Soil microbial community responses to fire

by

Sam Fox

A.S., Darton State College, 2013
B.A., University of New Mexico, 2015

AN ABSTRACT OF A DISSERTATION

submitted in partial fulfillment of the requirements for the degree

DOCTOR OF PHILOSOPHY

Division of Biology
College of Arts and Sciences

KANSAS STATE UNIVERSITY
Manhattan, Kansas

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Abstract

Fires, both wild and prescribed, have lasting impacts on the landscape and environment. Factors such as fire return interval, timing, and fire intensity and severity all play a role in the direct and indirect impacts fires have on the soil microbial communities (bacteria and fungi). Soil microbes play vital roles in soil stability, nutrient exchange, and many other ecosystem functions. Understanding how fires impact these communities is important for future land management decisions, especially in areas predicted to have more frequent and severe fires. In my dissertation, I first provide a synthetic review of what is currently known about the subject of fire impacts on fungi. This includes ecological frameworks, fungal fire traits, key fire-responsive fungal species, and community dynamics and trajectories. While this review is detailed and explores many facets of fungal responses to fire, I also address areas that still need to be explored, such as functional gene analysis following a fire, and having more controlled fire experiments. Second, I explored how fire frequency impacts the microbial communities residing in different soil horizons- A (topmost), E, and B (bottommost) as well as abiotic attributes that may be indirect drivers of community dynamics such as; Total N, Total C, SOM, inorganic N, P, and pH. For this project, we utilized an experimental infrastructure that had sixty years of continuously maintained, controlled fire regimes. This experiment included replicated experimental units that had been burned annually, every two years, and every four years, as well as a fire exclusion treatment that had not been burned in over sixty years. We observed that fire frequency impacts the microbial communities, but does so mainly in the topmost soil profile. The fire exclusion treatment differed from others when we compared the topmost soil horizons (where most microbial activity occurs). In almost all of our community and abiotic parameters, the fire interval manipulation treatments differed in the topmost A horizon, whereas the two deeper horizons E and B, had only a few parameters that differed between the fire interval treatments. Lastly, I investigate effects of low and high severity fires in a mid- to long-term experiment. This experiment manipulated fire severity and compared high and low severity fires to determine how the microbial communities change over a six-year time span. We also collected samples before the fire samples to enable comparisons to samples after fire to assess community recovery. My results suggested that the high-severity fires had a greater impact on the microbial communities compared to the low severity fires for both bacteria and fungi. Within the high

severity fire sites, the communities remained distinct six years post-fire. In the low severity treatments, the communities started to resemble those before the fire, especially richness and diversity of the bacterial communities. This project allowed us to gain valuable understanding in microbial community trajectories following fire, and could aid in planning future restoration projects. Taken together, my dissertation research has allowed us to answer whether and how fire severity and frequency impact the soil microbial community. Indicator taxon analyses that I employed in both studies, identified taxa that seem to drive the community distinctions amongst the treatments, such as fungal taxa, *Anthrocobia, Morchella, Pholiolata*, and *Pyronema* which are described as pyrophilous taxa in my synthetic review. My dissertation research strongly indicates that microbial communities change with fire events and that these responses depend on fire interval and severity contexts. Whilst my studies provide considerable insight into the microbial responses to fire, the underlying reasons why they respond still remain complex and poorly understood. In all, fire changes soil chemistry, plant physiology and community composition, soil fauna, and many other system attributes that interact with microbial communities in soil. Exploring which of the many potential drivers are most important for microbial community fire responses and recovery remain a lingering area of research that needs to be explored.

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Dedication

I would like to dedicate this work to my nieces, Bobbie Jaie and Nora Locke.

Always stay wild and weird.

Preface

The contents of this dissertation are in collaboration with Ari Jumpponen and others who have aided in these projects. Chapter 2 has been submitted and conditionally accepted to *Mycologia* and is formatted according to their requirements; it is a collaborative effort by eight researchers with expertise in fungal responses to fire.

Chapter 1 - Introduction

Fires have been utilized as a management tool to promote plant diversity and encourage vegetation regrowth or pyrodiversity for thousands of years by indigenous people (Huffman 2013; Trauernicht et al. 2016). Due to European settlement, much of this traditional ecological knowledge of fire management was lost and discontinued, which led to evident landscape changes. These landscape changes have included loss of plant diversity, and in many places, a gradual build-up of fuel loads. In the 20th century, a public view of fire being "bad" increased policies to support of fire suppression, especially in the western United States (Pyne 1997; Brunson and Shindler 2004; Berry 2007). These policies, and an increase in human population and thus, increase in wildland-urban interface (Andela et al. 2017) have led to unprecedented "Mega Fires" in the western United States that burn hotter and longer (Williams 2013), and are encouraged by ongoing droughts of the region (Loehman et al. 2018).

Fires, regardless of whether prescribed or wildfire, are heterogeneous due to topography, weather, soil moisture, plant community composition, and fuel accumulation. The heterogeneity of fire results in landscape mosaics (Agee JK 1998), or patches of different fire severity in which the fire impacts areas of a landscape differently leading subsequently to different successional trajectories of community recovery following fire. This patchiness and variability in successional states across the landscape leads to pyrodiversity, or "the degree of variation in post-fire landscape characteristics within or among fires (Jones and Tingley 2021)." Pyrodiversity can also change based on fire-return interval, where a fire-frequented system will likely respond differently compared to a fire suppressed system.

While aboveground systems and their pyrodiversity have been studied extensively, much of how fire impacts belowground systems has only been explored in the last 60 years including high throughput DNA sequence analyses within the last 20 years. Several pioneering studies on this subject have found that pyrodiversity above ground also translated to the below ground system (Choromanska and DeLuca 2002; Hart et al. 2005; Hamman et al.2007; Holden and Treseder 2013), but pyrodiversity can vary based on fire type, sampling time, sampling procedure, and system, leaving much to be investigated.

Studies of fungi responding to fire observed through fruiting bodies date back to the early 1900s. This is especially true for known pyrophilous fungi like morels (Sturgis 1905). However, these fungi are only a small portion of fungal diversity within the soils. Shifts in the fungal community after fire results in a loss of some community members (Fire-sensitive). In contrast, some taxa are able to resist the direct or indirect effects of fire (Fire-resistant), whereas some others expedite their lifecycle and produce fruiting bodies (Fire-responsive) after a fire, and yet others that require fire to complete their life cycles (Fire-adapted). In addition to these categories, there are also fungi that can invade the system via dispersal or emerge from local refugia (See Chapter 2).

The microbial communities, both bacterial and fungal, are important for soil stability, nutrient and mineral exchange, symbiotic relationships with plants, and food for microfauna. Understanding how these communities respond to different types of fire, different fire regimes, and different fire systems is important for overall ecosystem health and management. The results from these studies further the understanding of these community responses and address potential gaps in the field of microbial community dynamic responses to fire.

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Chapter 2 - Fire as a Driver of Fungal Diversity – a Synthesis of Current Knowledge

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Keywords: Pyrophilous fungi; fire adaptations; endemism; community dynamics; fire frameworks; fire severity.

Abstract

Fires occur in most terrestrial ecosystems where they drive changes in the traits, composition, and diversity of fungal communities. Fires range from rare, stand-replacing wildfires to frequent, prescribed fires used to mimic natural fire regimes. Fire regime factors, including burn severity, fire intensity, and timing vary widely and likely determine how fungi respond to fires. Despite the importance of fungi to post-fire plant communities and ecosystem functioning, attempts to identify common fungal responses and their major drivers are lacking. This synthesis addresses this knowledge gap, and ranges from fire adaptations of specific fungi to succession and assembly fungal communities as they respond to spatially heterogenous burning within the landscape. Fires impact fungi directly and indirectly through their effects on fungal survival, substrate and habitat modifications, changes in environmental conditions, and/or physiological responses of the hosts with which fungi interact. Some specific pyrophilous, or "fire-loving", fungi often appear after fire. Our synthesis explores whether such taxa can be considered cosmopolitan, and whether they are truly fire-adapted, or simply opportunists adapted to rapidly occupy substrates and habitats made available by fires. We also discuss the possible inoculum sources of post-fire fungi and explore existing conceptual models and ecological frameworks that may be useful to generalize fungal fire responses. We conclude with identifying research gaps and areas that may best transform the current knowledge and understanding of fungal responses to fire.

1. Introduction

Every year, an estimated 570 million hectares of land burns globally, altering the storage and cycling of carbon and nutrients as well as the composition and function of ecosystems (Bond-Lamberty et al. 2007; Bowman et al. 2009; Pellegrini et al. 2018). In many locations, contemporary fire regimes (*e.g.*, fire frequency, seasonality, and intensity) have diverged from historical averages as a result of climate change, land use, and human encroachment at wildland-urban interfaces (Westerling et al. 2006; Miller et al. 2009; Dennison et al. 2014; Andela et al. 2017; Bento-Gonçalves and Vieira 2020). The impact of changing fire regimes on ecosystem function will partly be determined by the organismal fire responses. Fungal responses are likely critical as they provision essential ecosystem services.

Fungal communities respond to fire with resultant significant effects on ecosystem functioning and nutrient cycling (Dooley and Treseder 2012; Holden and Treseder 2013; Knelman et al. 2017). In ecosystems that rarely experience wildfires, infrequent fires can drive dramatic fungal community shifts that may take years (Gutknecht et al. 2010) or even decades (Dooley and Treseder 2012) to recover. In contrast, other ecosystems are maintained by frequent fires that may be necessary to also maintain fungal communities. Partly because of this variation in fire histories and regimes, we lack a synthetic understanding of the primary drivers of fungal fire responses. This understanding, however, is essential to better predict how fire-induced shifts of fungal communities may alter ecosystem functions. Decoupling drivers and fungal responses, however, is not straightforward. Fire changes an array of ecosystem components (Certini 2005), many of which are inherently linked. For example, changing fire regimes drive corresponding shifts in ecosystem carbon and nutrient cycles by changing plant communities, removing plant biomass (both live and dead), direct combustion of soil organic legacies including carbon (C) and nitrogen (N), altering fuel loads, and impacting soil microbial communities (*e.g.*, Ojima et al. 1994; Kauffman et al. 1995; Baird et al. 1999; Muqaddas et al. 2015; Pellegrini et al. 2015; Mack et al. 2021). Drivers that may underlie the responses of fungal communities are complex and likely include i) direct heat-induced mortality from fire; ii) abrupt changes to substrates and nutrient availability (Kaye and Hart 1998; Wang et al. 2012); iii) long-lasting indirect changes in environmental conditions (Chen and Cairney 2002; Reazin et al. 2016); and, iv) altered physiology or mortality of plant hosts on which some fungi depend (Haase and Sackett 1998;

Schwilk et al. 2009). Simultaneous shifts in plant responses (from individual plant physiology to entire communities), substrates for fungal decomposers, and soil nutrient availability (including immobilization, losses through combustion and volatilization, and release through organismal mortality) all complicate generalizing fungal fire ecology, particularly across widespread variation in fire regimes and ecosystems.

Here, we identify and address the gaps in our understanding of fungi and fungal communities in the context of fire. Our central goal is to define a unifying framework that can help integrate patterns across numerous independent studies and identify generalities in fungal fire ecology. Towards this goal (See Figure 2.1), we aim to i) evaluate direct and indirect drivers for fungal responses to fire, outlining how these differ among ecosystems, fire regimes, and fungal guilds; ii) explore existing ecological frameworks and evaluate how well they may apply to fungi and fungal communities; iii) define fungal traits related to fire, then explore how they are reflected in key pyrophilous taxa, their distributions, and more broadly among fungal guilds; and, iv) discuss the origin of post-fire fungi – not in the evolutionary context, but rather in terms of strategies for dispersal and dormancy.

Few of our objectives are resolved definitively but rather provide insights that fall into a variety of context dependencies, many based on fire characteristics (Figure 2.2). In describing different fire characteristics, we follow the existing conventions (Keeley 2009; He et al. 2019) such that we use fire intensity to describe the energy released by a fire whereas fire/burn severity describes the consumption of organic matter to discriminate between fire intensity and burn severity – the two key "*fire regime factors*." Not all fires are created equal and variation in fires based on intensity are well documented (Figure 2.1, 2.2): low intensity fires that are common in many systems may have only minimal ecosystem effects, whereas high intensity fires often result in substantial mortality and dramatically transform substrates. Similarly, fungal guilds experience fires differently. Biotrophic fungi (mutualists and antagonists alike) are not only affected directly by the fire but also by the responses of their host. Saprotrophic fungi and pathogens may respectively benefit from newly available, fire-generated substrates and weakened hosts that are stressed by fire. In detailing these diverse responses, this synthesis can serve as common foundation for future

research, provoke debate, and ultimately stimulate a deeper understanding of fungi and their responses to fire.

2. Direct vs. indirect drivers

Fire characteristics (*e.g.,* intensity, duration) and fire regime (*e.g.*, frequency, fire return interval) vary widely and may determine the relative impact of fires on fungi (Figure 2.2). We first focus on the mechanisms by which fire acts as a selective force on fungi and fungal communities. Most fires reach lethal temperatures only in the topmost soil profiles where a large portion of soil biological activity takes place (Neary et al. 1999; Smith et al. 2016). Even without direct mortality, indirect fire effects may ultimately be just as strong a selective pressure for fungi, and their importance may increase with time since fire (Hart et al. 2005), both in the short (*e.g.*, transient increases in availability of inorganic N and phosphorus (P)) and long term (*e.g.*, loss of litter or changes in plant community composition).

2.1 Direct impacts: Fires may kill fungi directly and can provide a strong selective pressure for fungal evolution. Some fungi can survive temperatures greater than 50°C and even up to 145°C (Seaver 1909), albeit 60°C for one minute has been commonly considered lethal for most soil organisms (Neary et al. 1999). The food industry considers fungi heat-resistant if they can survive 75°C for 30 min (Samson et al. 2004). Clearly, simple fit-for-all thresholds require revision. Pingree and Kobziar (2019) questioned the 60°C threshold in a meta-analysis of biological responses to soil heating as such thresholds severely misrepresent the great heterogeneity in soil characteristics, organismal tolerances, and the complexity of heat transfer in the substrate. Lethal temperatures may also depend on environmental conditions like soil moisture that may control heat transfer (Dunn et al. 1985). Sustained exposure to lethal temperatures is common in both wildfires and prescribed fires in forests, but less so in grasslands (Archibald et al. 2013). Repeated exposure to fires can dictate fungal responses. For example, wood-inhabiting fungi in fire-prone habitats in the boreal systems experience half the mortality compared to fungi in similar systems that rarely burn (Carlsson et al. 2012), potentially as a result of less fuel accumulation and therefore lower burn severities. Frequent fires may also drive fungal adaptations including heat-resistant spores and sclerotia, and even fire-induced germination and growth (see fungal traits below). The maximum temperatures that fungi experience are moderated by fungal habitats, fuel accumulation,

soil type, soil water content, and soil depth, as steep thermal gradients occur from the surface downward (Bruns et al. 2020). Lethal temperatures most likely occur in burning litter as indicated by clear declines of saprotrophic fungi after fire (Semenova-Nelsen et al. 2019; Pulido-Chavez et al. 2021). In contrast, mineral soils are often better insulated from heat transfer, particularly deeper in the soil profile (Massman 2012; Smith et al. 2016) with smaller post-fire fungal community shifts in mineral than organic horizons (Semenova-Nelsen et al. 2019; Hopkins et al. 2021). Similarly, downed wood and surviving plant tissues (*e.g.,* leaves, roots) can provide insulation that protects substrate- or tissue-inhabiting fungi from heat-induced mortality, exemplifying a "fire refugium" (see Meddens et al. 2018). In addition, some post-fire "blooms" of fungi may be due to the loss of substrate or host plants, which triggers a fruiting response (Fujimura et al. 2005; Kuo et al. 2014; Hughes et al. 2020b).

Fire consumption of plants and debris represent direct losses of fungal habitats and available substrates (Bowman et al. 2009). Plant mortality often results in the death of plant-associated fungi, including mycorrhizal fungi (Dove and Hart 2017), even if fungi themselves are insulated from heating. For example, mycorrhizal fungi on roots may die if host trees are killed in wildfires and new compatible hosts are unavailable. Many obligate mycorrhizal fungi will not persist in the absence of a host (Collier and Bidartondo 2009) unless they produce resistant propagules that can persist in the spore bank (Glassman et al. 2015b). Fire has played a key role in plant diversification, and plant fire adaptations likely provide novel morphological structures (Keeley et al. 2011) that may host (and protect) specialized fungi. Decomposer fungi in wood, plant litter, and other substrates may similarly be lost when fire consumes them, although heat-generated convection winds may also serve as an important dispersal mechanism (Camacho et al. 2018) and as a potential means to escape fire-induced mortality. For fungi dependent upon plant hosts and substrates lost in severe fires, recolonization may not be possible until these niches recover (Hart et al. 2005). If fungi are not completely consumed by fire, environmental shifts can also drive important changes to fungal physiology, growth, and community composition.

2.2 Indirect impacts: Fire can modify soil physical properties in a variety of ways (Neary et al. 1999; Certini 2005) and impact fungi indirectly. For example, fires can affect hydrology through decreased soil water retention, increased surface runoff and sediment loading to surface water

(DeBano 2000). Moderate to high severity fires often increase soil hydrophobicity that indirectly impacts soil fungal communities (Seaton et al. 2019) by creating a discrete and water-repellent front parallel to the surface that can decrease soil permeability for up to two years (Imeson et al. 1992). Fire can also modify soil color, which may influence fungi through impacts on albedo. For example, soil charring by a severe fire can blacken a layer 1-15cm thick (Ulery and Graham 1993). By removing vegetation fires also reduce light interception and change albedo, and combined, these effects can increase soil temperatures and alter evapotranspiration in ways that indirectly influence fungal communities (Hart et al. 2005).

Fire can also impact fungi indirectly by modifying soil chemistry and nutrient availability. Fire tends to increase soil pH as organic acids denature during heating (Certini 2005). Increased soil pH affects the bioavailability of most cations and can also strongly modify fungal communities (Glassman et al. 2017b). Depending on severity, fires can cause immediate losses in N and C through combustion, but often produce flushes of bioavailable N and P (Neary et al. 1999). A meta-analysis of 185 datasets from 87 studies between 1995 and 1999 found that fire increased soil ammonium (NH_4^+) by 94% and nitrate (NO_3^-) by 152% (Wan et al. 2001). Increase in N availability could significantly alter the compositions of both mycorrhizal and saprotrophic fungi (Cox et al. 2010; Morrison et al. 2016; Tahovská et al. 2020). Fires often result in a short-term enrichment of available P (Serrasolsas and Khanna 1995) because burning drives conversion of soil organic P to orthophosphate (Cade-Menun et al. 2000). Increased P bioavailability will likely influence fungi, particularly AM fungi which are important in mobilizing P for their plant hosts (Whiteside et al. 2019) but whose colonization declines when more P is available (Treseder 2004). Apart from fungi alone, these fire-induced stoichiometric shifts may also alter fungal symbiotic functions (Mouginot et al. 2014) and their competitive interactions with saprotrophic fungi (Frey 2019).

Fire impacts on total C and N storage are less clear than impacts on nutrient availability and differ within the soil profile: litter and the topmost horizons are most impacted whereas deeper mineral soils are insulated. One meta-analysis concluded that forest fires across a variety of ecosystems increased mineral soil C and N (Johnson and Curtis 2001), a response attributed to C sequestration of charcoal and post-fire colonization by N fixing vegetation. Another that focused

exclusively on temperate forests, however, concluded that fires reduced soil C and N (Nave et al. 2011). These losses were largely from the organic layer, whereas mineral soil organic C was unchanged. Changes to these key components can alter stoichiometry which dictates fungal physiology, growth, and community composition. Fires can also indirectly affect fungal community composition by transforming wood and leaf litter to pyrogenic organic matter (PyOM; Knicker 2011), which may serve as a food source for particular fungi (Kymäläinen et al. 2015; José et al. 2018)(Kymäläinen et al. 2015; José et al. 2018) or increase C storage due to its recalcitrance (Santín et al. 2015).

Finally, fires can indirectly impact fungal communities by modifying fungal food web connections and fungal habitat availability. Fires often reduce microbial biomass (Dooley and Treseder 2012), but fire-generated necromass may provide nutritional opportunities for surviving fungi (Bruns et al. 2020). Fires affect the biomass and composition of soil dwelling invertebrates (Pressler et al. 2019; Certini et al. 2021) which may have cascading impacts on fungal communities (Lavelle et al. 1997). Broader microbial mortality from fire, including bacteria and protists, may reduce competition for surviving fungi (El-Abyad and Webster 1968a; Zak and Wicklow 1980) or represent a loss of a key members of important ecological guilds such as ectomycorrhizal symbionts (Yang et al. 2020) or saprotrophs (Semenova-Nelsen et al. 2019). Like extinctions on small islands, wildfires may also drive fungal extirpations in isolated reserves if large, high severity fires disrupt or remove propagule sources that sustain their populations (Peay et al. 2007; Glassman et al. 2017a). For fungi restricted to fire-frequented ecosystems, however, their persistence may depend on maintaining frequent, low severity fires as it does for many endemic plants and animals.

3. Ecological frameworks applicable to fungal fire ecology

Our central goal is to help define a general ecological framework for fire fungi, and many existing frameworks may be usefully adapted. Most are derived from studies focusing on plants and have been vetted by field and experimental research over several decades. A unified conceptual framework has been recently proposed to predict and characterize temporal dynamics of microbiomes specifically (Stegen et al. 2018). Although this broad, unified framework that considers biotic and abiotic history, internal dynamics, and external forcing factors may

ultimately be useful, we choose to focus on established frameworks that are either specific to fire ecology or have been widely adopted to characterize community dynamics. We explore three ecological frameworks that may provide useful comparisons: i) fire-derived heterogeneity (*i.e.*, pyrodiversity) as a driver of fungal biodiversity; ii) trait-based frameworks that may predict fungal community responses to fire; and, iii) community assembly/succession frameworks that recognize fire impacts on fungal communities and their dynamics.

3.1 Fire as a driver of pyrodiversity/biodiversity: Fire-derived heterogeneity, collectively called pyrodiversity (Martin and Sapsis 1991; He et al. 2019), facilitates niche diversity in time and space to organisms including fungi. Both plant and animal biodiversity often increase with pyrodiversity (Jones and Tingley 2021), which is driven by a variation in fire characteristics including fire type, intensity, pattern, seasonality, and fire history (He et al. 2019). For example, differences in fire severity across the landscape may help maintain a wide range of organismal traits, including those tightly linked to fire (*e.g.,* fruiting in response to fire or extirpation with severe fire) and those only weakly impacted by fire. Further, some organisms may be only minimally affected by fire as a result of "fire refugia" (Meddens et al. 2018), protected by landscape attributes (*e.g.*, topography) and substrate/habitat (plant tissues or position in the soil profile). Niches created by this fire variation across space and time likely increase fungal richness on the landscape level, even if fire itself reduces richness within small landscape patches.

Pyrodiversity interacts with abiotic and biotic factors, including topography, moisture, and vegetation, that also shape fungal niche space resulting in heterogeneous landscape mosaics (Hiers et al. 2009). Because these parameters interact before, during, and after a fire event, disentangling pyrodiversity and fungal diversity is difficult. Fungal diversity clearly changes in response to fire (Holden et al. 2013; Dove and Hart 2017), and these changes are not uniform across the landscape mosaic that fire creates (Agee 1998; Kong et al. 2019). A study of fire impacts in Oregon ponderosa pine forests found that fungal communities were distinct among plots that experienced different fire severities within the landscape (Reazin et al. 2016). In addition, dominance within the fungal community changes through time as burned areas recover and produce heterogeneous belowground mosaics of biotic and abiotic conditions (Huffman and

Madritch 2018) or as plant communities transition through distinct post-fire successional trajectories (see Hart et al. 2005). As with plants and other sessile organisms (He et al. 2019), it is likely that the diverse landscape mosaics created by fire provide distinct habitats (in time and space) where fungi with different and unique trait combinations can survive.

Evidence that fire-created mosaics increase heterogeneity for fungal communities varies among systems, fire attributes, and the scale of observation. Fire characteristics, and fire severity in particular, have been key in addressing the diversifying or homogenizing effects of fire on biodiversity. High severity fires have long been considered a homogenizing force in ecosystems (Turner et al. 1994; Holling et al. 1996; Allen and Holling 2008), particularly for plants. Such individual fires are often stand-replacing, resulting in substantial plant mortality and ecosystem homogenization ("resetting the successional clock"), knocking vast areas back to a uniform successional stage (Baskin 1999), and promoting plant communities dominated by few ruderal species (Burkle et al. 2015). However, the ecosystem and scale of analyses impact the conclusions drawn about spatial variation in fire effects. Fires may homogenize the landscape, particularly at small spatial scales, killing aboveground vegetation and producing even-aged patches (Allen and Holling 2008; Velle et al. 2014). Following the 1988 Yellowstone National Park fire, however, different burn intensities "reset" the dominant pre-fire vegetation and landscape units to different successional stages, such that post-fire landscape was as patchy and as variable as the pre-fire landscape (Baskin 1999). Wildfire effects on both vegetation and fungi likely depend on pre-fire heterogeneity itself, with more homogenous systems such as the Yellowstone lodgepole pine (*Pinus contorta*) system showing less homogenization from fire. In contrast, while the frequent low severity fires may be essential to maintain ecosystem attributes and plant diversity in many grassland and savannah ecosystems, their impacts on heterogeneity and fungal diversity remains less clear. Lower fungal richness in experimental tallgrass prairie units that burn more frequently (Carson et al. 2019) would suggest fungal sensitivity to repeated burning (*e.g.*, Dooley and Treseder 2012; Pressler et al. 2019) and thus less pyrodiversity on a landscape level.

The few studies that can directly assess fungal community heterogeneity following fires suggest that fire regimes and ecosystem differences are important. Large fuel quantities and subsequent severe fires lead to decline in fungal richness but also to communities distinct from surrounding

areas with less severe burns (Reazin et al. 2016) therefore adding to fungal community variation across the landscape. It is still uncertain how long communities responding to severe fires remain distinct and if they represent unique successional trajectories, but chronosequence studies suggest that the fire-generated landscape units likely persist for years and perhaps even decades (Holden et al. 2013; Sun et al. 2015; Pérez-Valera et al. 2018). In contrast, prescribed burning in both pine savanna (medium severity) and tallgrass prairie (low severity) changed soil fungal communities as well, but plots were no more or less similar to one another when burned than when not burned that year (Hopkins et al. 2021). Frequent prescribed fires in these systems (*i.e.,* every 1-3 years) may maintain heterogeneity. As with other ecosystems components (Ligon et al. 1986; Steen et al. 2013b, 2013a; Kowal et al. 2014), varying fire intervals may affect fungal communities (Oliver et al. 2015) and help maintain landscape level heterogeneity and high fungal beta-diversity (Carson et al. 2019). In some systems and scales, fires can maintain ecosystem heterogeneity, and that of fungal communities, but more data are clearly needed.

In addition to landscape-scale heterogeneity, soil is inherently heterogeneous (Cardinale et al. 2000). Fires may promote fungal community heterogeneity across the soil profile as a result of the rapid heat attenuation with depth. Fire-generated heat pulses are greatest near the surface and the heat pulses gradually decline with soil depth (Campbell et al. 1994; Massman 2012). Importantly, heat penetration also depends on soil water content (dry soils conduct heat poorly compared to wet soils) and on the depth and combustibility of the organic layer (Valette et al. 1994; Reardon et al. 2007; Kreye et al. 2016). While severe fires likely eliminate much of the soil biota - including fungi – from the upper few centimeters of soil (Semenova-Nelsen et al. 2019), dormant organisms residing in deeper soil strata can be stimulated by moderate heat (Massman 2012) – the so-called ‘goldilocks zone,’ wherein the fire temperature/duration is within "optimal range" for stimulation (Bruns et al. 2020). Fungal community shifts following prescribed fires were much greater in litter compared to the soil layer just below (to 2cm) in sandy, pine savanna soils (Semenova-Nelsen et al. 2019). Following wildfires in mixed forests of the Great Khingan Mountains in Mongolia, ectomycorrhizal fungi declined in richness (<40%) in the organic soil horizon but not in the deeper mineral layers, whereas saprotrophic fungi had no depth-dependent fire responses (Yang et al. 2020). More work is clearly needed to generalize these patterns, which likely reflect both direct and indirect fire effects.

Fire impacts on soil properties and plants may also indirectly drive diverse fungal responses to fire across the soil profile. High temperatures can combust large proportions of the ligno-cellulosic biomass near the surface, transforming some into partially burned pyrogenic organic material (Keiluweit et al. 2010). Substrate removal and transformation are not homogeneous and the governing factors vary even at small, local scales (Kreye et al. 2016). Fuel accumulation, landscape and ecosystem attributes, as well as fire history and characteristics likely dictate the generation of heterogeneous mosaics of unburned and pyrogenic substrates across the soil profile. Fire generates and deposits alkaline ash that modifies pH, particularly in the surface soils (Certini 2005). At the landscape scale, increased pH seems to interact with fire severity to determine fungal community responses to boreal wildfires (Day et al. 2019; Whitman et al. 2019), but differential pH impacts on fungi across the soil profile remain unexplored. Other fire-responsive soil attributes (soil inorganic N, soil organic matter) tend to shift most at the soil surface, with effects declining with depth. Plant rooting strategies are also diverse and create heterogenous niches throughout the soil profile. Fire-caused plant mortality may remove specific habitats for plant-associated fungi, resulting in replacement by saprotrophic fungi. For example, tree mortality following a boreal wildfire had a greater impact on fungal communities than the surface fire severity (Pérez-Izquierdo et al. 2021). In many fire-frequented systems, plants have key belowground adaptations to fire that may create additional habitat heterogeneity for fungi across the soil profile. To our knowledge, little research has addressed whether fungi can specialize on fire-adapted belowground plant organs. More explicit belowground research that parse fire effects on soil layers, plant tissues, and fungal niches may help better explain resultant fungal biodiversity and their responses after fire.

3.2 Trait-based frameworks for fungal fire responses: In many fire-frequented ecosystems, animals (see Smith and Lyon 2000) and plants (see Brown et al. 2000) possess a diversity of adapted fire-traits that may be paralleled in fungi. Arthropods and nematodes share many of the same environments (and scale) with fungi. These organisms generally exhibit fire intensity and burn severity dependent mortality, including biodiversity shifts from these and other fire regime factors (Certini et al. 2021). Although still poorly understood, some of these organisms are fire-responsive (Certini et al. 2021) and many of their responses are driven by fire-related changes in substrates also used by fungi. However, because many animals can move to escape the worst fire

effects, we may expect that plant adaptations are most relevant to fungal fire adaptations. Plant fire adaptations include resprouting from epicormic buds, fire-induced seed release (*i.e.*, serotiny), heat-triggered germination, and fire-resistant structures like thick bark (Keeley et al. 2011). These adaptations generally focus either on surviving fire or on releasing offspring that can take advantage of the post-fire environment. Thermotolerant fungi (Fergus 1964; Rippon et al. 1980; Redman et al. 1999; Suryanarayanan et al. 2011) parallel fire-resistant plants, and include fire-adapted plant-fungal associations (Baynes et al. 2011). Thermotolerant fungi can also produce heat-resistant compounds (Singsaas 2000; Sharkey et al. 2001), including laccases (Hildén et al. 2007) and trehalose (Tereshina 2005). Further, some species, such as those in the genera *Anthracobia* and *Pyronema* (Pyronemataceae), fruit frequently and in great abundance after fires (Seaver 1909; Petersen 1970). Although less well described mechanistically than plant reproductive adaptations to fire, this suggests that fire-induced reproduction is likely an important fire strategy for fungi.

Grime's trait-based model, originally developed for animals and later applied to plants, considered disturbance, stress, and competition the main drivers of life history evolution (Grime 1977, 2002) and ultimately succession. In this model, disturbance-responsive organisms are r-selected strategists (ruderal taxa) that rapidly access nutrients, quickly colonize and reproduce, are non-combative, and therefore ephemeral on the disturbed landscape. Stress tolerant or S-selected strategists colonize more slowly but persist under conditions most other organisms cannot tolerate; they too possibly occur soon after disturbance. As succession proceeds, combative C-strategists with superior competitive abilities defend their territory and dominate in the crowded niche space when resources are scarce. Grime (1988) identified CSR parallels between plants and fungi and adaptations of the model have been successfully applied to mycorrhizal fungal communities (Chagnon et al. 2013) and carbon traits of microbes (including fungi; Malik et al. 2020). The CSR framework has been adapted in an attempt to generalize fungal responses to disturbance (Pugh and Boddy 1988) and to fire specifically (Whitman et al. 2019; Enright et al. 2021). Pyrophilous fungi may follow CSR, combining the attributes of taxa that thrive in the post-fire environment because of traits that either permit survival through the fire (*e.g.*, heat resistant/tolerant spores), facilitate rapid growth (*e.g.*, rRNA gene copy numbers), or allow utilization of the post-fire substrates (*e.g.*, metabolic pathways that permit aromatic C degradation) (Whitman et al. 2019; Enright et al. 2021).

These and other contemporary trait-based approaches seek to avoid density-dependence and acknowledge complex and diverse life cycles (Andrews 1992; Reznick et al. 2002; Crowther et al. 2014). Fungi have unique life-histories and developmental phases that can differ in function and dispersal, so the whole organism (throughout its entire life) may not fit a single trait category (*i.e*., CSR; Zanne et al. 2020). Still, r-selected *traits* or r-selected *life phases* may yet prove useful to describe fungi that respond to fire and establish expediently in post-fire environments and systems, whereas s-selected *traits* or s-selected *life phases* may be more applicable to organisms that persist in the post-fire environments. It is also of note that no single characteristic or trait may apply generally to dynamic communities that occupy post-fire environments. Early bacterial communities establishing soon after a fire in pine forests were dominated by spore-forming, easily dispersing taxa, whereas later post-fire communities were dominated by oligotrophs in an environment characterized by sparsely available soil organic matter (Ferrenberg et al. 2013). Moreover, some empirical evidence supports fire facilitation of opportunistic, fast-growing, and readily dispersed ruderal, r-selected fungi which are slowly replaced by competitive, slower-growing, k-selected specialists (Reznick et al. 2002; Peay et al. 2009).

