeras and low frequency OTUs (OTUs that were comprised of 1 sequence, ≤ 2 sequences, ≤ 5 sequences, and ≤ 10 sequences), as well as observed (S_{Obs}) and extrapolated (Chao 1) richness, diversity (1-D) and evenness (E_D) in two paired MiSeq amplicon libraries generated with the non-proofreading (Phire) and proofreading (Phusion) polymerases. Wilcoxon test is the signed rank test testing the null hypothesis $H_0: Y_{Phire} = Y_{Phusion}$, where Y is a measured response. Note that all results are congruent with parametric paired t -tests (not shown). Significant responses are highlighted in boldface ($P < 0.05$) or in italics ($0.05 \leq P < 0.10$). (*) $0.05 \leq P < 0.10$; * $0.01 \leq P < 0.05$; ** $0.001 \leq P < 0.01$; *** $P < 0.001$.

Mean \pm st dev	Phire	Phusion	Wilcoxon Test (df = 23)
Chimeras (%)	2.70 \pm 1.51	2.72 \pm 1.34	W = 4.00 ^{ns}
N Seqs = 1 (%)	0.68 \pm 0.14	0.51 \pm 0.11	W = -141.50***
N Seqs = 2 (%)	1.01 \pm 0.21	0.80 \pm 0.19	W = -148.00***
N Seqs = 5 (%)	1.66 \pm 0.37	1.40 \pm 0.35	W = -138.50***
N Seqs = 10 (%)	2.42 \pm 0.60	2.09 \pm 0.48	W = -140.00***
Good's Coverage	0.98 \pm 0.001	0.98 \pm 0.001	W = 14.00 ^{ns}
Richness (S_{Obs})	758.39 \pm 53.09	734.86 \pm 56.35	W = -104.00**
Richness (Chao 1)	1049.49 \pm 70.03	1040.26 \pm 86.69	W = -22.00 ^{ns}
<i>Diversity (1-D)</i>	<i>0.98 \pm 0.01</i>	<i>0.98 \pm 0.01</i>	W = 66.00 ^(*)
Evenness (E_D)	0.056 \pm 0.012	0.060 \pm 0.01	W = 98.00**

Appendix B - Supplemental Information for Chapter 3

Tables

Table B.1 Primer and DNA-tag (Multiplexing IDentifiers; MID) sequences used for sample specific PCR and sample identification in MiSeq ITS2 amplicon libraries generated.

Forward primer	fITS7	GTGARTCATCGAATCTTTG
Reverse primer	ITS4	TCCTCCGCTTATTGATATGC
MID	Sample	
TCCCTTGTCTCC	Phusion_1_2w_1	
ACGAGACTGATT	Phusion_2_3w_2	
TACCGCTTCTTC	Phusion_3_c_3	
ATCACCAGGTGT	Phusion_4_6s_4	
TGGTCAACGATA	Phusion_6_c_5	
ATCGCACAGTAA	Phusion_7_6s_6	
GTCGTGTAGCCT	Phusion_8_3w_7	
GATTATCGACGA	Phusion_9_3w_8	
ATCCTTTGGTTC	Phusion_10_6s_9	
GCCTAGCCCAAT	Phusion_11_2w_10	
ACCGGTATGTAC	Phusion_12_3w_11	
GATGTATGTGGT	Phusion_13_3w_12	
TGCATACACTGG	Phusion_14_3s_13	
AGTCGAACGAGG	Phusion_15_c_14	
ACCAGTGACTCA	Phusion_16_2w_15	
GAATACCAAGTC	Phusion_17_3s_16	
GTAGATCGTGTA	Phusion_18_3w_17	
TAACGTGTGTGC	Phusion_19_6s_18	
ACTCCTTGTGTT	Phusion_21_c_19	
CCAATACGCCTG	Phusion_22_2w_20	
ACTTGGTGTAAG	Phusion_23_3w_21	
TCACCTCCTTGT	Phusion_24_3w_22	

CAAACAACAGCT Phusion_25_3s_23

GCAACACCATCC Phusion_26_3s_24

Table B.2 A complete list of soil fungi OTUs present in the ITS2 MiSeq Illumina dataset with their taxonomic assignments and sequence counts.

OTU	Phylum	Class	Order	Family	Genus	Species	Count
Otu0001	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Umbelopsidaceae	Umbelopsis	Umbelopsis dimorpha	28163
Otu0002	Basidiomycota	Wallemiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	unclassified	16897
Otu0003	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	8635
Otu0004	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Umbelopsidaceae	unclassified Umbelopsidaceae	Umbelopsidaceae sp	7794
Otu0005	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	7297
Otu0006	Basidiomycota	Tremellomycetes	Tremellales	Tremellales family Incertae sedis	Cryptococcus	Cryptococcus podzolicus	7213
Otu0007	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	unclassified	5223
Otu0008	Ascomycota	Eurotiomycetes	unclassified	unclassified	unclassified	unclassified	5176
Otu0009	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	unclassified Atheliaceae	unclassified	4985
Otu0010	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	4239
Otu0011	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula cascadenis	3721
Otu0012	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp ARIZ AZ0501	3582
Otu0013	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	2535
Otu0014	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	unclassified Trichocomaceae	uncultured Thermoascus	2915
Otu0015	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	2773
Otu0016	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp aurim729	2835
Otu0017	Zygomycota	Zygomycota class Incertae sedis	Mortierellales	Mortierellaceae	Mortierella	Mortierella minutissima	2724
Otu0018	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	Trechispora sp LISU178537	2212
Otu0019	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula crustosa	2404
Otu0020	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	Suillus cothurnatus	2350
Otu0021	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp aurim729	2458

Otu0022	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	ungal sp ARIZ AZ0501	2403
Otu0023	Basidiomycota	Agaricomycetes	Geastrales	Geastraceae	Geastrum	Geastrum sp TNS KH JPN10 626	2207
Otu0024	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	2152
Otu0025	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Catathelasma	Catathelasma ventricosum	2104
Otu0026	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Tylospora	Tylospora sp	1983
Otu0027	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula acrifolia	1958
Otu0028	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Umbelopsidaceae	unclassified Umbelopsidaceae	Umbelopsidaceae sp	1932
Otu0029	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	1979
Otu0030	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	1827
Otu0031	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	Inocybe aff perlata TENN 062740	1799
Otu0032	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	1874
Otu0033	Zygomycota	Zygomycota class Incertae sedis	Mortierellales	Mortierellaceae	Mortierella	unclassified	1878
Otu0034	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	1476
Otu0035	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	Cortinarius mucosus	1733
Otu0036	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	ungal sp aurim729	1874
Otu0037	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	Thelephoraceae sp H176	1660
Otu0038	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactifluus	Lactarius bertillonii	1711
Otu0039	Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	Rhizopogon fuscrobens	1494
Otu0040	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	ungal sp ARIZ AZ0501	1387
Otu0041	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactifluus	Lactarius bertillonii	1727
Otu0042	Ascomycota	Leotiomycetes	Geoglossales	Geoglossaceae	Geoglossum	Geoglossum difforme	1611
Otu0043	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	1507
Otu0044	Zygomycota	Zygomycota class Incertae sedis	Mortierellales	Mortierellaceae	Mortierella	Mortierella elongata	1225
Otu0045	Basidiomycota	Microbotryomycetes	unclassified Microbotryomycetes	unclassified Microbotryomycetes	unclassified Microbotryomycetes	Microbotryomycetes sp	1421
Otu0046	Zygomycota	Zygomycota class Incertae sedis	Mortierellales	Mortierellaceae	Mortierella	Mortierella simplex	1304

Otu0047	Zygomycota	Zygomycota class Incertae sedis	Mortierellales	Mortierellaceae	Mortierella	Mortierella verticillata	1413
Otu0048	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	1290
Otu0049	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	unclassified Atheliaceae	Atheliaceae sp	1071
Otu0050	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactarius	Lactarius subplinthogalus	1281
Otu0051	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	unclassified	1342
Otu0052	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	1084
Otu0053	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Cuphophyllus	Cuphophyllus lacmus	1277
Otu0054	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	Basal lineages	1008
Otu0055	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	1121
Otu0056	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	Basal lineages	1016
Otu0057	Basidiomycota	Agaricomycetes	Agaricales	Hydnangiaceae	Laccaria	Laccaria trichodermophora	1178
Otu0058	Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	Ascomycota sp 4 RB 2011	1196
Otu0059	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungus sp ARIZ AZ0501	1090
Otu0060	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	unclassified	808
Otu0061	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	986
Otu0062	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	1074
Otu0063	Basidiomycota	Agaricomycetes	Cantharellales	Hydnaceae	Hydnum	unclassified	886
Otu0064	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungus sp ARIZ AZ0501	1069
Otu0065	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	1132
Otu0066	Basidiomycota	Agaricomycetes	Agaricales	Mycenaceae	Mycena	Mycena sp pink	1165
Otu0067	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	Cortinarius pseudorubricosus	1218
Otu0068	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	Cortinarius caperatus	1097
Otu0069	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	Basal lineages	1157
Otu0070	Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	Rhizopogon pseudoroseolus	1232
Otu0071	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	687
Otu0072	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	unclassified	832

Otu0073	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	unclassified	991
Otu0074	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactarius	Lactarius deceptivus	943
Otu0075	Basidiomycota	Tremellomycetes	Tremellales	Tremellales family Incertae sedis	Cryptococcus	Cryptococcus podzolicus	967
Otu0076	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	unclassified	unclassified	859
Otu0077	Zygomycota	Zygomycota class Incertae sedis	Mortierellales	Mortierellaceae	Mortierella	Mortierella verticillata	790
Otu0078	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	907
Otu0079	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe reidii	869
Otu0080	Ascomycota	Leotiomycetes	Geoglossales	Geoglossaceae	Geoglossum	Geoglossum simile	896
Otu0081	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Tricholoma	unclassified	655
Otu0082	Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	uncultured Basidiomycota	872
Otu0083	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	749
Otu0084	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	768
Otu0085	Zygomycota	Zygomycota class Incertae sedis	Mortierellales	Mortierellaceae	Mortierella	unclassified	778
Otu0086	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula cf cyanoxantha BB2004 251	806
Otu0087	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	671
Otu0088	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	unclassified	808
Otu0089	Basidiomycota	Agaricomycetes	Boletales	Boletaceae	unclassified	unclassified	759
Otu0090	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	Amanita pantherina	810
Otu0091	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactarius	unclassified	859
Otu0092	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified	unclassified	unclassified	804
Otu0093	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Umbelopsidaceae	unclassified Umbelopsidaceae	Umbelopsidaceae sp	830
Otu0094	Zygomycota	Zygomycota class Incertae sedis	Mortierellales	Mortierellaceae	Mortierella	unclassified	798
Otu0095	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	173
Otu0096	Basidiomycota	Agaricomycetes	Agaricales	Mycenaceae	Mycena	Mycena aff pura TL8052	790
Otu0097	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	unclassified	765
Otu0098	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	662

Otu0099	Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	uncultured Basidiomycota	789
Otu0100	Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	Metarhizium	unclassified	720
Otu0101	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp aurim729	750
Otu0102	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	Inocybe cf splendens EL21906	748
Otu0103	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula vesca	679
Otu0104	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	unclassified	711
Otu0105	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	Suillus cothurnatus	722
Otu0106	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	unclassified	778
Otu0107	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	512
Otu0108	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	712
Otu0109	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrophorus	Hygrophorus cf subalpinus TRTC156469	595
Otu0110	Basidiomycota	Agaricomycetes	Agaricales	Strophariaceae	Hebeloma	Hebeloma cylindrosporum	503
Otu0111	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified	unclassified	unclassified	22
Otu0112	Basidiomycota	Agaricomycetes	Cantharellales	Hydnaceae	Sistotrema	Sistotrema sp	617
Otu0113	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	Cortinarius quarciticus	643
Otu0114	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe laeta var. flava	643
Otu0115	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactarius	Lactarius deceptivus	659
Otu0116	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Piloderma	unclassified	741
Otu0117	Ascomycota	Pezizomycetes	Pezizales	Tuberaceae	Tuber	Tuber shearii	636
Otu0118	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	638
Otu0119	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe cf conica	638
Otu0120	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	637
Otu0121	Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	leotiomyces sp 2 RB 2011	664
Otu0122	Ascomycota	Eurotiomycetes	Eurotiales	Elaphomycetaceae	Elaphomyces	Elaphomyces sp	601
Otu0123	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	524
Otu0124	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe laeta var. flava	623

Otu0125	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavaria	Clavaria acuta	606
Otu0126	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Byssocorticium	Byssocorticium pulchrum	556
Otu0127	Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	Trichoderma spirale	581
Otu0128	Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	uncultured Basidiomycota	563
Otu0129	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	158
Otu0130	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	531
Otu0131	Basidiomycota	Agaricomycetes	Polyporales	unclassified Polyporales	unclassified Polyporales	uncultured Trechispora	552
Otu0132	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	unclassified Herpotrichiellaceae	Herpotrichiellaceae sp	508
Otu0133	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Tylospora	Tylospora sp	524
Otu0134	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	Cortinarius quarcticus	612
Otu0135	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	Trechispora sp LISU178537	586
Otu0136	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	unclassified	581
Otu0137	Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	uncultured ectomycorrhiza Basidiomycete	569
Otu0138	Zygomycota	Zygomycota class Incertae sedis	Mortierellales	Mortierellaceae	unclassified	unclassified	551
Otu0139	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula cf cyanoxantha BB2004 251	616
Otu0140	Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	Rhizopogon pseudoroseolus	531
Otu0141	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	575
Otu0142	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	402
Otu0143	Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified	483
Otu0144	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	unclassified Clavariaceae	uncultured Clavulinopsis	385
Otu0145	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	518
Otu0146	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	507
Otu0147	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	518

Otu0148	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	484
Otu0149	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	492
Otu0150	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	411
Otu0151	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	463
Otu0152	Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	Rhizopogon pseudoroeseolus	490
Otu0153	Ascomycota	Pezizomycetes	Pezizales	Pezizaceae	Peziza	Peziza sp RH1250	456
Otu0154	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Tricholoma	Tricholoma portentosum	460
Otu0155	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	470
Otu0156	Basidiomycota	Agaricomycetes	Geastrales	Geastraceae	Geastrum	unclassified	453
Otu0157	Basidiomycota	Agaricomycetes	Sebacinales	unclassified Sebacinales	unclassified Sebacinales	Sebacinales sp 1 CG 2012	467
Otu0158	Zygomycota	Zygomycota class Incertae sedis	Mortierellales	Mortierellaceae	Mortierella	unclassified	413
Otu0159	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	450
Otu0160	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactifluus	Lactarius bertillonii	482
Otu0161	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrophorus	Hygrophorus cf subalpinus TRTC156469	400
Otu0162	Basidiomycota	Agaricomycetes	Gomphales	Gomphaceae	Ramaria	unclassified	465
Otu0163	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	416
Otu0164	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified Sebacinaceae	uncultured Tremellodendron	417
Otu0165	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavulinopsis	Clavulinopsis luteoalba	427
Otu0166	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	355
Otu0167	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Tylospora	Tylospora sp	445
Otu0168	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavaria	Clavaria zollingeri	428
Otu0169	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	366
Otu0170	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	452
Otu0171	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula cf cyanoxantha BB2004 251	374
Otu0172	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	416
Otu0173	Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Cryptococcus	Cryptococcus terricola	402

Otu0174	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Tricholoma	Tricholoma portentosum	402
Otu0175	Basidiomycota	Agaricomycetes	unclassified Agaricomycetes	unclassified Agaricomycetes	unclassified Agaricomycetes	Agaricomycetes sp	442
Otu0176	Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	leotiomyceta sp 2 RB 2011	390
Otu0178	Basidiomycota	Wallemiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	unclassified	267
Otu0179	Zygomycota	Zygomycota class Incertae sedis	Mortierellales	Mortierellaceae	Mortierella	Mortierella exigua	388
Otu0180	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	311
Otu0181	Basidiomycota	Wallemiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	unclassified	216
Otu0182	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula cascadenis	365
Otu0183	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	374
Otu0184	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified Sebacinaceae	Sebacinaceae sp	386
Otu0185	Basidiomycota	Agaricomycetes	Atheliales	unclassified Atheliales	unclassified Atheliales	Atheliales sp	321
Otu0186	Basidiomycota	Agaricomycetes	Gomphales	Gomphaceae	unclassified Gomphaceae	uncultured Ramaria	345
Otu0187	Basidiomycota	Agaricomycetes	Agaricales	Agaricales family Incertae sedis	Camarophylloopsis	Camarophylloopsis sp SGT 2012	182
Otu0188	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	unclassified	347
Otu0189	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe laeta var. flava	321
Otu0190	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	334
Otu0191	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Leucoagaricus	Leucoagaricus sp Weber 6019	355
Otu0192	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Thelephora	Thelephora terrestris	373
Otu0193	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe pratensis var. pratensis	324
Otu0194	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Tylospora	Tylospora sp	371
Otu0195	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	344
Otu0196	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	unclassified	unclassified	391
Otu0197	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	317
Otu0198	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	175
Otu0199	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	unclassified	unclassified	326