Fungal adaptations to fire may be more akin to general adaptations to disturbance (Shade et al. 2012; Griffiths and Philippot 2013). Although lacking a synthetic review, fungi respond to many different disturbances including earthquakes (Lin et al. 2019), lava (Nara et al. 2003), glacial movement (Jumpponen et al. 2002; Dresch et al. 2019), mining (Zak 1992; Crognale et al. 2017), air pollution (Arnolds 1991), and agriculture (Miller and Lodge 2007). Rapid growth is advantageous after these disturbances and is a strategy shared by many pyrophilous fungi. For example, species in the Pyronemataceae genera *Pyronema* and *Anthracobia* have been documented to quickly overgrow burned areas (Claridge et al. 2009). Growth is a measure of species performance in a particular environment but is difficult to standardize for comparisons (Bárcenas-Moreno and Bååth 2009) and could eventually be tied to metabolic activity (Zanne et al. 2020). Pyrophilous fungi may also allocate resources to escape post-fire environments through reproduction or transitioning to other life history phases. For example, homothallic *Pyronema* spp. can produce ascocarps within a week in the lab (Traeger et al. 2013) and rapidly after natural (Seaver 1909) or experimental fires (Bruns et al. 2020). Some pyrophilous fungi rapidly produce and disperse asexual mitospores (El-Abyad and Webster 1968b) while fruiting bodies can produce

large numbers of meiospores, both of which may accumulate over time as spore banks in fire-prone areas (Warcup and Baker 1963). Thus far such spore banks following fire have been documented for mycorrhizal fungi (Glassman et al. 2016a) but may not be present for other (*e.g.*, saprotrophic) fungi. We posit that an effective fire adaptation is for spores to lie dormant until cued by fire, whether by heat, smoke, chemicals, reduced toxins, released compounds, or pH change (Wicklow 1988). The tradeoff is that without fire or a comparable trigger, the dormant propagules remain inactive and these fungi could risk local extinction. Many fungi that respond to fire may be a subset of a broader disturbance-adapted fungal group, and therefore models that focus on disturbance may be useful for understanding fungal fire traits and post-fire community changes.

3.3 Community assembly/succession frameworks: Community assembly models (Diamond 1975; Cole 1983; Hunt Jr 1991) have also been adopted for fungal communities (Jumpponen and Egerton-Warburton 2005) and may be useful in predicting fungal community responses to fire, similar to their use for bacterial post-fire dynamics (Ferrenberg et al. 2013). Assembly rules outline the constraints – or series of filters – that select community members from local or regional species pools (Weiher and Keddy 2001) and identify ecological processes that lead to assembled communities (Drake et al. 1993). These "filter models" incorporate organismal dispersal and/or residence and constraints of organismal establishment and persistence in the communities (Keddy 1992). Fire may be a key "filter" with fungal dispersal, establishment, and persistence traits determining post-fire community assembly. The application of community assembly to fungi has already helped explain community patterns in fungal wood decomposers (Fukami et al. 2010) and arbuscular mycorrhizal fungi (Maherali and Klironomos 2012). In addition, priority effects, where early arrival of some taxa alters the success of later arriving taxa, occur in nectar yeasts inhabiting insect-pollinated flowers (Peay et al. 2012) and fungal endophytes following disturbance (Sikes et al. 2016). Trait-based assembly models may be useful to determine post-fire fungal communities as fire-associated mortality (severity dependent) reduces fungal competition in ways that also shape post-fire community assembly. Further, abiotic and plant host changes from fire also may be important filters for the post-fire fungal assembly (Hart et al. 2005), and most of this research has focused on fungal community succession.

Succession describes the process of community assembly and post-fire fungal succession has been considered extensively. Following a fire, fungal communities respond rapidly within days or few weeks (Reazin et al. 2016), albeit the post-fire communities may remain distinct from those present before fire for years or decades (Dooley and Treseder 2012; Pulido-Chavez et al. 2021). Fire alters fungal successional dynamics (*e.g.,* Pressler et al. 2019; Smith and Wan 2019; Lombao et al. 2020) that may be related to a number of factors including: i) population mortality and differential community recovery driven by dispersal, colonization probabilities, and priority effects; ii) shifting edaphic conditions that facilitate emergent niche partitioning in surviving fungi; iii) differential utilization of pyrogenic substrates (*e.g.,* biochar or fire-generated necromass); or, iv) perhaps, collections of taxa that act in concert as interacting fire resilient sub-communities (*i.e.*, consortia; Paerl and Pinckney 1996). All of these may be operating simultaneously, and it seems certain that their relative importance to post-fire fungal succession differs based on fire regime, ecosystem, and a range of related environmental factors. However, successional models may be useful to generalize the combined effect of these factors on fungal community changes after fire.

It is tempting to view post-fire community shifts as deterministic (e.g., Clements 1916; Petersen 1970) within the context of a temporal system recovery, but the relative importance of different community assembly processes (*e.g.*, neutral and niche- or filter-based processes) may shift with time since a fire (Ferrenberg et al. 2013). Early assembly of post-fire fungal communities may also strongly influence subsequent trajectories, potentially paralleling "initial floristics" succession models for plants (Drury and Nisbet 1973). Evidence for fungal priority effects following fire to our knowledge, however, has not been experimentally explored. Distinct fire traits (*e.g.*, heat-stimulated spores or heat-resistant (pseudo-sclerotia) and "refugia" habitats (Meddens et al. 2018) almost certainly provide non-random "initial" taxa for post-fire fungal communities. Together these provide additional functional, temporal, and spatial complexity to the successional dynamics that result in distinct potential post-fire successional trajectories.

Most commonly, fungal succession following wildfires in infrequently burned systems is treated simply as community "recovery," interlocked with other ecosystem properties. The regrowth of vegetation and rebuilding of substrates can limit the pace of fungal succession (Hart et al. 2005; Duhamel et al. 2019), and drive contrasts between systems where these processes occur slowly

(*e.g.*, forested, colder biomes) and those where vegetation can recover rapidly (*e.g.*, temperate grasslands) after fires. With vegetation regrowth come organic legacies, such as the accumulation of litter and organic matter on which saprotrophic fungi rely and which promotes mycorrhizal acquisition of nutrients (Sun et al. 2015; Alem et al. 2020). In contrast, many have pointed out that mycorrhizal fungi often facilitate post-disturbance vegetation recovery (*e.g.*, Read 1989; Cazares et al. 2005). A key factor still to unravel is how feedbacks between fungi, plant communities and soil nutrients operate to govern fungal succession after fire. Fire-frequented systems may provide important experimental systems in which fire itself can be manipulated but may prove conservative models because recurrent fires represent a strong selective force. In these systems, nutrients are often scarce and fire is not a disturbance but a necessity for ecosystem stability. Vegetation and fungi are often fire resistant, fire resilient (see section on categories of pyrophilous fungi below), both, or even depend on fire for reproduction and completion of their life cycles (see section on pyrophilous fungi below). Two key areas for future research are to target the temporal dynamics of fungal communities at short time scales immediately after fire as well as time series that incorporate fire regime, pre-fire conditions, short-term fungal dynamics, and successional dynamics that occur over longer time frames.

3.4 Consortium-based framework: Some fungi clearly thrive in fire-impacted systems, yet it remains poorly understood whether fire-responsive consortia that include fungi exist. Consortia are collections of taxa that coincide temporally, coexist spatially, and interact functionally (Koenig et al. 2011). These consortia represent organismal sub-communities within a larger community but include only members that respond interdependently and synergistically. If such fire-responsive consortia existed, they may be adapted to respond to fire through cooperation and/or nutritional interdependencies (*i.e.*, syntrophisms). Evidence and examples of syntrophism include communities wherein members directly or indirectly facilitate access to resources otherwise unavailable to some consortium members (Zhang et al. 2018; Wei et al. 2019). For example, post-fire communities may include fungal specialists capable of using the biochar or other pyrogenic substrates (Warnock et al. 2007; Anderson et al. 2011) that thereby facilitate other consortia members unable to use these resources directly. A challenge is to disentangle if whole communities are driven by defined processes following fire, or if observed responses are merely the sum of individual responses. Despite the potential value of incorporating consortium frameworks in

ecology, this is not routinely done (*but see* Weber et al. 2006; Tian et al. 2014). Where groups of fire fungi are considered together, analyses and inference generally rely on phylogenetic frameworks (*e.g.*, shifts in abundances of fungal genera or families in response to fire) (Enright et al. 2021) or functional categories (*e.g.*, saprobes, symbiotrophs) (Brown et al. 2019; Semenova-Nelsen et al. 2019). While such analyses are important to better understand fungal fire responses, they do not account for consortia, whose members likely represent different lineages, functional groups, or even kingdoms. As a result, these approaches likely overlook syntrophic or other interdependent associations. Ecologically relevant, engineered consortia can facilitate detailed mechanistic understanding of community dynamics and function (Erbilgin et al. 2017; Zhang et al. 2018) and pure-cultured community members from fire-affected ecosystems may afford a detailed understanding that can inform system-wide processes and post-fire dynamics.

Many questions remain on fungal fire ecology and rigorous consideration of existing models for other organisms and their fire responses seems fruitful. Assessing whether these models – be those pyrodiversity, trait-based, or focused on assembly processes – are appropriate for fungi in multiple ecosystems is critical to try to generalize fungal fire responses and dynamics. Fungi are unique, diverse, and interconnected with other organisms and substrates, making this task complicated. Identifying general fire-adapted traits in fungi is fundamentally complicated by the many simultaneous biotic and abiotic post-fire changes as well as the diversity of fungal lifestyles, life stages, and dormancy. For plant-associated fungi, decoupling the fungal responses to altered host physiology and to the direct effects of fire is a challenge that will likely require ingenious experimental arrangements or laboratory studies that allow us to determine their changing relative importance across hosts, fire gradients, and soils. Models that explicitly consider multidimensional fungal traits seem the most likely to advance generalizable frameworks to understand fungal fire adaptations, life-history, community structure, and ultimately function. Finally, simplified manipulative pyrocosm systems that have recently been developed (Bruns et al. 2020) may permit detailed investigations of fungal communities – or consortia if such exist – and their responses to fire. Renewed experimentation with individual fungi and fungal consortia in laboratory and mesocosms can provide key data to better generalize fungal responses to fire.

4. Fire-specific fungal traits and pyrophilous fungi

Organisms respond to fires in many ways. Although nearly exclusive to burned areas, some fire-responsive species may also fruit in unburned habitats but flush in large numbers after a fire. However, it is often unclear what are the traits that define fire-resistant, fire-tolerant, fire-responsive, or fire-adapted fungi – or how these broad categorizations differ. We approach these questions through carefully selected examples and consider whether lifestyles that include dormant propagules that may persist through fires should be incorporated. Much of what we currently know about fungi and their fire adaptations or fire-related traits comes from records of fungal fruiting or – more recently – from molecular analyses of substrates exposed to fire. As a result, the fire-related traits are usually indirectly inferred from such data and direct observations of morphological and/or physiological adaptations are few.

Fungal adaptations to fire cannot be examined without explicit consideration of maximum temperatures and duration of heating in the substrate – soil or living plant tissues and litter – or organismal differences in their heat tolerance. A recent meta-analysis of biological responses to soil heating suggests use of duration-temperature models to explore fungal inactivation to better represent the selective pressure such that the cumulative and additive effects of substrate heating could better identify fire-adapted taxa (Pingree and Kobziar 2019). Regardless of how organismal heat tolerances are described, the pyrophilous fungi that we discuss below can survive or even thrive in the post-fire conditions, even though fire duration, intensity or severity are rarely measured in their immediate surroundings or substrates.

4.1 Defining fungal responses to fire: A number of terms (phoenicoid, pyrophilous, anthracophilous, carbonicolous, fireplace fungi, post-fire fungi) have been applied to those specialized fungi that appear after wildfires, in autoclaved soils or on volcanic ash (Petersen 1970; Carpenter and Trappe 1985; Carpenter et al. 1987; Dix and Webster 1995; Fujimura et al. 2005). For most of these fungi, the life history traits that allow long-term survival in the absence of fire but trigger the sudden initiation of post-fire growth or reproduction remain elusive. However, a prerequisite is that pyrophilous fungal mycelia and/or propagules must either be resistant to heat, have propagules in the "goldilocks zone," (Bruns et al. 2020), or rapidly invade burned soils from an external source (Kobziar et al. 2018). Many pyrophilous species that fruit and proliferate rapidly after a fire are in the ascomycete order Pezizales (*Anthracobia*, *Geopyxis carbonaria*, *Morchella*,

Peziza, *Pyronema*, *Scutellinia*, *Sphaerosporella, Tricharina* (Fujimura et al. 2005; Hughes et al. 2020b, 2020a; Figure 2.3); although some pyrophilous basidiomycetes exist (*e.g.*, *Pholiota carbonicola = Pholiota highlandensis, Lyophyllum atratatum* (Matheny et al. 2018; Steindorff et al. 2021). In some cases, the fungal lifestyle may shift from mycorrhizal to saprotrophic following fire (Greene et al. 2010) and often from basidiomycete- to ascomycete-dominated communities (Cairney and Bastias 2007). Fire-derived changes to substrates, including pH, nutrient availability, or competitor mortality, can stimulate fungal species that respond positively across post-fire landscapes for days, weeks, and months. The traits that associate with these responses are inferred for fungi on burns, but empirical data remain limited to a few traits for a few taxa.

4.2 Categories of pyrophilous fungi: Building from previous efforts (Moser 1949; Raudabaugh et al. 2020), we aim to categorize pyrophilous fungi. Here, we categorize pyrophilous fungi as fire-resistant, fire-responsive and fire-adapted - fully acknowledging that these classifications overlap, that some taxa may belong in more than one category, and that the traits we use to define these categories may apply to more than one category.

Fire-resistant - We define fire-resistant fungi as those that are heat-resistant for some aspect of their life cycle. However, fire-resistance may also occur as a consequence of buried propagules that are insulated from excessive heat by substrates. For example, buried sclerotia of some *Morchella* spp. (Figure 2.3B) can survive wildfires (Greene et al. 2010; Baynes et al. 2011) and some fungi likely have persistent, heat-resistant spores, for example *Rhizopogon olivaceotinctus* (Figure 2.3K; Baar et al. 1999; Glassman et al. 2016; Bruns et al. 2019), *Ascobolus carbonarius*, and *Trichophaea abundans* (conidia and ascospores; El-Abyad and Webster 1968b), whereas others may survive as mycelia in mycorrhizae or soil as exemplified by *Wilcoxina rehmii* (Pulido-Chavez et al. 2021). The basidiomycetes *Basidioascus* and *Geminibasidium*, isolated from soil samples, are both heat-resistant and xerotolerant (Nguyen et al. 2013; Enright et al. 2021; Hopkins et al. 2021). The first fungi to fruit after a wildfire are often those with large fire/heat resistant sclerotia or pseudosclerotia (McMullan-Fisher et al. 2011). Without specific fire-resistance experiments, the term **fire-tolerant** is also used, albeit less frequently, to describe fungi found in fire-dependent ecosystems (Dooley and Treseder 2012; Hansen et al. 2019). Such fungi may even be symbionts and have a cooperative tolerance with their plant host (Baynes et al. 2011). While

there is some literature devoted to fungal heat tolerance, fewer studies exist on other chemical and edaphic fire-driven changes in the soil (Pingree and Kobziar 2019).

Fire-responsive - Fire responsive taxa are those triggered to grow and/or fruit by heat or by chemical changes caused by heat (*e.g.*, *Anthracobia, Neurospora*, *Pyronema*). Fire events also tend to increase air-borne spore counts in general with numbers peaking after more than a week after such events (Camacho et al. 2018). However, it remains unclear whether this indicates fire responsiveness. Fire-induced convections of heated air mass and environmental conditions that are favorable for fires may promote the spore release. Alternatively, fire events and conditions favorable for fires may simply disperse spores that would have been released regardless of the fire. Be that as it may, the greater air-borne spore abundances after fires is an interesting dispersal mechanism as is the potential stimulation of spore germination by heated air. Such combined effects might provide an explanation for the rapid appearance of many pyrophilous fungi soon after fire. For example, in moist tropical areas, *Neurospora* appears quickly on burned vegetation (Emerson 1948; Dix and Webster 1995). Similarly, in temperate climates, the operculate Pezizales, (*e.g.*, *Anthracobia* – Figure 2.3D; *Pyronema* Figure 2.3J) rapidly fruit after severe fires. However, dispersal and stimulation by heated convection air mass is likely not the only process at work. Soil sampling suggests that *Pyronema* is normally present in soils at low frequencies but increases rapidly after a fire in soil (Bruns et al. 2020). In this case, spores are not only heat resistant, but their rapid growth appears to be triggered in heat-treated soils (El-Abyad and Webster 1968b). Similarly, Warcup and Baker (1963) found that heat stimulates spore germination for *Anthracobia melaloma* (Figure 2.3D) as well as some aspergilli and penicilli. Many of these fire-responsive species may also be fire-resistant – some may have been locally insulated from fire-generated heat pulses and respond to other indirect stimuli such as nutrient release or reduced competition. While evidence strongly suggests that some fungi are fire responsive and stimulated by fire, it remains unclear if spores can be stimulated to germinate by the heated air mass thus resulting in positive fire response.

Fire-adapted – Fire-adapted fungi are those with specific traits related to fire and that may require fire to complete their life cycle (*e.g.*, *Pholiota carbonicola* (Figure 2.3E), *Sphaerosporella* spp.). Several fungi discussed above also possess clear fire-adaptations, including heat-stimulated spore

production/germination or heat-resistant sclerotia or spores. Fungal traits parallel those of many fire-adapted plants where frequent fires enable some part of their life cycle. Serotinous pines, for example, release seeds after a fire, many *Eucalyptus* spp. produce epicormic buds from the protected vascular cambium tissues (Burrows 2002) and *Quercus suber* (cork oak) protects buds by the thickness of its bark (Burrows and Chisnall 2016). Recent studies with the pyrophilous basidiomycete *Pholiota carbonicola* (Figure 2.3E) demonstrated that it may persist as an endophyte of mosses and fruit only when the host is burned (Raudabaugh et al. 2020). In like manner, *Sphaerosporella* spp. endophytes and/or mycorrhizal partners of *Pinus pungens*, a fire-adapted Appalachian endemic tree, are undetectable in unburned soils, but after a fire, increase in abundance in burned soil and fruit (Hughes et al. 2020a). More work is needed to identify the drivers that allow fungi to either resist or respond to fire, including whether such adaptations are to direct fire effects or the many abiotic and biotic changes fire causes in ecosystems.

4.3 Fire responses of fungal guilds and taxa: Fire can affect fungi differently depending on their ecological guild. For fungi in tight associations with their plant hosts, fire responses can depend mainly on the host responses. Mycorrhizal fungi (Dove and Hart 2017) and many decomposers often decline substantially following fire (Brown et al. 2013; Day et al. 2019; Semenova-Nelsen et al. 2019), albeit these responses depend on fire severity and position in the soil profile. As detailed above, landscape-scale variation in fire severity likely plays an important role in determining the mosaic of hosts for many fungi. In turn, host availability can impact fungal community dynamics by determining inoculum sources that maintain or re-establish the fungal community, whether it be from spore banks, living mycelium that survives in refugia, or new propagules arriving from outside the burn.

Most studied are mycorrhizal fungal responses, which vary widely and likely reflect their diversity. Fires tend to decrease overall mycorrhizal fungal richness (Dove and Hart 2017). A decline that can persist a decade or more in systems impacted by high severity fire (Pulido-Chavez et al. 2021). The dependence of mycorrhizal responses on fire characteristics and ecosystem attributes is another key factor that make broad generalizations so difficult. Certain ectomycorrhizal taxa dominate soon after fire. The ascomycete *Pustularia*, for example, was a dominant ectomycorrhizal fungus two years after high severity fires in Washington ponderosa pine stands

(Pulido-Chavez et al. 2021). Several other ectomycorrhizal genera clearly colonize roots shortly after fire, including *Thelephora, Phialophora, Pustularia, Amphinema* and *Wilcoxina* (Bent et al. 2011; Kalucka and Jagodzinski 2016; Pulido-Chavez et al. 2021). In Pinaceae-dominated systems, *Suillus* and *Rhizopogon* species often colonize young seedlings on both unburned and burned sites where they may arise early from spore banks or via animal vectors (Ashkannejhad and Horton 2006; Glassman et al. 2016). Similarly, *Hebeloma anthracophilum* appears restricted to fire-impacted sites, although its ectomycorrhizal status needs confirmation, as do some putatively ectomycorrhizal ascomycetes on burns (*e.g.*, species of Pezizales in Fujimura et al. 2005). Fire also reduces the overall richness of AM fungi in many systems, yet several taxa increase in abundance (spores or sequences) following fire (Dove and Hart 2017), responses potentially linked to those of their hosts.

Although less researched following fire, changes in fungal pathogens may either reflect the loss of available hosts or opportunities to infect hosts with compromised disease resistance and/or damaged by fire (Brown et al. 2019; Semenova-Nelsen et al. 2019; Dove et al. 2021). Most surveys provide evidence for the latter. Several taxa in the plant pathogen genus, *Teratosphaeria*, were key indicators of burned plots (Semenova-Nelsen et al. 2019) in pine savannas. Potential fungal pathogens in aspen leaves resprouting after fire were four-fold higher compared to similarly aged leaves in unburned sites (Dove et al. 2021). In Western North America, fungal forest pathogens often disperse to damaged trees via insects (Parker et al. 2006). Just as with insect defoliation (Saravesi et al. 2015), defoliation by fire likely alters plant host C allocation leading to fungal community responses belowground of many different functional groups. Fungal parasites of other taxa (*e.g.,* animals, insects, other fungi) may also shift after fire, but are even more poorly studied than plant pathogens. Almost certainly these responses are not homogeneous and likely depend on the dispersal limitations or the fire regimes (*e.g.,* frequency, severity) of the systems in which the fungi have coevolved with their hosts.

Finally, some presumed saprobes (post-fire ascomycetes such as *Anthracobia* (Figure 2.3D) and *Pyronema* (Figure 2.3J)) appear unique to burned environments. Fire responses of saprobic fungi are likely complex, because of the many abiotic and biotic factors that rapidly and simultaneously shift because of a fire. Fire results in a heat pulse and may lead to sterilization of soil – at least in

the topmost layers, if large volumes of fuel have accumulated (*e.g.*, slash piles, large down wood) (Busse et al. 2010; Smith et al. 2016). Some wood-inhabiting fungi reportedly have heat-resistant mycelia which can favor them in fire-prone or post-fire environments (Carlsson et al. 2012). The heat pulse can also change the nutrient and substrate environment (Certini 2005) and produce necromass that may serve as a substrate for a number of specialized saprobes. Clearly, there is a need to distinguish between the taxa that use pyrogenic materials and opportunists that exploit resources made available by the death of others. Differentiating these may help us better generalize saprobic fungal responses to fire. While variation within these functional guilds challenges our ability to generalize, these examples highlight fungi in different functional guilds that all thrive after fire. We suggest these functionally different fungi may be central players in fire-adapted fungal consortia.

4.4 Cosmopolitan vs. endemic pyrophilous fungi: Wildland fires are globally prevalent (Scott 2008). Yet, it remains unclear whether particular taxa of pyrophilous fungi have a widespread distribution or individual fungal lineages have arisen in different ecosystems. Many fungal taxa that respond positively to fire were also observed after the volcanic eruptions of Mount St. Helen's, 1981-1983 (Carpenter et al. 1987), perhaps because of similarities with fire: increased soil pH, altered soil chemistry, and abundant necromass. Across different fire events, however, the same taxa are not consistently present, highlighting the variety of uncertainties and unknowns about fungal fire ecology and fungal responses to fire. For example, *Pyronema* spp. are often considered pyrophilous (Petersen 1970; Bruns et al. 2020), yet they are not always present after a fire (Brown et al. 2019; Semenova-Nelsen et al. 2019; Hopkins et al. 2021). It remains uncertain whether these differences stem from biome and system distinctions or mere absence of communities or propagules that strongly and positively respond to fire.

Many pyrophilous fungi are thought widely distributed (Larson et al. 2016) but distribution data are sparse. Limited post-fire collections among ecosystems and following fires of different severities compromise our ability to assess distributions of post-fire fungi. The problem is exacerbated by three key issues: i) geographic sampling that is biased towards Australia, North America, and Europe; ii) the paucity of molecular data for pyrophilous fungi and inaccurate or uncertain identifications in the literature and GenBank; and, iii) the lack of expertise to accurately

identify pyrophilous fungi, especially within the Pezizales, which dominate early post-fire fruiting. Sampling itself can often be challenging. Wildfires are unpredictable and the specific timing of prescribed fires depends on weather. Further, burns are heterogenous and the timing of pyrophilous fungus responses varies as a direct result. Even obtaining permits to sample recently burned areas can be difficult because these landscapes may be dangerous or inaccessible for long periods of time. Given these challenges, it is difficult to ascertain which pyrophilous taxa are truly cosmopolitan. Below, we exploit existing literature on pyrophilous fungi, alongside available morphological and DNA sequence data to determine if there is evidence of ubiquity (Table A 1). We focus on three genera for which more data exists. We aim to err on the side of caution as we fully acknowledge that 'absence of evidence is not evidence of absence' - a note particularly fitting here.

Anthracobia (Pyronemataceae; Ascomycota): Widely considered an obligate pyrophilous taxon (Larsen 1975), *Anthracobia*'s life cycle (like many post-fire fungi) in the absence of fire is largely unknown and may involve saprotrophic or endophytic stages. All *Anthracobia* spp. seem pyrophilous with the exception of "Taxonomic species B" which fruits on cow dung (Larsen 1975). *Anthracobia* spp. have been reported fruiting in North America following the Washington State Mount St. Helens eruption (Claridge et al. 2009) and wildfires in the western (Fujimura et al. 2005; Claridge et al. 2009) and eastern United States (Hughes et al. 2020b). They have also been observed fruiting after wildfires in Australia (Warcup 1990; McMullan-Fisher et al. 2011), the United Kingdom (Wilberforce 2005), and Denmark (Dix and Webster 1995). From this limited evidence, we conclude that the genus *Anthracobia* may have a cosmopolitan distribution. The details on the distribution of species within the genus *Anthracobia* are included in Supplementary Materials (Table A 2).

Morchella (Morchellaceae; Ascomycota): Field guides tend to treat the true morels as a few, widely distributed species and frequently use incorrect European names for North American taxa (O'Donnell et al. 2011). Certainly, the genus *Morchella* appears to have a cosmopolitan distribution with reports from North America and Europe (Richard et al. 2015), South and Central America (Baroni et al. 2018), Israel (Masaphy et al. 2008; Masaphy and Zabari 2013), Turkey (Taşkın et al. 2012), China (Du et al. 2012) and Australia (Elliott et al. 2014). It remains less certain

whether this is true for congeneric species - particularly so for those considered pyrophilous. Most *Morchella* spp. are not fire responsive (Kuo et al. 2012). Of those that are pyrophilous, some may be obligately so (fruiting only after a fire, fire-adapted), whereas others are facultative (fruiting enhanced by fire, fire-responsive - O'Donnell et al. 2011). Reported pyrophilous *Morchella* spp. include (but are not limited to) *M. tomentosa* (Stefani et al. 2010; Kuo et al. 2012), *M. sextelata* (Kuo et al. 2012), *M. septimelata* = *Mel-7* of O'Donnell 2011 (Kuo et al. 2012), *M. capitata* (*M. exuberans*; Kuo et. al 2012), and *M. eximia* (*M. anthracophila*; Richard et al. 2015). In the eastern U.S., *M. exuberans* fruited in a *Pinus pungens* forest following a wildfire (Miller et al. 2017) and *M. importuna* was collected after a fire in a burned pine forest in Sichuan, China (Li et al. 2017). Li et al. (2017) consider *M. importuna* as a fire-responsive taxon "involved in nutrient acquisition", but Kuo et al. (2012) describe this species as growing in planters and on wood chips in landscaping. *Morchella conica* was observed in pine plantations in Israel five months after a fire (Masaphy et al. 2008). These reports highlight the broad interest in pyrophilous *Morchella* as well as the taxonomic challenges that are inherent in generalizing their fire responses.

It is likely that fire adaptation is convergent in *Morchella* (O'Donnell et al. 2011). Current estimates of the evolution of a clade of fire-adapted morels dates to the Oligocene 25 million years ago (O'Donnell et al. 2011). Three species from this clade observed in Turkey (*Mel7, 9, 10*) appear to be endemic to western North America (Taşkın et al. 2012), perhaps transferred with pine plantings in Turkey. The *M. elata* subclade provides key examples of the diversity of fire-responses within a subclade (O'Donnell et al. 2011). Two species, *Mel*-7 and *Mel*-9, are obligate post-fire species, whereas *Mel*-10 appears to be facultatively fire-responsive. In contrast, *Mel*-6 and *Mel*-12 are *Bromus tectorum* endophytes able to increase host seed production and biomass. Interestingly, infected plants produced seed that was better adapted to fire (Baynes et al. 2011). Overall, we conclude that the genus *Morchella* is cosmopolitan but only some of the congeneric species seem pyrophilous. Known pyrophilous *Morchella* spp. seem not cosmopolitan, but instead limited in distribution to specific ecosystem(s).

Pyronema (Pyronemataceae; Ascomycota): Evidence that the genus *Pyronema* is pyrophilous dates back more than a century (Seaver 1909). Like *Anthracobia* and *Morchella*, several *Pyronema*

spp. are globally distributed and appear rapidly after fires. High throughput sequencing (HTS) data in the Western US, for example, suggest that *Pyronema* spp. are highly abundant as mycelium in soils immediately post-fire (Reazin et al. 2016; Bruns et al. 2020). *Pyronema* species were nearly undetectable via HTS of unburned soils, but *Pyronema domesticum* surged to 58% and *P. omphalodes* to 7% of ITS1 sequences after experimental fires in laboratory pyrocosms (Bruns et al. 2020). *Pyronema* spp., however, were not detected with HTS of ITS2 amplicons (Ihrmark et al. 2012) after wildfire in the Southern Appalachians (Brown et al. 2019) or prescribed fires of Longleaf pine savannas (Semenova-Nelsen et al. 2019) and prairies (Hopkins et al. 2021), even when other Pyronemataceae were present. Available evidence suggests that the genus *Pyronema* is spotty in its distribution even in relation to fire and likely requires a threshold of fire severity to bloom.

Pyronema omphalodes (Figure 2.3J) and *P. domesticum* are the two most likely candidates for cosmopolitan fire fungi. Both have been reported as fireplace fungi in northern Europe (Petersen 1970). A *Pyronema* sp. (reported as *P. omphalodes* in Warcup 1990) fruited in high abundance after wildfires in *Eucalyptus* forests in Australia (Warcup 1990) and *P. omphalodes* (= *P. confluens*) has been reported to fruit after fires across the USA in Iowa, New York, and North Dakota (Seaver 1909). After a 2016 wildfire in Tennessee, *P. omphalodes,* but not *P. domesticum,* was recovered both as ascomata on burned soil (Hughes et al. 2020b) and as ITS2 sequences from severely burned soils but not in great abundance and only in hemlock/pine areas (Hughes unpublished data). Other studies report that *P. domesticum* and *P. omphalodes* accounted for approximately 60% of ITS1 sequences after a mega-fire burned down a *Pinus ponderosa* forest in the California Sierra Nevada (Glassman unpublished data) and after a high severity fire burned a California Chaparral shrubland (Figure 2.4). *Pyronema domesticum* ITS1 sequences also increased 100-fold in frequency after experimental fires in an Oregon *P. ponderosa* forest (Reazin et al. 2016). From available literature and molecular data, we conclude that *P. domesticum* occurs in Europe and Western North America, whereas *P. omphalodes* may have a broader distribution including eastern and western North America, Europe, and Australia. Thus, *P. omphalodes* may be a true cosmopolitan dominating post-fire landscapes ranging in host diversity (Eucalyptus and Pine forests, Chaparral) and globally from Australia to Europe to western North America. Details on the distribution of species within the genus *Pyronema* is included in (Table A.1).

Available data and literature strongly suggest that while pyrophilous genera are likely globally distributed, congeneric species may often have much more limited ranges. Admittedly, our conclusions are based on limited data and likely biased towards Europe, North America and Australia. We posit that it is likely that there are also locally adapted and endemic pyrophilous taxa. For example, *Rhizopogon olivaceotinctus* (Rhizopogonaceae, Figure 2.3K) is a hypogeous, putatively pyrophilous basidiomycete that forms ectomycorrhizae with western North American pines and appears to be endemic to these forested systems. *Rhizopogon olivaceotinctus* dominated root colonization after the 1995 Vision Fire burned down a *Pinus muricata* forest (Baar et al. 1999) and after the 2013 Rim Fire burned down a *Pinus ponderosa* forest (Glassman et al. 2016), both in California. Its great abundance in the roots of juvenile trees is likely due to its ability to produce and maintain prolific thermotolerant spore banks in soil (Bruns et al. 2019). Many more endemic pyrophilous fungi may exist that are thus far at best known only as sequences in community surveys or more likely, wholly undescribed.

It is increasingly clear that detection and identification of pyrophilous fungi, including defining their endemism, depends on the timing of the fire and subsequent fungal surveys because pyrophilous fungi follow distinct temporal trajectories. For example, the intensive temporal sampling in the year following the 2018 Holy Fire in southern California demonstrates marked shifts in soil fungal abundance over time (Figure 2.4; Glassman unpublished data). Within the first several weeks post-fire, the basidiomycete yeast *Geminibasidium* dominated (data not shown), but then quickly declined as the ascomycete *P. domesticum* spiked in abundance. After a month, other ascomycetes (*Aspergillus* and *Penicillium*; Aspergillaceae) increased in abundance (Figure 2.4). Whilst we do not wish to argue that all these taxa are pyrophilous, soil heating experiments suggest thermotolerance of some aspergilli and penicilli (Warcup and Baker 1963) as well as *Geminibasidium* (Nguyen et al. 2013) and *Pyronema* (Bruns et al. 2020). Similar post-fire taxa were also found in ~monthly sampling following prescribed fires in both Longleaf pine savanna (Florida) and tallgrass prairie sites (Kansas), including Aspergillaceae, Pyronemataceae, and *Geminibasidium* (Hopkins et al. 2021). It remains uncertain if these taxa occur following a fire because of their thermotolerance or if they have alternate strategies such as fast post-fire colonization, response to fire-generated necromass, or release of cytoplasmic contents after

organismal death. More time series data – both on finer temporal scales as well as over longer periods post-fire – are necessary to help identify and determine the ubiquity of pyrophilous taxa.

In conclusion, a few cosmopolitan pyrophilous taxa likely exist, but more sampling is necessary in Africa, South America, and Asia to confirm if they are truly cosmopolitan. Most data are limited to single post-fire sampling of fruiting bodies or HTS data based on short ITS fragments with limited taxonomic resolution. Thus, it remains a challenge to validate distribution based on the available data. To better understand the pyrophilous taxon distribution, molecular data including nrITS sequences must be linked to morphological descriptions for vouchered pyrophilous fungi worldwide. Such data and collections would also facilitate detailed studies aiming to resolve whether putative species are cryptic complexes that may include endemic taxa.

5. Sources and dispersal of pyrophilous fungi

Sparse empirical data currently limit our understanding of the early post-fire dynamics of fungal communities (but see Hopkins et al. 2021). Instead, most post-fire fungal successions rely on space for time substitutions (*e.g.,* chronosequences), or sample after enough time has passed that important fungal responses may have been missed (Dove and Hart 2017; Pressler et al. 2019; Yang et al. 2020). While providing critical data on which our understanding (and much of this paper) are based, so far all fail to identify inoculum sources in the post-fire landscape. These sources may determine immediate fungal fire responses and, if priority effects are important, longer term community assembly.

Fungi must either survive fire or recolonize soon after to establish the diverse and functionally important post-fire communities. Fungal spores can and likely do arrive aerially any time after the fire. Interestingly, recent evidence suggests that fungal spores can also arrive to burn sites aerially via smoke vectors (Kobziar et al. 2018; Moore et al. 2021). Low density propagule pools likely exist that are stimulated by heat and/or the resultant changes in soil chemistry. Additional mycelial reservoirs are possible in unburned roots (Vrålstad et al. 1998; Dighton 2003), other plant tissues (Wang et al. 2016), and bryophytes (Raudabaugh et al. 2020), or may survive as sclerotia or tubers (McMullan-Fisher et al. 2011). However, the relative importance of these sources – whether from external sources (*i.e.,* allochthonous), or dormant propagules and/or surviving mycelia already at

the site (*i.e.*, autochthonous) – remains uncertain (Figure 2.2). Post-fire communities establish rapidly after a fire (Reazin et al. 2016, Bruns et al. 2020), suggesting that the initial community likely includes a large component of resident, resistant propagules. Even at small scales – in mesocosms or campsite fire pits – pyrophilous fungi either establish vegetative mycelia or fruit abundantly (Adamczyk et al. 2012; Bruns et al. 2020), providing additional support for the importance of local propagule pools in the establishment of pyrophilous fungal communities. The importance of other mycelial reservoirs may still be important as well.

What reservoirs may be present within the system after fire? Soil heating reduces vegetative mycelium, particularly in the organic and upper mineral soil layers (Cairney and Bastias 2007; Dooley and Treseder 2012). However, mycelial inocula can be derived from cryptic life stages in unburned plant parts (Raudabaugh et al. 2020), or in roots of dying trees (Dighton 2003). Within plants, fire causes declines in colonization that coincide with compositional changes in mycorrhizal associates. When measured *in situ*, mycorrhizal colonization often declines following fire, whereas colonization measured in bioassays does not (Dove and Hart 2017). This difference may indicate shifts in pools of organisms that either survive to colonize new roots *versus* those that establish from resident propagule pools. Many post-fire fungi may form new mycorrhizal associations soon after a fire (Egger and Paden 1986; Vrålstad et al. 1998; Dahlberg 2002) and we posit these are more likely to establish from resident spore banks rather than from surviving mycelia in soil (Baar et al. 1999; Glassman et al. 2016). Some ectomycorrhizal fungi already in soils clearly produce heat-resistant spores (Peay et al. 2009) explaining the increase in their abundance after experimental or natural soil heating (Izzo et al. 2006; Peay et al. 2010; Glassman et al. 2016).

Early colonization may be from autochthonous reservoirs, but recent work has confirmed the importance of fire to fungal dispersal and showed clear pathways for post-fire dispersal into fire-impacted sites. Fires in the Mediterranean increased airborne fungal spores, with a peak ~10 days after fires (Camacho et al. (2018) and abundant fungal propagules aerosolized within smoke plumes that followed prescribed fires in Florida pyrogenic ecosystems (Kobziar et al. 2018). These studies suggest that pathogenic and non-pathogenic fungal dispersal may be fire-stimulated. More work is clearly needed on microbial aerobiology in relation to fire (Moore et al. 2021). Small

mammals (Johnson 1995; Trappe et al. 2005) and invertebrates (Vašutová et al. 2019) may also carry fungal spores to and from burned sites. Pyrophilous mycophagous insects are attracted to recently burned areas (Wikars 2002) and, as noted above, are important in the post-fire spread of fungal tree diseases (Parker et al. 2006). Beyond specific forest pests, however, how important they are as fungal vectors for dispersing spores remains unknown.

Current understanding of pyrophilous fungi is based mainly on records of fruiting. Undeniably, vegetative establishment and mycelial resource exploitation must precede the observed fruiting further highlighting the expedient pyrophilous fungal responses. The fire-fungal traits section above details how fire stimulates sporulation, growth, and fruiting in several different species. Based on this rapid fruiting and mycelial expansion inferred from molecular data, we posit that most pyrophilous fungi recorded as fruiting bodies emerge from resident inocula. More broadly, sources that establish the distinct post-disturbance fungal communities following fire are largely unresolved. Post-fire species may survive as mycelium (Vrålstad et al. 1998), have inactive spores present in soil that germinate only after exposure to fire (*e.g.,* El-Abyad and Webster 1968b; Jalaluddin 1969), or may establish from air-borne propagules (Chen and Cairney 2002) or from plant reservoirs (Raudabaugh et al. 2020). We speculate that post-fire communities, now overwhelmingly characterized using molecular tools, are most likely a combination of air-borne sources and – to a larger extent – a rapid vegetative expansion from either a heat-resistant or deep-buried propagule banks and perimeters of the intensely burned areas that lead to the community turnover resulting from the rapid responses to fire. These speculations are consistent with observations of low frequency detection of the post-fire dominants in the pre-fire communities and the very fast establishment of the post-fire community. Many open questions remain about the necessary morphological, genomic, and physiological adaptations that underlie the fungal responses to fire-generated stimuli.

6. Conclusions

Fire effects on ecosystem properties and biodiversity are increasingly important research areas as fire frequencies and burn severities increase in many areas because of climate change and an expansion of the wildland-urban interface. Our synthesis explores the impacts of fire on fungal communities and their diversity. It is important to improve our understanding of fire in the Earth

system by focusing on non-plant organisms, which are generally overlooked in fire ecology. Our goal was to highlight fungal fire traits, key pyrophilous fungi, and fungal community dynamics initiated by fire, identifying key research gaps along the way. Applying existing frameworks for fungal fire responses is challenging because of the many unique life history traits fungi possess. Developing matrices of trophic, dispersal and metabolic traits may serve as an effective tool to characterize the largely unknown diversity of pyrophilous fungi (Zanne et al. 2020). Although this synthesis shows how much we have learned about fungi that commonly appear in fire-impacted systems, the temporal component is often lacking from our research. Experiments that combine pre-fire conditions and repeated sampling in time series are sorely needed. Combining sequencing approaches with vouchered specimen collections in this research is also critical to better link DNA-based community responses to specific cosmopolitan pyrophilous taxa. Such studies can also help differentiate immediate community dynamics from longer term successional trajectories to distinguish fungi that exploit fire-impacted systems and provide essential ecosystem functions at different time scales. Such experiments might best be combined with mechanistic tests that help explain how specific fungi proliferate in post-fire environments. Another key area that is lacking data is fungal community functional responses to fire. Are shifting communities functionally distinct or redundant? Do fire-resultant changes in substrates lead to novel functional attributes in these communities? Post-fire fungi appear poorer at decomposition in some systems (Semenova-Nelsen et al. 2019, Hopkins et al. 2020), but is this a general phenomenon? The current explosion of environmental meta-omics tools may permit substantial insight in how to better tackle these challenging questions (*e.g.*, Nelson et al. 2021). Ultimately, we argue that much progress can be made by relatively simple laboratory experiments that focus on identifying crucial pyrophilous traits. This is particularly the case if such minimalistic experiments are combined with carefully designed experiments in mesocosm systems or in field manipulations.

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Chapter 2 Tables and Figures

Figure 2.1 Conceptual Model of Fungal Fire Systems

A conceptual model demonstrating the ecosystem and fire regime attributes that contribute to structuring the pre-fire fungal communities and to the fire behavior and its impacts on fungal community dynamics. While some systems (*e.g.*, grasslands) may be maintained by fires, others *(e.g.*, temperate and boreal coniferous forests) experience fires infrequently. These ecosystem attributes are linked with fuel accumulation and fire intensity or severity, highlighting the numerous context dependencies that preclude universal general statements about fungal fire responses. This work discusses various ecological frameworks that can be applied to better understand fungal responses to fire including trait- or consortium-based frameworks as well as those that link pyrodiversity or community assembly and succession. Only some members of the fungal communities are directly impacted by fire or fire-induced mortality. Others are impacted indirectly and may primarily respond to changes in substrates or environmental conditions, whereas others yet respond to loss hosts or changes in their physiology. Post-fire fungal communities are composed of fungi that may rely on local refugia and spore banks or newly enter aerially, perhaps even within the smoke plumes. A subset of these fungi are pyrophilous and respond positively to fire or prevailing conditions in the post-fire environment. Illustration by Ellen Meyer.

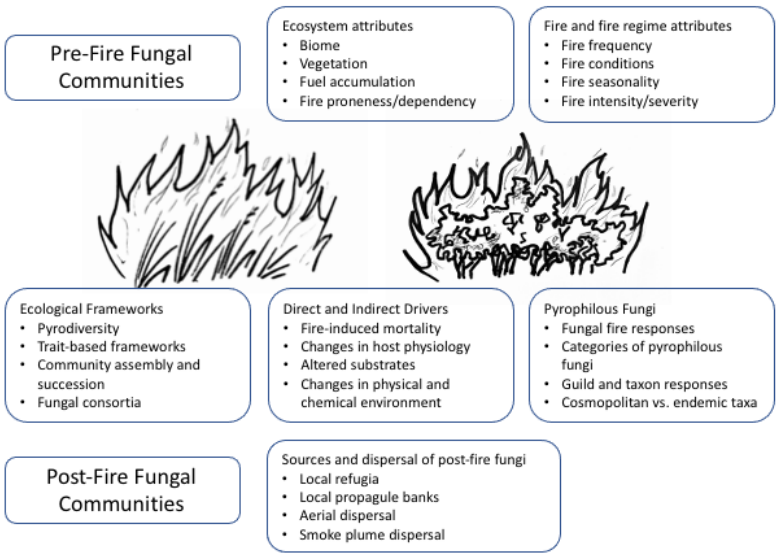


Figure 2.2 Conceptual Model of Fungal Community Responses to Fire

A conceptual model highlighting the interdependencies of system and environmental contexts and resultant variability in fungal community responses to fire. Ecosystems differ and environmental conditions vary in fire regimes and conditions. Direct fire-induced mortality as well as indirect effects including changes in soil chemistry and structure, removal of hosts and substrates, or the altered competitive balance among the resident organisms impact fungal communities and change their composition. Post-fire communities are a result of survival of fire resistant fungi as well as those that are protected by refugia or those that are able to return after fire from local and distant sources. Pyrophilous fungi are often stimulated by fires and increase in abundance following a fire event. Assembly of the fungal communities in the median and long-term can be considered in the contexts of successional dynamics and assembly rules or theoretical frameworks that incorporate these concepts.

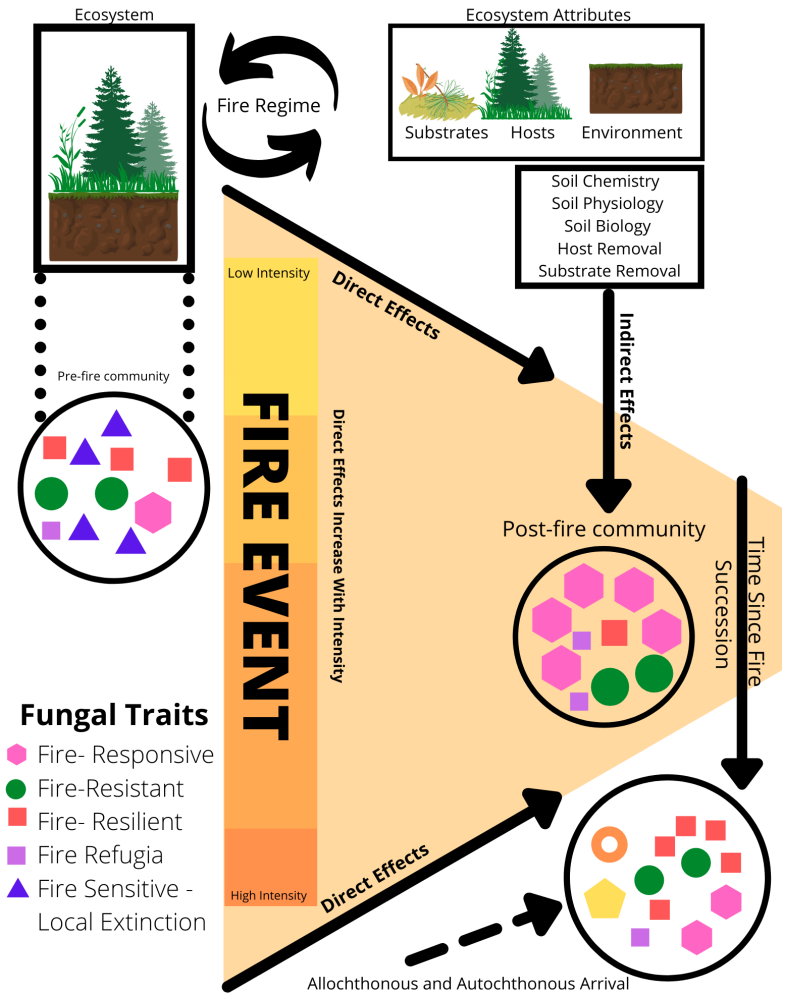
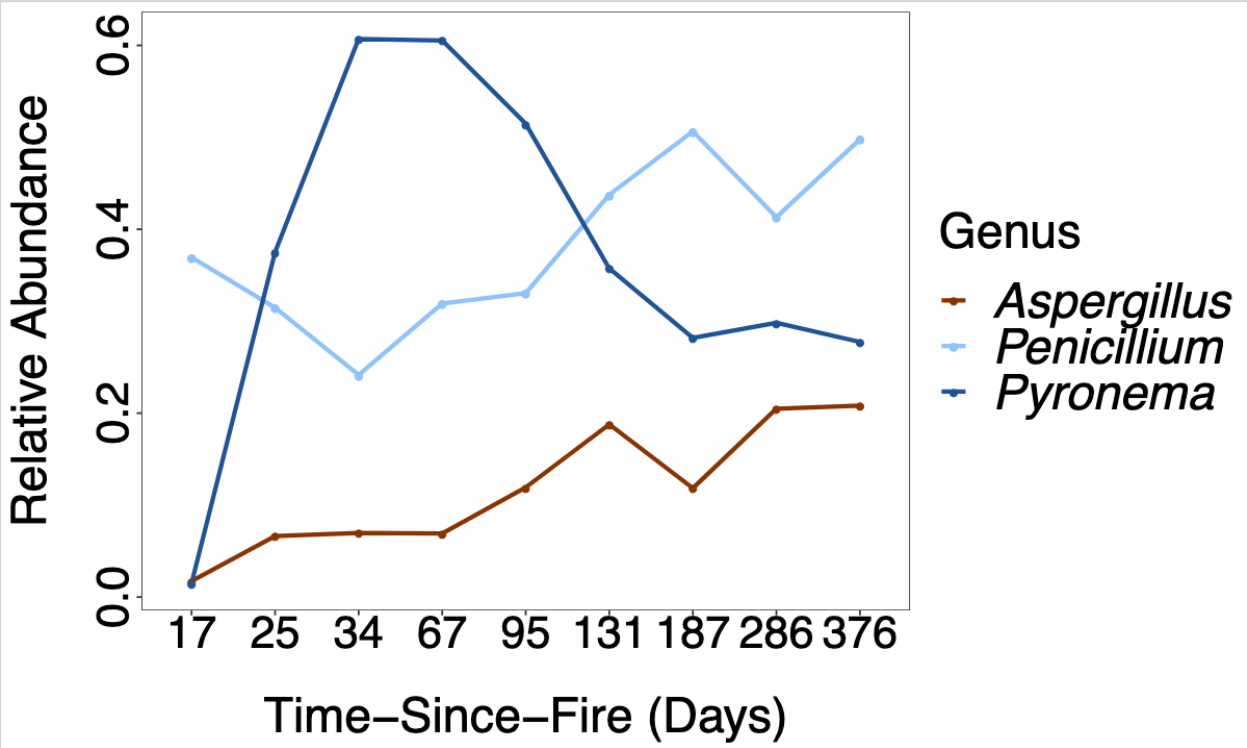


Figure 2.3 Examples of Fruiting Pyrophilous Fungi

Examples of common ascomata and basidiomata found after fires, including prescribed burns and wildfires in the eastern and western United States. A) *Peziza echinospora* – following 2016 wildfire in Great Smoky Mountains National Park – photo by K. Hughes B) *Morchella cf septimelata* (CLC3670(MONT)) following 2017 Meyers Fire, MT – photo by C. Cripps. C) Flush of undescribed *Clitocybe* spp. following 2018 prescribed fire at St. Joseph Bay State Buffer Preserve, FL – photo by J. Huffman D) *Anthracobia cf. melaloma* (TENN-F-071502) following 2016 wildfire at Great Smoky Mountains National Park – photo by B. Matheny. E) *Pholiota carbonaria* – following 2017 prescribed fire at Wade Tract near Thomasville, GA – photo by B. Sikes. F) *Pachylepyrium carbonicola* following 2001 Fridley Fire, MT wildfire – photo by C. Cripps. G) *Geopyxis carbonaria* (CLC2304(MONT)) following 2006 Jungle Fire, MT wildfire – photo by C. Cripps. H) *Hygrocybe conica* (TENN-F-071517) following 2016 wildfire at Great Smoky Mountains National Park – photo by B. Matheny. I) *Tricharina praecox* – following 2013 Rim Fire (wildfire), California – photo by T. Bruns. J) *Pyronema omphalodes* following 2014 Rim Fire, CA – photo by T. Bruns. K) *Rhizopogon olivaceotinctus* following 2013 Vision Fire in Pt. Reyes, CA – photo by T. Bruns.

Figure 2.4 Relative sequence abundance of top three genre following a fire

Relative ITS2 sequence abundance (using Illumina Miseq) of top three most abundant genera after the 2018 Holy Fire burned down a Manzanita (*Arctostaphylos* sp) dominated Chaparral in southern California. Sampling occurred nine times between two weeks and approximately one year post-fire. Glassman lab unpublished data.



Chapter 3 - Over a Half Century of Prescribed Fire Interval Manipulations Alter Microbial Communities in the Upmost Soil Horizon in Florida Longleaf Pine System

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Key Words: fire; community ecology; bacteria; fungi; forest

Abstract

Prescribed fires are common in forest management, yet we lack a clear picture of how different fire frequencies impact soil systems. Here, we present evidence of microbial community and soil chemistry shifts following sixty years of continuous prescribed fire interval manipulation at the Olustee Experimental Forest in Northeastern Florida. We investigated three fire interval treatments (1year, 2 years, and 4 years) in addition to a comparable control treatment without fire in over sixty years. Excluding the O horizon that was absent in the most frequent fire treatments, we sampled three mineral soil horizons (A, E, and B) to elucidate prescribed fire impacts across the soil profile. Our results indicate that only the topmost A horizon was affected by the fire interval manipulations, whereas the deeper E and B horizons were minimally impacted. Richness of both bacterial and fungal communities in recurring fire treatments was higher than, and their community composition different from, those in the fire exclusion control in the A horizon. Similar to the biotic soil attributes, fire interval treatments altered soil chemistry only in the A horizon: the

frequent prescribed burns (one-, two-, four-year fire intervals) had higher total nitrogen, total carbon, phosphorus, and NH_4^+ than the fire exclusion treatment; the soil chemistry of the deeper E and B horizons did not differ among the treatments. The soil chemistry correlated with the microbial community composition, especially when comparing the more frequent burns to the fire exclusion treatment. Indicator taxon analyses identified fire-responsive bacteria and fungi, such as *Ktedonobacteria* sp. and an unclassified ascomycete that were abundant in the fire exclusion treatment and the ectomycorrhizal *Russula* spp. that were most abundant in the annual burn treatment. The different fire intervals also impacted fungal guilds suggesting shifts in community function. The fire exclusion treatment was enriched with ectomycorrhizal, lichenized, and wood saprotrophic fungi, whereas the annual burn treatment was enriched with arbuscular mycorrhizal fungi compared to the other treatments. Given the many roles of microbial communities in soil systems, our results suggest that recurring prescribed fires change the soil microbial communities and their function as well as soil chemistry, although mainly only in the uppermost soil horizon.

Introduction

Prescribed fires are a common forest management practice implemented to reduce fuel loads and to restore fire-adapted landscapes (Ryan et al. 2013). Fire suppression in fire-adapted landscapes can lead to compositional shifts in resident communities, biogeochemical cycling, and overall biodiversity (Bond et al. 2005; Donovan and Brown 2007; Pressler et al. 2019; Certini et al. 2021). Prescribed fires have been widely used for centuries in the United States, and such fires are typically less severe than wildfires. Traditional ecological knowledge of prescribed burning is still used by Native Americans to promote certain plants, as some require fire to germinate (Agee 1996; Anderson 2005). Currently however, many sociopolitical issues and inadequate funding often preclude fire restoration in the United States (Ryan et al. 2013). These issues include increase in cropland, grazing land for livestock, and increase in human population that has led to an increase in wildland-urban interface that makes fire management difficult, with an estimated loss of ~25% of burn area (both prescribed and wildland) from 1998-2015. (Andela et al. 2017). Over 70% of the land that is burned using prescribed fire in the United States is located in the southern states that are dominated by longleaf pine forest (Kolden 2019).

Many prescribed fire studies have focused on responses in plant communities or soil chemistry (Certini 2005). In contrast, studies focusing on soil-inhabiting bacteria, archaea and micro-eukaryote communities and their responses to prescribed fire are fewer (Certini et al. 2021). These organisms provide important ecosystem functions such as nutrient cycling and carbon sequestration (Crowther et al 2019). In the past few years, however, research focusing on microbial community fire responses has increased (Dove and Hart 2017; Pressler 2019; Certini 2021). Thus far though, only a few studies have aimed to elucidate how fires impact microbial communities and the soil chemistry in different soil horizons (Yang et al. 2020; Qin and Liu 2021), particularly so in experimental manipulations that have been maintained over extended periods of time. Most studies commonly sample only the top 10cm of the soil because most of the abiotic and biotic activities occur there and fire impacts are most obvious there (Certini 2005; Joergensen and Emmerling 2006). As a result, the impacts of maintained prescribed fire regimes on deeper horizons in the soil profile have received little attention.

In this study, we exploited a unique 60-year experiment to gain further insight into how fires impact soil chemistry as well as bacterial and fungal communities in soil. Our primary goals were to (1) understand how the different fire intervals impact the soil chemistry and microbial communities and (2) investigate how soil chemistry and microbial communities in different soil horizons (A, E, and B) respond to the fire interval manipulations in the long term. We hypothesized (1) that the frequent fire intervals would result in microbial communities and soil chemistry attributes distinct from those present in soils where fire had been excluded in the long term and (2) that the soil chemistry and microbial communities in the top-most mineral horizon (the A horizon) would be the most responsive to recurring prescribed fires compared to the other two horizons (E and B).

Materials and Methods

Study site

The experiment is located in the Olustee Experimental Forest within the Osceola National Forest in Baker County in Northeastern Florida (30°14’17” N, 82°24’41” W). This experimental forest

is one of 19 maintained by the USDA Forest Service Southern Research Station. It was established in 1931, originally used to study naval stores (resin products used for water-proofing). Overstory vegetation at the site is dominated by longleaf pine (*Pinus palustris* Mill). Understory vegetation at the site is characterized by shrubs such as *Quercus minima* (Sargent) Small (runner oak), *Serenoa repens* (Bartr.) Small (saw palmetto), *Ilex glabra* (L.) Gray (gallberry), and *Lyonia ferruginea* (Walter) Nutt. (fetterbush), along with a diverse array of grasses and herbs in the ground layer vegetation (Glitzenstein et al. 2003). Soils at the site are derived from marine sediments and classified as sandy, siliceous, thermic Ultic Alaquods (Sapelo series) (Watts 1996; Soil Survey Staff 2004).

Experimental design

We utilized a research infrastructure established in 1958 that has been continuously maintained by the USDA Forest Service Southern Research Station since its initiation – for a total of sixty years at the time of our sampling in 2018. The objective of this broad long-term study was to evaluate long- and short-term vegetation responses to prescribed fire occurring at different return intervals (annual, every 2 years, every 4 years, and an unburned control). We will use T1, T2, T4, and T60 for these treatments from here on. The experiment is arranged in six blocks dispersed over a slight moisture gradient. Each block has one replicate of each of the four fire treatments. Each treatment in the experimental design was replicated in a 0.8 ha plot in each of the six blocks for a total of 24 plots across the six blocks and four fire interval treatments. All plots had been established in a longleaf pine stand that was approximately 50 years old at the time of establishment, and that had experienced limited fire management before this experiment. Since 1958, experimental prescribed fires have been consistently conducted on schedule.

Soil sampling

We sampled soils in January 2018 within a week before the prescribed burns were to take place. Our sampling took place during a year when all burn treatments synchronized such that all prescribed burns were scheduled for burning and all burn intervals were as close to complete as possible. In other words, plots that were scheduled for annual burn cycles had been burned approximately 12 months ago, whereas those scheduled for four-year intervals had been burned approximately 48 months ago.

To get a representative sample of the 0.8 ha plots, we selected seven representative dominant canopy trees (longleaf pine in all plots, although there are dominant hardwoods in some of the long-term unburned plots) avoiding edges of the plot. From each of these seven trees, 3 m south of the bole, we collected an auger core using a bucket auger, and sampled soils from the middle of the A, E and B horizons (Figure B 2). The depths of the horizons varied due to the differences in the water table at the site. The O horizon was discarded, where present, because it was absent in the annually burned treatment. Within each plot, the samples were composited into one by soil horizon and homogenized manually for a total of 72 samples across the 24 plots and three sampled horizons. The homogenized, pooled samples were transferred into Ziploc bags, placed on dry ice and shipped overnight to Kansas State University for analyses. Upon arrival at Kansas State University, the soil samples were stored at -20°C until further processing.

At processing, the soil samples were thawed and passed through a 2mm sieve to remove roots and large fragments. Each sample was divided into three aliquots: 1) 10g for DNA extractions and molecular analyses of soil-inhabiting bacterial and fungal communities, 2) 50 ml for soil chemistry analyses; and, 3) 10g for gravimetric soil moisture analysis. The remaining soil was archived in 50ml Falcon tubes at -20°C. All samples were stored in a -20C freezer until further analyses.

Soil Chemistry

Soil chemistry analyses were conducted by the Kansas State University Soils Testing Lab. 50ml Falcon tubes full of frozen soil (weights varied) were submitted for testing. These soils were prepared by drying overnight at 60°C and then ground to pass through a 2mm sieve. Subsamples of these soils were used for analyses of pH, Total C, Total N, Bray Phosphorous, readily available inorganic N (NH_4^+ and NO_3^-), and Soil Organic Matter (SOM). The following methods were used to analyze the soils. Using a 1:1 (w:w) soil slurry of 10g of soil and deionized water, the pH was measured using an automated system. Bray P, the potentially plant available P, was measured using HCl-ammonium fluoride extractant from 2g of dried soil and a colorimetric assay. The inorganic forms of nitrogen (NH_4^+ and NO_3^-) were extracted from 2g of dried soil using 1M of KCl and Cd reduction for NO_3^- (Gelderman and Beegle 1998) and run in separate channels in a flow analyzer to measure the ions simultaneously. Using 0.35g of dried soil, Total C and Total N

were measured using a LECO TruSpec CN combustion analyzer (LECO, St. Joseph, MI). Using a modified version of methods from Combs and Nathan (1998), SOM was measured using loss on ignition wherein 1g of soil was dried at 150°C for 2h and ignited at 400°C for 3h.

DNA extraction, PCR amplification, and sequencing

DNA was extracted from all samples within six months of sampling. Environmental DNA was extracted from ~10g subsamples using PowerMax Soil DNA Isolation Kit (MoBio, Carlsbad, California) following the manufacturer's instructions and stored at -20°C until PCR amplification. The DNA was quantitated with an ND2000 spectrophotometer (NanoDrop Technologies, Wilmington, Delaware) and standardized to 0.4ng/ul for PCR amplification of the bacterial hypervariable V4 region of the small subunit of the ribosomal RNA gene (16S) and the fungal Internal Transcribed Spacer (ITS2) region of the ribosomal RNA gene cluster. These targets were chosen because they are highly variable and optimal for the short paired-end Illumina MiSeq sequences. The amplicons were generated with 12bp barcoded primers of the forward 515f and reverse 806r primers for bacterial 16S (Caporaso et al. 2012) and the forward primer fITS7 (Ihrmark et al. 2012) and reverse primer ITS4 (White et al. 1990) for fungal ITS2 region. All PCRs were performed in triplicate 50 ul reaction volumes with the following amounts: 5µl dNTPs (200µM), 5µl each primer (1µM each), 10µl Phusion 5X HF Buffer with 7.5mM $MgCl_2$, 10µl DNA (4ng), 14.5µl molecular grade water, and 0.5µl (1 unit) Phusion Green Hot Start II DNA polymerase (ThermoScientific, Pittsburg USA). Proofreading polymerase was chosen to minimize generation of amplification artifacts (Oliver et al. 2015). Bacterial PCR reactions began with an initial denaturation for 30s (98°C), followed by 25 cycles of 98°C for 10s denaturing, 30s of annealing (50°C), 1 min extension (72°C), and concluded with a 10-min final extension at (72°C). Fungal PCR reactions began with an initial denaturation for 30s (98°C), followed by 30 cycles of 98°C for 10s denaturing, 54°C for 30s annealing, 72°C for 1min extension, followed by a final 10min extension at 72°C. We used *Saccharomyces cerevisiae* for a fungal positive control and *Escherichia coli* for a bacterial positive control. Molecular grade RNA- and DNA-free H_2O was used as a negative control. All PCR products were visualized in 1.5% agarose gel to ensure the successful amplification of correct size DNA fragments.

A total of 30µl of each of the three technical replicates were combined for a total of 90µl of the PCR product for amplicon purification with the Mag-Bind RxnPure Plus Magnetic Bead Clean-up solution (Omega Bio-Tek, Norcross, Georgia) using a modified manufacturer protocol with a 1:1 ratio of PCR product to the magnetic bead solution and rinsed three times with 80% EtOH. Following clean-up, a total of 200ng for bacteria and 220ng for fungi of DNA were pooled for sequencing. Illumina adapters and indices were added in four PCR cycles using KAPA Hyper Prep Kit (Roche, Pleasenton, California), and 0.5µg starting DNA. The libraries were sequenced (2 x 300 cycles) using the Illumina MiSeq Personal Sequencing System at the Integrated Genomics Facility (Kansas State University, Manhattan KS USA). The sequence data are available through the Sequence Read Archive under the BioProject #; BioSamples #.

Sequence analysis

Sequence data were processed using the bioinformatic program mothur (v.1.38.0; Schloss et al., 2009). For both bacteria and fungi, sequences were contiged, primer sequences trimmed, and any sequences with ambiguous bases or more than 8 homopolymers (fungi) and 7 homopolymers (bacteria) were filtered out. Fungal sequences were then truncated to the shortest sequence length in the data set (237bp), and pre-clustered to minimize platform generated biases (Huse et al. 2010). Bacterial sequences were aligned using the SILVA (release 132; www.arb-sil- va.de) reference alignment followed by pre-clustering. Bacterial and fungal sequences were screened for chimeras using VSEARCH (Rognes et al. 2016), and sequences presumed chimeric were filtered out. Sequences were classified using mothur implemented Naïve Bayesian Classifier (Wang et al., 2007) against the UNITE database (v6; Kõljalg et al. 2013) for fungi and the RDP training set (v10) for bacteria. Non-target lineages were removed as well as any sequences that could not be classified. Operational taxonomic units (OTUs) were then clustered into OTUs using Vsearch for fungi and nearest neighbor algorithm for bacteria. We calculated Good's coverage, observed (S_{obs}) and extrapolated (Chao1) richness, Shannon's Diversity (H') and Shannon's evenness (E_H) using mothur.

Statistical Analysis

Statistical analyses were conducted using R version 3.6.3 (R Core Team, 2020) and R studio version 1.1.143. Data were examined for normality and homogeneity of variance, and factors were

logarithmically transformed as needed. We first analyzed our full dataset in a global Analysis of Variance (ANOVA) with fire interval and soil horizon as main effects in addition to their interaction (fire interval x horizon) to test whether or not fire interval effects may vary depending on the soil horizon. As a result of significant interaction terms in many of these analyses, we decided to continue our analyses separately for each soil horizon to better focus on and understand the fire interval effects within each of the three sampled soil horizons. To do this, we used one-way ANOVA to test for the effects of fire interval treatments on bacterial and fungal richness, diversity, and evenness as well as on the soil chemistry variables that we measured. Where the ANOVA tests indicated differences among the treatments, we utilized Tukey's Honestly Significant Difference (HSD) post-hoc pairwise comparisons to identify which of the four fire interval treatments might underlie those differences.