Otu0200	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	Tomentella lilacinogrisea	299
Otu0201	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Sagenomella	Sagenomella sp	318
Otu0202	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe conica	352
Otu0203	Basidiomycota	Agaricomycetes	Cantharellales	Hydnaceae	Sistotrema	unclassified	351
Otu0204	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Umbelopsidaceae	unclassified Umbelopsidaceae	Umbelopsidaceae sp	200
Otu0205	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Camarophyllus	Camarophyllus borealis	115
Otu0206	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	347
Otu0207	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Umbelopsidaceae	Umbelopsis	unclassified	297
Otu0208	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe laeta var. flava	325
Otu0209	Basidiomycota	Wallemiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	unclassified	327
Otu0210	Basidiomycota	Wallemiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	unclassified	303
Otu0211	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	unclassified	335
Otu0212	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	Trechispora sp LISU178537	349
Otu0213	Basidiomycota	Agaricomycetes	Cantharellales	Clavulinaceae	Clavulina	Clavulina sp EMF53	323
Otu0214	Ascomycota	Leotiomycetes	Geoglossales	Geoglossaceae	Trichoglossum	unclassified	316
Otu0215	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	291
Otu0216	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactifluus	unclassified	279
Otu0217	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentellopsis	unclassified	326
Otu0218	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula sp 7 RG 2012	315
Otu0219	Basidiomycota	Microbotryomycetes	unclassified Microbotryomycetes	unclassified Microbotryomycetes	unclassified Microbotryomycetes	Microbotryomycetes sp	352
Otu0220	Basidiomycota	Wallemiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	Geminibasidium donsium	328
Otu0221	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp ARIZ AZ0501	316
Otu0222	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	305
Otu0223	Zygomycota	Zygomycota class Incertae sedis	Mortierellales	Mortierellaceae	Mortierella	Mortierella cystojenkinii	298
Otu0224	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	334
Otu0225	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	295

Otu0226	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	327
Otu0227	Ascomycota	Pezizomycetes	Pezizales	Tuberaceae	Tuber	Tuber separans	357
Otu0228	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	184
Otu0229	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	334
Otu0230	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	319
Otu0231	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula sp 7 RG 2012	301
Otu0232	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	290
Otu0233	Basidiomycota	Agaricomycetes	Geastrales	Geastraceae	Geastrum	Geastrum saccatum	292
Otu0234	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	289
Otu0235	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	306
Otu0236	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula sp MHM015	319
Otu0237	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	253
Otu0238	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactifluus	unclassified	277
Otu0239	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	122
Otu0240	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	294
Otu0241	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	315
Otu0242	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	246
Otu0243	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	156
Otu0244	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Tretomyces	Tretomyces lutescens	272
Otu0245	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	unclassified	unclassified	270
Otu0246	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	Suillus cothurnatus	293
Otu0247	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Mucoraceae	Mucor	Mucor moelleri	272
Otu0248	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	Cortinarius vernus	268
Otu0249	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	306
Otu0250	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	unclassified	287
Otu0251	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	Basal lineages	246
Otu0252	Zygomycota	Zygomycota class Incertae sedis	Mortierellales	Mortierellaceae	Mortierella	unclassified	299
Otu0253	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	265

Otu0254	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	259
Otu0255	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	237
Otu0256	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	unclassified	unclassified	104
Otu0257	Basidiomycota	Agaricomycetes	Agaricales	unclassified Agaricales	unclassified Agaricales	Agaricales sp	240
Otu0258	Zygomycota	Zygomycota class Incertae sedis	Mortierellales	Mortierellaceae	Mortierella	Mortierella alpina	252
Otu0259	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Tricholoma	Tricholoma ulvinenii	268
Otu0260	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	265
Otu0261	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	unclassified	221
Otu0262	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	266
Otu0263	Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	Ascomycota sp 4 RB 2011	274
Otu0264	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	unclassified	256
Otu0265	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	236
Otu0266	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	224
Otu0267	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavulinopsis	Clavulinopsis luteoalba	224
Otu0268	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	unclassified Atheliaceae	Atheliaceae sp	222
Otu0269	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified	unclassified	unclassified	254
Otu0270	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Piloderma	Piloderma sp 5 RT 2012	209
Otu0271	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	237
Otu0272	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	Sebacina	Sebacina sp	228
Otu0273	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	236
Otu0274	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentellopsis	Tomentellopsis echinospora	248
Otu0275	Basidiomycota	Wallemiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	unclassified	231
Otu0276	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe aff coccinea	221
Otu0277	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	185
Otu0278	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	unclassified	237
Otu0279	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	Tomentella stiposa	238
Otu0280	Zygomycota	Zygomycota class Incertae sedis	Mortierellales	Mortierellaceae	Mortierella	Mortierella biramosa	200

Otu0281	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	242
Otu0282	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	207
Otu0283	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	40
Otu0284	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	unclassified	233
Otu0285	Basidiomycota	Agaricomycetes	Agaricales	Mycenaceae	Mycena	Mycena pura	209
Otu0286	Ascomycota	Leotiomycetes	Geoglossales	Geoglossaceae	unclassified	unclassified	241
Otu0287	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	unclassified	219
Otu0288	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentellopsis	Tomentellopsis echinospora	62
Otu0289	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	149
Otu0290	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Ramariopsis	Ramariopsis helvola	171
Otu0291	Basidiomycota	Wallemiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	unclassified	227
Otu0292	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	199
Otu0293	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	90
Otu0294	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactifluus	Lactifluus cf volemus 04 166	202
Otu0295	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified Sebacinaceae	unclassified	129
Otu0296	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	207
Otu0297	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	Inocybe rimosa	227
Otu0298	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Byssocorticium	Byssocorticium caeruleum	206
Otu0299	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	248
Otu0300	Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	unclassified	unclassified	186
Otu0301	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	unclassified	193
Otu0302	Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	Ascomycota sp BBC	185
Otu0303	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	198
Otu0304	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Umbelopsidaceae	Umbelopsis	Umbelopsis isabellina	228
Otu0305	Ascomycota	Eurotiomycetes	unclassified	unclassified	unclassified	unclassified	207

Otu0306	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified	unclassified	212
Otu0307	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	unclassified	212
Otu0308	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	unclassified	206
Otu0309	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp ARIZ AZ0501	184
Otu0310	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Tretomyces	Tretomyces lutescens	158
Otu0311	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	144
Otu0312	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	Suillus cothurnatus	177
Otu0313	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	173
Otu0314	Basidiomycota	Agaricomycetes	Auriculariales	unclassified Auriculariales	unclassified Auriculariales	uncultured Hyaloriaceae	151
Otu0315	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	180
Otu0316	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	215
Otu0317	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Sagenomella	unclassified	174
Otu0318	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Pseudotomentella	Pseudotomentella atrofusca	196
Otu0319	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	197
Otu0320	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified Sebacinaceae	Sebacinaceae sp	161
Otu0321	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula pectinatoides	178
Otu0322	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Tricholoma	Tricholoma ulvinenii	193
Otu0323	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe aff coccinea	182
Otu0324	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	205
Otu0325	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	211
Otu0326	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	179
Otu0327	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified	unclassified	187
Otu0328	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	131
Otu0329	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	145
Otu0330	Basidiomycota	Agaricomycetes	Boletales	Boletaceae	Chalciporus	Chalciporus trinitensis	157
Otu0331	Basidiomycota	Wallemiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	unclassified	158
Otu0332	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	191

Otu0333	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactarius	Lactarius subplinthogalus	159
Otu0334	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp mh32602	170
Otu0335	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Tylospora	Tylospora sp	180
Otu0336	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	unclassified	179
Otu0337	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified	unclassified	unclassified	136
Otu0338	Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	Sphaerosporella	Sphaerosporella sp	177
Otu0339	Basidiomycota	Agaricomycetes	Agaricales	Mycenaceae	Mycena	Mycena sp pink	182
Otu0340	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	167
Otu0341	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	173
Otu0342	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	Cortinarius ectypus	118
Otu0343	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	183
Otu0344	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Clitocybe	Clitocybe subditopoda	140
Otu0345	Basidiomycota	Agaricomycetes	Sebacinales	unclassified	unclassified	unclassified	153
Otu0346	Basidiomycota	Agaricomycetes	Auriculariales	unclassified Auriculariales	unclassified Auriculariales	uncultured Hyaloriaceae	163
Otu0347	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Lycoperdon	unclassified	99
Otu0348	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	unclassified	unclassified	110
Otu0349	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	165
Otu0350	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	unclassified	168
Otu0351	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	162
Otu0352	Basidiomycota	Agaricomycetes	Sebacinales	unclassified Sebacinales	unclassified Sebacinales	Sebacinales sp 2 CG 2012	158
Otu0353	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	unclassified	142
Otu0354	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	Trechispora sp LISU178537	163
Otu0355	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	unclassified Atheliaceae	unclassified	181
Otu0356	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	152
Otu0357	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	134
Otu0358	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	144

Otu0359	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	59
Otu0360	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe quieta	131
Otu0361	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	Sebacina	Sebacina sp RT 2012	149
Otu0362	Basidiomycota	Agaricomycetes	Polyporales	Xenasmataceae	Xenasmatella	Xenasmatella sp	146
Otu0363	Basidiomycota	Agaricomycetes	Agaricales	unclassified Agaricales	unclassified Agaricales	Agaricales sp	174
Otu0364	Basidiomycota	Agaricomycetes	Boletales	Boletaceae	unclassified	unclassified	117
Otu0365	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	135
Otu0366	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	153
Otu0367	Basidiomycota	Agaricomycetes	unclassified Agaricomycetes	unclassified Agaricomycetes	unclassified Agaricomycetes	uncultured Agaricomycetes	130
Otu0368	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavaria	Clavaria vermicularis	155
Otu0369	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	120
Otu0370	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Umbelopsidaceae	unclassified Umbelopsidaceae	uncultured Umbelopsis	135
Otu0371	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	148
Otu0372	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	unclassified	unclassified	146
Otu0373	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified Sebacinaceae	unclassified	149
Otu0374	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	134
Otu0375	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	125
Otu0376	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	unclassified	134
Otu0377	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	Suillus cothurnatus	151
Otu0378	Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	unclassified Ceratobasidiaceae	unclassified	139
Otu0379	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactarius	unclassified	130
Otu0380	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	133
Otu0381	Basidiomycota	Agaricomycetes	Sebacinales	unclassified	unclassified	unclassified	136
Otu0382	Basidiomycota	Agaricomycetes	Agaricales	Agaricales family Incertae sedis	Camarophylloopsis	Camarophylloopsis sp SGT 2012	124
Otu0383	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	unclassified	139
Otu0384	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula cf cyanoxantha BB2004 251	149

Otu0385	Basidiomycota	Agaricomycetes	Polyporales	Meruliaceae	Hyphoderma	Peniophorella pallida	140
Otu0386	Basidiomycota	Agaricomycetes	Geastrales	Geastraceae	Geastrum	Geastrum saccatum	131
Otu0387	Ascomycota	Pezizomycetes	Pezizales	Tuberaceae	Tuber	Tuber shearii	43
Otu0388	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	105
Otu0389	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	unclassified Trichocomaceae	uncultured Thermoascus	131
Otu0390	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	132
Otu0391	Ascomycota	Leotiomycetes	Geoglossales	Geoglossaceae	Glutinoglossum	Glutinoglossum glutinosum	125
Otu0392	Basidiomycota	Atractiellomycetes	Atractiellales	unclassified Atractiellales	unclassified Atractiellales	Atractiellales sp 95	112
Otu0393	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	137
Otu0394	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	89
Otu0395	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	124
Otu0396	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	Inocybe rimosa	135
Otu0397	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	unclassified Tricholomataceae	Tricholomataceae sp	129
Otu0398	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	137
Otu0399	Basidiomycota	Agaricomycetes	Cantharellales	Botryobasidiaceae	Botryobasidium	Botryobasidium laeve	133
Otu0400	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	Suillus cothurnatus	155
Otu0401	Basidiomycota	Agaricomycetes	unclassified Agaricomycetes	unclassified Agaricomycetes	unclassified Agaricomycetes	Agaricomycetes sp	152
Otu0402	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactarius	unclassified	125
Otu0403	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	unclassified Tricholomataceae	Tricholomataceae sp	140
Otu0404	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	130
Otu0406	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	128
Otu0407	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe aff coccinea	116
Otu0408	Basidiomycota	Wallemiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	Geminibasidium donsium	157
Otu0409	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	unclassified	140
Otu0410	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	139
Otu0411	Ascomycota	Pezizomycetes	Pezizales	Tuberaceae	Tuber	Tuber shearii	139

Otu0412	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	unclassified	unclassified	124
Otu0413	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungus sp 833 YZ 2011	133
Otu0414	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Byssocorticium	Byssocorticium atrovirens	139
Otu0415	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungus sp shylm91	140
Otu0416	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	unclassified	147
Otu0417	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	Trechispora sp	63
Otu0418	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula cessans	133
Otu0419	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	unclassified	152
Otu0420	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula aff sanguinea UC 1859522	135
Otu0421	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	132
Otu0422	Basidiomycota	Agaricomycetes	Boletales	Boletaceae	unclassified	unclassified	104
Otu0423	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	unclassified	96
Otu0424	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	Suillus cothurnatus	110
Otu0425	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	unclassified	118
Otu0426	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	unclassified	117
Otu0427	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	144
Otu0428	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	103
Otu0429	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	unclassified	140
Otu0430	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula laurocerasi	120
Otu0431	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	25
Otu0432	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	129
Otu0433	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	Inocybe sp TENN61398	126
Otu0434	Basidiomycota	Agaricomycetes	Polyporales	unclassified Polyporales	unclassified Polyporales	uncultured Polyporales	105
Otu0435	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	118
Otu0436	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	136
Otu0437	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	123
Otu0438	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	116
Otu0439	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	94

Otu0440	Basidiomycota	Wallemiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	unclassified	98
Otu0441	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	121
Otu0442	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	unclassified	unclassified	117
Otu0443	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactifluus	Lactifluus cf volemus 04 166	126
Otu0444	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	123
Otu0445	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	Inocybe rimosa	109
Otu0446	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	unclassified	111
Otu0447	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	Suillus cothurnatus	81
Otu0448	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	102
Otu0449	Ascomycota	Eurotiomycetes	Eurotiales	Elaphomycetaceae	Elaphomyces	Elaphomyces sp	96
Otu0450	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Gliophorus	Gliophorus unguinosus	113
Otu0451	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	107
Otu0452	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula aff sanguinea UC 1859522	103
Otu0453	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	Inocybe aff perlata TENN 062740	93
Otu0454	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Piloderma	Piloderma sp 5 RT 2012	128
Otu0455	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus	Agaricus sp F2389	118
Otu0456	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	105
Otu0457	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	81
Otu0458	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	87
Otu0459	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavulinopsis	Clavulinopsis corniculata	103
Otu0460	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified	unclassified	unclassified	106
Otu0461	Basidiomycota	Agaricomycetes	Gastrales	Geastraceae	Geastrum	Geastrum saccatum	90
Otu0462	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified	unclassified	101
Otu0463	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	89
Otu0464	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	Suillus cothurnatus	102
Otu0465	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	unclassified	105

Otu0466	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	85
Otu0467	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	91
Otu0468	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	102
Otu0469	Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	unclassified	unclassified	102
Otu0470	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	95
Otu0471	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	unclassified	101
Otu0472	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	78
Otu0473	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified	unclassified	92
Otu0474	Basidiomycota	Agaricomycetes	Agaricales	unclassified Agaricales	unclassified Agaricales	Agaricales sp	89
Otu0475	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	unclassified	88
Otu0476	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	93
Otu0477	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe pratensis var. pratensis	83
Otu0478	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	101
Otu0479	Basidiomycota	Agaricomycetes	Polyporales	unclassified Polyporales	unclassified Polyporales	uncultured ectomycorrhiza Polyporales	97
Otu0480	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	105
Otu0481	Ascomycota	Eurotiomycetes	Eurotiales	Elaphomycetaceae	Elaphomyces	Elaphomyces decipiens	84
Otu0482	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	80
Otu0483	Ascomycota	Pezizomycetes	Pezizales	Tuberaceae	unclassified	unclassified	95
Otu0484	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	100
Otu0485	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	Cortinarius semisanguineus	84
Otu0486	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	83
Otu0487	Basidiomycota	Agaricomycetes	Gomphales	Gomphaceae	Ramaria	unclassified	96
Otu0488	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	unclassified	90
Otu0489	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Tylospora	Tylospora sp	97
Otu0490	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	unclassified	96
Otu0491	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified	unclassified	unclassified	91