To analyze and infer responses in the bacterial and fungal community composition to the fire interval treatments by horizon, we used the R package vegan (Oksanen et al. 2019). We derived Bray-Curtis distance matrices and compared treatments using PERMANOVA, adonis2() function (McArdle andAnderson 2001) within the vegan package. These community data were visualized using Non-Metric Multidimensional Scaling (NMDS) ordinations using packages ggplot2 (Wickham 2016) and ggpubr (Kassambara 2020). To understand the differences in compositional responses amongst the microbial communities based on fire interval, we utilized the pairwiseAdonis packages (Martinez Arbizu 2020). To investigate the dispersion (community convergence or divergence) amongst the communities, we used betadisper() within the vegan package (Anderson et al. 2006). We also fit our soil chemistry data to environmental vectors into our NMDS ordinations using the envfit() command in the vegan package. To investigate which OTUs were disproportionately more abundant in one treatment compared to others, we utilized multiplatt() command of the indicspecies package (De Cáceres and Legendre 2009; De Cáceres et al. 2010). Similar to the community analyses, we investigated the indicator OTUs by soil horizon.

To derive functional attributes of the fungal community members, we used FUNGuild (Nguyen et al. 2016) to assign our fungal OTUs to ecological guilds and trophic modes. FUNGuild is a python based program that utilizes the FUNGuild database. With these data, we conducted one-way ANOVA and Tukey's HSD post-hoc tests to understand the how specific ecological guilds

(arbuscular mycorrhizae (AM), ectomycorrhizae (EcM), lichenized fungi, and saprotrophs) differed among the fire interval treatments and among the soil horizons. We chose these specific fungal guilds because they may be particularly sensitive to fire (Holden and Treseder 2013; Semenova-Nelson et al. 2019; Certini et al. 2021).

Results

Soil Chemistry

Many soil chemistry responses to fire depended on the soil horizon as indicated by the fire interval x soil horizon interactions in our two-way ANOVAs for Total N ($F_{6,61}$=4.85; P<0.001), Total C ($F_{6,61}$=5.29; P<0.001), NH_4^+ ($F_{6,61}$=5.17; P<0.001), and SOM ($F_{6,61}$= 2.52; P=0.03). In contrast, soil pH ($F_{6,61}$=0.91; P=0.50), Bray-P ($F_{6,61}$=0.85; P=0.54), or NO_3^- ($F_{6,61}$=1.20; P=0.32) had no evidence of fire interval x soil horizon interactions (Table B 1). The observed interactions were a result of largely exclusive fire interval manipulation effects on the soil chemistry in the topmost A horizon; we found no evidence for treatment effects on soil chemistry in the deeper E and B horizons. In our one-way ANOVAs, in which we analyzed each horizon separately, Total N ($F_{3,19}$= 6.08; P= 0.004), Total C ($F_{3,19}$= 6.50; P=0.003), Bray-P ($F_{3,19}$= 18.37; P<0.001), and NH_4^+ ($F_{3,19}$= 5.87; P=0.005) differed among the treatments in the topmost A horizon and were lower in the T60 treatment than in the other treatments (T1, T2, and T4) (Figure 3.1; A-G). Further, pH varied among the treatments ($F_{3,19}$=5.14; P=0.009) and was lower in T1 and T60 than in T2 and T4 (Figure 3.1; C).

Bacterial Communities

The full bacterial dataset contained initially 12,212,699 sequences. After quality control and subsampling, we included a total of 6,680,050 reads in the analyses. Good's coverage (99.4 ± 0.48 %) indicated that the bacterial communities were sampled adequately. The bacterial communities were dominated by Acidobacteria (36.0%), Verrucomicrobia (35.7%), and Proteobacteria (26.6%); followed by Actinobacteria (12.8%), Planctomycetes (6.8%), Chloroflexi (5.3%), Firmicutes (2.6%), Chlamydiae (1.3%), and other less frequent phyla that were <1% (totaling 2.6%). A small proportion (~3.0%) of the bacterial data remained unclassified beyond Domain Eubacteria.

Bacterial richness, diversity and evenness varied among the fire interval treatments and soil horizons. However, in contrast to soil chemistry, we observed no evidence for fire interval x soil horizon interaction for bacterial richness, diversity or evenness ($F_{6,60}$<1.84; P>0.11) in our two-way ANOVAs. Our by-horizon, one-way ANOVAs indicated that, within the A horizon, fire suppression led to lower bacterial richness and diversity: observed (S_{obs}) ($F_{3,19}$=15.23; P<0.001) and extrapolated (Chao1) ($F_{3,19}$=10.43; P<0.001) richness, as well as Shannon's diversity (H') ($F_{3,19}$=7.51; P=0.002) were lower in T60 than in the other fire interval treatments (Figure 2.A-2.C). There was no evidence for fire interval treatment effects for evenness (E_H) ($F_{3,19}$=1.43; P=0.27) (Figure 3.2 D). In contrast to the A horizon, in the E horizon, only bacterial evenness (E_H) differed ($F_{3,20}$=3.58; P=0.03) among the fire interval treatments and was lower in T60 than in T1, whereas the intermediate fire interval manipulations differed from neither (Figure 3.2 H). In the bottommost B horizon, we observed no evidence for any fire interval treatment effects on bacterial richness and diversity ($F_{3,19}$<2.32; P>0.11).

We visualized the bacterial community data using NMDS ordinations (Figure 3.4 A-C). Permutational analogs of analysis of variance (PERMANOVA) indicated that the bacterial community responses to fire interval manipulations likely depended on the soil horizon as indicated by the marginally significant ($F_{6,60}$= 1.54; P=0.054) fire interval x soil horizon interaction. Analyses by soil horizon indicated that the bacterial communities responded to fire interval treatments in the A ($F_{3,19}$ = 2.52; P=0.002) and E ($F_{3,20}$ = 1.98; P=0.02) horizons, but not in the bottommost B ($F_{3,19}$=0.87; P=0.65) horizon. Pairwise PERMANOVAs indicated that bacterial communities in the shortest fire interval treatments (Table 3.1) differed from T60 and that T1 also differed from T4 in the A horizon (Table 3.1). In the E horizon, all three prescribed burn treatments (T1-T4) differed from the fire exclusion (T60) treatment (Figure 3.4). The pairwise dispersion tests provided no evidence for bacterial community convergence or divergence among the fire treatments in the A horizon ($F_{3,19}$=0.99; P=0.42), E ($F_{3,20}$=0.15; P=0.93), or B Horizon ($F_{3,19}$=0.86; P=0.48).

Our indicator taxon analyses identified OTUs underlying the observed community differences between the fire intervals and soil horizons. Like our community data, we divided the data based

on horizon to focus on how fire intervals may have impacted community members. In the A horizon, a total of 27 bacterial indicator OTUs were disproportionately more abundant in T1, three in T2, none in T4, and eight in T60 (Table B 6). The most abundant indicators for T1 were OTUs representing unclassified bacteria (29.6% of T1 indicators' abundance) and *Acidobacteria* (22.2% of T1 indicators' abundance). *Verrucomicrobia* represented 33.3% of the total abundance of the indicators for T2 of the A horizon. The most abundant indicator for T60 treatment in the A horizon was OTU1918 (*Ktedonobacteria)* with a total 26% of the abundance of indicators for the T60 treatment within the A horizon. In the E horizon, there were 11 indicator OTUs for T1, seven for T2, one for T4, and 45 for T60. In T1, *Firmicutes* accounted for nearly half of the indicators abundance, accounting for 46%. Of the seven indicators in T2, OTU3859, *Gammaproteobacteria,* was the most abundant indicator, accounting for 25% of the indicators' abundance. The most abundant indicator for T60 in the E horizon was OTU450 (*Gammaproteobacteria*), 20% of the indicators' abundance for the T60 treatment in the E horizon. In the bottom-most B horizon, we identified a total of six indicator OTUs for T1, ten for T2, one for T4, and eighteen with T60. In the annual burn treatment (T1), *Alphaproteobacteria* (2 of the six indicators) and *Actinobacteria* (1 indicator) were the most abundant indicators with 7 counts each. OTU1098 (*Chlamydiae*) was the most abundant indicator for T2 accounting for 26% of the abundance of indicators in the treatment. Similar to the A and E horizons, the indicators with the most OTU counts occurred in the T60 treatment. OTU2766, belonging to *Alphaproteobacteria*, was the most abundant indicator for T60 in the B horizon (Table B 6).

Our analyses of the environmental correlates for bacterial communities indicated that all measured soil chemistry variables correlated ($R^2 > 0.29$, $P < 0.026$) with the bacterial community composition (Figure B 3; Table B 4) in the A horizon. The correlates with the highest coefficients were Bray-P (R^2=0.52; P=0.002) and SOM (R^2=0.54; P=0.002). Similarly, in the E horizon, all soil chemistry measurements correlated ($R^2 > 0.25$, $P < 0.038$) with the bacterial communities except pH (R^2=0.21; P=0.097). Soil NO_3- (R^2=0.61; P=0.004) and Total C (R^2=0.47; P=0.014) were the correlates with highest coefficients in the E horizon. The environmental correlates of the bacterial communities were fewer in the bottommost B horizon, where only pH (R^2=0.36; P=0.017) and NH_{4+} (R^2=0.32; P=0.023) correlated with the community data (Figure B 3; Table B 4).

Fungal Communities

The fungal dataset initially contained 3,225,289 sequences. After quality control and subsampling, the final sequence count was 1,510,145. Similar to bacteria, the fungal diversity was well represented in our sampling as indicated by Good's coverage (99.8 ± 0.51%). The fungal data were strongly dominated by Basidiomycota (54.2%) and Ascomycota (41.0%). Relatively few sequences represented the arbuscular mycorrhizal fungi, the Glomeramycota (0.8%), or the basal, early diverging fungi formerly assigned to Zygomycota (1.4%), Rozellomycota (0.3%), and Chytridiomycota (> 0.1%). A small proportion (2.4%) of the data remained unclassified beyond Kingdom Fungi.

Similar to bacteria, we observed no evidence for fire interval x soil horizon interaction in our two-way ANOVAs for fungal observed (S_{obs} – $F_{6,60}$=1.67; P=0.14) or extrapolated (Chao1 – $F_{6,60}$=1.84; P=0.11) richness. In contrast, there was an interaction for diversity (H' – $F_{6,60}$=2.76; P=0.019) and evenness (E_H – $F_{6,60}$=2.94; P=0.014). In subsequent one-way ANOVAs, in which we analyzed each soil horizon separately, observed (S_{obs} – $F_{3,19}$= 7.62; P=0.001) and extrapolated richness (Chao1 – $F_{3,19}$=8.27; P=0.001) as well as Shannon's diversity (H' – $F_{3,19}$= 11.69; P<0.001) and evenness (E_H – $F_{3,19}$= 9,47; P<0.001) differed among the fire interval treatments in the topmost A horizon (Figure 3.3 A-D). Pairwise comparisons indicated that richness (Sobs, Chao1) was lower in T60 than in any of the burn treatments (T1-T4) (Figure 3.3 A; 3.3 B). In the A horizon, diversity and evenness were lower in T1 and T60 than in T2 and T4 treatments. Similar to the bacterial analyses, there were no fire interval treatment effects on fungal richness and diversity in the E horizon (Figure 3.3 E-H). Even though fungal observed (S_{obs} – $F_{3,19}$=2.11; P=0.133) and extrapolated richness (Chao1 – $F_{3,19}$=2.12; P=0.132) did not differ among the fire intervals in the bottommost B horizon, in contrast to bacteria that did not respond to fire treatments, fungal diversity (H' – $F_{3,19}$=5.21; P=0.008) and evenness (E_H – $F_{3,19}$=4.77; P=0.012) in T1 and T2 were higher than in the T4 and T60 treatments (Figure 3.3 K; 3.3 L).

Fungal community responses to fire interval treatments differed among the soil horizons as indicated by the fire interval x soil horizon interaction (PERMANOVA: $F_{6,60}$=1.39; P=0.005). In subsequent analyses and in contrast to bacterial communities, fire interval treatments differed in

each of the three soil horizons: A horizon ($F_{3,19}$=3.05; P=0.001); E horizon ($F_{3,20}$=1.63; P=0.001); B horizon ($F_{3,19}$=1.61; P=0.01). Pairwise comparisons indicated that in the A horizon, all burn treatments (T1-T4) differed from the fire exclusion treatment (T60), and fungal communities in T2 and T4 were distinct from T1 (Table 3.2; Figure 3.5 A). In the E horizon, T1 and T2 treatments, but not T4, differed from T60 and the T1 communities also differed from T4 communities (Figure 3.5 B). In the bottommost B horizon, the T1 and T2 treatments differed from the T4 and T60 treatments (Figure 3.5 C). Similar to the bacterial analyses, we observed no evidence for community convergence or divergence in the fungal communities among the four fire interval manipulations in any of the three soil horizons: A ($F_{3,19}$=1.13; P=0.36), E ($F_{3,19}$=1.77; P=0.18), or B horizon ($F_{3,19}$=0.35; P=0.78).

We analyzed the environmental correlates for fungal communities. In the A horizon, all soil chemistry measurements correlated with the fungal community composition except SOM and NO_3^- (Figure B 4, Table B 5). Bray-P (R^2=0.72; P=0.001) and soil pH (R^2=0.49; P=0.002) and were the correlates with highest coefficients in the A horizon reflecting their observed low values in the T60 treatment. In the E horizon, NO_3^- was the only fungal community correlate (R^2=0.31; P=0.046) (Figure 3.3 B). In the B horizon, only pH (R^2=0.48; P=0.002) and Total C (R^2=0.27; P=0.041) correlated with fungal communities, even though neither differed among the fire interval treatments in this horizon (Figure B 4.C).

We utilized the indicator taxon analyses to identify those fungi that may have been disproportionately more abundant in one treatment than in others (Table B 7). Similar to our other analyses, we analyzed the indicators separately for each soil horizon. In the A horizon, we identified 63 indicators for T1, 24 for T2, 12 for T4, and 37 for T60 (Supplemental Table 5). The most abundant indicators for the A horizons were (T1) OTU 13*, Russula,* which accounted for 64% of the T1 indicators' abundance in the A horizon, (T2) OTU 134 *Humidicutis,*62% of T2 inidicators' abundance, (T4) OTU 878 *Basidiodendron* sp.*,* 88 of 378 OTU counts and (T60) OTU 1953, *Trechispora coharens*, 24560 of 43825 OTU counts. The E horizon had a total of twenty indicators for T1, three for T2, ten for T4 and 34 for T60. The most abundant indicator OTUs for the E horizon were (T1) OTU 13 *Russula*, accounting for 82% of the indicators' abundance for T1 of the E horizon, (T2) unclassified fungi, 50% of the indicators' abundance, (T4)

Herpotrichiellaceae sp 27% of the inidicators' abundance and (T60) unclassified *Clavariaceae,*25% of the indicators' abundance for T60 of the E horizon. In the B horizon, there was a total 51 indicators for T1, 13 for T2 and 2 for T4 and T60 each. The most abundant indicator taxa for B horizon were: (T1) OTU 13, *Russula*, 20% of the indicators' abundance for T1 of the B horizon, (T2) unclassified *Pleosporales* 26% of the indicators' abundance (T4) unclassified Fungi for both indicators with a total of 156 counts and (T60) *Talaromyces* 52% of the indicators' abundance for T60 of the B horizon. Notably, OTU 13 representing the EcM genus *Russula* was among the T1 treatment indicators in all three soil horizons. In the A and E horizons in the fire exclusion treatment, OTUs representing unclassified ascomycetes were most abundant.

To gain insight into fungal ecological roles and their responses to fire interval manipulations across the soil profile, we utilized FUNGuild. Of the total of 2,624 fungal OTUs, a total of 1,484 (57%) OTUs could not be assigned to a guild or trophic modes. Further, some OTUs were assigned to more than one guild. When this occurred, we used the one listed first. Of the 1,140 FUNGuild assigned OTUs, we chose to focus on the two most common trophic modes: saprotrophs and symbiotrophs (representing 735 OTUs in total). This refined dataset included twelve guilds (Figure B 5 and 6). Among those, we analyzed the five most abundant guilds. Because these data were a subset from the full dataset, they do not reflect our richness and diversity measurements.

We utilized two-way ANOVAs with fire interval and soil horizon and their interaction included in the model for each of the five guilds. The wood saprotroph guild was the only guild with a fire interval x soil horizon interaction ($F_{6,60}$=5.49; P<0.001) suggesting that only its response to fire intervals depended on the soil horizon. In contrast, AM ($F_{6,60}$=0.38; P=0.886) and EcM ($F_{6,60}$=1.07; P=0.389) fungi, as well as lichenized fungi ($F_{6,60}$=1.40; P=0.230) and undefined saprotrophs ($F_{6,60}$=0.60; P=0.727) had no evidence for interactions. We then used one-way ANOVAs within each guild and soil horizon to gain further insight into how the fire intervals may have impacted guilds within each horizon (Figure 3.6 A D). Overall, four of the five guilds analyzed in detail responded to burn interval treatments in the A horizon, whereas responses to burn intervals were fewer in the deeper E and B horizons. Undefined saprotrophs did not respond to burn intervals in any of the three analyzed soil horizons. In the A horizon, the AM fungi differed among the burn treatments ($F_{3,20}$=3.87; P=0.025). This was attributable to the greater abundance of AM fungi in

T1 than in T4 and T60. The AM fungi also differed among the burn interval treatments in the E ($F_{3,20}$=5.12; P=0.009) and B ($F_{3,20}$=6.67; P=0.003) horizons. In these soil horizons, the AM fungi were more abundant in T1 than in the other fire interval treatments. The EcM fungi also differed among the burn interval treatments in the A horizon ($F_{3,20}$=4.40; P=0.02). In contrast to AM fungi, the EcM fungi were more abundant in fire exclusion treatment (T60) than in T2 and T4. The EcM fungi did not differ among the burn interval treatments in the E ($F_{3,20}$=2.45; P=0.09) or B horizons ($F_{3,20}$=1.53; P=0.24). Lichenized fungi also differed in the A horizon ($F_{3,20}$=3.17; P=0.046), a result of their higher abundance in T60 than in T1 and T2. However, there was no strong evidence of responses in deeper E ($F_{3,20}$=2.85; P=0.063) or B horizons ($F_{3,20}$= 0.88; P=0.466). The wood saprotrophs varied among the burn interval treatments in the A horizon ($F_{3,20}$= 6.19; 0.004), where their abundance was greater in T60 than in T1 and T2. The wood saprotrophs also differed among the burn interval treatments in the E horizon ($F_{3,20}$=3.35; P=0.039), though only marginally in pairwise comparisons that suggested their greater abundance in T60 than in T2 and T4. In contrast to these four guilds, the undefined saprotrophs did not vary among the burn interval treatments in the A ($F_{3,20}$=0.68; P=0.571), E ($F_{3,20}$=1.66; P=0.207), or B ($F_{3,20}$=0.72; P=0.552) horizon.

Discussion

Our results indicate that prescribed fire intervals impact the soil-inhabiting bacterial and fungal communities and the soil chemistry, especially in the topmost A horizon. These results come with the caveat that we lack the O horizon, which likely contain a great deal of nutrients and microbial biomass. The O horizon has been sampled previously for soil chemistry analysis in Dicosty et al. (2006), and our results of the A, E, and B horizons are consistent with their results. In contrast, such responses deeper in the soil profile are subtler if not absent. In addition to fire responses that depended on soil horizon, our study highlights potential ecosystem context dependencies. For example, contrary to previous studies that report losses in soil C and N pools as a result of frequent fires (Neary et al. 1999; Holden and Treseder 2013; Pelligrini et al. 2018), our results indicate that the more frequent prescribed burn treatments may lead to higher Total C, Total N, Bray-P, SOM, and NH_4^+ in mineral soil. In a review on prescribed fire soil properties, Alcañiz et al. (2018) concluded that there is no clear trend of soil chemical responses to fire. Rather, responses in soil chemistry depend on the system, plant community composition, as well as, fire regime and fire

characteristics such as fire frequency, intensity, and severity (Pressler et al. 2019). Overall, our results corroborate and fall in line with other studies in coastal pine systems and agree on differences between frequent fires and complete fire exclusion as well as on often minimal differences among the frequent burn intervals (McKee 1982; Binkley et al.1992; Lavoie et al. 2010; Coates et al. 2018).

Our analyses supported our hypothesis that the soil chemistry and microbial communities in the top-most mineral horizon (the A horizon) are more responsive to recurring prescribed fires compared to the deeper soil horizons (the E and B horizons). It is remarkable that after six decades of continuously maintained fire manipulations, very few abiotic and biotic attributes were distinct among the complete fire exclusion and annual prescribed burning in the deepest soil horizons. These observations highlight the rapid heat pulse attenuation within the soil profile (Massman 2012; Smith et al. 2016; Bruns et al. 2020) and the resultant minimal impacts on soil chemistry and/or organisms deep in the soil profile that may be buffered from the short-term changes caused by fire. Long-term fire exclusion led to lower Total C and N as well as lower Bray-P and NH_4^+ in the A horizon compared to the three treatments that included relatively frequent (up to every four years) prescribed burning. We also observed a decrease in Total C and N (with a non-significant increase in the B horizon) and an increase in pH with increasing in soil depth. Previous studies that have analyzed soil chemistry by horizon found similar results. Importantly, carbon asserts a substantial control on microbial abundance and distribution in soil (Eilers et al. 2012; Jiao et al. 2018; and Xue et al. 2020). Our analyses of environmental correlates corroborate the importance of soil carbon for soil-inhabiting bacteria and fungi. Both SOM and Total C correlated with bacterial communities in the two top-most soil horizons (A, E) and with fungal communities in the topmost A horizon. It is of note, however, that in the A horizon nearly all measured abiotic soil attributes correlated with the bacterial and fungal community composition. For example, Total C, Total N and Bray-P were strongly correlated with bacterial communities, and soil pH and Bray-P with fungal communities in the A horizon. Although soil pH is an important driver for bacterial communities in particular (Rousk et al. 2010; Xue et al. 2020), it was not among those with highest coefficients, perhaps emphasizing the substantial effects that recurring fires may have on top soils and their chemistry.

Bacterial and fungal richness responded to prescribed fire frequency similarly in the A horizon. Fire exclusion had resulted in lower richness and both bacterial and fungal richness was lowest in the long-term fire exclusion treatment. Our results contrast Perez-Valera et al. (2018) who observed higher microbial richness in the unburned sites, but this is likely to our system being fire dependent (Kolden 2019). However, our observed responses in richness were limited to the top-most A horizon as there was no evidence for similar richness responses in either the E or B horizons. Microbial richness typically declines with soil depth (Jumpponen et al. 2010; Fierer et al. 2013; Santalahti et al. 2016). However, in contrast to other studies (Santalahti et al. 2016, Jumpponen et al. 2010), fungal richness and evenness were higher in the B horizon, particularly in the treatments with most frequent fires (T1 and T2) (Figure 3) – a pattern potentially attributable to the sandy coastal soils in our study area.

Our analyses of community composition supported our original hypothesis that fire exclusion would result in soil microbial communities distinct from those observed in the long-term prescribed fire treatments. Bacterial communities were distinct among the fire interval treatments in the A and E horizon as the communities in the most frequently burned treatments (T1, T2) differed from the fire exclusion treatments. Interestingly, bacterial communities of the top-most A horizon in the most frequent fire treatment (T1) also differed from the less frequent fire treatment (T4). These observations suggest that even relatively small differences in maintained fire frequencies can have consequences for soil communities in the long term. Similarly to bacteria, fungal communities also responded compositionally to maintained fire frequencies. In a similar pine ecosystem in Florida, Semenova-Nelson et al. (2019) also observed that burned and unburned fire treatments have distinct fungal communities. Overall, our results are consistent with others (Brown et al. 2013; Oliver et al. 2015) who have reported that recurring prescribed fires alter fungal communities compositionally. However, although the fungal communities differed compositionally among the fire interval treatments in all three horizons, in the deeper E and B horizons only the shortest fire intervals (T1 and T2) maintained communities different from the fire exclusion treatment. These results support earlier speculation (Brown et al. 2013; Oliver et al. 2015) that the longer fire intervals – here every four years – may permit system transition to conditions comparable to those without fire.

We utilized indicator taxon analyses to identify taxa that responded the different fire intervals. In general, we observed a number of potential indicators, particularly for the fire exclusion treatment, suggesting that many taxa disappear or become less frequent in systems experiencing greater fire frequencies. Among these indicators was a bacterial OTU assigned to *Ktendonobacteria* – the most abundant indicator for T60 in the A horizon. A chronosequence study of wildfire effects on bacteria in Canadian permafrost soils reported an increase of this bacterium in sites that were at least three years post fire (Zhou et al. 2020; Certini et al. 2021) suggesting it as an example of a bacterial taxon that is fairly intolerant of fire. In all three soil horizons the ectomycorrhizal fungi assigned to the genus *Russula* were the most abundant indicators for the most frequent fire treatment (T1). Several studies have indicated *Russula* spp. to be fire responsive, or more abundant following fire (Salo and Kouki 2018; Taudière et al. 2017; Rasmussen et al. 2018; Oliver 2020; Dove et al. 2021), whereas others reported *Russula* spp. to decrease in abundance following fire, therefore, fire sensitive (Dove et al. 2021; Pérez-Izquierdo et al. 2021). The differences in congeneric responses of *Russula* spp. may indicate ecosystem and context dependencies, or could potentially be species-specific responses to fire and conditions in the post-fire environments.

Although our indicator taxon analyses highlighted an EcM taxon as one more commonly responding positively to recurring fire, our functional guild analyses corroborated other studies (Dove et al. 2021; Castaño et al. 2020) that have concluded that EcM fungi overall are sensitive to fire and consequently decline in abundance after fire. Our guild-level analyses indeed indicated that EcM fungi were more abundant in the absence of recurring fire. In contrast to other studies (Day et al. 2019; Smith et al. 2020), we did not group all mycorrhizal fungi together, but rather analyzed EcM and AM fungi separately. Our data suggest contrasting responses of AM and EcM fungi. While EcM were most abundant in the fire exclusion treatment, the AM fungi were most abundant in the annual burn treatment (T1) in all three soil horizons that we analyzed here. Our results corroborate those by Treseder et al. (2004), who also observed greater AM fungus abundance in recently burned sites than in the less frequently burned sites. These observations likely reflect changes in the plant communities on which these fungi depend on. The fire exclusion sites tend to include a greater number of ectomycorrhizal plants compared to the frequently burned sites that may include a greater proportion of AM hosts (Hart et al. 2005). In addition, some of our guild-level analyses provided intuitive results. For example, wood saprotrophs were most abundant

in the fire exclusion treatment in the A horizon – an observation likely attributable to the more abundant woody substrates available in the absence of fire. Overall, these results support our hypothesis of community responses but also highlight the potential functional shifts in fungal communities.

Conclusions

Our use of this 60-year experiment allowed us to gain insight into how fires impact soils. Our study provided evidence that different fire intervals lead to changes in both soil chemistry and microbial communities. Importantly, these effects were most strongly visible in the topmost soil horizon and – set aside the community composition that differed often even in the bottommost horizon – largely limited to the A horizon. We cannot pinpoint the ultimate drivers that underlie these community changes or whether they are attributable to direct effects of the fire regime differences or subsequent changes in abiotic factors such as soil chemistry, particularly changes in soil carbon and organic matter that were often among the strongest correlates of the soil-inhabiting communities. Our study allowed us to demonstrate that prescribed fire regimes can impact the soil-inhabiting communities and that even relatively small differences in fire frequencies (annual vs. every four years) may have consequences on soil attributes. Importantly, our fungal guild analyses also strongly suggest that these community changes may also lead to changes in system wide functions as demonstrated by the declines in EcM fungi and increases in the AM fungi or wood decomposing fungi. This unique opportunity enabled a great insight into how soils are impacted by long-term management practices. To our knowledge, as of current, there are no comparable studies that have dissected fire effects on bacterial and fungal community or on soil chemistry across the soil profile like we have. While most biological activity occurs in the top 10cm of soils due to the abundance of roots and microbial activity (Eilers et al. 2012), having insight into the deeper horizons aids in our understanding of the long-term fire impacts.

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Chapter 3 Tables and Figures

Figure 3.1 Soil Chemistry Boxplots

Total nitrogen (%), total carbon (%), pH, Bray-Phosphorous (ppm), NO_3 (ppm) and NH_4^+ (ppm) of the four different fire treatments (T1, T2, T4, T60) for the 3 soil profiles A horizon-**A:G**, E horizon-**H:N**, B horizon-**O:U**). Also included are the results of the Tukey HSD Test as indicated by the letters above the boxes of the boxplot.

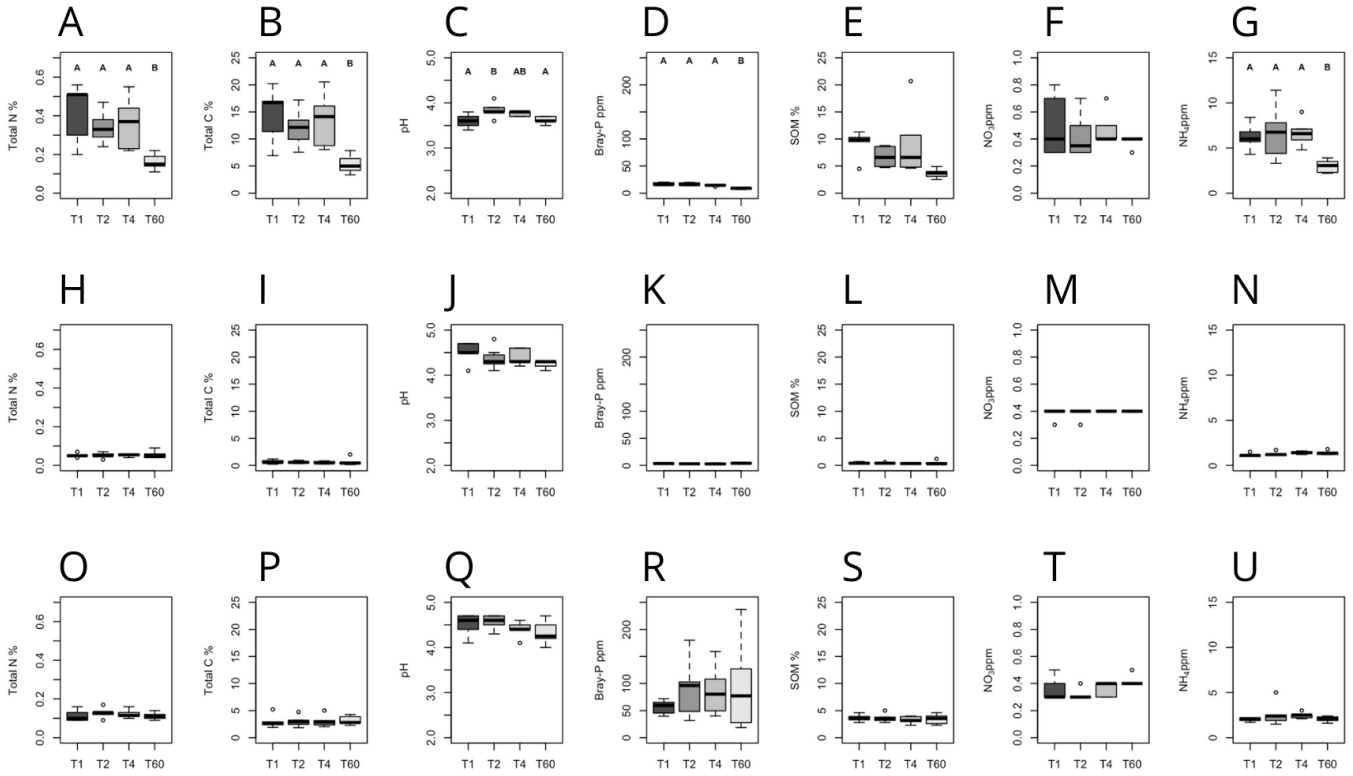

Figure 3.2 Bacterial Boxplots

Observed(S_{obs}), extrapolated richness (Chao1), Shannon's diversity (H'), and Shannon's evenness (E_H) of the four different fire treatments (T1, T2, T4, T60) for the 3 soil profiles (A horizon-**A:D**, E horizon-**E:H**, B horizon-**I:L**). Also included are the results of the Tukey HSD Test as indicated by the letters above the boxes of the boxplot.