Otu0492	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	64
Otu0493	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	95
Otu0494	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrophorus	Hygrophorus hypothejus	106
Otu0495	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	Tomentella fibrosa	83
Otu0496	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	70
Otu0497	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	88
Otu0498	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Pseudotomentella	Pseudotomentella sp	106
Otu0499	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	114
Otu0500	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	92
Otu0501	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	81
Otu0502	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	unclassified	unclassified	88
Otu0503	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	82
Otu0504	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	81
Otu0505	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	unclassified	unclassified	96
Otu0506	Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	unclassified	unclassified	82
Otu0507	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	unclassified	unclassified	86
Otu0508	Ascomycota	Dothideomycetes	unclassified	unclassified	unclassified	unclassified	81
Otu0509	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	27
Otu0510	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	unclassified	81
Otu0511	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	87
Otu0512	Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	unclassified	94
Otu0513	Ascomycota	Eurotiomycetes	unclassified	unclassified	unclassified	unclassified	55
Otu0514	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	unclassified Clavariaceae	uncultured Clavulinopsis	88
Otu0515	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp shylm91	33
Otu0516	Ascomycota	Pezizomycetes	Pezizales	Pezizaceae	Peziza	Peziza sp RH1250	77
Otu0517	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	64
Otu0518	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	74
Otu0519	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	95
Otu0520	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus	Agaricus sp F2389	85

Otu0521	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	Inocybe cf splendens EL21906	80
Otu0522	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	87
Otu0523	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	79
Otu0524	Basidiomycota	Agaricomycetes	Agaricales	Entolomataceae	Entoloma	unclassified	78
Otu0525	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp shylm91	12
Otu0526	Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	Ascomycota sp 4 RB 2011	92
Otu0527	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Ramariopsis	Ramariopsis helvola	74
Otu0528	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	79
Otu0529	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	64
Otu0530	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	87
Otu0531	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Leucoagaricus	unclassified	77
Otu0532	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	81
Otu0533	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	unclassified	78
Otu0534	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified	unclassified	67
Otu0535	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	Inocybe mixtilis	85
Otu0536	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	84
Otu0537	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	82
Otu0538	Ascomycota	Eurotiomycetes	Eurotiales	unclassified	unclassified	unclassified	78
Otu0539	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavaria	Clavaria acuta	58
Otu0540	Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	Trichoderma hamatum	81
Otu0541	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	52
Otu0542	Zygomycota	Zygomycota class Incertae sedis	Mortierellales	unclassified	unclassified	unclassified	76
Otu0543	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified	unclassified	84
Otu0544	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Camarophyllus	Camarophyllus borealis	57
Otu0545	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	78
Otu0546	Basidiomycota	Agaricomycetes	Agaricales	Mycenaceae	Mycena	Mycena sp pink	74
Otu0547	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	78
Otu0548	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	84

Otu0549	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified	unclassified	unclassified	76
Otu0550	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula crustosa	68
Otu0551	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified	unclassified	unclassified	71
Otu0552	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	47
Otu0553	Ascomycota	Pezizomycetes	Pezizales	Tuberaceae	unclassified	unclassified	64
Otu0554	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	unclassified Atheliaceae	unclassified	68
Otu0555	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	unclassified Tricholomataceae	uncultured Mycena	84
Otu0556	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	Suillus cothurnatus	51
Otu0557	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified Chaetothyriales	unclassified Chaetothyriales	Chaetothyriales sp Pd X nig 7	79
Otu0558	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp shylm91	59
Otu0559	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Umbelopsidaceae	Umbelopsis	Umbelopsis dimorpha	67
Otu0560	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	Sebacina	Sebacina dimitica	80
Otu0561	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	76
Otu0562	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp shylm91	74
Otu0563	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	76
Otu0564	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	unclassified Atheliaceae	Atheliaceae sp	81
Otu0565	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	unclassified	61
Otu0566	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified	unclassified	77
Otu0567	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	unclassified	76
Otu0568	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified Chaetothyriales	unclassified Chaetothyriales	Chaetothyriales sp Pd X nig 7	56
Otu0569	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	75
Otu0570	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	74
Otu0571	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	73
Otu0572	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavaria	Clavaria acuta	76
Otu0573	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp shylm91	13
Otu0574	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	62

Otu0575	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	Suillus cothurnatus	71
Otu0576	Basidiomycota	Agaricomycetes	Polyporales	Meruliaceae	Hyphoderma	Peniophorella pallida	74
Otu0577	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactarius	unclassified	36
Otu0578	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified Sebacinaceae	Sebacinaceae sp	84
Otu0579	Ascomycota	Leotiomycetes	Geoglossales	Geoglossaceae	Glutinoglossum	Glutinoglossum glutinosum	65
Otu0580	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	unclassified	64
Otu0581	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	73
Otu0582	Ascomycota	Pezizomycetes	Pezizales	Tuberaceae	Tuber	Tuber separans	54
Otu0583	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	73
Otu0584	Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae	Pestalotiopsis	unclassified	77
Otu0585	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	51
Otu0586	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	61
Otu0587	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	63
Otu0589	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	44
Otu0590	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	unclassified Atheliaceae	unclassified	73
Otu0591	Basidiomycota	Agaricomycetes	Hysterangiales	Phallogastraceae	Protubera	Protubera canescens	72
Otu0592	Basidiomycota	Agaricomycetes	Agaricales	Bolbitiaceae	Conocybe	Conocybe gigasperma	63
Otu0593	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified	unclassified	73
Otu0594	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	unclassified	unclassified	74
Otu0595	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	62
Otu0596	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	70
Otu0597	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	Suillus cothurnatus	58
Otu0598	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	65
Otu0599	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	50
Otu0600	Basidiomycota	Agaricomycetes	Cantharellales	Clavulinaceae	unclassified	unclassified	70
Otu0601	Basidiomycota	Agaricomycetes	Agaricales	unclassified Agaricales	unclassified Agaricales	Agaricales sp	77
Otu0602	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	62

Otu0603	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	67
Otu0604	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	56
Otu0605	Ascomycota	Lecanoromycetes	Ostropales	Stictidaceae	Cryptodiscus	unclassified	46
Otu0606	Basidiomycota	Agaricomycetes	Agaricales	Entolomataceae	Entoloma	Entoloma sp SACHS	63
Otu0607	Ascomycota	Eurotiomycetes	Eurotiales	unclassified	unclassified	unclassified	59
Otu0608	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	61
Otu0609	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	unclassified	66
Otu0610	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified	unclassified	unclassified	52
Otu0611	Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	Agaricomycotina sp	68
Otu0613	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	59
Otu0614	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	unclassified	56
Otu0615	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	72
Otu0616	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	unclassified	unclassified	54
Otu0617	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	unclassified	29
Otu0618	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavulinopsis	Clavulinopsis luteoalba	62
Otu0619	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	59
Otu0620	Ascomycota	Pezizomycetes	Pezizales	Pezizaceae	Peziza	Peziza irina	68
Otu0621	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe conica	58
Otu0622	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	unclassified	unclassified	46
Otu0623	Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	ascomycete sp OB2C2	46
Otu0624	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	64
Otu0625	Basidiomycota	Wallemiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	unclassified	64
Otu0626	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Tylospora	Tylospora sp	62
Otu0627	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified	unclassified	unclassified	74
Otu0628	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	47
Otu0629	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	58
Otu0630	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	58
Otu0631	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	53
Otu0632	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	69

Otu0633	Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	Rhizopogon fuscorubens	52
Otu0634	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentellopsis	unclassified	63
Otu0635	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	Suillus cothurnatus	58
Otu0636	Basidiomycota	Agaricomycetes	Agaricales	Mycenaceae	Mycena	Mycena sp pink	60
Otu0637	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	41
Otu0638	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	51
Otu0639	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	unclassified	52
Otu0640	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	Tomentella stuposa	45
Otu0641	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	66
Otu0642	Ascomycota	Leotiomycetes	Geoglossales	Geoglossaceae	Geoglossum	unclassified	17
Otu0643	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	61
Otu0644	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Piloderma	Piloderma sp 5 RT 2012	63
Otu0645	Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	unclassified	unclassified	48
Otu0646	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	65
Otu0647	Ascomycota	Pezizomycetes	Pezizales	Tuberaceae	Tuber	Tuber separans	50
Otu0648	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	62
Otu0649	Basidiomycota	Agaricomycetes	Cantharellales	Hydnaceae	Sistotrema	Sistotrema sp	34
Otu0650	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	63
Otu0651	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	55
Otu0652	Basidiomycota	Agaricomycetes	Agaricales	Entolomataceae	Clitopilus	unclassified	65
Otu0653	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe aff coccinea	55
Otu0654	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	66
Otu0655	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	Amanita flavoconia	57
Otu0656	Basidiomycota	Agaricomycetes	Cantharellales	Clavulinaceae	unclassified	unclassified	55
Otu0657	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	unclassified Atheliaceae	unclassified	45
Otu0658	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Tylospora	Tylospora sp	45
Otu0659	Basidiomycota	Agaricomycetes	Agaricales	Mycenaceae	Mycena	Mycena pura	49
Otu0660	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	56
Otu0661	Ascomycota	Eurotiomycetes	unclassified	unclassified	unclassified	unclassified	58

Otu0662	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	55
Otu0663	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	Amanita solaniolens	53
Otu0664	Ascomycota	Pezizomycetes	Pezizales	unclassified	unclassified	unclassified	35
Otu0665	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	55
Otu0666	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula virescens	60
Otu0667	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavaria	Clavaria acuta	62
Otu0668	Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	unclassified	unclassified	67
Otu0669	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	49
Otu0670	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	53
Otu0671	Ascomycota	Pezizomycetes	Pezizales	Tuberaceae	Tuber	Tuber separans	69
Otu0672	Ascomycota	Eurotiomycetes	unclassified	unclassified	unclassified	unclassified	49
Otu0673	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	Inocybe rimosa	60
Otu0674	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactarius	Lactarius subplinthogalus	49
Otu0675	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	Tomentella fibrosa	56
Otu0676	Ascomycota	Pezizomycetes	Pezizales	Tuberaceae	Tuber	Tuber separans	52
Otu0677	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	52
Otu0678	Basidiomycota	Agaricomycetes	Cantharellales	Clavulinaceae	unclassified	unclassified	53
Otu0679	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	unclassified	26
Otu0680	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	unclassified	54
Otu0681	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	55
Otu0682	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified Sebacinaceae	Sebacinaceae sp	47
Otu0683	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Umbelopsidaceae	unclassified	unclassified	56
Otu0684	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Cunninghamellaceae	Cunninghamella	Cunninghamella elegans	46
Otu0685	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	unclassified	29
Otu0686	Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	Ascomycota sp 1 LX 2012	47
Otu0687	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Umbelopsidaceae	Umbelopsis	Umbelopsis sp	26

Otu0688	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	49
Otu0689	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	unclassified Atheliaceae	unclassified	47
Otu0690	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	unclassified	58
Otu0691	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	63
Otu0692	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	62
Otu0693	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	62
Otu0694	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	22
Otu0695	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	57
Otu0696	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula laurocerasi	46
Otu0697	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe cf conica	29
Otu0698	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	36
Otu0699	Ascomycota	Pezizomycetes	unclassified Pezizomycetes	unclassified Pezizomycetes	unclassified Pezizomycetes	Pezizomycetes sp genotype 528	47
Otu0700	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe aff coccinea	43
Otu0701	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	50
Otu0702	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	45
Otu0703	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	54
Otu0704	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	45
Otu0705	Basidiomycota	Microbotryomycetes	unclassified Microbotryomycetes	unclassified Microbotryomycetes	unclassified Microbotryomycetes	Microbotryomycetes sp	59
Otu0706	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	38
Otu0707	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	51
Otu0708	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	53
Otu0709	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	51
Otu0710	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	43
Otu0711	Basidiomycota	Agaricomycetes	Agaricales	Mycenaceae	Mycena	unclassified	48
Otu0712	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	60
Otu0713	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	59
Otu0714	Basidiomycota	Agaricomycetes	unclassified Agaricomycetes	unclassified Agaricomycetes	unclassified Agaricomycetes	Agaricomycetes sp	50

Otu0715	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	Tomentella punicea	53
Otu0716	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	55
Otu0717	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Neohygrocybe	Neohygrocybe ingrata	46
Otu0718	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified	unclassified	39
Otu0720	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	44
Otu0721	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	46
Otu0722	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	48
Otu0723	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	44
Otu0724	Basidiomycota	Agaricomycetes	Auriculariales	unclassified Auriculariales	unclassified Auriculariales	uncultured Auriculariales	51
Otu0725	Fungi phylum Incertae sedis	Fungi class Incertae sedis	Fungi order Incertae sedis	Fungi family Incertae sedis	Mallocybe	Mallocybe unicolor	16
Otu0726	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Cuphophyllus	Cuphophyllus flavipes	52
Otu0728	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	46
Otu0729	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	50
Otu0730	Basidiomycota	Agaricomycetes	Agaricales	Strophariaceae	Pholiota	Pholiota spumosa	56
Otu0731	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	Trechispora sp LISU178537	56
Otu0732	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	47
Otu0733	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	48
Otu0734	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	44
Otu0735	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	50
Otu0736	Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetales family Incertae sedis	Candida	unclassified	51
Otu0737	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified	unclassified	unclassified	49
Otu0738	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp ARIZ AZ0501
Otu0739	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactifluus	unclassified	11
Otu0740	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	40
Otu0741	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	54
Otu0742	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavaria	Clavaria acuta	40

Otu0743	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	45
Otu0744	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	48
Otu0745	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe laeta var. flava	53
Otu0746	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	41
Otu0747	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	46
Otu0748	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	46
Otu0749	Basidiomycota	Agaricomycetes	Geastrales	Geastraceae	Geastrum	unclassified	44
Otu0750	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	33
Otu0751	Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	Bionectria	Bionectria ochroleuca	40
Otu0752	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	48
Otu0753	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	41
Otu0754	Basidiomycota	Agaricomycetes	Auriculariales	unclassified Auriculariales	unclassified Auriculariales	uncultured Hyaloriaceae	35
Otu0755	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	48
Otu0756	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	41
Otu0757	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	48
Otu0758	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	31
Otu0759	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	43
Otu0760	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	51
Otu0761	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	28
Otu0762	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	39
Otu0763	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Camarophyllus	Camarophyllus borealis	53
Otu0764	Basidiomycota	Agaricomycetes	Agaricales	Mycenaceae	Xeromphalina	Xeromphalina sp	29
Otu0765	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	40
Otu0766	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	unclassified Atheliaceae	unclassified	50
Otu0767	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	42
Otu0768	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified Sebacinaceae	Sebacinaceae sp	28

Otu0769	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	39
Otu0770	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	47
Otu0771	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	40
Otu0772	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	42
Otu0773	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	Amanita brunnescens	42
Otu0774	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	46
Otu0775	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	41
Otu0776	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	47
Otu0777	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	36
Otu0778	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	unclassified Atheliaceae	unclassified	44
Otu0779	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	Suillus cothurnatus	39
Otu0780	Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	unclassified Orbiliaceae	uncultured Dactylella	38
Otu0781	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Umbelopsidaceae	Umbelopsis	unclassified	46
Otu0782	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	36
Otu0783	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	Thelephoraceae sp B110	40
Otu0784	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Lycoperdon	Lycoperdon ericaeum	37
Otu0785	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	46
Otu0786	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	40
Otu0787	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	29
Otu0788	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp ARIZ AZ0501	39
Otu0789	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	41
Otu0790	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	37
Otu0791	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	Thelephoraceae sp Ct 6	47
Otu0792	Basidiomycota	Agaricomycetes	Cantharellales	Clavulinaceae	unclassified	unclassified	34
Otu0793	Chytridiomycota	Chytridiomycetes	Spizellomycetales	Spizellomycetaceae	unclassified	unclassified	45

Otu0794	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	Cortinarius mucosus	43
Otu0795	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	22
Otu0796	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Tylospora	Tylospora sp	40
Otu0797	Basidiomycota	Agaricomycetes	Geastrales	Geastraceae	Geastrum	Geastrum sp TNS KH JPN10 626	35
Otu0798	Basidiomycota	Agaricomycetes	Auriculariales	unclassified Auriculariales	unclassified Auriculariales	uncultured Hyaloriaceae	36
Otu0799	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	unclassified Tricholomataceae	unclassified	30
Otu0800	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	17
Otu0801	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified	43
Otu0802	Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae	Pestalotiopsis	Pestalotiopsis mangiferae	35
Otu0803	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp ARIZ AZ0501	40
Otu0804	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	40
Otu0805	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	39
Otu0806	Ascomycota	Leotiomycetes	Geoglossales	Geoglossaceae	Geoglossum	Geoglossum sp	40
Otu0807	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	34
Otu0808	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	38
Otu0809	Basidiomycota	Agaricomycetes	Agaricales	Strophariaceae	Hebeloma	Hebeloma sacchariolens	26
Otu0810	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	Thelephoraceae sp H176	36
Otu0811	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Lycoperdon	Lycoperdon lambinonii	36
Otu0812	Basidiomycota	Tremellomycetes	Trichosporonales	Trichosporonaceae	Asterotremella	Asterotremella humicola	11
Otu0813	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Leucoagaricus	Leucoagaricus sp ECV 2010c	27
Otu0814	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	unclassified	36
Otu0815	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	Tomentella fibrosa	42
Otu0816	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	unclassified	34
Otu0817	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	38
Otu0818	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	42
Otu0819	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	44

Otu0820	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	47
Otu0821	Ascomycota	Pezizomycetes	Pezizales	Tuberaceae	unclassified	unclassified	38
Otu0822	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp shylm91	37
Otu0823	Basidiomycota	Agaricomycetes	Agaricomycetes order Incertae sedis	Agaricomycetes family Incertae sedis	Resinicium	Resinicium furfuraceum	25
Otu0825	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	25
Otu0826	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	26
Otu0827	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp shylm91	35
Otu0828	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	Inocybe calospora	48
Otu0830	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	unclassified Atheliaceae	unclassified	36
Otu0831	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula laurocerasi	35
Otu0832	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	42
Otu0833	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	42
Otu0834	Ascomycota	Pezizomycetes	Pezizales	Tuberaceae	Tuber	unclassified	30
Otu0835	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	unclassified	unclassified	41
Otu0837	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	35
Otu0838	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	14
Otu0839	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	40
Otu0840	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	31
Otu0841	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	unclassified	29
Otu0842	Basidiomycota	Agaricomycetes	Agaricales	Strophariaceae	Gymnopilus	unclassified	36
Otu0843	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	38
Otu0844	Basidiomycota	Agaricomycetes	Corticiales	Corticaceae	unclassified Corticaceae	unclassified	16
Otu0845	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	16
Otu0846	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	Cortinarius diasemospermus	31
Otu0847	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	unclassified	unclassified	39
Otu0848	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Cuphophyllus	Cuphophyllus lacmus	37
Otu0849	Ascomycota	Eurotiomycetes	Eurotiales	Elaphomycetaceae	Elaphomyces	unclassified	43

Otu0850	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	20
Otu0851	Ascomycota	Eurotiomycetes	unclassified	unclassified	unclassified	unclassified	32
Otu0852	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	unclassified Russulaceae	unclassified	17
Otu0853	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	39
Otu0854	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	38
Otu0855	Zygomycota	Zygomycota class Incertae sedis	Mortierellales	unclassified Mortierellales	unclassified Mortierellales	Mortierellales sp 03VT04	25
Otu0856	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	39
Otu0857	Ascomycota	Eurotiomycetes	Eurotiales	Elaphomycetaceae	Elaphomyces	unclassified	34
Otu0858	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	unclassified	unclassified	31
Otu0859	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	21
Otu0860	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	32
Otu0861	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified Sebacinaceae	unclassified	29
Otu0862	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	26
Otu0864	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	unclassified	31
Otu0865	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	Amanita flavoconia	40
Otu0866	Ascomycota	Sordariomycetes	unclassified Sordariomycetes	unclassified Sordariomycetes	unclassified Sordariomycetes	Sordariomycetes sp ODKB8	27
Otu0867	Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	unclassified	unclassified	35
Otu0868	Basidiomycota	Agaricomycetes	Agaricales	Mycenaceae	Mycena	unclassified	34
Otu0869	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	Trechispora sp LISU178537	32
Otu0870	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	41
Otu0871	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	38
Otu0872	Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	unclassified	unclassified	36
Otu0873	Basidiomycota	Tremellomycetes	Tremellales	Tremellales family Incertae sedis	Cryptococcus	Cryptococcus podzolicus	36
Otu0874	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	34
Otu0875	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	34
Otu0876	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	unclassified	14

Otu0877	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	27
Otu0878	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavulinopsis	Clavulinopsis corniculata	23
Otu0879	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	33
Otu0880	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe conica	33
Otu0881	Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	Metarhizium	Metarhizium sp	33
Otu0882	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	31
Otu0883	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	27
Otu0884	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	35
Otu0885	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	Inocybe rimosa	38
Otu0886	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	35
Otu0887	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	unclassified	20
Otu0888	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	Inocybe caesariata	13
Otu0891	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Camarophyllus	Camarophyllus borealis	28
Otu0892	Basidiomycota	Agaricomycetes	Cantharellales	Botryobasidiaceae	Botryobasidium	Botryobasidium sp	36
Otu0893	Basidiomycota	Agaricomycetes	Cantharellales	Clavulinaceae	Clavulina	Clavulina sp EMF53	32
Otu0894	Basidiomycota	Wallemiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	unclassified	38
Otu0895	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified Sebacinaceae	unclassified	31
Otu0896	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus	Agaricus subrutilescens	36
Otu0897	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	Glomus sp PB	37
Otu0898	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	unclassified	30
Otu0899	Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	unclassified	unclassified	35
Otu0900	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified	unclassified	unclassified	30
Otu0901	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	unclassified	34
Otu0902	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	33
Otu0903	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	28
Otu0904	Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	unclassified	unclassified	15
Otu0906	Basidiomycota	Tremellomycetes	Tremellales	Tremellales family Incertae sedis	Cryptococcus	Cryptococcus podzolicus	32
Otu0907	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	38

Otu0908	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	28
Otu0909	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	30
Otu0910	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	33
Otu0911	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	unclassified	34
Otu0912	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	34
Otu0913	Basidiomycota	Agaricomycetes	Auriculariales	unclassified Auriculariales	unclassified Auriculariales	uncultured Auriculariales	15
Otu0914	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	Russula densifolia	26
Otu0915	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	unclassified	unclassified	29
Otu0916	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	32
Otu0917	Chytridiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	29
Otu0918	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	37
Otu0919	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	30
Otu0920	Glomeromycota	unclassified	unclassified	unclassified	unclassified	unclassified	36
Otu0921	Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	unclassified	unclassified	31
Otu0922	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	unclassified	31
Otu0923	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	unclassified	31
Otu0924	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	33
Otu0925	Ascomycota	Dothideomycetes	Pleosporales	Mytilinidiaceae	unclassified Mytilinidiaceae	uncultured Lophium	26
Otu0926	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	unclassified	unclassified	35
Otu0927	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	unclassified	26
Otu0928	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	34
Otu0929	Ascomycota	Eurotiomycetes	Eurotiales	Elaphomycetaceae	Elaphomyces	Elaphomyces sp	30
Otu0930	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified Sebacinaceae	Sebacinaceae sp	29
Otu0931	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified	unclassified	35
Otu0932	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	25
Otu0933	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	37

Otu0934	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	22
Otu0936	Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	unclassified Pyronemataceae	uncultured Wilcoxina	36
Otu0938	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	33
Otu0939	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	20
Otu0940	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	31
Otu0941	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	18
Otu0942	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactarius	unclassified	16
Otu0943	Ascomycota	Pezizomycetes	Pezizales	Tuberaceae	unclassified	unclassified	33
Otu0944	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Tylospora	Tylospora sp	37
Otu0945	Ascomycota	Leotiomycetes	Geoglossales	Geoglossaceae	Geoglossum	unclassified	33
Otu0946	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	unclassified Atheliaceae	Atheliaceae sp	24
Otu0947	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavaria	Clavaria acuta	30
Otu0948	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified	unclassified	28
Otu0949	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	28
Otu0950	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	23
Otu0951	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified Chaetothyriales	unclassified Chaetothyriales	Chaetothyriales sp	29
Otu0952	Zygomycota	Zygomycota class Incertae sedis	Mortierellales	Mortierellaceae	Mortierella	unclassified	26
Otu0953	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Byssocortium	Byssocortium pulchrum	27
Otu0954	Basidiomycota	Agaricomycetes	Polyporales	unclassified Polyporales	unclassified Polyporales	uncultured Trechispora	20
Otu0955	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	Amanita longistriata	31
Otu0956	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	33
Otu0957	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	25
Otu0958	Basidiomycota	Tremellomycetes	Trichosporonales	Trichosporonaceae	Trichosporon	Trichosporon porosum	24
Otu0959	Basidiomycota	Agaricomycetes	Geastrales	Geastraceae	Sphaerobolus	Sphaerobolus stellatus	28
Otu0960	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	14
Otu0961	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	Inocybe agordina	32

Otu0962	Ascomycota	Pezizomycetes	unclassified Pezizomycetes	unclassified Pezizomycetes	unclassified Pezizomycetes	Pezizomycetes sp genotype 545	27
Otu0963	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	25
Otu0964	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	20
Otu0965	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavaria	Clavaria zollingeri	17
Otu0966	Glomeromycota	unclassified	unclassified	unclassified	unclassified	unclassified	22
Otu0967	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	27
Otu0968	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	unclassified Hygrophoraceae	uncultured Hygrophorus	26
Otu0969	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Cladophialophora	Cladophialophora potulentorum	25
Otu0970	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	unclassified	19
Otu0971	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified	unclassified	unclassified	19
Otu0972	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	21
Otu0973	Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	unclassified	unclassified	36
Otu0974	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	16
Otu0975	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	29
Otu0976	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	26
Otu0977	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	Suillus variegatus	24
Otu0978	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	Inocybe calospora	21
Otu0979	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	27
Otu0980	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	22
Otu0981	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	Cortinarius phoeniceus	18
Otu0983	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	23
Otu0984	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Callistosporium	unclassified	29
Otu0985	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	unclassified Atheliaceae	Atheliaceae sp	24
Otu0986	Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Xylaria	unclassified	27
Otu0987	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	26
Otu0988	Basidiomycota	Agaricomycetes	Boletales	unclassified	unclassified	unclassified	25
Otu0989	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Umbelopsidaceae	Umbelopsis	unclassified	27

Otu0990	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactifluus	unclassified	17
Otu0991	Basidiomycota	Agaricomycetes	Agaricales	unclassified Agaricales	unclassified Agaricales	Agaricales sp	33
Otu0992	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	25
Otu0993	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Leucoagaricus	Leucoagaricus jubilaei	37
Otu0994	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactifluus	Lactifluus oedematopus	28
Otu0995	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	33
Otu0996	Glomeromycota	unclassified	unclassified	unclassified	unclassified	unclassified	22
Otu0997	Basidiomycota	Wallemiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	unclassified	24
Otu0998	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	28
Otu0999	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	22
Otu1000	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	32
Otu1001	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	20
Otu1002	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	20
Otu1003	Ascomycota	Pezizomycetes	Pezizales	Tuberaceae	unclassified Tuberaceae	Tuberaceae sp	16
Otu1004	Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	Ascomycota sp 4 RB 2011	17
Otu1006	Basidiomycota	Agaricomycetes	Agaricales	Mycenaceae	Mycena	Mycena sp pink	26
Otu1007	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Cladophialophora	unclassified	27
Otu1008	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	23
Otu1009	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified Sebacinaceae	unclassified	25
Otu1010	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Epicoccum	Epicoccum nigrum	27
Otu1011	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	30
Otu1012	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	25
Otu1013	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	26
Otu1014	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	unclassified	24
Otu1015	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavaria	Clavaria vermicularis	20

Otu1016	Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	Ascomycota sp N067	20
Otu1017	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	26
Otu1018	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	30
Otu1019	Basidiomycota	Wallemiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	unclassified	20
Otu1020	Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetales family Incertae sedis	Candida	unclassified	15
Otu1021	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	20
Otu1022	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	27
Otu1023	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactarius	Lactarius subplinthogalus	18
Otu1024	Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	Rhizopogon fuscorubens	18
Otu1025	Zygomycota	Zygomycota class Incertae sedis	Mortierellales	unclassified Mortierellales	unclassified Mortierellales	Mortierellales sp	32
Otu1026	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentellopsis	Tomentellopsis zygoesmoides	23
Otu1027	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	Tomentella sublilacina	24
Otu1029	Basidiomycota	Agaricomycetes	Auriculariales	unclassified Auriculariales	unclassified Auriculariales	uncultured Hyaloriaceae	26
Otu1030	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	19
Otu1031	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	19
Otu1032	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	21
Otu1033	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	26
Otu1034	Basidiomycota	Wallemiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	unclassified	23
Otu1035	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	Trechispora sp LISU178537	15
Otu1036	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Umbelopsidaceae	Umbelopsis	Umbelopsis autotrophica	25
Otu1037	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	14
Otu1038	Ascomycota	Pezizomycetes	unclassified Pezizomycetes	unclassified Pezizomycetes	unclassified Pezizomycetes	unclassified	20
Otu1039	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	17
Otu1040	Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	unclassified Orbiliaceae	uncultured Dactylella	30

Otu1041	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	unclassified Atheliaceae	uncultured Atheliaceae	17
Otu1042	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	22
Otu1043	Ascomycota	Pezizomycetes	Pezizales	Pezizaceae	unclassified Pezizaceae	Pezizaceae sp	28
Otu1044	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	21
Otu1045	Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	unclassified	unclassified	16
Otu1046	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	20
Otu1047	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	unclassified	19
Otu1048	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	22
Otu1050	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified Chaetothyriales	unclassified Chaetothyriales	Chaetothyriales sp	20
Otu1051	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp shyln91	15
Otu1052	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp ARIZ AZ0501	28
Otu1053	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	19
Otu1054	Basidiomycota	Agaricomycetes	Agaricales	Mycenaceae	Mycena	Mycena epipterygia	25
Otu1055	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Tylospora	Tylospora sp	17
Otu1056	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	21
Otu1058	Basidiomycota	Agaricomycetes	Agaricales	Mycenaceae	Mycena	unclassified	16
Otu1059	Glomeromycota	unclassified	unclassified	unclassified	unclassified	unclassified	22
Otu1061	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	24
Otu1062	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	26
Otu1064	Ascomycota	Eurotiomycetes	Eurotiales	Elaphomycetaceae	unclassified Elaphomycetaceae	Elaphomycetaceae sp	20
Otu1065	Ascomycota	Leotiomycetes	Geoglossales	Geoglossaceae	Trichoglossum	unclassified	26
Otu1066	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp shyln91	18
Otu1067	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	21
Otu1068	Basidiomycota	Agaricomycetes	Agaricales	Mycenaceae	Mycena	Mycena sp pink	15
Otu1069	Basidiomycota	Agaricomycetes	Agaricales	Mycenaceae	Mycena	Mycena sp pink	22
Otu1070	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	14
Otu1071	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	24

Otu1072	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	30
Otu1073	Zygomycota	Zygomycota class Incertae sedis	Mucorales	unclassified Mucorales	unclassified Mucorales	uncultured Umbelopsis	24
Otu1074	Basidiomycota	Agaricomycetes	Agaricales	Entolomataceae	Entoloma	Entoloma sp SACHS	20
Otu1075	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	19
Otu1076	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavaria	Clavaria acuta	18
Otu1077	Ascomycota	Pezizomycetes	unclassified	unclassified	unclassified	unclassified	23
Otu1078	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	19
Otu1079	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	18
Otu1080	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe conica	24
Otu1081	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	25
Otu1082	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Cystodermella	Cystodermella granulosa	22
Otu1083	Ascomycota	Leotiomycetes	Geoglossales	Geoglossaceae	Geoglossum	unclassified	24
Otu1084	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	unclassified Atheliaceae	Atheliaceae sp	23
Otu1085	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	21
Otu1086	Basidiomycota	Agaricomycetes	Polyporales	unclassified Polyporales	unclassified Polyporales	uncultured Trechispora	22
Otu1087	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	15
Otu1088	Ascomycota	Pezizomycetes	unclassified	unclassified	unclassified	unclassified	21
Otu1089	Ascomycota	Leotiomycetes	Geoglossales	Geoglossaceae	Trichoglossum	Trichoglossum octopartitum	26
Otu1090	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	23
Otu1091	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	17
Otu1092	Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	unclassified	unclassified	18
Otu1093	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentellopsis	Tomentellopsis zygoesmoides	12
Otu1094	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	16
Otu1095	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	17
Otu1096	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	18
Otu1097	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	17
Otu1098	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	16

Otu1099	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	19
Otu1100	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	18
Otu1101	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	16
Otu1102	Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	unclassified	unclassified	24
Otu1103	Basidiomycota	Agaricomycetes	Cantharellales	Botryobasidiaceae	Botryobasidium	Botryobasidium botryosum	23
Otu1104	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	Tremellodendron	Tremellodendron pallidum	19
Otu1105	Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	uncultured Basidiomycota	22
Otu1106	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	17
Otu1107	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	Tomentella lilacinogrisea	24
Otu1108	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	26
Otu1109	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	19
Otu1110	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	18
Otu1111	Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	Ascomycota sp 1 LX 2012	24
Otu1112	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	19
Otu1113	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	unclassified	unclassified	20
Otu1114	Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	leotiomyces sp 2 RB 2011	22
Otu1115	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	21
Otu1116	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp shylm7	15
Otu1117	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	16
Otu1118	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Tylospora	Tylospora sp	19
Otu1119	Ascomycota	Eurotiomycetes	unclassified	unclassified	unclassified	unclassified	13
Otu1120	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	21
Otu1121	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	18
Otu1123	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	Trechispora sp LISU178537	17

Otu1124	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	21
Otu1126	Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	unclassified	unclassified	20
Otu1127	Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	Ascomycota sp 4 RB 2011	18
Otu1128	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	23
Otu1129	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	17
Otu1130	Ascomycota	Sordariomycetes	Sordariomycetes order Incertae sedis	Plectosphaerellaceae	Verticillium	unclassified	13
Otu1131	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinales Group B	unclassified Sebacinales Group B	Sebacinales Group B sp	21
Otu1132	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Amphinema	Amphinema sp GO 2009 307	22
Otu1133	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	26
Otu1134	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	unclassified	13
Otu1135	Glomeromycota	unclassified Glomeromycota	unclassified Glomeromycota	unclassified Glomeromycota	unclassified Glomeromycota	uncultured Glomeromycota	19
Otu1136	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Lepiota	Lepiota cf phaeosticta TN51705	22
Otu1137	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	22
Otu1138	Glomeromycota	unclassified	unclassified	unclassified	unclassified	unclassified	17
Otu1139	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	25
Otu1140	Ascomycota	Saccharomycetes	Saccharomycetales	unclassified	unclassified	unclassified	13
Otu1141	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	22
Otu1142	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	18
Otu1143	Basidiomycota	Agaricomycetes	Boletales	Boletaceae	Chalciporus	unclassified	20
Otu1144	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe conica	21
Otu1145	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	20
Otu1146	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	22
Otu1147	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	11
Otu1148	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	17
Otu1149	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	unclassified	14
Otu1150	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	11