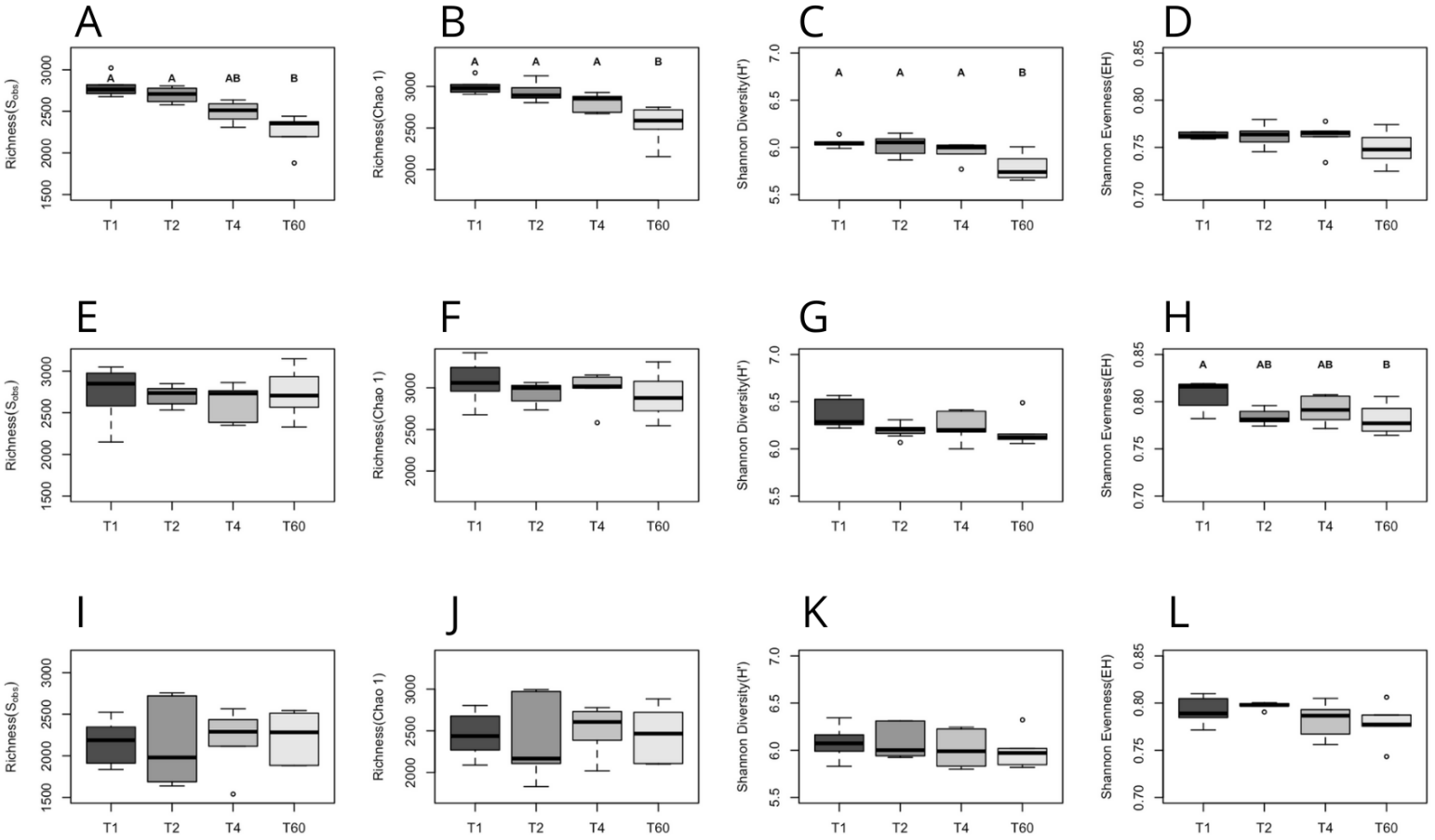

Figure 3.3 Fungal Boxplots

Observed(S_{obs}), extrapolated richness (Chao1), Shannon's diversity (H'), and Shannon's evenness (E_H) of the four different fire treatments (T1, T2, T4, T60) for the 3 soil profiles (A horizon-**A:D**, E horizon-**E:H**, B horizon-**I:L**). Also included are the results of the Tukey HSD Test as indicated by the letters above the boxes of the boxplot.

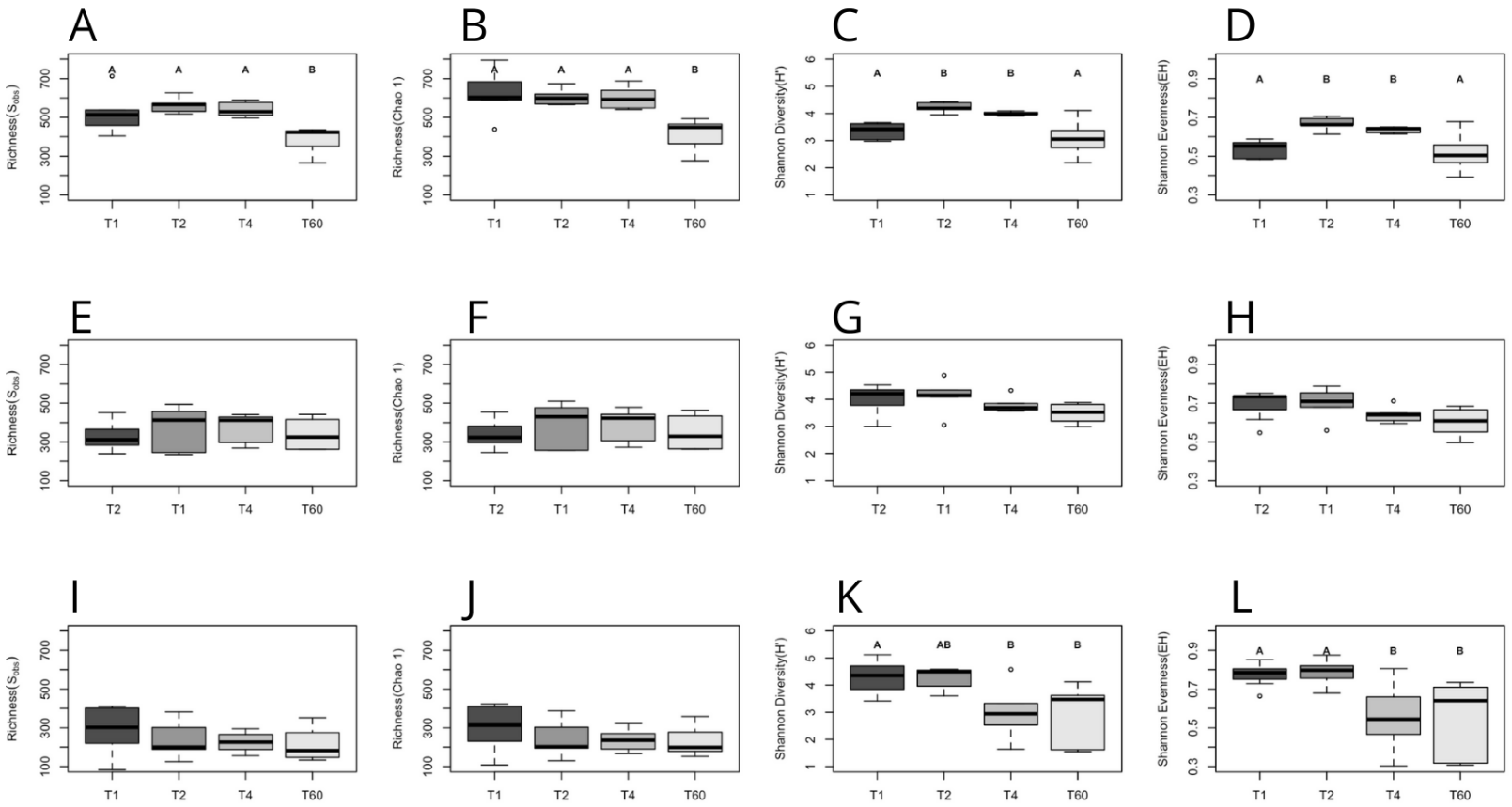

Figure 3.4 Bacterial Non-Metric Multidimensional Scaling (NMDS) Ordination Spider plots

Bacteria Non-Metric Multidimensional Scaling (NMDS) ordination spider plots of the four burn treatments (T1, T2, T4, T60) within the three soil horizons [**A** - A horizon (stress=0.09), **B** - E horizon (stress=0.07), **C** - B horizon (stress=0.10)]. Legs indicate community dispersion from centroid.

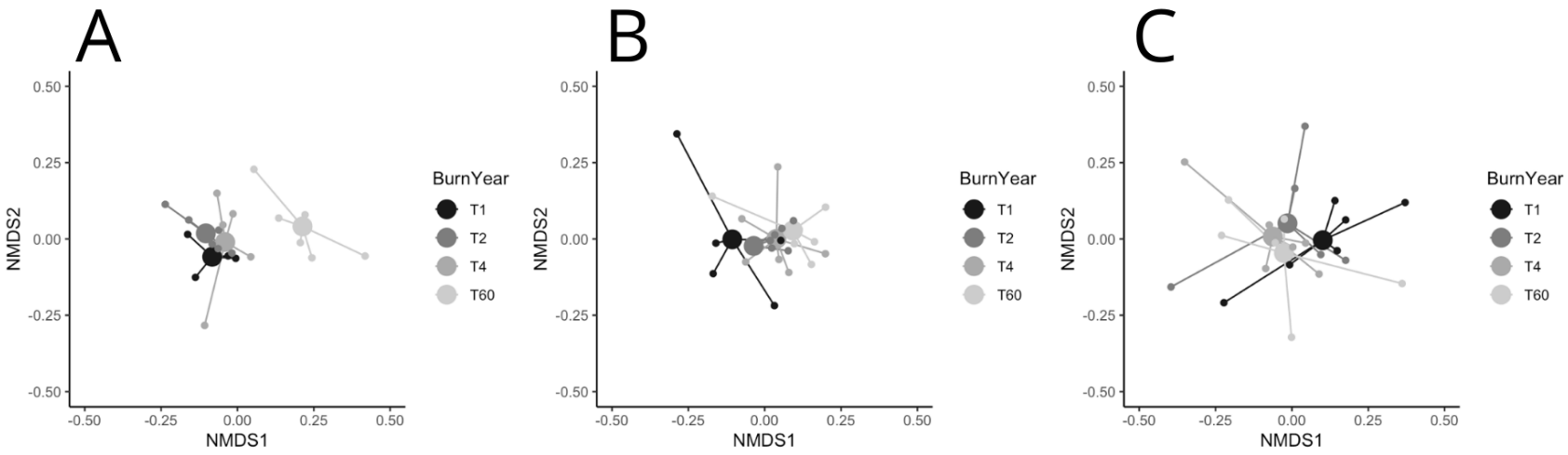

Figure 3.5 Fungal Non-Metric Multidimensional Scaling (NMDS) Ordination Spider plots

Fungi Non-Metric Multidimensional Scaling (NMDS) ordination spider plots of the four burn treatments (T1, T2, T4, T60) within the three soil horizons [**A** - A horizon (stress=0.17), **B** - E horizon (stress=0.18), **C** - B horizon (stress=0.13)]. Legs of spider indicate community dispersion from centroid.

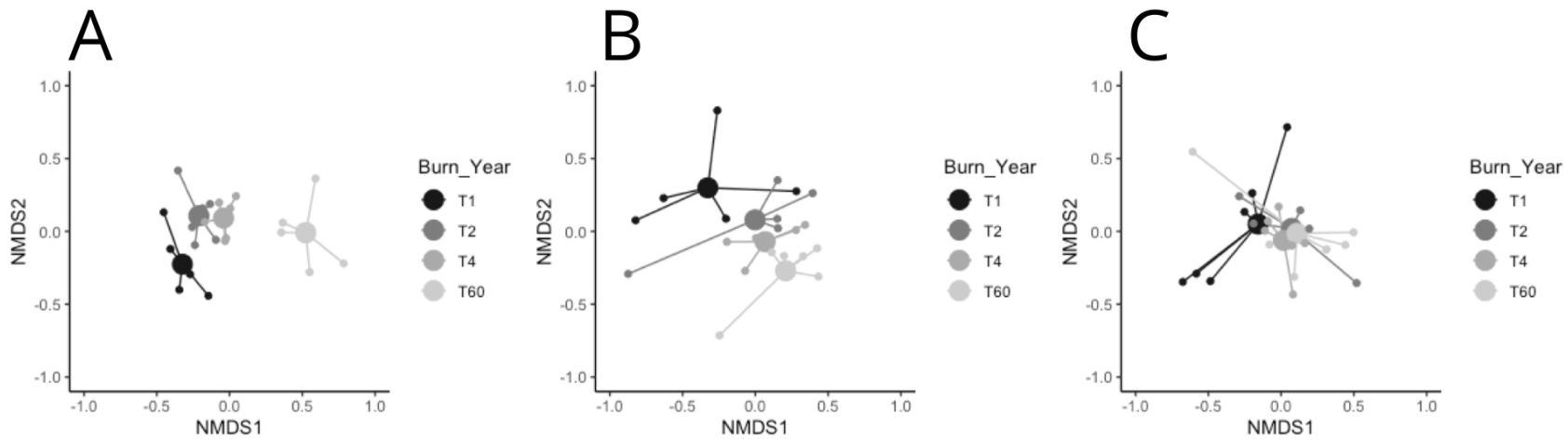

Figure 3.6 Abundance and percentage of guilds

Functional guilds abundance for each horizon based on burn treatment (**A, B,** and **C**) with standard error bars. Guild percentage based on burn year and horizon (**D**).

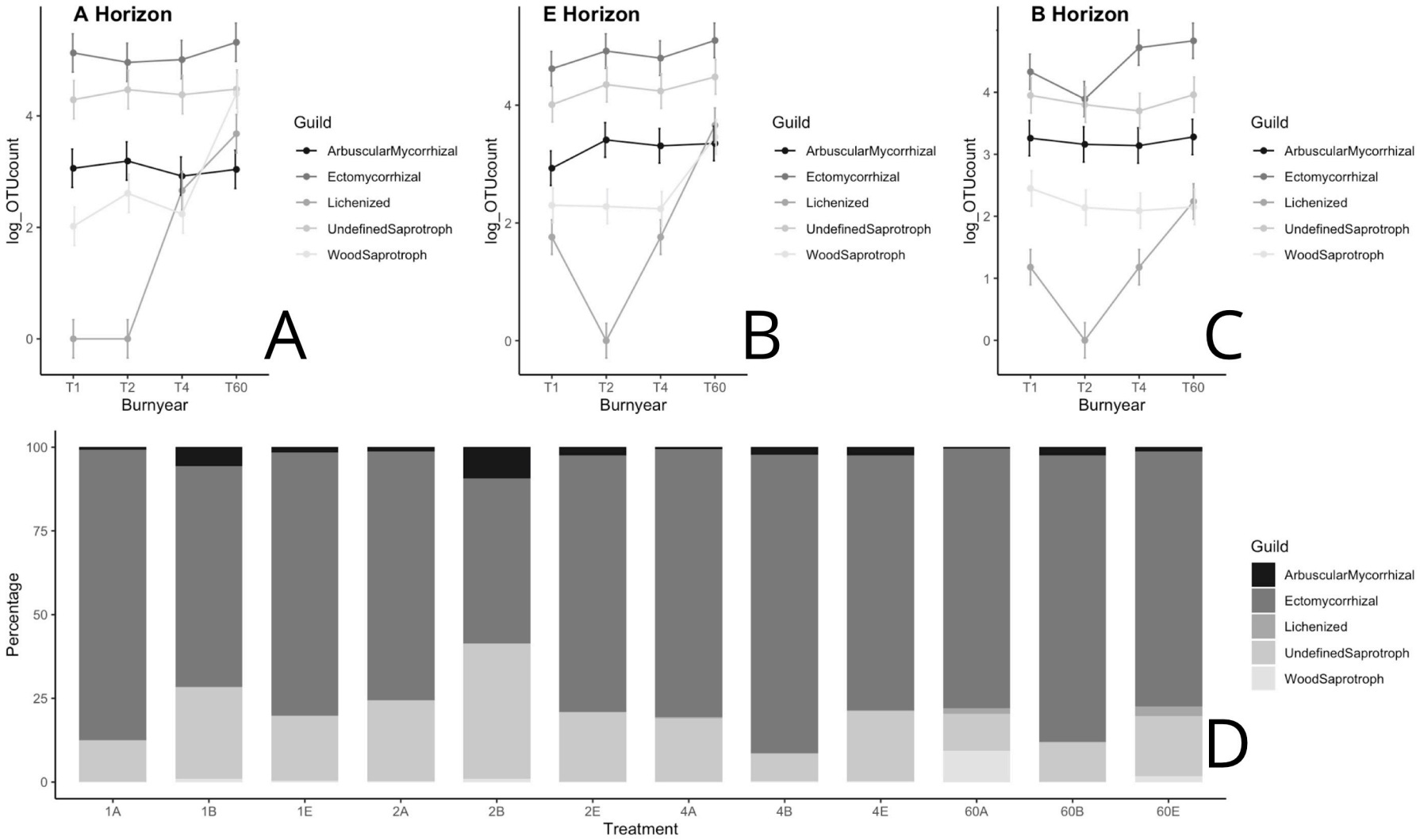

Table 3.1 Bacterial pairwise PERMANOVA

Bacterial pairwise permutational analysis of variance (PERMANOVA) results for bacterial community by horizon. Bold values indicate significance (P<0.05) differences amongst burn intervals.

PAIRWISE COMPARISON	A HORIZON			E HORIZON			B HORIZON		
	F	**R^2**	**P**	**F**	**R^2**	**P**	**F**	**R^2**	**P**
T1-T2	1.52	0.14	0.145	1.47	0.13	0.121	0.52	0.05	0.905
T1-T4	**3.21**	**0.26**	**0.016**	0.74	0.08	0.533	1.18	0.11	0.267
T1-T60	**3.61**	**0.29**	**0.007**	**3.62**	**0.29**	**0.022**	1.65	0.14	0.091
T2-T4	1.67	0.14	0.114	0.99	0.08	0.464	0.49	0.05	0.854
T2-T60	**3.27**	**0.25**	**0.003**	**2.04**	**0.16**	**0.047**	0.80	0.08	0.592
T4-T60	1.8	0.15	0.059	**3.12**	**0.24**	**0.012**	0.61	0.06	0.889

Table 3.2 Fungal pairwise PERMANOVA

Fungal pairwise permutational analysis of variance (PERMANOVA) results for bacterial community by horizon. Bold values indicate significance ($P<0.05$) differences amongst burn intervals.

PAIRWISE COMPARISON	A HORIZON			E HORIZON			B HORIZON		
	F	**R^2**	**P**	**F**	**R^2**	**P**	**F**	**R^2**	**P**
T1-T2	**1.51**	**0.14**	**0.049**	1.25	0.11	0.097	1.39	0.13	0.061
T1-T4	**1.59**	**0.15**	**0.045**	**2.33**	**0.21**	**0.005**	**2.02**	**0.17**	**0.015**
T1-T60	**4.26**	**0.32**	**0.003**	**2.39**	**0.21**	**0.005**	**1.88**	**0.16**	**0.005**
T2-T4	1.31	0.12	0.117	1.25	0.10	0.127	**2.00**	**0.18**	**0.027**
T2-T60	**5.01**	**0.33**	**0.004**	**1.44**	**0.12**	**0.036**	**1.66**	**0.15**	**0.041**
T4-T60	**5.04**	**0.33**	**0.002**	1.25	0.11	0.214	0.75	0.70	0.675

Chapter 4 - Soil-inhabiting Bacterial and Fungal Community Trajectories Remain Distinct Six Years after Low or High Severity Fire

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Key words: fire, community ecology, bacteria, fungi, forest

Abstract

Wildfires burn large areas of forested land annually, and they are projected to increase in frequency and intensity. These wildfires are not uniform. Rather, they burn in patches that vary in severity based on edaphic and environmental factors as well as fuel quality and quantity. Although much research has focused on how fires impact soil-inhabiting bacteria and fungi, a knowledge gap still exists in understanding the community trajectories that follow fires of different severities. Here, we tracked bacterial and fungal communities before and up to six years after experimental fire severity manipulations in Ponderosa pine stands in the Pringle Falls Experimental Forest located in the Deschutes National Forest in Oregon, USA. We investigated high and low severity burns, sampling soils before the fire, one week post-fire, as well as two years, four years, and six years post-fire. Our results indicate that both bacterial and fungal communities after a high severity fire are distinct from those before fire and remain so six years following fire in richness, diversity, and composition. In contrast, the low severity fire treatments did not have as clear a distinction following the fire. Two years post-fire, richness and diversity were comparable to pre-fire conditions, whereas community composition remained distinct throughout the six years. We employed indicator taxon analyses to identify taxa that positively responded to fire. These analyses

highlighted bacterial phylum Firmicutes as well as the fungal genera *Anthrocobia*, *Morchella*, and *Pholiota* as taxa that included operational taxonomic units that increased post-fire. Fungal guild analyses indicated an initial decrease in ectomycorrhizal fungi post-fire but two years post-fire the ectomycorrhizal abundances exceeded those before the fire. Additionally. plant pathogenic fungi dramatically increased following the high severity burn treatment. With the ongoing increase in wildland fires in the western United States, understanding the soil microbial community trajectories following varying fire severities is vital to the forest system recovery and management.

Introduction

In recent years, wildfires have increased in intensity and frequency, especially within the Western United States. In the past ten years, an average of 62,805 wildfires burned approximately three million hectares annually in the United States (Hoover and Hanson 2021). Environmental change adds compounding factors, such as drier conditions (Westerling et al. 2006), land use change (Andela et al. 2017), and the increasing wildland-urban interface (Bento-Gonçalves and Vieira 2020) that have led to the observed increase in wildland fires. Wildfires do not burn evenly. Rather, they create landscape mosaics (Agee 1998) in which fire severity within the landscape may vary depending on topography, weather, and plant community coverage. These landscape mosaics lead to an increase in pyrodiversity of the system (Martin and Sapsis 1992; Jones and Tingley 2021), or an increase in variation of the post-fire ecosystem. Patchy variation in burn severities and other fire behavior attributes across a landscape are aspects of pyrodiversity that can also include fire return interval, seasonality, size of fire, and intensity (Jones and Tingley 2021). Because of this uneven burning in the patch mosaics, recovery of biological communities following a fire can vary substantially, leading to a potential increase in biodiversity as well (Reazin et al. 2016).

Much of the wildland fire research has focused on aboveground responses to the varying fire severities across a landscape, but how the soil microbial communities respond to fires of different intensities remains a knowledge gap (but see Holden et al. 2016; Reazin et al. 2016). Studies that explore wildfire responses often lack pre-fire conditions and rely on space for time substitution, *i.e.*, chronosequence approaches (*e.g.*, Dooley and Treseder 2012; Sun et al. 2015), or time series comparisons of post-fire dynamics alone (*e.g.*, Hopkins et al. 2021; Pulido-Chavez et al. 2021).

This can lead to challenges in understanding the community dynamics, and how communities may change when facing a fire. Many studies have focused on immediate responses (within <3 months) (Goberna et al. 2012; Lucas-Borja et al. 2019; Barrerio and Díaz-Raviña. 2021) but following microbial communities through years of recovery has been rarely attempted (but see Pulido-Chavez et al. 2021). Further, these studies mainly consider fires homogeneous across the landscape and often fail to account for differences in fire severities (but see Brown et al. 2019).

We dissected soil-inhabiting bacterial and fungal communities before and up to six years following fires of two different severities. We aimed to answer the following three broad research questions: (1) how does the fire severity impact the bacterial and fungal communities over time; (2) are there important indicator taxa underlying the community dynamics; and, (3) do these indicators differ based on fire severity? We hypothesized that (1) the different fire severity treatments would result in distinct communities following the fire event; (2) the communities would maintain distinct trajectories over time; and, (3) distinct fire-responsive or pyrophilous taxa would follow a high severity fire but not low severity fire.

Materials and Methods

Study Site

We utilized a research infrastructure established in the Pringle Falls Experimental Forest (43º42'N, 121º37'W) located in the Deschutes National Forest in Oregon, USA. Previous studies utilizing this research infrastructure have reported early fungal community responses (Reazin et al. 2016), mycorrhizal fungus community responses (Cowan et al. 2016), heat pulse transfer (Smith et al. 2016) as well as long-term silviculture research (Youngblood 2011). The experiment was located within a prescribed burn area of ~199ha dominated by ponderosa pine (*Pinus ponderosa* Douglas ex. C Lawson). The understory in the area is mainly dominated by snowbrush ceonothus (*Ceonothus velutinus* Doug. Ex Hook) and bitterbrush (*Purshia tridentata* Pursh*)* (Cowan et al. 2016; Reazin et al. 2016). The soils are well drained, loamy with coarse sand and include volcanic ash deposits from the Mount Mazama eruption ~7,000 years ago (Youngblood et al. 2004). The soils are classified as Xeric Vitricryands according to the La Pine Soil Series.

Experimental Design

Because the experimental arrangement has been described previously (Cowan et al. 2016; Reazin et al. 2016; Smith et al. 2016), we only provide a brief description here. In 2011, the stand was thinned and harvested timber used to construct "mega-logs" to imitate large downed logs (~1.5-2m wide, 8-10m long, 1m high). These logs were left to cure until the burn treatments took place two years later. In 2013, ten blocks were established, each containing a plot of "mega-logs" to mimic combustion of large downed logs – a high burn (HB) severity – and an adjacent plot without additional fuel – a low burn (LB) severity. A prescribed burn was conducted on May 14th, 2013. This broadcast burn ignited both the LB and HB treatments.

Soil Sampling

We included the early samples used by Reazin et al. (2016) and continued to repeatedly sample this experiment on a biannual basis to better understand the temporal dynamics of soil-inhabiting bacterial and fungal communities after fires of different severities. The ten HB and LB plots were sampled five days before ignition (T0) and one week (T1) after fire as described in Reazin et al. (2016). We returned to repeat the soil sampling two (T2), four (T4), and six years (T6) after the fire and sampled in early growing season in late May or early June to minimize the possible temporal effects stemming from within season dynamics. Because no organic horizon (O horizon) was present in the HB treatments, the O horizon was removed where present and one core (10cm depth, 5cm diameter) of mineral soil was sampled at each plot. Soil samples were homogenized, collected into 15mL Falcon tubes, and transported on ice until stored at -20ºC ~24 hours later. The frozen soil samples were shipped on dry ice to Kansas State University for molecular analyses and stored at -20ºC until DNA extraction. In total, we acquired twenty samples (10 LB and 10 HB) at each sampling time point (T0-T6), for a total of one hundred soil samples across the five sampling events.

DNA Extraction, PCR Amplification, and Sequencing

Total genomic DNA was extracted from ~0.25g soil subsamples using PowerSoil DNA Isolation Kit (MoBio, Carlsbad, California, USA) following manufacturer's protocol. The DNA was quantitated with an ND2000 spectrophotometer (NanoDrop Technologies, Wilmington, Delaware) and standardized to 12.5ng/ul for PCR amplification. The hypervariable V4 region of the bacterial

16S ribosomal RNA gene was amplified using forward 515f and reverse 806r primers (Caporaso et al. 2012). The fungal Internal Transcribed Spacer (ITS2) region was amplified using the forward fITS7 (Ihrmark et al. 2012) and reverse ITS4 primers (White et al. 1990). We used two-step PCR protocol to avoid potential 3' primer bias as described in Berry et al. (2011). The primary PCR reactions with proof-reading Pfu polymerase (Oliver et al. 2015) were performed in triplicate 50ul reactions volumes with the following amounts/concentrations: 10ul (125ng) DNA template, 5ul dNTPs (200uM), 5ul each primer (1uM each), 10ul Phusion 5X HF Buffer with 7.5mM $MgCl_2$, 14.5 molecular grade water, and 0.5ul (1 unit) Phusion Green Hot Start II DNA polymerase (ThermoScientific, Pittsburg, Pennsylvania, USA). Primary bacterial PCR reactions began with an initial denaturing for 30s (98ºC), followed by 30 cycles of 98 ºC for 10s denaturing, 30s of annealing (50 ºC), 1 min extension (72 ºC), and concluded with a 10-min final extension. Primary fungal PCR reactions began with an initial denaturing for 30s (98 ºC), followed by 30 cycles of 98 ºC for 10s denaturing, 54 ºC for 30s annealing, 72 ºC for 1 min extension followed by a final 10-min extension at 72 ºC.

The three primary PCR technical replicates were cleaned using AMPure XP (Beckman Coulter, Brea, California, USA) following a modified manufacturer's protocol. A total of 30ul of each of the three technical replicates was combined for a total of 90ul of PCR product per sample. We used a 1:1 ratio of PCR product to magnetic bead solution and rinsed three times with 80% EtOH. Following the amplicon clean-up, secondary PCR was performed in a single 50ul reaction using the same primers as the primary PCR but with 12bp molecular identifiers (Caporaso et al. 2012). All secondary PCR reactions were performed in single 50ul reactions using the same concentrations/amounts of reagents. The PCR reaction conditions were also identical with the exception only five PCR cycles. The secondary PCR amplicons were cleaned similarly to the primary PCR products and quantitated using the ND2000 spectrophotometer. A total of 200ng of each sample was pooled for bacterial or fungal sequencing. Illumina adapters and indices were added in four PCR cycles, using KAPA Hyper Kit (Roche, Pleasenton, California, USA), and 0.5ug starting DNA. The libraries were sequenced (2 x 300 cycles) using the Illumina MiSeq Personal Sequencing System at the Integrated Genomics Facility (Kansas State University, Manhattan, Kansas, USA). The sequence data are available through the Sequence Read Archive under the BioProject #; BioSamples#.

Sequence Analysis

Sequence data were analyzed using mothur bioinformatic pipeline (v. 1.38.0; Schloss et al. 2009). Bacterial and fungal sequences were contiged, primer sequences trimmed, and any sequences with ambiguous bases or with homopolymers longer than 7bp were filtered out. Fungal sequences were then truncated to the shortest sequence length in the dataset (295bp). Sequence data were pre-clustered to minimize platform generated biases (Huse et al. 2010). Bacterial sequences were aligned using the SILVA (release 132; www.arb-sil-va.de) reference alignment. Bacterial and fungal sequences were screened for chimeras using VSEARCH (Rognes et al. 2016) and putative chimeras were culled. Sequences were classified using mothur implemented Naïve Bayesian Classifier (Wang et al. 2007) against the RDP training set (v.10) (bacteria) or the UNITE database (v6 Kõljalg et al. 2013) (fungi). Non-target lineages (Eukaryotes, mitochondria, chloroplast for bacteria and Protista, Plantae and Animalia for fungi) were removed as well as any sequences that could not be classified. Bacterial Operational Taxonomic Units (OTUs) were clustered into OTUs using nearest neighbor algorithm, whereas fungal OTUs were clustered using VSEARCH (Rognes et al. 2016). We iteratively (100 iterations) calculated Good's Coverage, observed richness (S_{obs}), Shannon's Diversity (H'), and Shannon's Evenness (E_H) using mothur.

Statistical Analyses

Statistical analyses were conducted using R version 3.6.3 (R Core Team, 2020) and R studio version 1.1.143. To better illustrate the community dynamics over time, we calculated response ratios using the equation $(t_i-t_0)/(t_i+t_0) = R$ where t_i represents samples collected post-fire within a non-replicated block, and t_0 is the pre-burn sample for that block. Response ratio (R) ranges from -1 to 1 with an expected mean of 0 when variable estimates for t_0 do not differ from t_i. Our samples are inherently paired because we sampled the same experimental units. As a result, we considered analyses of response ratios most appropriate to better follow how the communities may have changed over time.

We used analyses of variance (ANOVA) to test for differences in bacterial and fungal diversity, evenness, and richness metrics among the severity treatments and different sampling times. We also utilized the conservative pairwise Wilcoxon rank sum test to test whether the response ratios

of T1-T6 differed from zero (T0) for any of the sampling points. We first analyzed our full dataset using global ANOVA with burn severity (HB and LB) and sampling time (T0, T1, T2, T4, and T6)) as main effects as well as their interaction (severity x time) to explore how the fire severity impacts the community metrics through time. We also chose to analyze the two burn severities separately to more explicitly focus on the community trajectories over time in each of the two fire severities. To do this, we utilized one-way ANOVAs and Tukey's Honestly Significant (HSD) post-hoc pairwise comparisons to test how the five sampling time points differ from each other within each of the two severity treatments. To specifically test whether any of the post-fire (T1-T6) metrics differed from pre-fire (T0), we used pairwise Wilcoxon rank test.

To analyze and infer compositional responses of the bacterial and fungal communities to the fire severity and sampling time, we used the R package vegan (Oksanen et al. 2019). We derived Bray-Curtis distance matrices and compared treatments using PERMANOVA using adonis2() function (McArdle and Anderson 2001) within the vegan package. These community data were visualized using Non-Metric Multidimensional Scaling (NMDS) ordinations using packages ggplot2 (Wickham 2016) and ggpubr (Kassambra 2020). To understand the differences in compositional responses amongst the communities based on sampling years within the two different fire severities, we utilized pairwiseAdonis package (Martinez Arbizu 2020). To investigate the dispersion (community convergence or divergence) amongst the communities, we used betadisper() function within the vegan package. To identify OTUs disproportionately more abundant in one treatment compared to others, we utilized multiplatt() command of the indicspecies package (De Caceres and Legendre 2009). For these indicator taxon analyses, we focused on the most abundant OTUs representing 10% of all the OTUs or a total 100 OTUs for fungi and 1,638 OTUs for bacteria. Similar to the community analyses, we investigated the indicator OTUs separately for each of the two fire severity treatments.

To derive functional attributes of the fungal community members, we used FUNGuild (Nguyen et al. 2016) to assign OTUs to ecological guilds and trophic modes. We utilized the the R package FUNGuildR (Furneaux and Song 2021) that uses the FUNGuild database to match taxon to functional guilds. With these data, we conducted one-way ANOVA and Tukey's HSD post-hoc tests to understand how specific ecological guilds, the top five most abundant of our dataset

(Animal Pathogens, Ectomycorrhizal, Endophytes, Plant Pathogens, and Undefined Saprotrophs), shift following different fire severities, and how the trajectories of the guilds change with time since fire.

Results

Bacterial Communities

The bacterial dataset initially contained 8,176,265 sequences. After quality control and subsampling, the final sequence count was 3,114,769. The final sequence data were assigned to 4,254 Operational Taxonomic Units (OTU). The bacterial communities were dominated by OTUs assigned to Proteobacteria (24%), OTUs unclassified beyond domain Bacteria (20%), followed by Actinobacteria (8%), Acidobacteria (7.2%), Bacteroidetes (7.4%), Planctomycetes (6.4%), Verucomicrobia, (5.6%), and other bacterial phyla (21.4%) that accounted for less than 5% each. Good's coverage (91.6±3.70%) indicated that the bacterial diversity was fairly well represented in our sampling.

Bacterial richness and diversity over time depended on the severity treatment as indicated by the severity x time interaction in our two-way ANOVAs for observed richness (S_{Obs} - $F_{4,85}$=4.17; P=0.004) as well as Shannon's diversity (H'- $F_{4,85}$=15.58; P<0.001) and evenness (E_H - $F_{4,85}$=8.82; P <0.001). As a result, we analyzed the two burn severities (HB/LB) separately using one-way ANOVAs. In the LB treatment, the observed richness ($F_{4,44}$=4.74; P=0.004), Shannon's diversity ($F_{4,44}$=7.51; P=0.001), and evenness ($F_{4,44}$=7.43; P=0.001) differed among the sampling times. The subsequent post-hoc tests (Tukey's HSD) indicated that richness and diversity at T1 were lower than at T2-T6 (Figure 4.1). Consistent with these analyses, the pairwise Wilcoxon rank sum tests that aimed to specifically address whether or not any post-fire estimators differed from the pre-fire estimators indicated that diversity and evenness at T1 (H' - P_{adj}=0.01; E_H – P_{adj} =0.01) were lower than before fire, and they were higher than before fire at T6 (E_H - P_{adj}=0.01) (Figure 4.1). The bacterial communities responded to the HB treatment more strongly than to the LB treatment. The observed richness ($F_{4,41}$=56.05; P<0.001) as well as Shannon's diversity ($F_{4,41}$=33.01; P<0.001) and evenness ($F_{4,41}$=15.57; P <0.001) differed among the sampling years. All diversity and richness estimators were lower at T1 than at T2, T4 or T6 (Tukey's HSD, P < 0.05) (Figure 4.1). In addition,

post-fire richness (T1-T6) was consistently lower than before fire (T0) based on pairwise Wilcoxon rank sum tests (Figure 4.1). Although all bacterial richness and diversity metrics at T1 were lower than those at T0 (Figure 4.1), this was not true for T2-T6 with the exception of richness.

We visualized the bacterial communities in the HB and LB treatments together using NMDS ordination (Figure C 1). The PERMANOVA indicated a severity x time interaction ($F_{4,85}$= 3.27; P=0.001) in those analyses suggesting that community responses over time depended on the fire severity treatment. We then analyzed the bacterial communities in the LB and HB treatments separately to better understand the community trajectories in each treatment (Figure 4.3). The communities differed among the sampling times in both LB (PERMANOVA: $F_{4,44}$=2.29; P=0.001) and HB (PERMANOVA: $F_{4,44}$=6.38; P=0.001; Table 4.1 and 4.2) treatments. Based on our pairwise PERMANOVA tests (Table 4.1), all time points different from each other in the LB except for T0 and T1, and all time points differed from each other in the HB treatment. Further, our pairwise community dispersion tests provided evidence for divergence among the fire severities ($F_{1,93}$=26.55; P<0.001) and sampling times ($F_{4,90}$=3.75; P=0.007). In separate analyses of each burn severity, post-fire T2 was more heterogeneous than T0, T1, T4, and T6 in the LB treatment ($F_{4,44}$=2.57; P=0.05; Pairwise 0.004<P>0.03). In contrast, we observed no evidence for community divergence/convergence in the HB treatment ($F_{4,41}$=0.17; P=0.95).

We used indicator taxon analyses (De Caceres and Legendre 2009) to identify OTUs that were disproportionately more abundant in any one sampling time compared to others (P≤0.05) (Table C 1 (HB) and 2 (LB)) Because LB and HB treatments did not differ pre-fire, but did so post-fire, we analyzed the HB and LB treatments separately. In the LB treatment, there were a total of 18 indicator OTUs before the fire (T0), *i.e.*, OTUs that declined or were absent after the fire. A majority of these indicators belonged to Firmicutes (11 or 61%), Proteobacteria (4 or 22%), or remained unclassified (2 or 11%). At T1, there were a total of 16 indicators, four of which belonged to the Phylum Proteobacteria, three to Firmicutes, three to Bacteroidetes (3), rest representing Actinobacteria, Acidobacteria, and Verrucomicrobia or remained unclassified. Additionally, there were 58 indicator OTUs for T2, 7 indicators for T4, and 98 indicators for T6. In sampling year 2 (T2), the majority of the indicators were unclassified (16 or 27%) or represented Planctomycetes (11 or 19%), Proteobacteria (8 or 14%), Parcubacteria (5 or 9%) or Actinobacteria (4 or 7%). In

the fourth sampling year (T4), there were 7 indicators distributed across Proteobacteria (2 or 28%), Actinobacteria (1 or 14%), Gemmatimonadetes (1or 14%) and Parcubacteria (1or 14%), or remained unclassified (2 or 28%). Indicators for the last sampling (T6) were mainly Acidobacteria (20 or 20%), Proteobacteria (18 or 18%), Bacteroidetes (17 or 17%), Verrucomicrobia (14 or 14%), and Actinobacteria (4 or 4%), or remained unclassified (9 or 9%). Indicators in the HB treatment were more numerous than those in the LB treatment. In the HB, the pre-fire condition (T0) had a total 1,277 indicator OTUs, a majority of which were common soil-inhabiting taxa including Proteobacteria (295 or 23%), unclassified (239 or 19%), Acidobacteria (137 or 11%), Planctomycetes (106 or 8%), Verrucomicrobia (100 or 8%), and Bacteroidetes (89 or 7%). This large number of indicators represents those that declined or were absent after the HB treatment. In the first post-fire sampling (T1), only one week after the fire, there were only ten indicators, all representing the Phylum Firmicutes. Of note, Firmicutes indicators were present both in T0 and T1 sampling time points (<5% of the indicators for treatments T0), but none of them overlapped between the two time points. The number of indicator OTUs increased in the next sampling (T2) in HB to 98 indicator OTUs, nearly half of which (37 or 38%) represented Phylum Proteobacteria. The number of indicators for the subsequent sampling events (T4-T6) was lower: 23 at T4 and 64 at T6. For both of these time points, unclassified taxa were the largest proportion of the indicators (35% for T4 and 27% for T6), followed by Proteobacteria (22% for T4 and 23% for T6).

Fungal Communities

The fungal dataset initially contained 10,695,355 sequences. After quality control and subsampling, the final sequence count was 7,606,822. The final sequences were assigned to 996 Operational Taxonomic Units (OTUs). These OTUs mainly represented Basidiomycota (43.4%) and Ascomycota (41.4%), only relatively few belonged to the Phylum Glomeramycota (1.7%), or basal taxa formerly assigned to Chytridiomycota (3.3%) and Zygomycota (10.2%). Good's coverage (99.96±0.08%) indicated that fungal diversity was well represented in our sampling.

Similar to bacteria, fungal community temporal dynamics depended on the fire severity treatment as indicated by the severity x time interactions in our two-way ANOVAs for observed richness (S_{obs} - $F_{4,87}$=3.05; P=0.021) as well as for Shannon's diversity (H'- $F_{4,87}$=9.38; P<0.001) and evenness (E_H - $F_{4,87}$=9.98; P <0.001). We subsequently analyzed each burn severity (LB/HB)

separately using one-way ANOVAs. In the LB treatment, responses in fungal richness ($F_{4,45}$=3.34; P=0.02), diversity ($F_{4,45}$=2.30; P=0.07) and evenness ($F_{4,45}$=1.49; P =0.22) were rare or absent and did not differ in post-hoc comparisons (Tukey's HSD: P > 0.05) among the post-fire samples (T1-T6) (Figure 3). However, richness, diversity, and evenness estimators at T1 were lower at T0 (S_{Obs} - P_{adj}=0.01; H' - P_{adj}=0.01; E_H - P_{adj}=0.01), whereas those for T2-T6 did not differ from the pre-fire (T0) samples (Wilcoxon Rank Sum Test P_{adj} > 0.05) (Figure 4.3). The richness and diversity responses in the HB differed from those in the LB: observed richness ($F_{4,42}$=21.93; P<0.001) as well as diversity ($F_{4,42}$=18.36; P<0.001) and evenness ($F_{4,42}$=13.80; P <0.001) differed among the sampling times. The richness, diversity and evenness were lower at T1 than at T2, T4 and T6 (Tukey's HSD: P < 0.05) (Figure 4.3). In addition, richness was lower in all post-fire samples (T1-T6) than before the fire (T0) (T1- P_{adj}<0.01; T2 - P_{adj}=0.009; T4 - P_{adj}=0.001; T6 P_{adj}=0.01). Fungal diversity (T1- P_{adj}<0.001; T2 - P_{adj}<0.001; T4 - P_{adj}=0.001; T6 P_{adj}=0.08) was consistently lower after (T1-T6) the high severity fire than before it, whereas this was not true for evenness (T1- P_{adj}=0.01; T2 - P_{adj}=0.01; T4 - P_{adj}=0.16; T6 - P_{adj}=1.0) that was lower at T1 and T2 than at T0 but not at T4 or T6 (Figure 4.3).

The NMDS ordination of LB and HB treatments together (Figure C 2) indicated a severity x time interaction (PERMANOVA: $F_{4,87}$= 2.37; P<0.01) suggesting that community trajectories over time depended on fire severity. Consistently with our other analyses, we visualized the fungal communities in the LB and HB treatments separately (Figure 4.4). The fungal communities differed among sampling times in both LB (PERMANOVA: $F_{4,45}$=3.01; P=0.001) and HB (PERMANOVA: $F_{4,42}$=4.37; 0.001) treatments. Pairwise PERMANOVAs indicated that sampling times in the LB treatment differed from each other except for T1 and T2 (Table 4.3 and 4.4) and that all sampling times in the HB treatment differed from each other. Similar to the bacterial communities, we first analyzed the LB and HB treatments together for dispersion. Our pairwise dispersion tests provided evidence for divergence based on burn treatment ($F_{1,95}$=14.87; P<0.01) and time ($F_{4,92}$=12.73; P<0.01) indicating that the HB treatment was more dispersed relative to the LB treatment and that all post-fire samples (T1-T6) were more dispersed than the pre-fire sample (T0) (Tukey's HSD P<0.01). In separate analyses of the HB and LB treatments, pairwise dispersion tests provided no evidence for convergence or divergence in the HB treatment ($F_{4,42}$=1.87; P=0.13) but suggested that sampling times differed in dispersion in the LB treatment

($F_{4,45}$=4.64; P=0.001). Specifically, T4 and T6 were relatively divergent compared to T0 and T1 (T4-T0 P=0.001; T6-T0 P=0.003; T4-T1 P=0.002; T6-T1 P=0.002), suggesting that the samples characterizing communities at T4-T6 were more heterogeneous than those at T0-T1. There was no evidence of dispersion compared to T2.

To gain insight into ecological roles of the fungal community constituents and their trajectories after high and low severity fires, we utilized FUNGuild (Nguyen et al. 2016). Of the total of 996 fungal OTUs, a total of 630 (63.3%) were assigned to a guild and trophic mode. Some were assigned to more than one guild; when this occurred, we used the one listed first. The 630 FUNGuild assigned OTUs were distributed across 21 guilds. We chose to focus on the five most abundant ones including undefined saprotrophs (34.8% of the 630 OTUs), ectomycorrhizae (25.4%), endophytes (10.5%), animal pathogens (5.9%), and plant pathogens (5.4%). Note that broader guild analyses were consistent as the remaining guilds were present in low abundances (Figure C 3).

There was strong evidence for fire severity x time interaction in our two-way ANOVAs for the undefined saprotrophs guild ($F_{4,87}$= 6.69; P<0.001), but not for any of the other abundant guilds, suggesting that only the saprotroph guild responses over time depended on fire severity. In the separate analyses of the two burn severities, ectomycorrhizal ($F_{4,45}$=5.35; P=0.001), endophyte ($F_{4,45}$=10.49; P<0.001), and undefined saprotroph ($F_{4,45}$=29.40; P<0.001) guilds differed in their abundances over time in the LB treatment, whereas animal ($F_{4,45}$=2.19; P=0.08) and plant pathogens ($F_{4,45}$=1.04; P<0.40) did not. Specifically, the ectomycorrhizal guild was less abundant in T2 than in T1 and T6 (Tukey's HSD; P < 0.05). The fungal endophyte guild within the LB treatment remained distinctly lower post-fire (T1-T6) compared to pre-fire (T0). The undefined saprotroph guild was most abundant in T1 and T2, but by T4 and T6 its abundance was lower than in T0 (Figure #). The HB treatment resulted in distinct temporal differences in four of the five most abundant guilds: ectomycorrhiza ($F_{4,42}$=6.26; P<0.001), endophyte ($F_{4,42}$=8.78; P<0.001), plant pathogen ($F_{4,42}$=3.05; P=0.03), and undefined saprotroph ($F_{4,42}$=18.43; P<0.001) guilds, whereas the animal pathogen guild did not vary over time ($F_{4,42}$=1.67; P=0.17). The ectomycorrhizal guild was more abundant in T2 than in other sampling times (T0-T1, T4-T6). Interestingly, the pre-fire (T0) and first post-fire (T1) did not differ (Tukey's HSD; P > 0.05).

Endophytic fungi never reached their pre-fire abundances; their abundance at T0 was higher than at any other time (T1-T6). Upon further investigation, these taxa (Helotiales; *Cadophora* and *Phialocephala*) are likely mycorrhizal symbionts of Ericaceae (Walker et al. 2011), many of which were consumed by the fire. The plant pathogens at T2 were more abundant than at T1. The undefined saprotrophs increased in abundance in T1. By T2, their abundance did not differ from the pre-fire conditions (T0) and continued to decline in subsequent samplings (T4–T6) (Figure 4.5).

In addition to the guild analyses, we utilized indicator taxon analyses for fungi. Like bacteria, we analyzed the LB and HB treatments separately to understand which taxa may underlie the community shifts following fire (Table C 3 and 4). There was a total of 54 indicator OTUs for T0 in the LB treatment. These represented Ascomycota (25 indicator OTUs), Basidiomycota (16) and Mucoromycota (13). Immediately after fire (T1), there were nine indicator OTUs representing Ascomycota (5), Basidiomycota (3) and Mucoromycota (1), including *Morchella* (2 OTUs), *Neurospora* (1 OTU), *Pholiota* (1 OTU), and and *Scutellinia* (1 OTU) – members of families (Pyronemataceae) and genera (*Morchella, Neurospora, Pholiota*) with pyrophilous species. Two years post-fire (T2), there were 15 indicators, Ascomycota (2 indicator OTUs), Basidomycota (11), and Chytridiomycota (2). *Pholiota brunnescens* (OTU17) was also an indicator for the T2 low burn treatment. There were 5 indicators for T4 including Ascomycota (2), Basidiomycota (2) and Chytridiomycota (2). For T6, there were a total of 19 indicator OTUs – 8 Ascomycota, 7 Basidiomycota, and 4 Mucoromycota. Like bacteria, indicator OTUs within the HB treatment were more numerous. The pre-fire sampling (T0) had a total of 118 indicators, 25 of which represented basal taxa formerly in the phylum Zygomycota, 56 Ascomycota, and 36 Basidiomycota and 1 Chytridiomycota. HB T1 indicators totaled to 16, and belonged to the Phylum Ascomycota (11), notably with *Scutellinia* and *Morchella* among the indicators, and Basidiomycota (5). Second post-fire sampling (T2) of the HB treatment had a total of 32 indicators, 15 in the Phylum Basidiomycota, including three OTUs matching *Pholiota highlandensis* based on NCBI's BLASTN (Zhang et al. 2000), 11 in Ascomycota, and six representing early diverging basal fungi (*Spizellomyces*, Chytridiomycota). Next to last sampling (T4) had 9 indicator OTUs, including 4 Ascomycota indicators, 4 Basidiomycota, and 1 Chytridiomycota. The final sampling (T6) included 13 indicators, 5 Ascomycota, 6

Basidiomycota, and 2 Chytridiomycota. We BLASTN (Zhang et al. 2000) analyzed representative sequences for indicators that belonged to families or genera with potentially pyrophilous species: OTUs 10 (*Scutellinia*) and 17 (*Pholiota*) that were indicators in both burn treatments at T1 and T2, respectively. Sequence representing OTU10 was 99.4 % similar to *Anthracobia* sp. (GenBank: MK840938.1) from a fire site (Matheny et al. 2018; Hughes et al. 2020). OTU17 was 100% similar to *Pholiota brunnescens* (GenBank: MG735303.1), and another indicator (OTU44) was 99.7% similar to *Pholiota highlandensis* (GenBank: MG735279.1), a putatively pyrophilous taxon (Matheny et al. 2018). Of note, OTUs 10 and 29, the *Anthracobia* sp. and *Morchella* sp. (*Morchella sextelata* GenBank: MN622794.1 or *Morchella importuna* (GenBank: MH982599.1), both 99.7% sequence similarity to our OTU) were both indicators in the LB and HB at T1 time point. Similarly, OTU17 (*Pholiota brunnescens*) was an indicator in both burn treatments at T2.

Discussion

Forest fires are projected to increase in frequency and severity (Jolly et al. 2015; Pritchard et al. 2017), with much of this increase attributable to drier conditions, lightning flash rates, and anthropogenic factors (Krawchuk et al. 2009). We aimed to gain further understanding of soil-inhabiting bacterial and fungal community responses to different burn severities over time in an experiment that aimed to mimic large timber combustion in a ponderosa pine ecosystem. Bacterial communities changed compositionally and declined in richness and diversity directly following the fire (T1). These communities that were sampled a week after the fire differed in richness from those present before the fire (T0) conditions as well as from those analyzed later (T2-T6), regardless of burn severity. Fungal communities immediately following the fire were also distinct in composition, lower in richness and diversity and were distinctly different from those in the later sampling time points, but only in the high severity burn treatment (HB). In contrast to fungal communities in the HB treatment and bacterial communities overall, fungal communities in the low burn severity (LB) treatment only differed from the pre-fire (T0) conditions at the first sampling following the fire (T1). Both bacteria and fungi in the LB treatment reached richness and diversity comparable to those before the fire within two years after the fire. These data suggest that bacterial and fungal richness and diversity rebound quickly after low severity fires, whereas

the fungal community composition does not. In contrast, the fungal richness, diversity or community composition in the HB treatments had not become similar to those before the fire by our last sampling six years after the fire treatments. Our observations are consistent with those suggesting rapid community shifts following a fire (Reazin et al. 2016) and others reporting that post-fire communities remain distinct for years (Dooley and Treseder 2012; Oliver et al. 2015; Pulido-Chavez et al. 2021).

Although our analyses identified mainly different post-fire indicators in the LB and HB treatments, some bacteria and fungi responded to low and high severity burn similarly as suggested by overlapping indicators between the two fire severity treatments. The indicator OTUs for the first post-fire sampling (T1) for HB treatments exclusively included bacteria in the phylum Firmicutes, indicating that this phylum was disproportionally more abundant soon after fire than either before the fire or later after it. Some Firmicutes respond to fire positively and our observations are consistent with others. For example, Lucas-Borja et al. (2019) reported an increase in Firmicutes after high severity experimental fires in a Mediterranean ecosystem. Similarly, Pérez-Valera et al. (2019) reported an increase in Firmicutes in a similar Mediterranean ecosystem only one day after fire. Finally, Prendergast-Miller et al. (2017) reported an increase in Firmicutes approximately one month after a wildfire in Australia. Taken together, Firmicutes seem to include organisms that increase in abundance soon after a fire in a variety of systems globally. In contrast to the few bacteria that increased in abundance after fire, many clearly declined in response to fire. Notably, our analyses of the HB treatment identified 1,277 indicators before fire (T0), in contrast to just ten indicators after fire (T1). Interestingly, all these early post-fire indicators belonged to Firmicutes, further highlighting members of Firmicutes as positively fire responsive. Consistently with our observations, Enright et al. (2021) also observed a dramatic shift towards a Firmicutes dominated community following mega-fires in the *Sequoia sempervirens* stands in California. Similar to our results, they also observed a large number of taxa declining after the fire including representatives of Proteobacteria, Bacteroidetes, and Verrucomicrobia that are often among the common Phyla in soil (e.g., Roesch et al. 2007; Lauber et al. 2009; Wei et al. 2018). These taxa were also among the dominant indicators before our high severity fire but absent as indicators immediately after the fire.

Fungal indicators provided a more detailed insight into the positively fire-responsive taxa. Three putative pyrophilous OTUs were among the indicators in both our low and high severity burn treatments. Among these was an OTU within the family Pyronemataceae that closely matched *Anthracobia* sp. in BLAST analysis of representative sequences. *Anthracobia* spp. have been reported to fruit after prescribed fires in eastern Oregon, USA (Fujimura et al. 2005) and wildfires in the Great Smokey Mountains in Tennessee, USA (Hughes et al. 2020) or in Australia (Claridge et al. 2009). Our results, and the results of these previous studies, suggest that *Anthracobia* spp. can vegetatively respond to fire, whether high or low severity, but may only fruit after moderate to high severity fires (Warcup 1990; Claridge et al. 2009). *Morchella* sp. was another post-fire indicator in both burn treatments. *Morchella* spp., commonly known as morels, are choice edibles, some of which fruit after fire (Sturgis 1905; Larson et al. 2016). Li et al. (2017) manipulated fuel loads for experimental fires of varying intensities to assess their impact on morel production. A species that our *Morchella* OTU matched in BLAST analyses was *M. importuna*, the species used in Li et al. (2017). They reported greatest morel production with the highest fuel loads, but that all fuel loads, even just the ground fires induced morel fruiting. These results are consistent with our analyses that indicate that this taxon increases in abundance after a fire, regardless of fire intensity. The last post-fire indicator taxon common to both of our two burn treatments was *Pholiota highlandensis,* which was present in the HB T2 and the LB T1 samplings. This indicator was also reported in abundance several months following the Great Smokey Mountains National Park's Chimney Top fire and continued to be detected more than a year after it was initially detected (Matheny et al. 2018). This species is also subject of the "body snatchers" hypothesis (Raudabaugh et al. 2020), in which *P. highlandensis* was proposed to symbiotically associate with bryophytes after a fire.

Our FUNGuild analyses also provided great insight into fungal community functional shifts through time. Many of our results corroborate those of others (Holden et al. 2016; Dove et al. 2021; Pulido-Chavez et al. 2021). Specifically, Holden et al. (2016) reported that following severe fire, mycorrhizal fungi decreased. Pulido-Chavez et al. (2021) similarly reported that approximately half as many ectomycorrhizal amplified sequence variants (ASVs) occurred in burned treatments compared to unburned treatments. Holden et al. (2016) also noted that following fire, there was a greater abundance of ascomyetes than basidiomycetes, many of the latter being

mycorrhizal. Our data and results broadly concur. However, and somewhat surprisingly, ectomycorrhizal fungi increased in abundance in both fire severity treatments and exceeded the abundance in the pre-fire sampling within two years of the fire and maintained those higher levels through the later samplings (Figure 4.5). After the fire, plant pathogen abundance initially decreased (T1) but subsequently dramatically increased (T2) in our high fire severity treatment. This increase in plant pathogens after a fire is similar to that reported in Dove et al. (2021), who – studying an Aspen system in central Utah – observed a four-fold increase in plant pathogens after a high intensity prescribed fire. Some endophytes of the Helotiales order, *Cadophora* and *Phialocephala,* are also ericoid mycorrhizal symbionts (Walker et al. 2011). We saw a large decline in these groups following fire. Similar results of a decline in *Cadophora* were also observed in (Glassman et al. 2016), after the Rim Fire in California. In contrast, a study in a Mediterranean ecosystem comparing different fire return intervals, found that *Cadophora finlandica* had greater abundance in the more frequently burned sites (~7 years), compared to the unburned and long fire return interval (Buscardo et al. 2012). They noted that this species greatly colonized the shrubs within that fire interval. The decline observed in our study is likely due to total fuel consumption of the shrubs in the high severity burn treatment.

Fires can directly induce mortality of some community members, whereas others may survive in the spore bank (Glassman et al. 2016) or in local refugia (Krawchuk et al. 2016; Meddens et al. 2018). However, decoupling the drivers of post-fire successional trajectories can be difficult (Meiners et al. 2015) because fire-induced changes in soil chemistry, soil moisture, nutrient availability, plant host physiology and availability, as well as propagule arrival via air, animal vectors, or water can lead to changes in the resident communities (Certini 2005, Certini et al. 2021). As a result of multiple concurrent changes in the soil environment, we are confined to speculating which factors may underlie our community responses; some of which are likely context dependent (Bittleston et al. 2020). The last sampling (T6), six years post-fire, perhaps best exemplifies this. Communities at this time appeared more distant from the pre-fire samples than other, earlier post-fire samples – a trajectory quite opposite of our predictions. Further, there was also evidence of divergence at T6 in both fire severity treatments relative to other sampling events in our fungal community dispersion analyses. To seek possible explanations for this unexpected result, we acquired drought data from the National Integrated Drought Information System (NIDIS) (Figure C 4) The T6 sampling in 2019 coincided with a level D3 (Extreme drought) in

Deschutes County, where our experiment is located. The other sampling time points coincided with D0 (Abnormally dry) to D2 (Severe drought), suggesting that variability in the environmental conditions may underlie these observations. While there may be a correlation between the extreme drought and the community divergence, we cannot state with confidence that this is the main driver of the community trajectory, just that it may be among them. Whilst time series studies are a valuable tool to understand system behaviors and dynamics in the short- and mid-term, they struggle with confounding temporal shifts analogous to the spatial confounding factors that are often used to criticize chronosequence or space for time substitution studies (see Walker et al. 2010). As site conditions, species availability, and species performance are three key aspects to understanding succession (Meiners et al. 2015), they may be as dynamic over time as they may be dynamic over space. However, many studies of temporal dynamics must compromise over scale and site availability. Walker et al. (2010) point out that chronosequences are not ideal for short or mid-term successional dynamics, a research gap that time series studies like the one presented here aim to fill. However, the underlying and confounding factors that change in the short and medium term must be considered in multi-year studies.

Conclusions

Exploitation of this unique experiment allowed us to gain insight into how different fire severities impact soil microbial communities. Our study strongly indicates that more severe fires have a greater impact on the soil-inhabiting bacterial and fungal communities both in the short and long term compared to low severity ground fire. This study allowed us to demonstrate and sample a system that mimics a wildfire that contains heterogeneous burn severities, and how the varying fires can lead to distinct community trajectories. Interestingly, whilst our fire treatments led to decrease in richness and negatively impacted many resident taxa – particularly after the high severity treatment, some bacteria and fungi clearly increased in their abundance following the fire. Our results identify several severe-fire indicators representing a bacterial Phylum Firmicutes and fungal genera *Anthrocobia*, *Morchella*, *Neurospora,* and *Pholiota.* Finally, our analyses of fungal guilds indicate functional shifts in the fungal communities and highlight the increase in ecologically important groups (ectomycorrhizal symbionts and plant pathogens) as well as decrease in others (Helotialean endophytes). These changes in plant associated fungal

communities highlight the tight linkages among the plant and fungal communities as well as the complex multidimensional system responses to fire.

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Chapter 4 Figures and Tables

Figure 4.1 Bacterial Boxplots

Observed richness (S_{obs}), Shannon's diversity (H'), and Shannon's evenness (E_H) of the four sampling time points (T1, T2, T4, T6) for the different fire treatments – Low Burn (**Left Column; A-C);** High Burn (**Right Column; D-F**). The results of the Tukey's HSD Test are indicated by the letters above the boxplots and of the Wilcoxon rank sum test are indicated by "*". The former tests the null hypothesis that differences between the pre-fire estimates and those at T1-T6 do not differ from each other ($P \geq 0.05$), whereas the latter tests the null hypotheses that each of the differences is equal to zero ($P \geq 0.05$) indicating that the estimates at T0 and Ti are not different from each other based on our response ratio, $\boldsymbol{(t_i-t_0)/(t_i+t_0) = R}$.

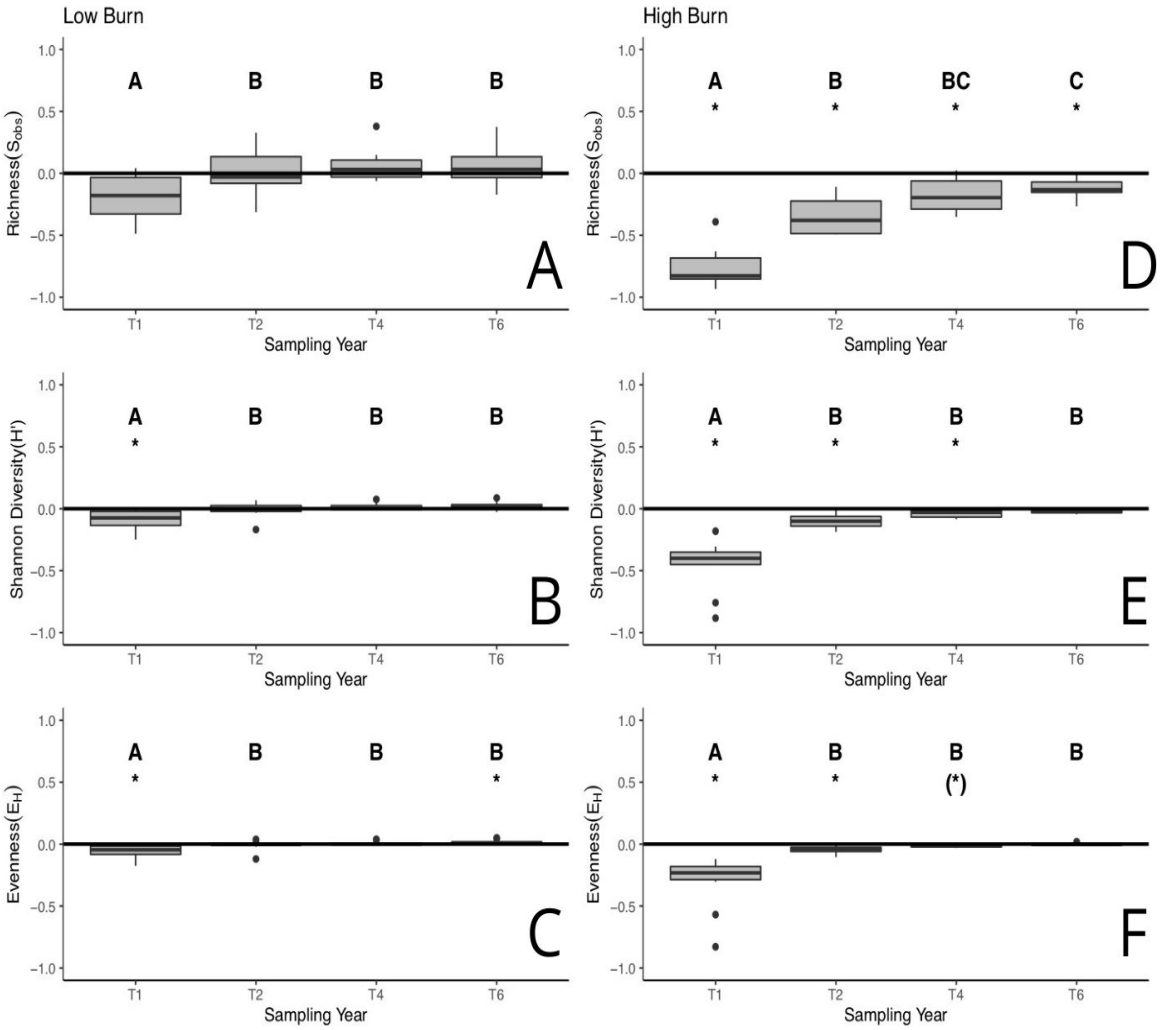

Figure 4.2 Fungal Boxplots

Observed richness (S_{obs}), Shannon's diversity (H'), and Shannon's evenness (E_H) of the four sampling time points (T1, T2, T4, T6) for the different fire treatments – Low Burn (**Left Column; A-C**); High Burn (**Right Column; D-F**). The results of the Tukey's HSD Test are indicated by the letters above the boxplots and of the Wilcoxon rank sum test are indicated by "*". The former tests the null hypothesis that differences between the pre-fire estimates and those at T1-T6 do not differ from each other ($P \geq 0.05$), whereas the latter tests the null hypotheses that each of the differences is equal to zero ($P \geq 0.05$) indicating that the estimates at T0 and Ti are not different from each other based on our response ratio, $\boldsymbol{(t_i-t_0)/(t_i+t_0) = R}$.

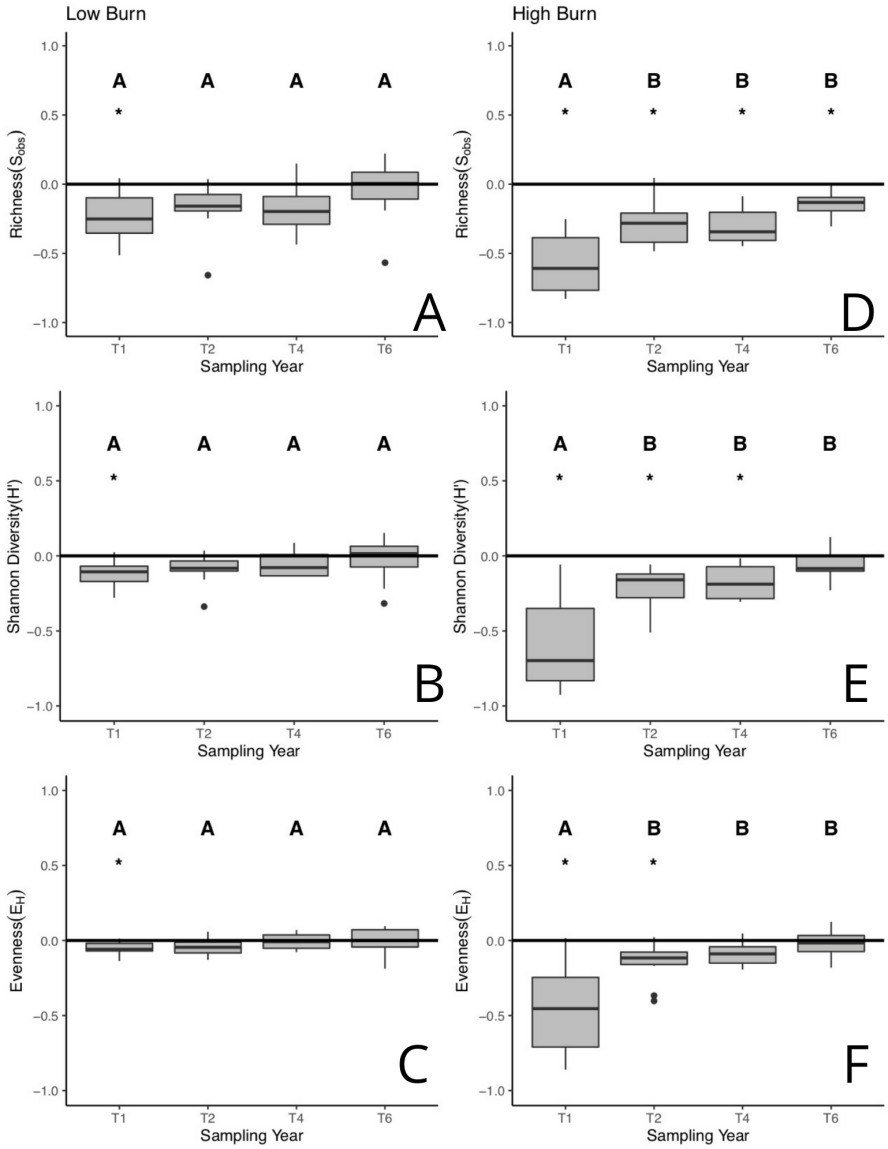

Figure 4.3 Bacterial NMDS spider plots

Bacterial Non-Metric Multidimensional Scaling (NMDS) ordination spider pots of the five sampling years (T0, T1, T2, T4, and T6) within the two fire severities [**A-**LB (stress= 0.14), **B-**HB (stress = 0.09)]. Legs indicate sample dispersion from centroid.