Otu1151	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified Chaetothyriales	unclassified Chaetothyriales	unclassified	18
Otu1152	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	15
Otu1153	Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	Agaricomycotina sp	18
Otu1154	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	unclassified	16
Otu1155	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	19
Otu1156	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	15
Otu1157	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	16
Otu1158	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	19
Otu1159	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	20
Otu1160	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Cunninghamellaceae	Gongronella	Gongronella sp 11 KF 2011a	19
Otu1161	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	20
Otu1162	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	uncultured Thelephoraceae	17
Otu1164	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	19
Otu1165	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Tylospora	Tylospora sp	18
Otu1166	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	24
Otu1167	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	13
Otu1169	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	Amanita flavoconia	18
Otu1170	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	22
Otu1171	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	unclassified	24
Otu1172	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	21
Otu1173	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	19
Otu1174	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	15
Otu1175	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	unclassified	22
Otu1176	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	18
Otu1177	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	14
Otu1179	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	15
Otu1180	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified	unclassified	unclassified	16

Otu1181	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	18
Otu1182	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Leucoagaricus	Leucoagaricus sp Weber 6019	19
Otu1184	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	unclassified	20
Otu1186	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	23
Otu1187	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	17
Otu1189	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	18
Otu1190	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified	unclassified	14
Otu1191	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp mh32602	12
Otu1192	Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	Agaricomycotina sp	16
Otu1194	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	19
Otu1195	Glomeromycota	unclassified	unclassified	unclassified	unclassified	unclassified	23
Otu1197	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	12
Otu1198	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	20
Otu1199	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Byssocorticium	Byssocorticium caeruleum	16
Otu1200	Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	unclassified	unclassified	11
Otu1201	Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	Agaricomycotina sp	19
Otu1202	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	Cortinarius vernus	17
Otu1203	Basidiomycota	Agaricomycetes	Gomphales	Gomphaceae	Ramaria	Ramaria sp TENN61341	20
Otu1204	Ascomycota	Lecanoromycetes	Ostropales	Stictidaceae	Cryptodiscus	unclassified	15
Otu1205	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	16
Otu1206	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	Thelephoraceae sp H176	18
Otu1207	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Tylospora	Tylospora sp	24
Otu1208	Ascomycota	Pezizomycetes	Pezizales	Tuberaceae	Tuber	Tuber sp AMRH136	16
Otu1209	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactifluus	Lactarius bertillonii	20
Otu1210	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	18
Otu1211	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	13

Otu1212	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	13
Otu1213	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	Inocybe cf splendens EL21906	16
Otu1214	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	20
Otu1215	Ascomycota	Dothideomycetes	Pleosporales	Pleosporales family Incertae sedis	unclassified	unclassified	18
Otu1216	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp ARIZ AZ0501	14
Otu1217	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinales Group B	unclassified Sebacinales Group B	Sebacinales Group B sp	18
Otu1219	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	12
Otu1220	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	18
Otu1221	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	17
Otu1222	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified	unclassified	unclassified	16
Otu1223	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	15
Otu1225	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	16
Otu1227	Basidiomycota	Agaricomycetes	Agaricales	Entolomataceae	Entoloma	unclassified	15
Otu1228	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified	unclassified	19
Otu1229	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp ARIZ AZ0501	11
Otu1231	Basidiomycota	Agaricomycetes	Agaricales	Mycenaceae	unclassified	unclassified	13
Otu1233	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Tricholoma	unclassified	13
Otu1234	Basidiomycota	Agaricomycetes	Sebacinales	unclassified	unclassified	unclassified	12
Otu1235	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	unclassified	unclassified	18
Otu1236	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	unclassified	16
Otu1237	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	17
Otu1238	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	17
Otu1239	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified Sebacinaceae	Sebacinaceae sp	15
Otu1240	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	19
Otu1241	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	unclassified	unclassified	14
Otu1242	Basidiomycota	Agaricomycetes	Boletales	Sclerodermataceae	Pisolithus	Pisolithus tinctorius Marx 270	18
Otu1243	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	15

Otu1244	Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	Metacordyceps	Pochonia chlamydosporia var spinulospora	15
Otu1245	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	Suillus brevipes	12
Otu1246	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	unclassified Atheliaceae	Atheliaceae sp	16
Otu1247	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	17
Otu1248	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	15
Otu1249	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	18
Otu1250	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	17
Otu1251	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Umbelopsidaceae	Umbelopsis	Umbelopsis sp	18
Otu1252	Basidiomycota	Agaricomycetes	Auriculariales	unclassified Auriculariales	unclassified Auriculariales	uncultured Auriculariales	14
Otu1253	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	Basal lineages	20
Otu1254	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	16
Otu1256	Basidiomycota	Agaricomycetes	Corticiales	Corticaceae	unclassified Corticaceae	uncultured Hyphoderma	14
Otu1257	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	21
Otu1258	Ascomycota	Eurotiomycetes	Eurotiales	Elaphomycetaceae	Elaphomyces	Elaphomyces sp 1 RB 2011	12
Otu1259	Basidiomycota	Agaricomycetes	Atheliales	unclassified	unclassified	unclassified	18
Otu1261	Ascomycota	Leotiomycetes	Leotiales	Leotiaceae	Leotia	Leotia atrovirens	13
Otu1263	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	15
Otu1264	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	Basal lineages	17
Otu1265	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	16
Otu1266	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	17
Otu1268	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	unclassified	12
Otu1272	Ascomycota	Eurotiomycetes	Eurotiales	Elaphomycetaceae	Elaphomyces	Elaphomyces maculatus	17
Otu1273	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	14
Otu1275	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	Suillus cothurnatus	18
Otu1276	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	16

Otu1278	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	14
Otu1279	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	14
Otu1281	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	16
Otu1282	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	17
Otu1284	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	Glomus sp PB	13
Otu1285	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinales Group B	unclassified Sebacinales Group B	Sebacinales Group B sp	15
Otu1286	Basidiomycota	Agaricomycetes	Agaricales	Mycenaceae	Mycena	Mycena epipterygia	16
Otu1289	Basidiomycota	Wallemiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	unclassified	12
Otu1290	Basidiomycota	Agaricomycetes	Gomphales	Gomphaceae	Ramaria	unclassified	20
Otu1292	Ascomycota	Leotiomycetes	Geoglossales	Geoglossaceae	Geoglossum	Geoglossum sp	11
Otu1295	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	15
Otu1298	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	Glomus sp 1v12 1	12
Otu1299	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	14
Otu1300	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	16
Otu1301	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	18
Otu1302	Basidiomycota	Agaricomycetes	unclassified Agaricomycetes	unclassified Agaricomycetes	unclassified Agaricomycetes	uncultured Agaricomycetes	15
Otu1303	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Byssocorticium	Byssocorticium pulchrum	13
Otu1305	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	11
Otu1306	Ascomycota	Eurotiomycetes	unclassified	unclassified	unclassified	unclassified	14
Otu1307	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	Cortinarius ectypus	16
Otu1310	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	14
Otu1311	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	12
Otu1312	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	15
Otu1317	Basidiomycota	Agaricomycetes	Cantharellales	unclassified	unclassified	unclassified	19
Otu1319	Ascomycota	Pezizomycetes	unclassified Pezizomycetes	unclassified Pezizomycetes	unclassified Pezizomycetes	Pezizomycetes sp genotype 545	12
Otu1320	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	15
Otu1321	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Leucoagaricus	Leucoagaricus sp Weber 6019	12

Otu1322	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	15
Otu1323	Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	uncultured Basidiomycota	19
Otu1324	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Tricholoma	Tricholoma portentosum	12
Otu1325	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	15
Otu1326	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified	unclassified	11
Otu1327	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	12
Otu1328	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavaria	Clavaria acuta	14
Otu1329	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	14
Otu1331	Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	ascomycete sp OB2C2	12
Otu1332	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	15
Otu1333	Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae	Lecanicillium	Lecanicillium psalliotae	14
Otu1335	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	unclassified	17
Otu1337	Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Parasola	unclassified	14
Otu1338	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	13
Otu1339	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Neohygrocybe	Neohygrocybe ingrata	12
Otu1340	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	16
Otu1341	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	12
Otu1342	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	12
Otu1343	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	Amanita pantherina	13
Otu1345	Glomeromycota	unclassified	unclassified	unclassified	unclassified	unclassified	16
Otu1346	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	unclassified	unclassified	15
Otu1347	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	unclassified	17
Otu1348	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	12
Otu1352	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	14
Otu1353	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	13
Otu1354	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	14
Otu1355	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	20

Otu1357	Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Hypocrea	Hypocrea virens	13
Otu1359	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	12
Otu1360	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	Trechispora sp LISU178537	13
Otu1361	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	20
Otu1363	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Umbelopsidaceae	unclassified Umbelopsidaceae	Umbelopsidaceae sp	13
Otu1366	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	15
Otu1367	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	13
Otu1368	Basidiomycota	Agaricomycetes	Cantharellales	unclassified	unclassified	unclassified	17
Otu1369	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	12
Otu1370	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	11
Otu1371	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	unclassified Atheliaceae	Atheliaceae sp	16
Otu1372	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Leucoagaricus	Leucoagaricus fragilissimus	11
Otu1373	Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	Basidiomycota sp B360	11
Otu1377	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	13
Otu1379	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified Sebacinaceae	unclassified	16
Otu1380	Ascomycota	Pezizomycetes	Pezizales	Tuberaceae	unclassified	unclassified	12
Otu1381	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	12
Otu1384	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	11
Otu1386	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	12
Otu1388	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	uncultured Thelephoraceae	15
Otu1390	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Tretomyces	Tretomyces lutescens	14
Otu1391	Basidiomycota	Agaricomycetes	Sebacinales	unclassified	unclassified	unclassified	12
Otu1396	Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	unclassified	11
Otu1397	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Umbelopsidaceae	Umbelopsis	Umbelopsis ramanniana	16

Otu1398	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	20
Otu1399	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	14
Otu1400	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	12
Otu1402	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	15
Otu1405	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified Sebacinaceae	Sebacinaceae sp A	16
Otu1406	Basidiomycota	Wallemiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	unclassified	12
Otu1407	Ascomycota	Pezizomycetes	Pezizales	Pezizaceae	unclassified Pezizaceae	Pezizaceae sp	14
Otu1408	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	11
Otu1409	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	12
Otu1410	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	12
Otu1412	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Tylospora	Tylospora sp	16
Otu1413	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified	unclassified	unclassified	13
Otu1415	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	12
Otu1416	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	unclassified Herpotrichiellaceae	uncultured Cladophialophora	15
Otu1419	Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	unclassified Basidiomycota	Basidiomycota cf Tremellales OTU 033	12
Otu1420	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	11
Otu1421	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	uncultured soil fungus	12
Otu1422	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	unclassified	12
Otu1425	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	Tomentella sp	12
Otu1426	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	fungal sp ARIZ AZ0501	13
Otu1427	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentellopsis	unclassified	12
Otu1428	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	14
Otu1430	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	12
Otu1431	Basidiomycota	Agaricomycetes	Gomphales	Gomphaceae	Ramaria	Ramaria sp TENN61341	14
Otu1435	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	13
Otu1438	Ascomycota	Pezizomycetes	unclassified	unclassified	unclassified	unclassified	11

Otu1439	Basidiomycota	Agaricomycetes	Agaricales	unclassified Agaricales	unclassified Agaricales	Agaricales sp	15
Otu1441	Ascomycota	Eurotiomycetes	unclassified	unclassified	unclassified	unclassified	15
Otu1443	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	Penicillium montanense	13
Otu1446	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	unclassified	12
Otu1447	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	unclassified	11
Otu1449	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	11
Otu1454	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	14
Otu1456	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	14
Otu1460	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe	unclassified	12
Otu1461	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Callistosporium	unclassified	12
Otu1463	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	Basal lineages	11
Otu1465	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	11
Otu1468	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	unclassified	17
Otu1470	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	Glomus sp 1v12 1	15
Otu1471	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Tricholoma	unclassified	12
Otu1475	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	13
Otu1476	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified	12
Otu1478	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	13
Otu1479	Basidiomycota	Agaricomycetes	Auriculariales	unclassified Auriculariales	unclassified Auriculariales	uncultured Hyaloriaceae	13
Otu1480	Basidiomycota	Agaricomycetes	Agaricales	Agaricales family Incertae sedis	Camarophylloopsis	Camarophylloopsis sp SGT 2012	16
Otu1481	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	14
Otu1483	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Neohygrocybe	Neohygrocybe ingrata	12
Otu1486	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	unclassified	13
Otu1490	Zygomycota	Zygomycota class Incertae sedis	Mucorales	Cunninghamellaceae	Absidia	Absidia caerulea	12
Otu1492	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	12
Otu1493	Basidiomycota	Agaricomycetes	Agaricales	Hydnangiaceae	Laccaria	unclassified	11

Otu1495	Basidiomycota	Agaricomycetes	Cantharellales	Botryobasidiaceae	unclassified Botryobasidiaceae	Botryobasidiaceae sp	11
Otu1496	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	15
Otu1498	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	12
Otu1500	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	Trechispora alnicola	11
Otu1507	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe conica	14
Otu1510	Zygomycota	Zygomycota class Incertae sedis	Mortierellales	Mortierellaceae	Mortierella	Mortierella sp FSU 10557	13
Otu1513	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	13
Otu1514	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	14
Otu1515	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	Talaromyces proteolyticus	17
Otu1517	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified Thelephoraceae	uncultured Thelephoraceae	13
Otu1518	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	11
Otu1522	Basidiomycota	Agaricomycetes	Auriculariales	unclassified Auriculariales	unclassified Auriculariales	uncultured Hyaloriaceae	13
Otu1526	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	11
Otu1528	Basidiomycota	Wallemiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	unclassified	12
Otu1531	Basidiomycota	Agaricomycetes	Polyporales	Meruliaceae	Hypochnicium	Hypochnicium michelii	13
Otu1533	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	14
Otu1539	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	11
Otu1544	Basidiomycota	Agaricomycetes	Cantharellales	Botryobasidiaceae	Botryobasidium	unclassified	11
Otu1545	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	unclassified Fungi	Basal lineages	11
Otu1547	Ascomycota	Eurotiomycetes	Eurotiales	unclassified	unclassified	unclassified	12
Otu1551	Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	unclassified Ascomycota	leotiomyceta sp 2 RB 2011	12
Otu1562	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	unclassified Clavariaceae	uncultured Clavulinopsis	11
Otu1567	Basidiomycota	Agaricomycetes	Polyporales	Xenasmataceae	Xenasmatella	Xenasmatella sp	11
Otu1571	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	11
Otu1573	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified	12
Otu1575	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	11

Otu1577	Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	unclassified Pyronemataceae	uncultured Wilcoxina	14
Otu1582	Basidiomycota	Agaricomycetes	Agaricales	Mycenaceae	Mycena	Mycena pura	14
Otu1584	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	11
Otu1595	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavulinopsis	Clavulinopsis corniculata	16
Otu1611	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	12
Otu1622	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	11
Otu1632	Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	unclassified	unclassified	11
Otu1633	Ascomycota	Pezizomycetes	unclassified Pezizomycetes	unclassified Pezizomycetes	unclassified Pezizomycetes	Pezizomycetes sp genotype 545	14
Otu1640	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Clitocybe	Clitocybe pruinosa	13
Otu1659	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	11
Otu1662	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	12
Otu1683	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentellopsis	Tomentellopsis echinospora	14
Otu1704	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified	13
Otu1711	Chytridiomycota	Chytridiomycetes	Spizellomycetales	Spizellomycetaceae	Powellomyces	Powellomyces sp DAOM 226231	11
Otu1715	Basidiomycota	Agaricomycetes	Gomphales	Gomphaceae	unclassified Gomphaceae	uncultured Ramaria	11
Otu1728	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	11
Otu1734	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	11
Otu1738	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified	12
Otu1739	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	11
Otu1746	Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Psathyrella	Psathyrella tenuicula	11
Otu1760	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unclassified	unclassified	11
Otu1771	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactarius	unclassified	11
Otu1778	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	Tomentella sp	11
Otu1810	Ascomycota	Eurotiomycetes	Verrucariales	unclassified Verrucariales	unclassified Verrucariales	uncultured Verrucariales	12
Otu1819	Ascomycota	Pezizomycetes	Pezizales	Tuberaceae	Tuber	Tuber separans	11

Table B.3 Indicator species analysis found a total of 77 indicator OTUs that occurred more frequently in a given treatment compared to others. Here is a list of all indicator OTUs with their associated taxonomic information, associated ecological role, and percent of total sequences for each treatment.