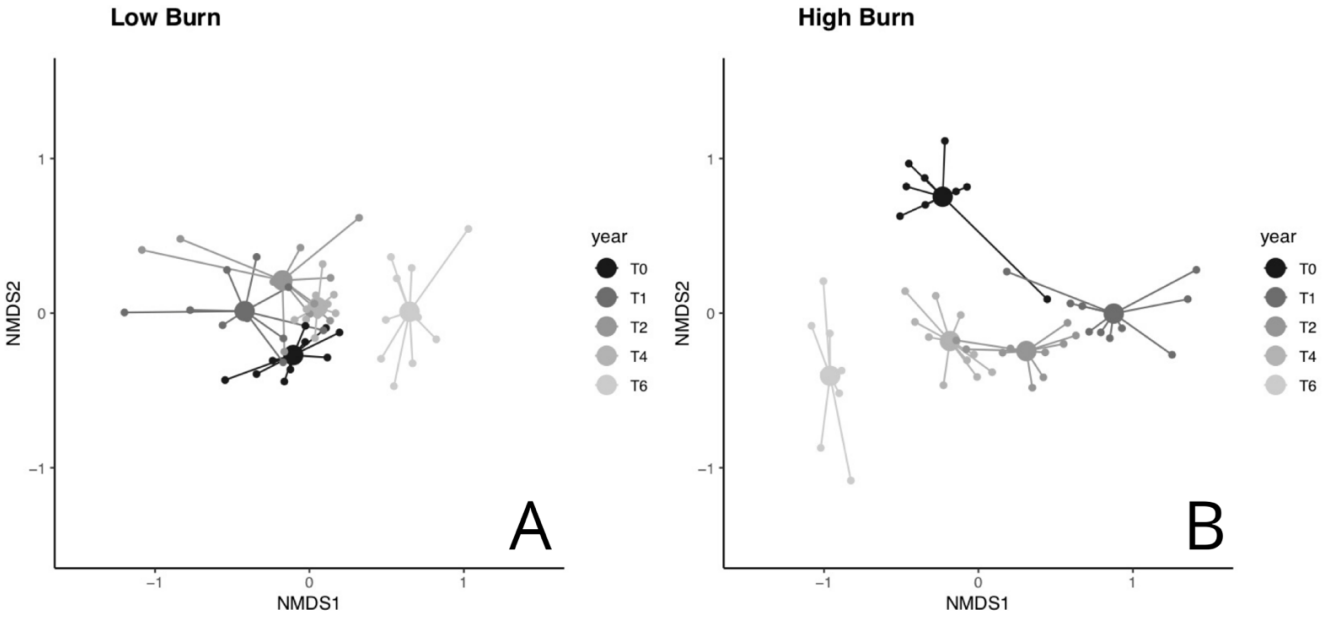

Figure 4.4 Fungal NMDS spider plots

Fungi Non-Metric Multidimensional Scaling (NMDS) ordination spider plots of the five sampling years (T0, T1, T2, T4, and T6) within the two fire severities [**A-**LB (stress=0.16), **B-**HB (stress=0.16)]. Legs of spider indicate community dispersion from centroid.

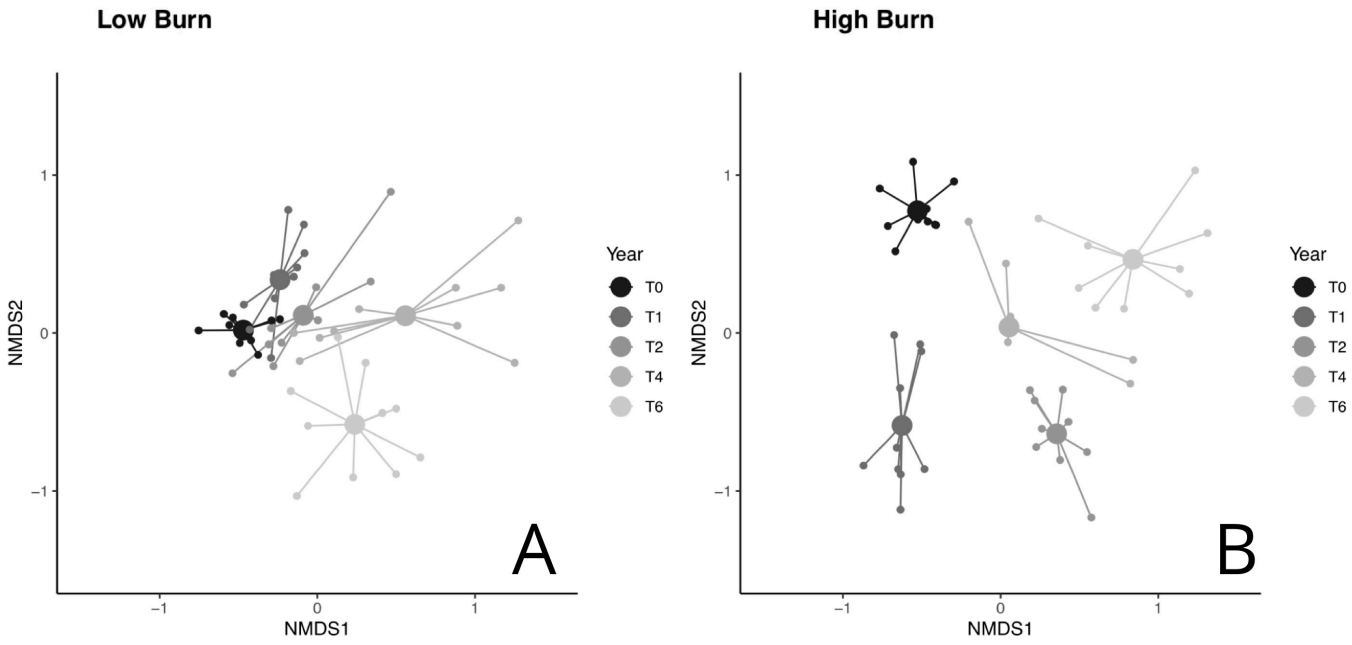

Figure 4.5 Functional Guild abundance and percentage

Functional guilds abundance for each burn severity; **A-Low Burn**, **B-High Burn**. Guild percentage based the five most abundant guilds **(C).**

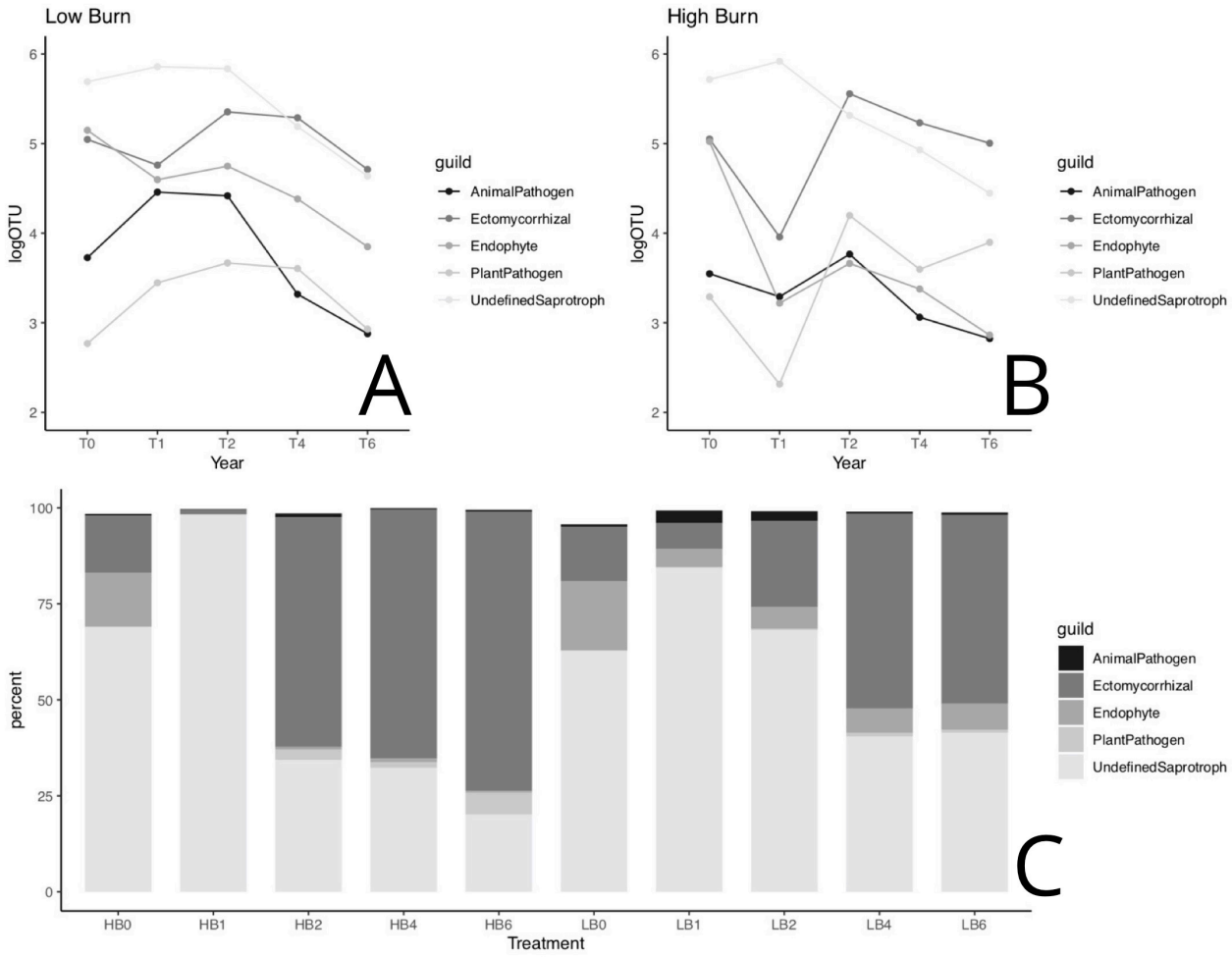

Table 4.1 High burn bacterial pairwise PERMANOVA results

Bacterial pairwise permutational analysis of variance (PERMANOVA) results for bacterial community by sampling year of the high burn treatment. Bold values indicate significance ($P<0.05$) differences amongst sampling years.

PAIRWISE COMPARISON	HIGH BURN		
	F	**R^2**	**P**
T0-T1	**9.32**	**0.34**	**0.001**
T0-T2	**7.90**	**0.33**	**0.001**
T0-T4	**5.27**	**0.23**	**0.001**
T0-T6	**4.02**	**0.20**	**0.001**
T1-T2	**7.83**	**0.32**	**0.001**
T1-T4	**9.65**	**0.35**	**0.001**
T1-T6	**8.14**	**0.34**	**0.001**
T2-T4	**4.16**	**0.21**	**0.001**
T2-T6	**4.48**	**0.24**	**0.001**
T4-T6	**1.90**	**0.11**	**0.001**

Table 4.2 Low burn bacterial pairwise PERMANOVA results

Bacterial pairwise permutational analysis of variance (PERMANOVA) results for bacterial community by sampling year of the low burn treatment. Bold values indicate significance ($P<0.05$) differences amongst sampling years.

PAIRWISE COMPARISON	LOW BURN		
	F	**R^2**	**P**
T0-T1	1.50	0.08	0.07
T0-T2	**3.00**	**0.15**	**0.001**
T0-T4	**3.51**	**0.16**	**0.001**
T0-T6	**2.29**	**0.11**	**0.002**
T1-T2	**1.76**	**0.09**	**0.01**
T1-T4	**1.82**	**0.09**	**0.003**
T1-T6	**1.88**	**0.09**	**0.01**
T2-T4	**2.10**	**0.11**	**0.002**
T2-T6	**2.65**	**0.13**	**0.001**
T4-T6	**2.57**	**0.12**	**0.003**

Table 4.3 High burn fungal pairwise PERMANOVA results

Fungal pairwise permutational analysis of variance (PERMANOVA) results for fungal community by sampling year of the high burn treatment. Bold values indicate significance ($P<0.05$) differences amongst sampling years.

PAIRWISE COMPARISON	HIGH BURN		
	F	**R^2**	**P**
T0-T1	**9.07**	**0.33**	**0.001**
T0-T2	**6.55**	**0.27**	**0.001**
T0-T4	**3.23**	**0.17**	**0.001**
T0-T6	**5.99**	**0.26**	**0.001**
T1-T2	**4.11**	**0.18**	**0.004**
T1-T4	**4.18**	**0.21**	**0.002**
T1-T6	**5.82**	**0.25**	**0.001**
T2-T4	**1.60**	**0.09**	**0.018**
T2-T6	**2.82**	**0.14**	**0.001**
T4-T6	**2.00**	**0.12**	**0.001**

Table 4.4 Low burn fungal pairwise PERMANOVA results

Fungal pairwise permutational analysis of variance (PERMANOVA) results for fungal community by sampling year of the low burn treatment. Bold values indicate significance ($P<0.05$) differences amongst sampling years.

PAIRWISE COMPARISON	LOW BURN		
	F	**R^2**	**P**
T0-T1	**1.82**	**0.09**	**0.024**
T0-T2	**1.69**	**0.09**	**0.015**
T0-T4	**2.81**	**0.13**	**0.001**
T0-T6	**5.50**	**0.23**	**0.001**
T1-T2	1.47	0.07	0.084
T1-T4	**3.06**	**0.14**	**0.001**
T1-T6	**5.66**	**0.24**	**0.001**
T2-T4	**1.65**	**0.23**	**0.023**
T2-T6	**4.25**	**0.19**	**0.001**
T4-T6	**2.13**	**0.10**	**0.001**

Chapter 5 - Conclusion

To better understand the effects of fire on soil microbial communities, this thesis research: 1) synthesized the literature on fungal responses to fire; 2) utilized an experimental pine forest system in Florida to gain insight into the impacts of different fire regimes; and, 3) utilized another fire intensity manipulation experiment in a Ponderosa pine system in Oregon. The acquired data strongly indicate that both different intensities and different fire regimes lead to distinct microbial communities following fire.

The synthesis of the current literature on fungal responses to fire, enabled categorization of fungi based on different traits, dissection of primary direct and indirect drivers of the fungal community assembly following a fire, exploration of how contemporary ecological frameworks may apply to fungal community responses to fire, and investigation of endemism of common and well-known pyrophilous fungi. This extensive synthetic work identified knowledge gaps on the subject of fungal responses to fire, including post-fire temporal dynamics and consensus on sampling strategies as well as fungal post-fire functional responses. The synthesis concludes with identification of research needs and proposals for mesocosm and field studies that may aid in a progress towards more comprehensive understanding of fungal fire responses.

The study investigating soil-dwelling bacterial and fungal responses to different fire intervals provided substantial insight into how these communities are impacted by more than a half century of continuous fire management. Among the most important finding from this study is the conclusion that fire exclusion – not the repeated fires at short intervals – resulted in a loss of both bacterial and fungal richness, potentially through the loss of pyrodiversity. In addition to the focus on fire intervals, analysis and dissection of three different soil horizons indicated that the abiotic and biotic responses across the soil horizons indeed differed Strong effects of repeated fires were nearly exclusively visible in the topmost, A horizon, whereas the deeper horizons appeared buffered against the effects of fire return interval manipulations – even after more than a half century of continuous faire interval manipulation. These results highlight the potential of prescribed burning as a tool to modify pyrodiversity and, subsequently, biodiversity in forested

systems, whilst also indicating system resilience against repeated fire disturbance deeper in the soil profile.

Wildfires in forested systems are increasing in frequency and intensity. With more intense fires come more severe changes to the soil microbial communities as highlighted in this thesis. The final study included here permitted experimental mimicking combustion of coarse woody debris in a wildfire. Fuel accumulation and thus also fire intensity or severity is patchy across a landscape – a key component in physical pyrodiveristy. The results indicated that more severe fires have greater and longer lasting effects on the soil microbial communities compared to less severe fire. Importantly, the patches differing in burn severity maintained distinct soil-inhabiting communities six years after the fire.

Fires impact the soil-inhabiting communities of bacteria and fungi. However, pinpointing the direct and indirect drivers that underlie these community transitions is difficult and often context dependent, and therefore beyond the scope of this work. Many questions remain to be answered about how microbial communities responds to fire. The results presented in this thesis and the results of future studies are vital to forest management, particularly when using prescribed fire management or considering restoration of sites impacted by wildfires.

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Appendix A - Supplemental Materials for Chapter 2.

Table A 1 Summary of pyrophilous species

Anthracobia (Pyronemataceae; Ascomycota):

Species distributions within the genus *Anthracobia*are uncertain. DNA nrITS+LSU sequences of *Anthracobia* spp. fruiting bodies recovered after a wildfire in an eastern USA mixed deciduous forest sorted into four clades (Hughes et al. 2020b). Morphologically, Clade 1 was *A. maurilabra*, whereas Clades 2 and 3 were *A. melaloma* and Clade 4 was *A. macrocystis*. NrITS +LSU sequences of Clades 1-3 were closely related but the data provided no evidence of recombination events suggesting a lack of interbreeding (Hughes et al. 2020). Collections identified as *A. maurilabra* (Clade 1) occur commonly throughout the northern hemisphere in Europe (Boudier 1907, Yao and Spooner 1996, Tóth 2003, MyCoPortal 2021) and the United States (MyCoPortal 2021). They also occur throughout the southern hemisphere in Argentina (Gamundí 2010, MyCoPortal 2021), Australia (Warcup 1990, Bridle and Catcheside), and Brazil (MyCoPortal 2021). Assuming that these records represent global panmictic populations and not potential cryptic taxa, *A. maurilabra* likely exemplifies a cosmopolitan pyrophilous taxon.

Anthracobia melaloma (Clades 2 and 3) has been suggested as cosmopolitan (Larson et al. 2016) but it may in fact represent two cryptic phylogenetic species. Morphospecies *A. melaloma* has been reported from several countries in Europe including Great Britain (Yao and Spooner 1996), Ireland, Czech Republic, France, Germany (all in Larson et al. 2016) and in North America including Washington state (Carpenter et al. 1987), Canada, and the eastern USA (Hughes et al. 2020b). It has also been collected in the southern hemisphere in Rhodesia (Larson et al. 2016) and Australia (Robinson et al. 2008). Molecular data, however, are sparse. Identical nrITS sequences for Clade 2 in GenBank include a lichen endophyte and a moss endophyte from North Carolina (JQ761457, MF943111) suggesting that Clade 2 may be an endemic taxon at some level. In contrast to Clade 2, nrITS sequences identical to Clade 3 represent data from Argentina (MT076107, wood sample), China (MN900600 – conifer endophyte, MT138665, KJ028787 as *Scutellinia*), and Lithuania (AY354274 – *Betula* stump). Thus, *A. melaloma sensu lato* is widely

distributed (Table 1) but an understanding of biogeographical partitioning based on molecular data is desperately needed.

Anthracobia macrocystis (Clade 4) morphospecies has been widely reported across the northern hemisphere ranging from Great Britain (Dennis 1954, Yao and Spooner 1996, Wilberforce 2005, Claridge et al. 2009), Turkey (Uzun et al. 2018), and Portugal (Natário et al. 2019) to Trinidad (Dennis 1954) and India (Yangdol et al. 2017). Available nrITS sequences exactly matching *A. macrocystis* collections from the Great Smoky Mountain National Park in eastern United States included those from Arizona (HM123462 – Lichen endophyte), Washington State (NG027605), California (MN724072-soil sample) and Ukraine (MH844571). Thus, *Anthracobia macrocystis* appears to have a Northern Hemisphere distribution (Larsen 1975), although there are rare reports of specimens with this species epithet from Australia and New Zealand (Table 1).

A fifth species of pyrophilous *Anthracobia*, *A. muelleri*, may have a predominantly southern hemisphere distribution (MyCoPortal 2021) including New Zealand, Australia, Columbia and Argentina (Table 1). Notwithstanding, MyCoPortal (2021) also records a few *A. muelleri* collections from Europe and North America.

Pyronema (Pyronemataceae; Ascomycota):
Pyronema omphalodes and *P. domesticum* are the two most likely candidates for cosmopolitan fire fungi. Both have been reported as fireplace fungi in northern Europe (Petersen 1970). A *Pyronema* sp. (reported as *P. omphalodes* in Warcup 1990) fruited in high abundance after wildfires in *Eucalyptus* forests in Australia (Warcup 1990) and *Pyronema omphalodes* (= *P. confluens*) has been reported to fruit after fires across the USA in Iowa, New York, and North Dakota (Seaver 1909). After a 2016 wildfire in Tennessee, *Pyronema omphalodes,* but not *P. domesticum,* was recovered both as ascomata on burned soil (Hughes et al. 2020b) and as ITS sequences from severely burned soils but not in great abundance (Hughes unpublished data). Other studies report that *P. domesticum* and *P. omphalodes* accounted for approximately 60% of ITS1 sequences after a mega-fire burned down a *Pinus ponderosa* forest in the California Sierra Nevada (Glassman unpublished data) and after a high severity fire burned a California Chaparral shrubland (Fig. 3). *Pyronema domesticum* ITS1 sequences also increased 100-fold in frequency after

experimental fires in an Oregon *P. ponderosa* forest (Reazin et al. 2016). From available literature and molecular data, we conclude that *P. domesticum* occurs in Europe and Western North America, whereas *P. omphalodes* may have a broader distribution including eastern and western North America, Europe, and Australia. Thus, *P. omphalodes* may be a true cosmopolitan dominating post-fire landscapes ranging in host diversity (Eucalyptus and Pine forests, Chaparral) and globally from Australia to Europe to western North America.

Table A 2 Distribution of pyrophilous species

Supplementary Table S2. Distribution of pyrophilous species within three genera of fungi, *Anthracobia*, *Morchella* and *Pyronema*.

Classification	Genus/Species	Distribution[1]
Ascomycota; Pezizales; Pyronemataceae	*Anthracobia macrocystis* (clade 4)	Australia, Europe including Portugal, Spain and the United Kingdom, New Zealand, North America
	Anthracobia maurilabra (clade 1)	Argentina, Australia, Brazil, Europe, North America
	Anthracobia melaloma (clade 2)	United States (Tennessee and North Carolina by ITS+LSU sequence data)
	*Anthracobia melaloma (*clade 3)	Argentina, Australia, Brazil, Europe including Lithuanian, Portugal, and the United Kingdom, Japan, North America South Africa
	Anthracobia muelleri	Argentina, New Zealand
Ascomycota; Pezizales; Pyronemataceae	*Pyronema domesticum*	Europe, United States
	Pyronema omphalodes (with 7 varieties)	Argentina, Australia, Europe, New Zealand, South Africa, United States
Ascomycota; Pezizales; Morchellaceae	*Morchella "elata" group Mel-10 (facultative)*	USA: Oregon, Washington Turkey (likely human transfer)
	Morchella "elata" group Mel-9	USA: Oregon, Turkey (likely human transfer)
	Morchella australiana	Australia
	Morchella capitata =Morchella exuberans	Western USA
	Morchella conica	Israel
	Morchella eximia =M. anthracophilia	Western USA

Appendix B - Supplemental Materials for Chapter 3

Figure B 1 Graphical Abstract

Different fire return intervals lead to differences in microbial communities, as well as soil chemistry. These differences are most pronounced in the top-most A horizon.

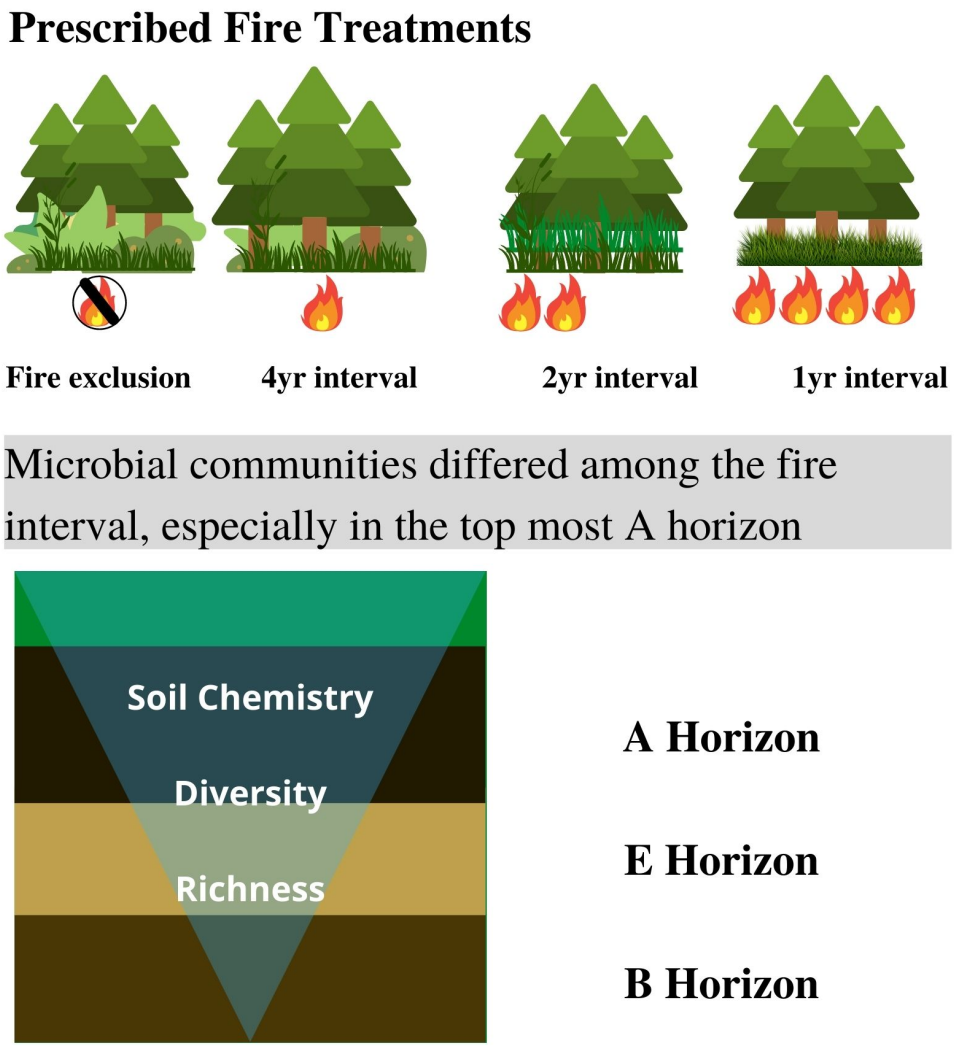

Figure B 1 Soil core with horizon labels

Photo credit: Melanie Taylor.

Figure B 2 Bacterial environmental correlation plots

Bacteria environmental correlation ordination plot of the four burn treatments within the three horizons: A – A horizon, B – E horizon, C – B horizon. Environmental correlate significance (P<0.05) indicated by vectors.

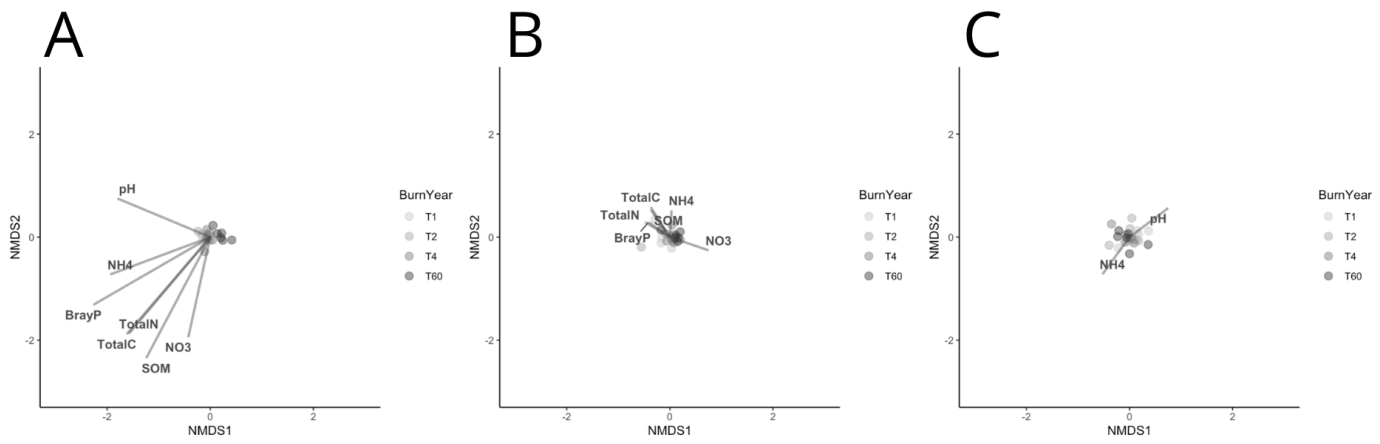

Figure B 3 Fungal environmental correlation ordination plots

Fungal environmental correlation ordination plot of the four burn treatments within the three horizons: **A** – A horizon, **B** – E horizon, **C** – B horizon. Environmental correlate significance ($P<0.05$) indicated by vectors.

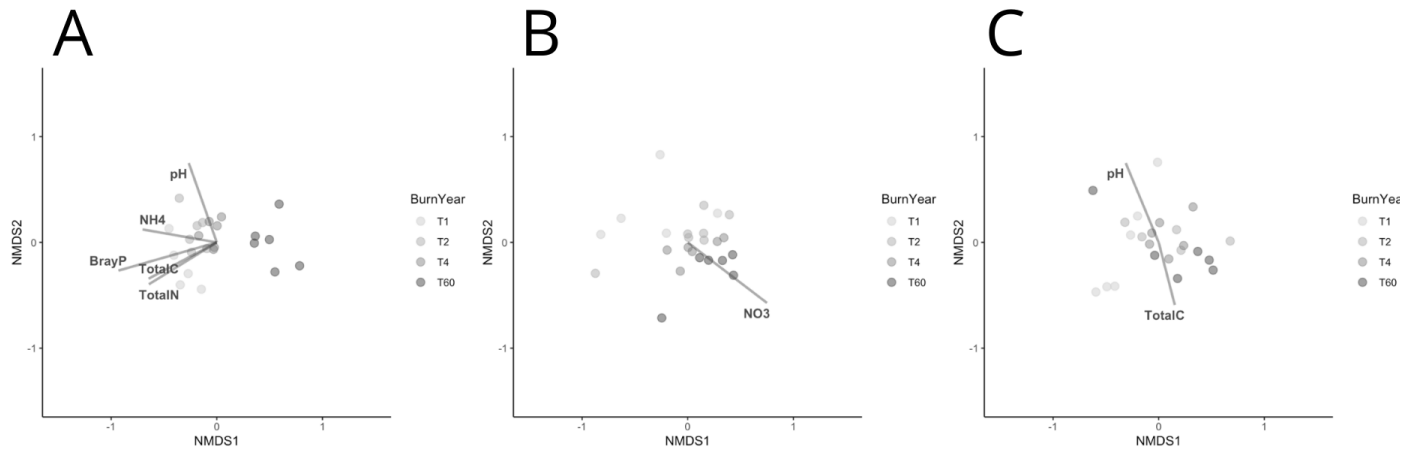

Figure B 4 Percentages of Guilds

The percentage of the twelve guilds that were either saprotroph or symbiotroph based on burn year and horizon

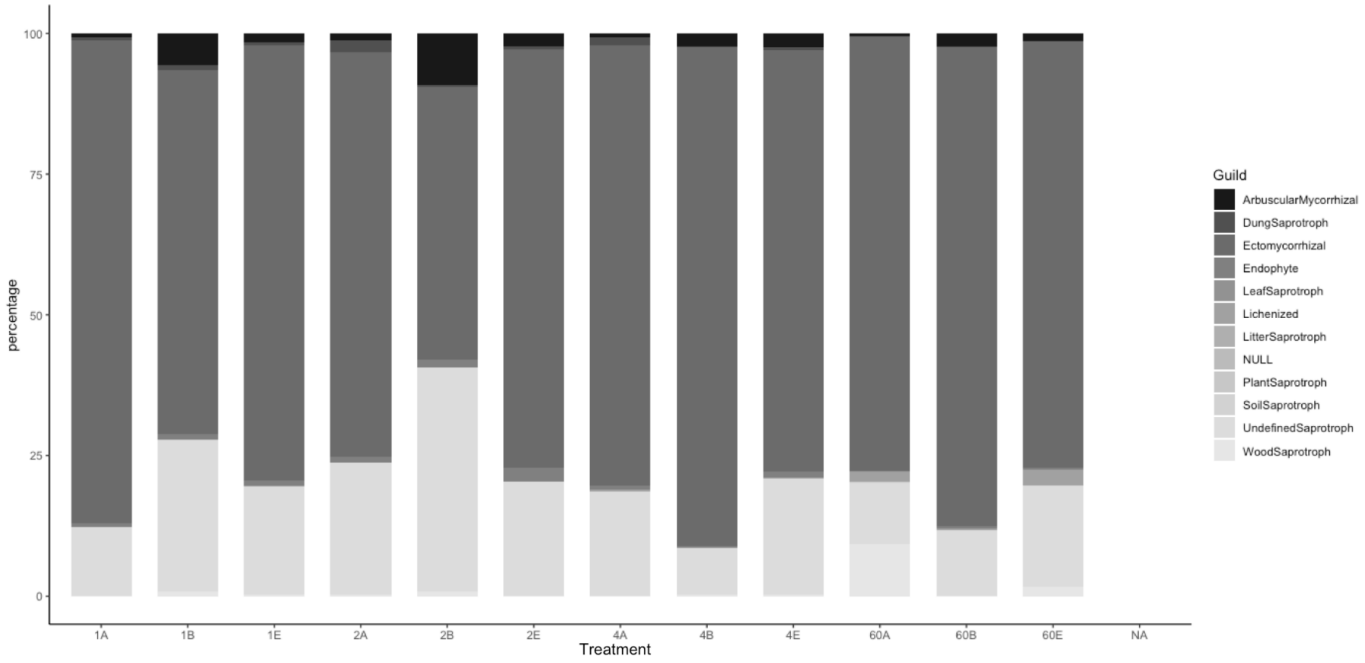

Figure B 5 Percentages of Saprotroph and Symbiotroph

The percentage of saprotrophs and symbiotrophs based on burn year and horizon.