Otu#	Treatment Indicator	p-value	Genus	Species	Ecological Role	Sequence Count	Total % Probability	Control % Mean \pm Std Dev	2W % Mean \pm Std Dev	3W % Mean \pm Std Dev	3S % Mean \pm Std Dev	6S % Mean \pm Std Dev
Control												
Otu0018	Control	0.0483	Trechispora	Trechispora sp	n/a	2212	0.634	0.085 \pm 0.07	0.008 \pm 0.011	0.018 \pm 0.047	0.019 \pm 0.035	0.01 \pm 0.017
Otu0036	Control	0.0301	unclassified Fungi	fungus sp	n/a	1874	0.537	0.085 \pm 0.065	0.016 \pm 0.029	0.005 \pm 0.009	0.002 \pm 0.001	0.021 \pm 0.038
Otu0064	Control	0.04	unclassified Fungi	fungus sp	n/a	1069	0.306	0.073 \pm 0.097	0.001 \pm 0.001	0.001 \pm 0.001	0 \pm 0	0.001 \pm 0.001
Otu0098	Control	0.0028	unclassified	unclassified	n/a	662	0.19	0.025 \pm 0.015	0.004 \pm 0.003	0.003 \pm 0.002	0.004 \pm 0.005	0.009 \pm 0.002
Otu0108	Control	0.0023	Russula	unclassified	ECM	712	0.204	0.028 \pm 0.005	0.002 \pm 0.002	0.003 \pm 0.003	0.006 \pm 0.009	0.01 \pm 0.008
Otu0112	Control	0.0045	Sistotrema	Sistotrema sp	ECM	617	0.177	0.018 \pm 0.011	0.003 \pm 0.003	0.006 \pm 0.004	0.006 \pm 0.005	0.005 \pm 0.003
Otu0142	Control	0.0223	Russula	unclassified	ECM	402	0.115	0.013 \pm 0.011	0.001 \pm 0.001	0.005 \pm 0.005	0.001 \pm 0.001	0.004 \pm 0.002
Otu0210	Control	0.0123	Geminibasidium	unclassified	n/a	303	0.087	0.016 \pm 0.016	0 \pm 0	0.001 \pm 0.001	0.001 \pm 0.001	0.003 \pm 0.006
Otu0218	Control	0.0105	Russula	Russula sp	ECM	315	0.09	0.014 \pm 0.007	0.001 \pm 0.002	0.001 \pm 0	0.004 \pm 0.007	0.002 \pm 0.002
Otu0221	Control	0.0271	unclassified Fungi	fungus sp	n/a	316	0.091	0.008 \pm 0.004	0.001 \pm 0.001	0.003 \pm 0.003	0.003 \pm 0.004	0.004 \pm 0.003
Otu0232	Control	0.0223	unclassified	unclassified	n/a	290	0.083	0.011 \pm 0.011	0.001 \pm 0.001	0.001 \pm 0.001	0.004 \pm 0.003	0.002 \pm 0.003
Otu0268	Control	0.0403	unclassified Atheliaceae	Atheliaceae sp	n/a	222	0.064	0.004 \pm 0.001	0.002 \pm 0.001	0.003 \pm 0.002	0.002 \pm 0.002	0.002 \pm 0.001
Otu0343	Control	0.0146	unclassified	unclassified	n/a	183	0.052	0.013 \pm 0.025	0 \pm 0	0 \pm 0	0 \pm 0	0 \pm 0

Otu0439	Control	0.0082	unclassified	unclassified	n/a	94	0.027	0.004 ± 0.002	0 ± 0	0 ± 0	0 ± 0	0.002 ± 0.002
Otu0686	Control	0.003	unclassified Ascomycota	Ascomycota sp	n/a	47	0.013	0.003 ± 0.003	0.001 ± 0.001	0 ± 0	0 ± 0	0 ± 0
Otu0729	Control	0.0109	unclassified	unclassified	n/a	50	0.014	0.002 ± 0.001	0.001 ± 0.001	0 ± 0	0 ± 0	0.001 ± 0.001
Otu0737	Control	0.0382	unclassified	unclassified	n/a	49	0.014	0.001 ± 0.001	0 ± 0.001	0 ± 0.001	0 ± 0	0.001 ± 0
Otu0790	Control	0.0065	unclassified	unclassified	n/a	37	0.011	0.002 ± 0.001	0 ± 0	0 ± 0	0 ± 0	0 ± 0.001
Otu0807	Control	0.0404	unclassified Verrucariales	uncultured Verrucariales	n/a	34	0.01	0.002 ± 0.004	0 ± 0	0 ± 0	0 ± 0	0 ± 0
Otu0835	Control	0.0409	unclassified	unclassified	n/a	41	0.012	0.002 ± 0.001	0 ± 0	0 ± 0	0.001 ± 0.001	0.001 ± 0.001
Otu0850	Control	0.0421	unclassified	unclassified	n/a	20	0.006	0.001 ± 0.001	0 ± 0	0 ± 0	0 ± 0	0 ± 0
Otu0984	Control	0.0317	Callistosporium	unclassified	n/a	29	0.008	0.001 ± 0.001	0 ± 0	0 ± 0.001	0 ± 0	0 ± 0
Otu0986	Control	0.0281	Xylaria	unclassified	saprobe	27	0.008	0.001 ± 0.001	0 ± 0	0 ± 0	0 ± 0	0.001 ± 0.001
Otu1139	Control	0.0036	unclassified	unclassified	n/a	25	0.007	0.001 ± 0.001	0 ± 0	0 ± 0.001	0 ± 0	0 ± 0
Otu1236	Control	0.0346	unclassified Thelephoraceae	unclassified	ECM	16	0.005	0.001 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
Otu1584	Control	0.0162	unclassified	unclassified	n/a	11	0.003	0.001 ± 0.001	0 ± 0	0 ± 0	0 ± 0	0 ± 0
2-year Winter												
Otu0165	2-year Winter	0.049	Clavulinopsis	Clavulinopsis luteoalba	n/a	427	0.122	0.001 ± 0.001	0.012 ± 0.007	0.005 ± 0.006	0.005 ± 0.006	0.003 ± 0.002
Otu0213	2-year Winter	0.0065	Clavulina	Clavulina sp	ECM	323	0.093	0 ± 0	0.019 ± 0.023	0.002 ± 0.003	0 ± 0	0 ± 0
Otu0233	2-year Winter	0.0358	Geastrum	Geastrum saccatum	n/a	292	0.084	0.001 ± 0	0.015 ± 0.025	0.001 ± 0.001	0.002 ± 0.001	0.001 ± 0.001
Otu0377	2-year Winter	0.0076	Suillus	Suillus cothurnatus	ECM	151	0.043	0 ± 0	0.005 ± 0.003	0.001 ± 0.001	0.002 ± 0.002	0.001 ± 0.001
Otu0401	2-year Winter	0.0441	unclassified Agaricomycetes	Agaricomycetes sp	n/a	152	0.044	0 ± 0	0.01 ± 0.02	0 ± 0	0 ± 0	0 ± 0
Otu0442	2-year Winter	0.0455	unclassified	unclassified	n/a	117	0.034	0 ± 0	0.007 ± 0.014	0 ± 0	0.001 ± 0.001	0 ± 0
Otu0501	2-year Winter	0.0228	unclassified	unclassified	n/a	81	0.023	0 ± 0	0.006 ± 0.01	0 ± 0	0 ± 0	0 ± 0

Otu0601	2-year Winter	0.0048	unclassified Agaricales	Agaricales sp	n/a	77	0.022	0 ± 0	0.003 ± 0.003	0.001 ± 0.001	0 ± 0	0 ± 0
Otu0714	2-year Winter	0.0069	unclassified Agaricomycetes	Agaricomycetes sp	n/a	50	0.014	0 ± 0	0.003 ± 0.005	0 ± 0	0 ± 0	0 ± 0
Otu0911	2-year Winter	0.0414	unclassified Thelephoraceae	unclassified	ECM	34	0.01	0 ± 0	0.002 ± 0.002	0 ± 0.001	0 ± 0	0 ± 0
Otu0938	2-year Winter	0.0231	unclassified Verrucariales	uncultured Verrucariales	n/a	33	0.009	0 ± 0	0.001 ± 0.002	0 ± 0	0 ± 0	0 ± 0
Otu0983	2-year Winter	0.0099	unclassified	unclassified	n/a	23	0.007	0 ± 0	0.001 ± 0.002	0 ± 0	0 ± 0	0 ± 0
Otu0991	2-year Winter	0.035	unclassified Agaricales	Agaricales sp	n/a	33	0.009	0 ± 0	0.002 ± 0.004	0 ± 0	0 ± 0	0 ± 0.001
Otu0992	2-year Winter	0.0216	unclassified	unclassified	n/a	25	0.007	0 ± 0	0.001 ± 0.001	0 ± 0	0 ± 0	0 ± 0
Otu1076	2-year Winter	0.01	Clavaria	Clavaria acuta	saprobe	18	0.005	0 ± 0	0.001 ± 0.001	0 ± 0	0 ± 0	0 ± 0
Otu1456	2-year Winter	0.032	unclassified	unclassified	n/a	14	0.004	0 ± 0	0.001 ± 0.001	0 ± 0	0 ± 0	0 ± 0
3-year Winter												
Otu0090	3-year Winter	0.0032	Amanita	Amanita pantherina	ECM	810	0.232	0.005 ± 0.005	0.007 ± 0.005	0.019 ± 0.011	0.006 ± 0.004	0.003 ± 0.002
Otu0132	3-year Winter	0.0229	unclassified Herpotrichiellaceae	Herpotrichiellaceae sp	n/a	508	0.146	0.005 ± 0.003	0.004 ± 0.003	0.01 ± 0.005	0.005 ± 0.002	0.003 ± 0.002
Otu0207	3-year Winter	0.0223	Umbelopsis	unclassified	n/a	297	0.085	0.001 ± 0.002	0.001 ± 0.001	0.007 ± 0.006	0.002 ± 0.003	0.002 ± 0.002
Otu0751	3-year Winter	0.0155	Bionectria	Bionectria ochroleuca	endophyte	40	0.011	0 ± 0	0 ± 0	0.001 ± 0.001	0 ± 0	0 ± 0.001
Otu0974	3-year Winter	0.0288	unclassified	unclassified	n/a	16	0.005	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
Otu0995	3-year Winter	0.0295	unclassified	unclassified	n/a	33	0.009	0 ± 0	0 ± 0	0.001 ± 0.003	0 ± 0	0 ± 0
Otu1018	3-year Winter	0.0281	unclassified	unclassified	ECM	30	0.009	0 ± 0	0 ± 0	0.001 ± 0.003	0 ± 0	0 ± 0
Otu1121	3-year Winter	0.0382	unclassified	unclassified	n/a	18	0.005	0 ± 0	0 ± 0	0.001 ± 0.001	0 ± 0	0 ± 0
Otu1221	3-year Winter	0.0306	unclassified	unclassified	n/a	17	0.005	0 ± 0	0 ± 0	0.001 ± 0.001	0 ± 0	0 ± 0
Otu1422	3-year Winter	0.0117	unclassified Thelephoraceae	unclassified	ECM	12	0.003	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
3-year Summer												

Otu0055	3-year Summer	0.0115	unclassified	unclassified	n/a	1121	0.321	0.003 ± 0.003	0.002 ± 0.001	0.016 ± 0.013	0.036 ± 0.032	0.008 ± 0.004
Otu0296	3-year Summer	0.0263	unclassified Verrucariales	uncultured Verrucariales	n/a	207	0.059	0 ± 0	0 ± 0	0 ± 0	0.014 ± 0.027	0 ± 0.001
Otu0400	3-year Summer	0.0267	Suillus	Suillus cothurnatus	ECM	155	0.044	0.001 ± 0.002	0 ± 0	0.002 ± 0.001	0.004 ± 0.003	0.002 ± 0.002
Otu0423	3-year Summer	0.0462	Suillus	unclassified	ECM	96	0.028	0.001 ± 0.001	0.001 ± 0	0.001 ± 0.001	0.002 ± 0.001	0.001 ± 0
Otu0629	3-year Summer	0.0345	unclassified	unclassified	n/a	58	0.017	0 ± 0	0 ± 0	0.001 ± 0	0.001 ± 0.001	0.001 ± 0.001
Otu0630	3-year Summer	0.0425	unclassified	unclassified	n/a	58	0.017	0 ± 0	0.001 ± 0	0.001 ± 0.001	0.002 ± 0.001	0 ± 0
Otu0759	3-year Summer	0.0196	unclassified	unclassified	n/a	43	0.012	0 ± 0	0 ± 0	0 ± 0	0.003 ± 0.006	0 ± 0
Otu1055	3-year Summer	0.0217	Tylospora	Tylospora sp	ECM	17	0.005	0 ± 0	0 ± 0	0 ± 0	0.001 ± 0.001	0 ± 0
Otu1431	3-year Summer	0.0486	Ramaria	Ramaria sp	n/a	14	0.004	0 ± 0	0 ± 0	0 ± 0	0.001 ± 0.001	0 ± 0
Otu1517	3-year Summer	0.0492	unclassified Thelephoraceae	uncultured Thelephoraceae	ECM	13	0.004	0 ± 0	0 ± 0	0 ± 0	0.001 ± 0.001	0 ± 0
Otu1611	3-year Summer	0.0218	unclassified Verrucariales	uncultured Verrucariales	n/a	12	0.003	0 ± 0	0 ± 0	0 ± 0	0.001 ± 0.001	0 ± 0
6-year Summer												
Otu0058	6-year Summer	0.0478	unclassified Ascomycota	Ascomycota sp	n/a	1196	0.343	0.004 ± 0.004	0.007 ± 0.01	0.006 ± 0.006	0.009 ± 0.013	0.053 ± 0.058
Otu0159	6-year Summer	0.021	unclassified Verrucariales	uncultured Verrucariales	n/a	450	0.129	0.006 ± 0.003	0.004 ± 0.004	0.003 ± 0.004	0.003 ± 0.003	0.013 ± 0.007
Otu0167	6-year Summer	0.0291	Tylospora	Tylospora sp	ECM	445	0.128	0.012 ± 0.01	0.001 ± 0.001	0.001 ± 0.001	0 ± 0	0.017 ± 0.008
Otu0322	6-year Summer	0.0061	Tricholoma	Tricholoma ulvinenii	ECM	193	0.055	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0.013 ± 0.026
Otu0445	6-year Summer	0.0139	Inocybe	Inocybe rimosa	ECM	109	0.031	0.002 ± 0.001	0.001 ± 0	0.001 ± 0.001	0.001 ± 0.001	0.003 ± 0.001
Otu0608	6-year Summer	0.0271	unclassified	unclassified	n/a	61	0.017	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0.004 ± 0.007
Otu0697	6-year Summer	0.041	Hygrocybe	Hygrocybe cf conica	n/a	29	0.008	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0.002 ± 0.004
Otu0700	6-year Summer	0.0486	Hygrocybe	Hygrocybe aff coccinea	n/a	43	0.012	0 ± 0.001	0 ± 0	0.001 ± 0.001	0.001 ± 0.001	0.001 ± 0.001
Otu0845	6-year Summer	0.0023	unclassified	unclassified	n/a	16	0.005	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0.001 ± 0

Otu0913	6-year Summer	0.0351	unclassified Auriculariales	uncultured Auriculariales	saprobe	15	0.004	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0.001 ± 0.001
Otu1065	6-year Summer	0.0403	Trichoglossum	unclassified	n/a	26	0.007	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0.002 ± 0.003
Otu1077	6-year Summer	0.0306	unclassified	unclassified	n/a	23	0.007	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0.001 ± 0.002
Otu1238	6-year Summer	0.0379	unclassified	unclassified	n/a	17	0.005	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0.001 ± 0.001
Otu1348	6-year Summer	0.0495	unclassified	unclassified	n/a	12	0.003	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0.001 ± 0.001

Appendix C- Supplemental Information for Chapter 3

Tables

Table C.1 Forward and reverse primer and DNA-tag sequences used for sample specific PCR and sample identification in 454-FLX Titanium amplicon library generated.

Forward primer	LROR	CCGCTGAACTTAAGCATAT
Reverse primer	LR3	CCGTGTTTCAAGACGGG
Barcode	Sample	
TCGATAGTGA	1_2w	
TCGCTGCGTA	2_3w	
TCTGACGTCA	3_C	
TGAGTCAGTA	4_6s	
TGTAGTGTGA	6_C	
TGTCACACGA	7_6s	
TGTCGTCGCA	8_3w	
ACACATACGC	9_3w	
CATACTCTAC	10_6s	
CGACACTATC	11_2w	
CGAGACGCGC	12_3w	
CGTATGCGAC	13_3w	
AGCTATCGCG	14_3s	
AGTCTGACTG	15_C	
AGTGAGCTCG	16_2w	
ATAGCTCTCG	17_3w	
ATCACGTGCG	18_3w	
ATCGTAGCAG	19_6s	
ATCGTCTGTG	21_C	
ATGTACGATG	22_2w	
ATGTGTCTAG	23_3w	
CACACGATAG	24_3w	

CACTCGCACG	25_3s
CAGACGTCTG	26_3s

Table C.2 A list of the genera present in the dataset after quality control and subsampling. Genera were assigned an ecological annotation which including the following ecologies: ecological groups: unclassified (UNC), unknown (UNK), saprobic (SAP), pathogenic (PAT), parasitic (PAR), entomopathogenic (ENT), arbuscular mycorrhizal (AM), and ECM. The number of sequences representing the genera present is also included (count).

Genus	ecology	Genus	Count
Acaulospora	AM	Acaulospora	4
Glomus	AM	Glomus	529
Albatrellus	ECM	Albatrellus	1
Amanita	ECM	Amanita	119
Amphinema	ECM	Amphinema	8
Boletellus	ECM	Boletellus	1
Chroogomphus	ECM	Chroogomphus	43
Clavulina	ECM	Clavulina	5
Coltricia	ECM	Coltricia	90
Cortinarius	ECM	Cortinarius	1
Craterellus	ECM	Craterellus	1
Descolea	ECM	Descolea	1
Gomphidius	ECM	Gomphidius	329
Hebeloma	ECM	Hebeloma	56
Hydnellum	ECM	Hydnellum	
Inocybe	ECM	Inocybe	81
Laccaria	ECM	Laccaria	
Lactarius	ECM	Lactarius	990
Piloderma	ECM	Piloderma	21
Pisolithus	ECM	Pisolithus	7
Quadrispora	ECM	Quadrispora	4
Rhizopogon	ECM	Rhizopogon	163
Russula	ECM	Russula	2463
Scleroderma	ECM	Scleroderma	24
Sebacina	ECM	Sebacina	10
Sebacinaceae	ECM	Sebacinaceae	1
Suillus	ECM	Suillus	121
Thaxterogaster	ECM	Thaxterogaster	
Thelephora	ECM	Thelephora	4
Tomentella	ECM	Tomentella	1184
Tomentellopsis	ECM	Tomentellopsis	2
Tremellodendron	ECM	Tremellodendron	8
Tricholoma	ECM	Tricholoma	135
Tuber	ECM	Tuber	236
Tylopilus	ECM	Tylopilus	16

Tylospora	ECM	Tylospora	72
uncultured_Amanitaceae	ECM	uncultured_Amanitaceae	397
uncultured_Cantharellaceae	ECM	uncultured_Cantharellaceae	521
uncultured_Russulaceae	ECM	uncultured_Russulaceae	2
uncultured_Sebacinaceae	ECM	uncultured_Sebacinaceae	20
uncultured_Thelephoraceae	ECM	uncultured_Thelephoraceae	315
Bensingtonia	ENT	Bensingtonia	14
Filobasidiella	PAR	Filobasidiella	1
Kriegeria	PAR	Kriegeria	207
Sclerotinia	PAR	Sclerotinia	6
Spiculogloea	PAR	Spiculogloea	1
Tremella	PAR	Tremella	1
Alternaria	PAT	Alternaria	13
Bionectria	PAT	Bionectria	21
Calonectria	PAT	Calonectria	129
Chalara	PAT	Chalara	48
Colletotrichum	PAT	Colletotrichum	109
Coniochaeta	PAT	Coniochaeta	341
Corynespora	PAT	Corynespora	7
Pestalotiopsis	PAT	Pestalotiopsis	157
Phomopsis	PAT	Phomopsis	2
Agaricus	SAP	Agaricus	1
Aphyllorphoralean	SAP	Aphyllorphoralean	3
Ascobolus	SAP	Ascobolus	3
Atractiella	SAP	Atractiella	1
Botryobasidium	SAP	Botryobasidium	1
Cerinomyces	SAP	Cerinomyces	7
Chaetomidium	SAP	Chaetomidium	52
Clathrus	SAP	Clathrus	2
Clavaria	SAP	Clavaria	10
Coprinellus	SAP	Coprinellus	1
Coriolopsis	SAP	Coriolopsis	1
Crepidotus	SAP	Crepidotus	6
Cudoniella	SAP	Cudoniella	487
Diplomitoporus	SAP	Diplomitoporus	
Endoperplexa	SAP	Endoperplexa	1
Flagelloscypha	SAP	Flagelloscypha	28
Gymnopilus	SAP	Gymnopilus	2
Gymnopus	SAP	Gymnopus	168
Henningsomyces	SAP	Henningsomyces	8
Heterochaete	SAP	Heterochaete	173
Kavinia	SAP	Kavinia	7
Lachnum	SAP	Lachnum	
Lagarobasidium	SAP	Lagarobasidium	2
Lophiostoma	SAP	Lophiostoma	
Lophiotrema	SAP	Lophiotrema	2
Lycoperdon	SAP	Lycoperdon	23
Mitrula	SAP	Mitrula	

Mycena	SAP	Mycena	392
Nolanea	SAP	Nolanea	10
Phaeodothis	SAP	Phaeodothis	2
Pluteus	SAP	Pluteus	2
Preussia	SAP	Preussia	3
Pseudohydnum	SAP	Pseudohydnum	
Pseudoomphalina	SAP	Pseudoomphalina	5
Pseudoplectania	SAP	Pseudoplectania	2
Ramariopsis	SAP	Ramariopsis	390
Ripartites	SAP	Ripartites	2
Serpula	SAP	Serpula	
Thelebolus	SAP	Thelebolus	
Trametes	SAP	Trametes	1
Vibrissea	SAP	Vibrissea	3112
Westerdykella	SAP	Westerdykella	2
Massariosphaeria	SAP/PAR	Massariosphaeria	1
Aulographina	UNC	Aulographina	1
Camarophylloopsis	UNC	Camarophylloopsis	4
Capnodiales_incertae_sedis	UNC	Capnodiales_incertae_sedis	1
Ceratobasidium	UNC	Ceratobasidium	1
Chytridium	UNC	Chytridium	56
Cladophialophora	UNC	Cladophialophora	232
Cosmospora	UNC	Cosmospora	
Cotylidia	UNC	Cotylidia	2
Didymella	UNC	Didymella	24
Elaphocordyceps	UNC	Elaphocordyceps	85
Eupenicillium	UNC	Eupenicillium	133
Fibulorhizoctonia	UNC	Fibulorhizoctonia	1
Gelasinospora	UNC	Gelasinospora	2
Guignardia	UNC	Guignardia	1
Gyromitra	UNC	Gyromitra	1
Hydropisphaera	UNC	Hydropisphaera	15
Hygrocybe	UNC	Hygrocybe	83
Hypocrea	UNC	Hypocrea	993
Lobulomyces	UNC	Lobulomyces	5
Lyophyllum	UNC	Lyophyllum	12
Malassezia	UNC	Malassezia	15
Metacordyceps	UNC	Metacordyceps	5
Micromphale	UNC	Micromphale	
Mutinus	UNC	Mutinus	1
Neurospora	UNC	Neurospora	
Penicillium	UNC	Penicillium	1
Peziza	UNC	Peziza	101
Phellinidium	UNC	Phellinidium	2
Phialophora	UNC	Phialophora	5074
Pholiota	UNC	Pholiota	21
Rhizophydium	UNC	Rhizophydium	31
Saccharomyces	UNC	Saccharomyces	22

Saccobolus	UNC	Saccobolus	
Schizothecium	UNC	Schizothecium	1
Spizellomyces	UNC	Spizellomyces	29
Urnula	UNC	Urnula	2
Amorphotheca	UNK	Amorphotheca	553
Amplistroma	UNK	Amplistroma	255
Anthostomella	UNK	Anthostomella	47
Anungitopsis	UNK	Anungitopsis	61
Aspergillus	UNK	Aspergillus	175
Asterotremella	UNK	Asterotremella	1
Atheliaceae	UNK	Atheliaceae	2
Boletinellus	UNK	Boletinellus	1
Capronia	UNK	Capronia	1
Caripia	UNK	Caripia	1
Carpoligna	UNK	Carpoligna	16
Catenomyces	UNK	Catenomyces	19
Chaetomella	UNK	Chaetomella	2
Chaetosphaeria	UNK	Chaetosphaeria	73
Chalciporus	UNK	Chalciporus	1
Cladosporium	UNK	Cladosporium	61
Classicula	UNK	Classicula	1
Clavulinopsis	UNK	Clavulinopsis	523
Columnosphaeria	UNK	Columnosphaeria	2
Coniochaetidium	UNK	Coniochaetidium	1
Conoplea	UNK	Conoplea	429
Cryptococcus	UNK	Cryptococcus	23
Cyphellophora	UNK	Cyphellophora	1
Cyrenella	UNK	Cyrenella	56
Devriesia	UNK	Devriesia	2
Diplodia	UNK	Diplodia	
Exophiala	UNK	Exophiala	13
Fibulobasidium	UNK	Fibulobasidium	8
Geastrum	UNK	Geastrum	165
Godronia	UNK	Godronia	1
Hamigera	UNK	Hamigera	11
Harknessia	UNK	Harknessia	2
Heimiomyces	UNK	Heimiomyces	1
Heleiosa	UNK	Heleiosa	2
Hilberina	UNK	Hilberina	19
Immersiella	UNK	Immersiella	4
Jaculispora	UNK	Jaculispora	3
Kappamyces	UNK	Kappamyces	17
Karlingiomyces	UNK	Karlingiomyces	
Kirschsteiniothelia	UNK	Kirschsteiniothelia	1
Lasiodiplodia	UNK	Lasiodiplodia	21
Lasiosphaeria	UNK	Lasiosphaeria	1
Laternea	UNK	Laternea	
Lentomitella	UNK	Lentomitella	8

Melanopsammella	UNK	Melanopsammella	378
Microdiplodia	UNK	Microdiplodia	1
Microthyrium	UNK	Microthyrium	3
Minimedusa	UNK	Minimedusa	2
Moesziomyces	UNK	Moesziomyces	1
Monoblepharella	UNK	Monoblepharella	1
Morchella	UNK	Morchella	5
Myxotrichum	UNK	Myxotrichum	125
Niesslia	UNK	Niesslia	2
Oedogoniomyces	UNK	Oedogoniomyces	5
Olpidium	UNK	Olpidium	1
Peyronellaea	UNK	Peyronellaea	1
Phlyctocytrium	UNK	Phlyctocytrium	1
Platygløea	UNK	Platygløea	1
Podochytrium	UNK	Podochytrium	1
Polyscytalum	UNK	Polyscytalum	13
Porothelium	UNK	Porothelium	5
Powellomyces	UNK	Powellomyces	22
Pseudoclitocybe	UNK	Pseudoclitocybe	2
Pseudozyma	UNK	Pseudozyma	
Pyrenochaeta	UNK	Pyrenochaeta	3
Rhinoclatiella	UNK	Rhinoclatiella	1
Rhizophlyctis	UNK	Rhizophlyctis	7
Rhopalogaster	UNK	Rhopalogaster	1
Sarcinomyces	UNK	Sarcinomyces	1
Sarcostroma	UNK	Sarcostroma	1
Scolecobasidiella	UNK	Scolecobasidiella	1
Sorocybe	UNK	Sorocybe	4
Synchytrium	UNK	Synchytrium	29
Tainosphaeria	UNK	Tainosphaeria	23
Tolypocladium	UNK	Tolypocladium	1
Torpedospora	UNK	Torpedospora	1
Toxicocladosporium	UNK	Toxicocladosporium	
Tricellulortus	UNK	Tricellulortus	
Triparticalcar	UNK	Triparticalcar	7
Troposporella	UNK	Troposporella	
Tsuchiyaea	UNK	Tsuchiyaea	308
unclassified	UNK	unclassified	3004
uncultured_Atheliaceae	UNK	uncultured_Atheliaceae	53
uncultured_Boletales_incertae_sedis	UNK	uncultured_Boletales_incertae_sedis	2
uncultured_Ceratobasidiaceae	UNK	uncultured_Ceratobasidiaceae	68
Valsaria	UNK	Valsaria	
Veronaea	UNK	Veronaea	6
Zygopleurage	UNK	Zygopleurage	2
Chromocleista	UNK	Chromocleista	11

Table C.3 A complete list of all 274 root-associated OTUs with their taxonomic associations and sequence counts.

OTU	Phylum	Class	Order	Family	Genus	Count
Otu001	Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	Phialophora	4954
Otu002	Ascomycota	Leotiomycetes	Helotiales	Vibrisseaceae	Vibrissea	2391
Otu003	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	2119
Otu004	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	1066
Otu005	Ascomycota	Sordariomycetes	Sordariales	Sordariaceae	unclassified	1202
Otu006	Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Hypocrea	973
Otu007	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	unclassified	856
Otu008	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactarius	511
Otu009	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	unclassified	542
Otu010	Basidiomycota	Agaricomycetes	Cantharellales	Cantharellaceae	uncultured_Cantharellaceae	517
Otu011	Ascomycota	Leotiomycetes	Helotiales	Vibrisseaceae	Vibrissea	659
Otu012	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactarius	419
Otu013	Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Cudoniella	478
Otu014	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	uncultured_Amanitaceae	386
Otu015	Ascomycota	Pezizomycetes	Pezizales	Sarcoscyphaceae	Conoplea	425
Otu016	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Mycena	338
Otu017	Ascomycota	Leotiomycetes	Leotiomycetes_incertae_sedis	Myxotrichaceae	Amorphotheca	370
Otu018	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavulinopsis	404
Otu019	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	415
Otu020	Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Melanopsammella	373
Otu021	Ascomycota	Sordariomycetes	Coniochaetales	Coniochaetaceae	Coniochaeta	337
Otu022	Basidiomycota	Tremellomycetes	Tremellales	Tremellaceae	Tsuchiyaea	293
Otu023	Basidiomycota	Agaricomycetes	Boletales	Gomphidiaceae	Gomphidius	326
Otu024	Basidiomycota	Agaricomycetes	Geastrales	Geastraceae	Geastrum	163
Otu025	Ascomycota	Sordariomycetes	Sordariomycetes_incertae_sedis	Amplistromataceae	Amplistroma	249
Otu026	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	uncultured_Thelephoraceae	302

Otu027	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Aspergillus	165
Otu028	Ascomycota	Pezizomycetes	Pezizales	Tuberaceae	Tuber	233
Otu029	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Gymnopus	167
Otu030	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Cladophialophora	218
Otu031	Ascomycota	Leotiomycetes	Leotiomycetes_incertae_sedis	Myxotrichaceae	Amorphotheca	174
Otu032	Basidiomycota	Agaricomycetes	Auriculariales	Exidiaceae	Heterochaete	173
Otu033	Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae	Pestalotiopsis	155
Otu034	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Calonectria	129
Otu035	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	260
Otu036	Ascomycota	Pezizomycetes	Pezizales	Pezizaceae	Peziza	99
Otu037	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Ramariopsis	143
Otu038	Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	121
Otu039	Basidiomycota	Microbotryomycetes	Microbotryomycetes_incertae_sedis	Microbotryomycetes_incertae_sedis	Kriegeria	128
Otu040	Basidiomycota	Agaricomycetes	Cantharellales	Clavulinaceae	unclassified	136
Otu041	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	106
Otu042	Ascomycota	Leotiomycetes	Leotiomycetes_incertae_sedis	Myxotrichaceae	Myxotrichum	118
Otu043	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Tricholoma	131
Otu044	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	113
Otu045	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	98
Otu046	Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	unclassified	118
Otu047	Basidiomycota	Agaricomycetes	Hymenochaetales	Hymenochaetaceae	Coltricia	87
Otu048	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavulinopsis	106
Otu049	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Eupenicillium	93
Otu050	Ascomycota	Dothideomycetes	Capnodiales	Davidiellaceae	Cladosporium	60
Otu051	Ascomycota	Sordariomycetes	Sordariomycetes_incertae_sedis	Glomerellaceae	Colletotrichum	104
Otu052	Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae	Elaphocordyceps	82
Otu053	Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Chaetomidium	51
Otu054	Ascomycota	Ascomycota_incertae_sedis	Ascomycota_incertae_sedis	Ascomycota_incertae_sedis	Anungitopsis	60
Otu055	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Ramariopsis	68

Otu056	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Ramariopsis	50
Otu057	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Ramariopsis	66
Otu058	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	83
Otu059	Basidiomycota	Cystobasidiomycetes	Cystobasidiomycetes_incertae_sedis	Cystobasidiomycetes_incertae_sedis	Cyrenella	53
Otu060	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	28
Otu061	Ascomycota	Leotiomycetes	Helotiales	Helotiales_incertae_sedis	Chalara	48
Otu062	Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	uncultured_Ceratobasidiaceae	67
Otu063	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Tylospora	65
Otu064	Ascomycota	Dothideomycetes	Capnodiales	unclassified	unclassified	45
Otu065	Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Chaetosphaeria	32
Otu066	Basidiomycota	Agaricomycetes	Boletales	Gomphidiaceae	Chroogomphus	43
Otu067	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Hebeloma	56
Otu068	Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Anthostomella	46
Otu069	Chytridiomycota	Chytridiomycetes	Chytridiales	Chytridiaceae	Chytridium	36
Otu070	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Mycena	35
Otu071	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	uncultured_Atheliaceae	34
Otu072	Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Didymella	24
Otu073	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	42
Otu074	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Inocybe	55
Otu075	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactarius	22
Otu076	Ascomycota	Sordariomycetes	Sordariomycetes_incertae_sedis	Sordariomycetes_incertae_sedis	Hilberina	19
Otu077	Basidiomycota	Microbotryomycetes	Microbotryomycetes_incertae_sedis	Microbotryomycetes_incertae_sedis	Kriegeria	38
Otu078	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Eupenicillium	24
Otu079	Chytridiomycota	Chytridiomycetes	Spizellomycetales	Spizellomycetaceae	Spizellomyces	22
Otu080	Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	Phialophora	33
Otu081	Ascomycota	Dothideomycetes	Pleosporales	Melanommataceae	unclassified	27
Otu082	Basidiomycota	Agaricomycetes	Agaricales	Lycoperdaceae	Lycoperdon	21

Otu083	Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetaceae	Saccharomyces	21
Otu084	Ascomycota	Leotiomycetes	Helotiales	Vibrissaceae	Vibrissea	18
Otu085	Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Tainosphaeria	23
Otu086	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Ramariopsis	36
Otu087	Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Chaetosphaeria	27
Otu088	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Flagelloscypha	27
Otu089	Ascomycota	Dothideomycetes	Botryosphaeriales	Botryosphaeriaceae	Lasiodiplodia	21
Otu090	Basidiomycota	Microbotryomycetes	Microbotryomycetes_incertae_sedis	Microbotryomycetes_incertae_sedis	Kriegeria	36
Otu091	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	22
Otu092	Basidiomycota	Agaricomycetes	Boletales	Sclerodermataceae	Scleroderma	24
Otu093	Basidiomycota	Agaricostilbomycetes	Agaricostilbales	Agaricostilbaceae	Bensingtonia	14
Otu094	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Hamigera	9
Otu095	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	uncultured_Thelephoraceae	10
Otu096	Basidiomycota	Agaricomycetes	Boletales	Boletaceae	Tylopilus	16
Otu097	Chytridiomycota	Chytridiomycetes	Chytridiales	Synchytriaceae	Synchytrium	16
Otu098	Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	Bionectria	20
Otu099	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria	13
Otu100	Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	unclassified	11
Otu101	Chytridiomycota	Chytridiomycetes	Rhizophydiales	Rhizophydiaceae	Rhizophydium	17
Otu102	Basidiomycota	Agaricomycetes	Agaricales	Entolomataceae	Nolanea	10
Otu103	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactarius	25
Otu104	Basidiomycota	Exobasidiomycetes	Malasseziales	Malasseziaceae	Malassezia	12
Otu105	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Piloderma	9
Otu106	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Ramariopsis	19
Otu107	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Eupenicillium	15
Otu108	Basidiomycota	Tremellomycetes	Tremellales	Tremellaceae	Cryptococcus	21
Otu109	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Inocybe	18
Otu110	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	11

Otu111	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	uncultured_Sebacinaceae	14
Otu112	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Lyophyllum	12
Otu113	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	uncultured_Atheliaceae	15
Otu114	Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	Phialophora	8
Otu115	Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Carpoligna	15
Otu116	Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Chaetosphaeria	7
Otu117	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Exophiala	11
Otu118	Basidiomycota	Agaricomycetes	Agaricales	Strophariaceae	Pholiota	21
Otu119	Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	Hydropisphaera	14
Otu120	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Mycena	12
Otu121	Ascomycota	Pezizomycetes	Pezizales	Sarcosomataceae	Pseudoplectania	2
Otu122	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	unclassified	12
Otu123	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Amphinema	8
Otu124	Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	7
Otu125	Ascomycota	Sordariomycetes	Sordariomycetes_incertae_sedis	Sordariomycetes_incertae_sedis	Polyscytalum	13
Otu126	Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	Metacordyceps	5
Otu127	Chytridiomycota	Chytridiomycetes	Chytridiales	Chytridiaceae	Chytridium	9
Otu128	Ascomycota	Leotiomycetes	Helotiales	Sclerotiniaceae	Sclerotinia	6
Otu129	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	5
Otu130	Blastocladiomycota	Blastocladiomycetes	Blastocladales	Catenariaceae	Catenomyces	8
Otu131	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	11
Otu132	Chytridiomycota	Chytridiomycetes	Spizellomycetales	Olpidiaceae	Powellomyces	8
Otu133	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	4
Otu134	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Piloderma	11
Otu135	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Aspergillus	7
Otu136	Basidiomycota	Tremellomycetes	Tremellales	Tremellaceae	Tsuchiyaea	7
Otu137	Ascomycota	Pezizomycetes	Pezizales	Morchellaceae	Morchella	4
Otu138	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Tricholoma	3

Otu139	Chytridiomycota	Chytridiomycetes	Chytridiales	Synchytriaceae	Synchytrium	7
Otu140	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	Tremellogendron	8
Otu141	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Cladophialophora	5
Otu142	Basidiomycota	Agaricomycetes	Agaricales	Schizophyllaceae	Porothelium	5
Otu143	Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	6
Otu144	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavulinopsis	6
Otu145	Chytridiomycota	Chytridiomycetes	Rhizophydiales	Kappamycetaceae	Kappamyces	3
Otu146	Ascomycota	Leotiomycetes	Leotiomycetes_incertae_sedis	Myxotrichaceae	Myxotrichum	5
Otu147	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	uncultured_Sebacinaceae	6
Otu148	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Cladophialophora	4
Otu149	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	7
Otu150	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	7
Otu151	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	6
Otu152	Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Chaetosphaeria	6
Otu153	Basidiomycota	Tremellomycetes	Tremellales	Sirobasidiaceae	Fibulobasidium	8
Otu154	Chytridiomycota	Chytridiomycetes	Spizellomycetales	Spizellomycetaceae	Spizellomyces	6
Otu155	Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_incertae_sedis	Corynespora	6
Otu156	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavaria	6
Otu157	Chytridiomycota	Chytridiomycetes	Spizellomycetales	Olpidiaceae	Powellomyces	5
Otu158	Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Immersiella	4
Otu159	Basidiomycota	Agaricomycetes	Agaricales	Schizophyllaceae	Henningsomyces	6
Otu160	Basidiomycota	Agaricomycetes	Geastrales	Geastraceae	unclassified	8
Otu161	Chytridiomycota	Chytridiomycetes	Rhizophydiales	Kappamycetaceae	Kappamyces	7
Otu162	Basidiomycota	Agaricomycetes	Gomphales	Gomphaceae	Kavinia	6
Otu163	Basidiomycota	Exobasidiomycetes	Malasseziales	Malasseziaceae	Malassezia	3
Otu164	Ascomycota	Sordariomycetes	Sordariomycetes_incertae_sedis	Sordariomycetes_incertae_sedis	Lentomitella	6

Otu165	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Chromocleista	6
Otu166	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	Sebacina	6
Otu167	Ascomycota	Leotiomycetes	Helotiales	Vibrissaceae	Vibrissea	5
Otu168	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Thelephora	4
Otu169	Ascomycota	Pezizomycetes	Pezizales	Ascobolaceae	Ascobolus	3
Otu170	Blastocladiomycota	Blastocladiomycetes	Blastocladales	Catenariaceae	Catenomyces	7
Otu171	Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	Phialophora	3
Otu172	Basidiomycota	Agaricomycetes	Boletales	unclassified	unclassified	4
Otu173	Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	8
Otu174	Chytridiomycota	Chytridiomycetes	Spizellomycetales	Spizellomycetaceae	Triparticalcar	4
Otu175	Basidiomycota	Agaricomycetes	Boletales	Pisolithaceae	Pisolithus	7
Otu176	Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Hypocrea	4
Otu177	Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	6
Otu178	Ascomycota	Dothideomycetes	Pleosporales	unclassified	unclassified	2
Otu179	Basidiomycota	Agaricomycetes	Agaricales	Crepidotaceae	Crepidotus	6
Otu180	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Camarophyllopsis	4
Otu181	Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	5
Otu182	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	4
Otu183	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Veronaea	3
Otu184	Chytridiomycota	Chytridiomycetes	Rhizophydiales	Rhizophydiaceae	Rhizophydium	6
Otu185	Chytridiomycota	Monoblepharidomycetes	Monoblepharidales	Oedogoniomycetaceae	Oedogoniomyces	5
Otu186	Chytridiomycota	Chytridiomycetes	Spizellomycetales	Spizellomycetaceae	Rhizophlyctis	6
Otu187	Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	5
Otu188	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Sorocybe	3
Otu189	Ascomycota	Dothideomycetes	Microthyriales	Microthyriaceae	Microthyrium	2
Otu191	Chytridiomycota	Chytridiomycetes	Lobulomycetales	Lobulomycetaceae	Lobulomyces	3
Otu192	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	uncultured_Amanitaceae	3

Otu193	Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae	Elaphocordyceps	3
Otu194	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Pyrenochaeta	3
Otu195	Chytridiomycota	Chytridiomycetes	Spizellomycetales	Olpidiaceae	Powellomyces	4
Otu197	Ascomycota	Sordariomycetes	Coniochaetales	Coniochaetaceae	Coniochaeta	2
Otu198	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	3
Otu199	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Ramariopsis	3
Otu200	Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	Phialophora	4
Otu203	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	5
Otu204	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Pseudoomphalina	4
Otu206	Basidiomycota	Cystobasidiomycetes	Cystobasidiomycetes_incertain_sedis	Cystobasidiomycetes_incertain_sedis	Cyrenella	3
Otu207	Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	Phialophora	2
Otu210	Ascomycota	Sordariomycetes	Sordariomycetes_incertain_sedis	Glomerellaceae	Colletotrichum	4
Otu211	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	4
Otu212	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	unclassified	4
Otu213	Basidiomycota	Agaricomycetes	Cantharellales	Cantharellales_incertain_sedis	Minimedusa	2
Otu216	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Gymnopilus	2
Otu217	Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	Phialophora	2
Otu218	Ascomycota	Leotiomycetes	Helotiales	Helotiales_incertain_sedis	Chaetomella	2
Otu220	Basidiomycota	Agaricomycetes	Hymenochaetales	Hymenochaetaceae	Coltricia	2
Otu222	Chytridiomycota	Chytridiomycetes	Spizellomycetales	Olpidiaceae	Powellomyces	4
Otu223	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	4
Otu224	Basidiomycota	Ustilaginomycetes	Ustilaginales	Ustilaginaceae	unclassified	3
Otu225	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	Sebacina	3
Otu227	Chytridiomycota	Chytridiomycetes	Rhizophydiales	Kappamycetaceae	Kappamyces	3
Otu228	Basidiomycota	Agaricomycetes	Polyporales	Polyporales_incertain_sedis	Aphyllorphoralean	3
Otu229	Basidiomycota	Classiculomycetes	Classiculales	Classiculaceae	Jaculispora	2
Otu230	Basidiomycota	Microbotryomycetes	Microbotryomycetes_incertain_sedis	Microbotryomycetes_incertain_sedis	Kriegeria	2

Otu231	Ascomycota	Pezizomycetes	Pezizales	Sarcosomataceae	Urnula	2
Otu232	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavaria	2
Otu234	Basidiomycota	Dacrymycetes	Dacrymycetales	Cerinomycetaceae	Cerinomyces	4
Otu236	Chytridiomycota	Chytridiomycetes	Rhizophydiales	Rhizophydiaceae	Rhizophydium	2
Otu237	Basidiomycota	Dacrymycetes	Dacrymycetales	Cerinomycetaceae	Cerinomyces	3
Otu238	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	3
Otu240	Chytridiomycota	Chytridiomycetes	Chytridiales	Chytridiaceae	Chytridium	3
Otu241	Basidiomycota	Agaricomycetes	Cantharellales	Clavulinaceae	Clavulina	4
Otu242	Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia	3
Otu244	Glomeromycota	Glomeromycetes	Diversisporales	Acaulosporaceae	Acaulospora	2
Otu246	Chytridiomycota	Chytridiomycetes	Rhizophydiales	Rhizophydiaceae	Rhizophydium	3
Otu247	Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Westerdykella	2
Otu248	Ascomycota	Leotiomycetes	Leotiomycetes_incertae_sedis	Myxotrichaceae	Amorphotheca	3
Otu249	Basidiomycota	Agaricomycetes	Boletales	Boletales_incertae_sedis	uncultured_Boletales_incertae_sedis	2
Otu250	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavaria	2
Otu253	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	unclassified	2
Otu256	Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Melanopsammella	2
Otu258	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	2
Otu260	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	3
Otu261	Chytridiomycota	Chytridiomycetes	Rhizophydiales	Kappamycetaceae	Kappamyces	2
Otu263	Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	Phialophora	3
Otu264	Blastocladiomycota	Blastocladiomycetes	Blastocladales	Catenariaceae	Catenomyces	2
Otu266	Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_incertae_sedis	Lophiotrema	2
Otu273	Chytridiomycota	Chytridiomycetes	Chytridiales	Synchytriaceae	Synchytrium	2
Otu275	Basidiomycota	Agaricomycetes	Phallales	Clathraceae	Clathrus	2
Otu276	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	2

Otu277	Basidiomycota	Agaricomycetes	Hymenochaetales	Schizoporaceae	Lagarobasidium	2
Otu279	Chytridiomycota	Chytridiomycetes	Spizellomycetales	Spizellomycetaceae	Triparticalcar	2
Otu280	Basidiomycota	Agaricomycetes	Agaricales	Lycoperdaceae	Lycoperdon	2
Otu284	Basidiomycota	Agaricomycetes	Russulales	Podoscyphaceae	Cotylidia	2
Otu285	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	2
Otu286	Basidiomycota	Tremellomycetes	Tremellales	Tremellaceae	Cryptococcus	2
Otu287	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Pseudoclitocybe	2
Otu288	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Veronaea	2
Otu290	Ascomycota	Sordariomycetes	Sordariomycetes_incertae_sedis	Amplistromataceae	Amplistroma	2
Otu291	Basidiomycota	Agaricomycetes	Agaricales	Schizophyllaceae	Henningsomyces	2
Otu292	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Quadrispora	2
Otu294	Ascomycota	Sordariomycetes	Diaporthales	Diaporthales_incertae_sedis	Harknessia	2
Otu297	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	2
Otu301	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Inocybe	2
Otu304	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	uncultured_Atheliaceae	2
Otu306	Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	Phialophora	2
Otu314	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Hamigera	2
Otu315	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Chromocleista	2
Otu318	Ascomycota	Sordariomycetes	Hypocreales	Niessliaceae	Niesslia	2
Otu321	Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Phaeodothis	2
Otu327	Basidiomycota	Agaricomycetes	Agaricales	Pluteaceae	Pluteus	2
Otu328	Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Zygopleurage	2
Otu329	Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	Phialophora	2
Otu332	Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	Phialophora	2
Otu333	Ascomycota	Sordariomycetes	Sordariomycetes_incertae_sedis	Sordariomycetes_incertae_sedis	Lentomitella	2
Otu337	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Ripartites	2
Otu338	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	unclassified	2
Otu340	Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	Phialophora	2

Otu343	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentellopsis	2
Otu345	Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Hypocrea	2

Figure C.4 A complete list of the 45 OTUs with their taxonomic associations and sequence counts determined to be ECM taxon by ecological annotations.

ECM OTUs	Phylum	Class	Order	Family	Genus	Count
Otu003	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	1465
Otu004	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	802
Otu008	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactarius	170
Otu010	Basidiomycota	Agaricomycetes	Cantharellales	Cantharellaceae	uncultured_Cantharellaceae	275
Otu012	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactarius	303
Otu014	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	uncultured_Amanitaceae	286
Otu023	Basidiomycota	Agaricomycetes	Boletales	Gomphidiaceae	Gomphidius	240
Otu026	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	uncultured_Thelephoraceae	228
Otu028	Ascomycota	Pezizomycetes	Pezizales	Tuberaceae	Tuber	150
Otu035	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	136
Otu038	Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	101
Otu041	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	86
Otu043	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Tricholoma	139
Otu044	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	74
Otu045	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	63
Otu047	Basidiomycota	Agaricomycetes	Hymenochaetales	Hymenochaetaceae	Coltricia	79
Otu060	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	7
Otu066	Basidiomycota	Agaricomycetes	Boletales	Gomphidiaceae	Chroogomphus	44
Otu067	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Hebeloma	39
Otu074	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Inocybe	27
Otu075	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactarius	46
Otu091	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	16
Otu092	Basidiomycota	Agaricomycetes	Boletales	Sclerodermataceae	Scleroderma	10

Otu095	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	uncultured_Thelephoraceae	10
Otu096	Basidiomycota	Agaricomycetes	Boletales	Boletaceae	Tylopilus	12
Otu103	Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Lactarius	8
Otu105	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Piloderma	10
Otu109	Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Inocybe	12
Otu110	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	7
Otu111	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	uncultured_Sebacinaceae	11
Otu133	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	Suillus	8
Otu134	Basidiomycota	Agaricomycetes	Atheliales	Atheliaceae	Piloderma	15
Otu138	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Tricholoma	2
Otu140	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	Tremellodendron	2
Otu143	Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	7
Otu147	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	uncultured_Sebacinaceae	4
Otu149	Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita	6
Otu168	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Thelephora	3
Otu173	Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	5
Otu175	Basidiomycota	Agaricomycetes	Boletales	Pisolithaceae	Pisolithus	8
Otu177	Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	4
Otu181	Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	5
Otu187	Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	5
Otu225	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	Sebacina	2
Otu241	Basidiomycota	Agaricomycetes	Cantharellales	Clavulinaceae	Clavulina	3