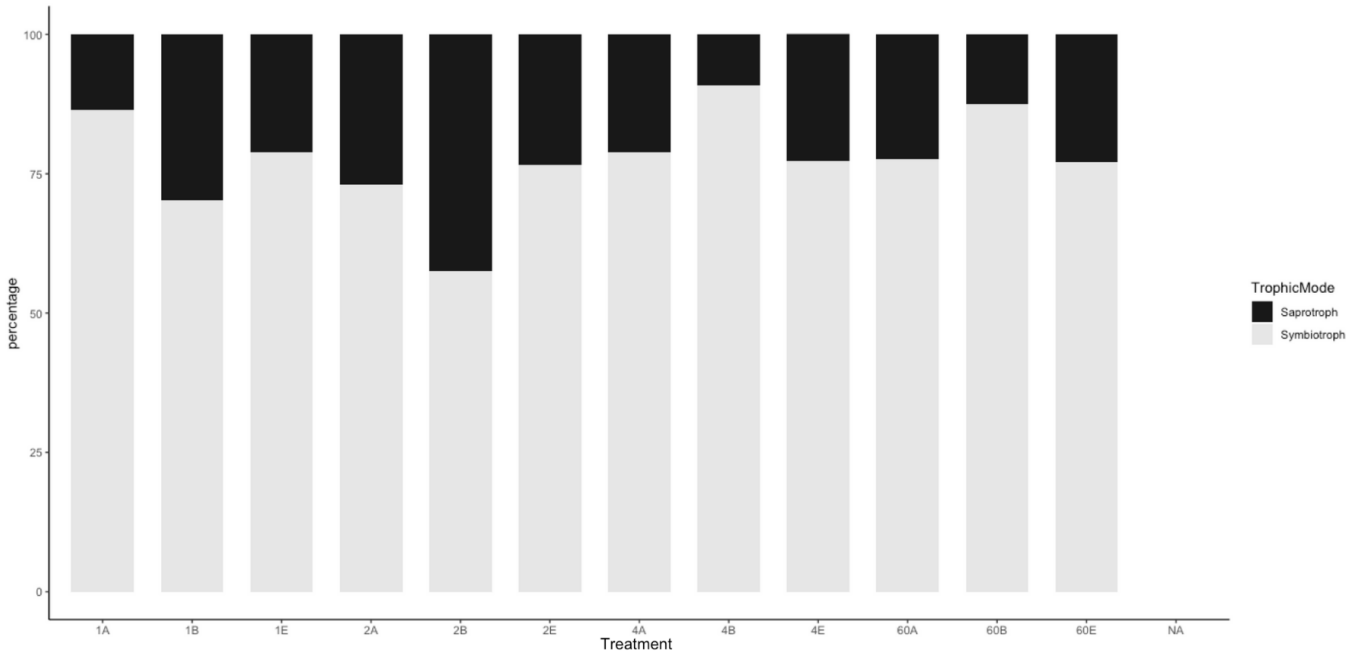

Table B 1 Soil Chemistry two-way interaction ANOVA results

Total N	**DF**	**F**	**P**
Burn Year	3	5.74	<0.001
Horizon	2	103.94	<0.001
Burn Year: Horizon	6	4.85	<0.001
Total C			
Burn Year	3	5.50	0.002
Horizon	2	126.59	<0.001
Burn Year: Horizon	6	5.29	<0.001
pH			
Burn Year	3	2.15	0.10
Horizon	2	67.22	<0.001
Burn Year: Horizon	6	0.91	0.50
Bray P			
Burn Year	3	0.25	0.86
Horizon	2	44.77	<0.001
Burn Year: Horizon	6	0.85	0.54
SOM			
Burn Year	3	2.67	0.05
Horizon	2	59.02	<0.001
Burn Year: Horizon	6	2.52	0.03
NO_3			
Burn Year	3	0.02	1.00
Horizon	2	3.58	0.03
Burn Year: Horizon	6	1.20	0.32
NH_4^+			
Burn Year	3	6.85	<0.001
Horizon	2	110.69	<0.001
Burn Year: Horizon	6	5.17	<0.001

Table B 2 Soil chemistry two-way interaction ANOVA results including "Block" as a factor

Total N	**DF**	**F**	**P**	**Total N**	**DF**	**F**	**P**
Horizon	2	63.96	<0.001	Burn Year	3	1.04	0.38
Block	5	0.73	0.61	Block	5	0.29	0.91
Horizon: Block	10	0.69	0.73	Burn Year: Block	15	0.24	1.00
Total C				**Total C**			
Horizon	2	75.35	<0.001	Burn Year	3	0.85	0.47
Block	5	0.65	0.66	Block	5	0.24	0.94
Horizon: Block	10	0.64	0.77	Burn Year: Block	15	0.21	1.00
pH				**pH**			
Horizon	2	63.01	<0.001	Burn Year	3	0.60	0.62
Block	5	1.73	0.14	Block	5	0.69	0.63
Horizon: Block	10	0.59	0.82	Horizon: Block	15	0.25	1.00
Bray P				**Bray P**			
Horizon	2	51.75	<0.001	Burn Year	3	0.09	0.96
Block	5	1.61	0.17	Block	5	0.50	0.78
Horizon: Block	10	1.46	0.18	Burn Year: Block	15	0.34	0.99
SOM				**SOM**			
Horizon	2	43.94	<0.001	Burn Year	3	0.77	0.51
Block	5	0.42	0.83	Block	5	0.23	0.95
Horizon: Block	10	0.55	0.84	Burn Year: Block	15	0.41	0.97
NO_3				**NO_3**			
Horizon	2	3.12	0.05	Burn Year	3	0.02	1.00
Block	5	0.47	0.80	Block	0.76	1.52	0.58
Horizon: Block	10	0.22	0.99	Burn Year: Block	15	2.80	0.003
NH_4^+				**NH_4^+**			
Horizon	2	60.55	<0.001	Burn Year	3	1.18	0.33
Block	5	0.33	0.89	Block	5	0.13	0.98
Horizon: Block	10	0.39	0.95	Burn Year: Block	15	0.28	0.99

Table B 3 Two way interaction results including "Block" as factor

Left column (**bacteria**); Right column (**fungi**) two-way interaction ANOVA results including "Block" as a factor.

S_{obs}	DF	F	P	S_{obs}	DF	F	P
Horizon	2	19.96	<0.001	Horizon	2	47.16	<0.001
Block	5	0.72	0.61	Block	5	2.07	0.08
Horizon: Block	10	0.67	0.75	Horizon: Block	10	0.40	0.94
S_{obs}				**S_{obs}**			
Burn Year	3	0.55	0.65	Burn Year	3	1.11	0.35
Block	5	0.50	0.78	Block	5	0.99	0.43
Burn Year: Block	15	0.71	0.76	Burn Year: Block	15	0.80	0.68
Chao1				**Chao1**			
Horizon	2	22.20	<0.001	Horizon	2	54.24	<0.001
Block	5	1.07	0.39	Block	5	1.77	0.14
Horizon: Block	10	0.68	0.74	Horizon: Block	10	0.38	0.97
Chao1				**Chao1**			
Burn Year	3	0.93	0.43	Burn Year	3	1.18	0.33
Block	5	0.76	0.58	Block	5	0.76	0.58
Burn Year: Block	15	0.84	0.63	Burn Year: Block	15	0.67	0.80
Shannon (H')				**Shannon (H')**			
Horizon	2	17.70	<0.001	Horizon	2	0.51	0.60
Block	5	0.91	0.48	Block	5	0.99	0.43
Horizon: Block	10	0.33	0.97	Horizon: Block	10	0.83	0.60
Shannon (H')				**Shannon (H')**			
Burn Year	3	2.46	0.73	Burn Year	3	8.36	<0.001
Block	5	0.78	0.57	Block	5	1.52	0.20
Burn Year: Block	15	0.91	0.56	Burn Year: Block	15	1.12	0.31
Shannon Evenness (E_H)				**Shannon Evenness (E_H)**			
Horizon	2	29.08	<0.001	Horizon	2	2.51	0.09
Block	5	1.07	0.39	Block	5	0.87	0.51
Horizon: Block	10	0.90	0.54	Horizon: Block	10	0.85	0.58

Shannon Evenness (E_H)				**Shannon Evenness (E_H)**			
Burn Year	3	2.05	0.12	Burn Year	3	19.96	<0.001
Block	5	0.56	0.73	Block	5	0.72	0.61
Burn Year: Block	15	0.76	0.71	Burn Year: Block	15	0.67	0.75

Table B 4 Bacterial environmental correlates with soil chemistry

Bacterial environmental correlation with soil chemistry results for bacterial community by horizon. Bold values indicate significance (P<0.05) differences amongst burn intervals.

CHEMISTRY PARAMETER	A HORIZON		E HORIZON		B HORIZON	
	R^2	**P**	**R^2**	**P**	**R^2**	**P**
TOTAL N	**0.4573**	**0.002**	**0.3084**	**0.034**	0.0984	0.363
TOTAL C	**0.4703**	**0.001**	**0.4663**	**0.014**	0.1438	0.206
PH	**0.2899**	**0.026**	0.2132	0.097	**0.3574**	**0.017**
PHOSPHORUS	**0.5243**	**0.002**	**0.2475**	**0.038**	0.2466	0.060
SOM	**0.5381**	**0.003**	**0.3997**	**0.032**	0.1050	0.350
NO_3	**0.3020**	**0.036**	**0.6134**	**0.004**	0.0155	0.843
NH_4^+	**0.3272**	**0.016**	**0.2651**	**0.024**	**0.3206**	**0.023**

Table B 5 Fungal environmental correlates with chemistry

Fungal environmental correlation with soil chemistry results for bacterial community by horizon. Bold values indicate significance ($P<0.05$) differences amongst burn intervals.

CHEMISTRY PARAMETER	A HORIZON		E HORIZON		B HORIZON	
	R^2	**P**	**R^2**	**P**	**R^2**	**P**
TOTAL N	**0.4391**	**0.008**	0.1038	0.305	0.1078	0.335
TOTAL C	**0.4118**	**0.010**	0.1698	0.155	**0.2720**	**0.041**
PH	**0.4877**	**0.002**	0.0532	0.515	**0.4819**	**0.002**
PHOSPHORUS	**0.7225**	**0.001**	0.1722	0.144	0.1669	0.174
SOM	0.2328	0.079	0.1666	0.174	0.1896	0.125
NO_3	0.1040	0.351	**0.3107**	**0.046**	0.0105	0.898
NH_4^+	**0.3921**	**0.007**	0.1132	0.300	0.0903	0.370

Table B 6 Bacterial indicator taxon analysis results

BAC A Horizon	Stat	P.value	Taxonomy
T1 Indicators			
Otu003245	0.937	0.002 **	AcidoAcidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu000839	0.918	0.001 ***	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004084	0.898	0.004 **	Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Gemmata(66);
Otu002196	0.887	0.006 **	Chloroflexi(100);KtedonoKtedonobacterales(100);Ktedonobacteraceae(100);Ktedonobacter(100);
Otu002640	0.884	0.004 **	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003445	0.872	0.003 **	AcidoAcidobacteria_Gp1(100);Gp1(100);Gp1_unclassified(100);
Otu003731	0.864	0.010 **	ActinoActinoAcidimicrobiales(100);Acidimicrobiales_unclassified(100);
Otu003028	0.861	0.042 *	Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu003122	0.86	0.013 *	Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu003439	0.816	0.024 *	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002494	0.796	0.042 *	ActinoActinoActinomycetales(100);Actinomycetales_unclassified(94);
Otu002588	0.791	0.043 *	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003206	0.78	0.047 *	ProteoAlphaproteoRhizobiales(100);Rhizobiales_unclassified(100);
Otu000783	0.764	0.030 *	ProteoAlphaproteoRhizobiales(100);Roseiarcaceae(100);Roseiarcus(100);
Otu000313	0.762	0.033 *	AcidoAcidobacteria_Gp2(100);Gp2(100);Gp2_unclassified(100);
Otu002836	0.753	0.047 *	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu000869	0.739	0.024 *	Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu000613	0.707	0.042 *	Chloroflexi(100);KtedonoKtedonobacterales(100);Ktedonobacteraceae(100);Ktedonobacter(100);
Otu000703	0.707	0.042 *	ProteoAlphaproteoRhizobiales(100);Methylocystaceae(100);
Otu000994	0.707	0.042 *	AcidoAcidobacteria_Gp2(100);Gp2(100);Gp2_unclassified(100);
Otu001182	0.707	0.038 *	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001408	0.707	0.042 *	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001649	0.707	0.038 *	ProteoProteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu002193	0.707	0.042 *	Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Gemmata(100);
Otu003167	0.707	0.029 *	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003537	0.707	0.035 *	AcidoAcidobacteria_Gp17(100);Gp17(100);Gp17_unclassified(100);

Otu003806	0.707	0.035 *	AcidoAcidobacteria_Gp5(100);Gp5(100);Gp5_unclassified(100);
T2 Indicators			
Otu002009	0.782	0.013 *	ProteoDeltaproteoMyxococcales(100);Cystobacteraceae(100);Anaeromyxobacter(100);
Otu003602	0.739	0.011 *	ProteoDeltaproteoMyxococcales(100);Labilitrichaceae(71);Labilithrix(71);
Otu002978	0.699	0.034 *	Verrucomicrobia(100);SpartoSpartobacteria_unclassified(100);Spartobacteria_unclassified(100);
T60 Indictors			
Otu003910	0.974	0.001 ***	ProteoAlphaproteoRhodospirillales(100);Acetobacteraceae(100);
Otu002933	0.939	0.002 **	ActinoActinoActinomycetales(100);Thermomonosporaceae(93);
Otu001981	0.914	0.002 **	Chloroflexi(100);KtedonoKtedonobacterales(100);Ktedonobacterales_unclassified(100);
Otu002122	0.899	0.004 **	Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Chlamydiales_unclassified(100);
Otu002232	0.897	0.002 **	AcidoAcidobacteria_Gp1(100);Acidipila(100);Acidipila_unclassified(100);
Otu003175	0.858	0.013 *	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004038	0.778	0.034 *	Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Simkaniaceae(100);Simkania(100);
Otu002467	0.707	0.035 *	AcidoAcidobacteria_Gp2(100);Gp2(100);Gp2_unclassified(100);
BAC E Horizon			
T1 Indicators			
Otu003161	0.863	0.001 ***	Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Simkaniaceae(62);Simkania(62);
Otu001434	0.837	0.004 **	AcidoAcidobacteria_Gp1(100);Acidobacteria_Gp1_unclassified(100);Acidobacteria_Gp1_unclassified(100);
Otu002607	0.825	0.010 **	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002449	0.814	0.006 **	Chloroflexi(100);KtedonoKtedonobacteria_unclassified(100);Ktedonobacteria_unclassified(100);
Otu002931	0.796	0.012 *	AcidoAcidobacteria_Gp1(100);Gp1(100);Gp1_unclassified(100);
Otu004075	0.75	0.015 *	Chloroflexi(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);
Otu003328	0.715	0.049 *	Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);

Otu001207	0.714	0.044 *	Firmicutes(100);Firmicutes_unclassified(100);Firmicutes_unclassified(100);Firmicutes_unclassified(100);
Otu003202	0.682	0.050 *	Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Chlamydiales_unclassified(100);
Otu002727	0.678	0.014 *	AcidoAcidobacteria_Gp13(100);Gp13(100);Gp13_unclassified(100);
Otu002889	0.675	0.038 *	ActinoActinoActinomycetales(100);Thermomonosporaceae(100);Actinoallomurus(100);
T2 Indicators			
Otu003859	0.77	0.044 *	ProteoGammaproteoGammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu004005	0.745	0.023 *	ProteoDeltaproteoMyxococcales(100);Myxococcales_unclassified(100);
Otu003800	0.719	0.043 *	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003515	0.681	0.022 *	Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu001578	0.655	0.046 *	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001738	0.655	0.046 *	Chloroflexi(100);KtedonoKtedonobacteria_unclassified(100);Ktedonobacteria_unclassified(100);
Otu002160	0.655	0.044 *	ProteoAlphaproteoRhodospirillales(100);Rhodospirillales_unclassified(100);
T4 Indicators			
Otu002182	0.882	0.013 *	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
T60 Indicators			
Otu002232	1	0.001 ***	AcidoAcidobacteria_Gp1(100);Acidipila(100);Acidipila_unclassified(100);
Otu002051	0.989	0.001 ***	candidate_division_WPS-2(100);candidate_division_WPS-2_unclassified(100);candidate_division_WPS-2_unclassified(100)
Otu001217	0.98	0.002 **	AcidoAcidobacteria_Gp1(100);Acidobacterium(100);Acidobacterium_unclassified(100);
Otu000450	0.97	0.001 ***	ProteoGammaproteoGammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu002924	0.925	0.001 ***	Verrucomicrobia(100);SpartoSpartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu003474	0.92	0.001 ***	Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu001334	0.915	0.001 ***	ActinoActinoActinomycetales(100);Actinomycetales_unclassified(86);
Otu003145	0.911	0.005 **	Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu002375	0.9	0.008 **	ProteoBetaproteoBetaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);

Otu003175	0.896	0.002 **	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002933	0.893	0.001 ***	ActinoActinoActinomycetales(100);Thermomonosporaceae(93);
Otu000899	0.889	0.016 *	Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Simkaniaceae(100);Simkania(100);
Otu002047	0.882	0.002 **	ProteoAlphaproteoRhodospirillales(100);Rhodospirillaceae(100);
Otu003583	0.866	0.003 **	Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Aquisphaera(100);
Otu001195	0.864	0.004 **	ProteoAlphaproteoAlphaproteobacteria_incertae_sedis(100);Rhizomicrobium(100);
Otu001812	0.864	0.004 **	ProteoAlphaproteoRhodospirillales(100);Acetobacteraceae(100);
Otu002969	0.855	0.016 *	Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);Parachlamydia(100);
Otu002226	0.844	0.004 **	ProteoAlphaproteoRhodospirillales(100);Rhodospirillales_unclassified(100);
Otu002131	0.837	0.037 *	AcidoAcidobacteria_Gp3(100);Acidobacteria_Gp3_unclassified(100);Acidobacteria_Gp3_unclassified(100);
Otu002707	0.824	0.012 *	ProteoProteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu002957	0.824	0.019 *	ProteoAlphaproteoRhodospirillales(100);Acetobacteraceae(100);
Otu002794	0.822	0.016 *	candidate_division_WPS-2(100);candidate_division_WPS-2_unclassified(100);candidate_division_WPS-2_unclassified(100)
Otu003894	0.819	0.009 **	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003910	0.816	0.004 **	ProteoAlphaproteoRhodospirillales(100);Acetobacteraceae(100);
Otu002832	0.815	0.012 *	Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu003018	0.815	0.010 **	ProteoDeltaproteoBdellovibrionales(100);Bdellovibrionaceae(100);Vampirovibrio(100);
Otu003402	0.805	0.043 *	ActinoActinoSolirubrobacterales(100);Conexibacteraceae(100);Conexibacter(100);
Otu002958	0.799	0.045 *	ProteoAlphaproteoRhodospirillales(100);Acetobacteraceae(100);Acidisoma(100);
Otu002662	0.788	0.005 **	Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu001981	0.786	0.023 *	Chloroflexi(100);KtedonoKtedonobacterales(100);Ktedonobacterales_unclassified(100);
Otu003758	0.775	0.009 **	Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu004018	0.767	0.038 *	ProteoGammaproteoLegionellales(100);Coxiellaceae(100);Aquicella(100);
Otu003265	0.762	0.030 *	ProteoAlphaproteoRhizobiales(100);Bradyrhizobiaceae(93);
Otu001465	0.752	0.019 *	ProteoAlphaproteoRhodospirillales(100);Acetobacteraceae(100);Acidisoma(100);
Otu003535	0.751	0.014 *	AcidoAcidobacteria_Gp1(100);Gp1(100);Gp1_unclassified(100);
Otu002903	0.746	0.012 *	AcidoAcidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu002929	0.729	0.041 *	ProteoAlphaproteoRhizobiales(100);Roseiarcaceae(100);Roseiarcus(100);
Otu002886	0.729	0.026 *	ProteoAlphaproteoRhodospirillales(100);Acetobacteraceae(100);

Otu003761	0.726	0.024 *	ProteoAlphaproteoRhodospirillales(100);Rhodospirillaceae(72);
Otu002625	0.716	0.016 *	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002856	0.714	0.029 *	ActinoActinoActinomycetales(100);Thermomonosporaceae(97);Actinoallomurus(71);
Otu001823	0.711	0.034 *	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003189	0.679	0.025 *	ProteoAlphaproteoAlphaproteobacteria_incertae_sedis(100);Rhizomicrobium(100);
Otu002360	0.663	0.049 *	ProteoProteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu003456	0.661	0.040 *	AcidoAcidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);

BAC B Horizon

T1 Indicators

Otu001541	0.756	0.008 **	ProteoAlphaproteoAlphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu003223	0.7	0.016 *	ProteoAlphaproteoRhodospirillales(100);Acetobacteraceae(100);
Otu001093	0.655	0.043 *	AcidoAcidobacteria_Gp3(100);Candidatus_Solibacter(100);Candidatus_Solibacter_unclassified(100);
Otu002506	0.655	0.038 *	Verrucomicrobia(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);
Otu003438	0.655	0.034 *	ActinoActinoActinomycetales(100);Actinomycetales_unclassified(100);
Otu004014	0.655	0.033 *	Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Chlamydiales_unclassified(100);

T2 Indicators

Otu001098	0.756	0.024 *	Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Chlamydiales_unclassified(86);
Otu002791	0.736	0.012 *	Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu002413	0.701	0.026 *	Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu001133	0.678	0.015 *	ProteoAlphaproteoAlphaproteobacteria_incertae_sedis(100);Rhizomicrobium(100);
Otu000351	0.632	0.038 *	AcidoAcidobacteria_Gp1(100);Gp1(100);Gp1_unclassified(100);
Otu001837	0.632	0.036 *	candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100)
Otu002267	0.632	0.036 *	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002633	0.632	0.037 *	ProteoAlphaproteoRhizobiales(100);Roseiarcaceae(100);Roseiarcus(100);
Otu003542	0.632	0.027 *	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);

Otu003854	0.632	0.047 *	Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
T4 Indicators			
Otu003524	0.69	.028 *	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
T60 Indicators			
Otu000715	0.913	0.002 **	ProteoGammaproteoGammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu002719	0.816	0.002 **	Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Simkaniaceae(99);Simkania(99);
Otu001792	0.789	0.006 **	candidate_division_WPS-2(100);candidate_division_WPS-2_unclassified(100);candidate_division_WPS-2_unclassified(100)
Otu003680	0.786	0.006 **	AcidoAcidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu001523	0.776	0.017 *	Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001638	0.769	0.019 *	ActinoActinoSolirubrobacterales(100);Solirubrobacterales_unclassified(54);
Otu001750	0.752	0.012 *	Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu001160	0.749	0.013 *	AcidoAcidobacteria_Gp13(100);Gp13(100);Gp13_unclassified(100);
Otu001319	0.73	0.012 *	AcidoAcidobacteria_Gp1(100);Gp1(100);Gp1_unclassified(100);
Otu003920	0.724	0.027 *	Chloroflexi(100);KtedonoKtedonobacterales(100);Ktedonobacteraceae(98);Ktedonobacter(98);
Otu001924	0.72	0.042 *	ProteoAlphaproteoAlphaproteobacteria_incertae_sedis(100);Rhizomicrobium(100);
Otu002040	0.707	0.031 *	ProteoDeltaproteoDeltaproteobacteria_unclassified(100);Deltaproteobacteria_unclassified(100);
Otu002766	0.707	0.031 *	ProteoAlphaproteoRhodospirillales(100);Rhodospirillaceae(100);
Otu001732	0.701	0.026 *	ProteoDeltaproteoMyxococcales(100);Labilitrichaceae(100);Labilithrix(100);
Otu002181	0.683	0.038 *	ProteoDeltaproteoMyxococcales(100);Myxococcales_unclassified(93);
Otu000626	0.679	0.037 *	ProteoGammaproteoGammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu001734	0.672	0.015 *	ProteoAlphaproteoRhodospirillales(100);Rhodospirillales_unclassified(77);
Otu001776	0.624	0.046 *	ActinoActinoSolirubrobacterales(100);Conexibacteraceae(100);Conexibacter(100);

Table B 7 Fungal Indicator taxon analysis results

FUN A Horizon

T1 Indicators

Otu0090	0.955	0.022 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Amanitaceae(100);g__Amanita(100);s__Amanita_rubescens(100);
Otu0194	0.893	0.011 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__unclassified_Agaricomycetes(100);f__unclassified_Agaricomycetes(100);g__unclassified_Agaricomycetes(100);s__Agaricomycetes_sp(100);
Otu0013	0.882	0.005 **	p__Basidiomycota(100);c__Agaricomycetes(100);o__Russulales(100);f__Russulaceae(100);g__Russula(100);
Otu0678	0.875	0.007 **	p__Ascomycota(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);
Otu1301	0.871	0.005 **	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(92);o__Chaetothyriales_unclassified(92);o__Chaetothyriales_unclassified(92);
Otu0059	0.869	0.006 **	p__Basidiomycota(100);c__Agaricomycetes(100);o__Boletales(100);f__Boletaceae(100);f__Boletaceae_unclassified(95);
Otu2299	0.862	0.006 **	p__Ascomycota(100);c__Dothideomycetes(100);o__Hysteriales(100);f__Gloniaceae(100);g__Cenococcum(100);s__Cenococcum_geophilum(72);
Otu0570	0.849	0.015 *	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);f__Herpotrichiellaceae_unclassified(100);
Otu2102	0.849	0.005 **	p__Basidiomycota(100);c__Agaricomycetes(100);o__Polyporales(100);f__Meruliaceae(100);g__Phlebia(100);s__Phlebia_sp_604(100);
Otu1598	0.828	0.006 **	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__unclassified_Chaetothyriales(100);g__unclassified_Chaetothyriales(100);s__Chaetothyriales_sp(100);
Otu2133	0.819	0.017 *	p__Ascomycota(100);c__Dothideomycetes(100);o__Hysteriales(100);f__Gloniaceae(100);g__Cenococcum(100);s__Cenococcum_geophilum(100);
Otu1559	0.804	0.005 **	p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(100);f__Pleosporales_family_Incertae_sedis(100);g__Phoma(100);s__Phoma_sp_A15(100);
Otu0098	0.775	0.008 **	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Cortinariaceae(100);g__Cortinarius(100);
Otu0324	0.775	0.004 **	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu0361	0.775	0.004 **	p__Ascomycota(100);c__Saccharomycetes(100);o__Saccharomycetales(100);f__Saccharomycetales_family_Incertae_sedis(100);g__Debaryomyces(100);s__Debaryomyces_prosopidis(100);
Otu0408	0.775	0.004 **	p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(100);f__Montagnulaceae(100);f__Montagnulaceae_unclassified(100);
Otu0460	0.775	0.004 **	p__Ascomycota(100);c__Sordariomycetes(100);o__Hypocreales(100);f__Cordycipitaceae(100);g__Cordyceps(100);s__Cordyceps_bassiana(100);
Otu0497	0.775	0.004 **	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Agaricaceae(100);g__Agaricus(100);s__Agaricus_bisporus(100);
Otu0777	0.775	0.004 **	p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Aspergillus(100);s__Aspergillus_niger(58);
Otu1319	0.775	0.007 **	p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(100);f__Sporormiaceae(100);f__Sporormiaceae_unclassified(94);
Otu1808	0.775	0.004 **	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__unclassified_Chaetothyriales(96);g__unclassified_Chaetothyriales(96);s__Chaetothyriales_sp(96);
Otu2122	0.775	0.004 **	p__Ascomycota(100);c__Dothideomycetes(100);o__Capnodiales(100);f__Mycosphaerellaceae(100);g__Ramichloridium(100);s__Ramichloridium_luteum(100);
Otu2208	0.775	0.003 **	p__Ascomycota(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);
Otu0168	0.773	0.021 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);o__Agaricales_unclassified(100);o__Agaricales_unclassified(100);
Otu0651	0.756	0.025 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);o__Agaricales_unclassified(100);o__Agaricales_unclassified(100);
Otu2000	0.756	0.019 *	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__unclassified_Chaetothyriales(95);g__unclassified_Chaetothyriales(95);s__Chaetothyriales_sp(95);
Otu1225	0.756	0.013 *	p__Ascomycota(100);p__Ascomycota_unclassified(97);p__Ascomycota_unclassified(97);p__Ascomycota_unclassified(97);p__Ascomycota_unclassified(97);
Otu2222	0.753	0.013 *	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(74);o__Chaetothyriales_unclassified(74);o__Chaetothyriales_unclassified(74);
Otu0085	0.747	0.028 *	p__Ascomycota(100);c__Saccharomycetes(100);o__Saccharomycetales(100);f__Saccharomycetaceae(100);g__Saccharomyces(100);s__Saccharomyces_cerevisiae(100);
Otu1531	0.742	0.049 *	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__unclassified_Chaetothyriales(79);g__unclassified_Chaetothyriales(79);s__Chaetothyriales_sp(79);
Otu1065	0.736	0.032 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Mycenaceae(100);g__Mycena(100);s__Mycena_sp(98);
Otu2110	0.735	0.015 *	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__unclassified_Chaetothyriales(100);g__unclassified_Chaetothyriales(100);s__Chaetothyriales_sp(100);
Otu1703	0.726	0.025 *	p__Basidiomycota(100);c__Agaricomycetes(86);c__Agaricomycetes_unclassified(86);c__Agaricomycetes_unclassified(86);c__Agaricomycetes_unclassified(86);
Otu2282	0.725	0.041 *	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__unclassified_Chaetothyriales(100);g__unclassified_Chaetothyriales(100);s__Chaetothyriales_sp(100);
Otu0978	0.724	0.032 *	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__unclassified_Chaetothyriales(100);g__unclassified_Chaetothyriales(100);s__Chaetothyriales_sp(100);
Otu1104	0.720	0.033 *	p__Ascomycota(100);c__Dothideomycetes(100);o__Capnodiales(100);o__Capnodiales_unclassified(100);o__Capnodiales_unclassified(100);

Otu0926	0.695	0.034 *	p__Ascomycota(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);
Otu2458	0.685	0.016 *	p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(100);o__Pleosporales_unclassified(100);o__Pleosporales_unclassified(100);
Otu0774	0.676	0.032 *	p__Ascomycota(100);p__Ascomycota_unclassified(97);p__Ascomycota_unclassified(97);p__Ascomycota_unclassified(97);p__Ascomycota_unclassified(97);
Otu0443	0.632	0.042 *	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu0706	0.632	0.044 *	p__Basidiomycota(53);p__Basidiomycota_unclassified(53);p__Basidiomycota_unclassified(53);p__Basidiomycota_unclassified(53);p__Basidiomycota_unclassified(53);
Otu0722	0.632	0.044 *	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu0750	0.632	0.042 *	p__Chytridiomycota(100);p__Chytridiomycota_unclassified(100);p__Chytridiomycota_unclassified(100);p__Chytridiomycota_unclassified(100);p__Chytridiomycota_unclassified
Otu0756	0.632	0.042 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Mycenaceae(100);g__Mycena(100);s__Mycena_sp(99);
Otu0758	0.632	0.041 *	p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(100);f__Montagnulaceae(100);f__Montagnulaceae_unclassified(91);
Otu0795	0.632	0.036 *	p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(100);f__Pleosporales_family_Incertae_sedis(100);g__Ascochyta(100);s__Ascochyta_sp(100);
Otu0855	0.632	0.042 *	p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(100);o__Pleosporales_unclassified(93);o__Pleosporales_unclassified(93);
Otu0905	0.632	0.044 *	p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(100);f__Phaeosphaeriaceae(100);g__Phaeosphaeria(100);s__Phaeosphaeria_triglochinicola(100);
Otu1079	0.632	0.044 *	p__Ascomycota(100);c__Dothideomycetes(100);o__Capnodiales(100);f__Davidiellaceae(100);g__Cladosporium(100);
Otu1237	0.632	0.042 *	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu1359	0.632	0.042 *	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu1497	0.632	0.042 *	p__Ascomycota(100);c__Sordariomycetes(100);o__Hypocreales(100);f__Hypocreaceae(100);g__Trichoderma(100);
Otu1550	0.632	0.044 *	p__Ascomycota(100);c__Dothideomycetes(100);o__Capnodiales(100);f__Mycosphaerellaceae(100);g__Cercospora(100);s__Cercospora_olivascens(60);
Otu1621	0.632	0.044 *	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);o__Chaetothyriales_unclassified(90);o__Chaetothyriales_unclassified(90);
Otu1833	0.632	0.042 *	p__Ascomycota(100);c__Sordariomycetes(100);o__Sordariales(100);f__Lasiosphaeriaceae(100);g__Podospora(100);s__Podospora_longicollis(100);
Otu1897	0.632	0.036 *	p__Ascomycota(100);c__Sordariomycetes(100);o__Hypocreales(100);f__Hypocreales_family_Incertae_sedis(100);g__Acremonium(100);s__Acremonium_sp_CCF3791(100);
Otu1898	0.632	0.042 *	p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Aspergillus(100);
Otu1960	0.632	0.043 *	p__Ascomycota(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);
Otu2075	0.632	0.042 *	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu2085	0.632	0.039 *	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);f__Herpotrichiellaceae_unclassified(100);
Otu2287	0.632	0.042 *	k__Fungi_unclassified(86);k__Fungi_unclassified(86);k__Fungi_unclassified(86);k__Fungi_unclassified(86);k__Fungi_unclassified(86);
Otu2312	0.632	0.041 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Mycenaceae(100);f__Mycenaceae_unclassified(100);
Otu2485	0.632	0.042 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Phallales(100);f__Phallaceae(100);g__Phallus(100);s__Phallus_rugulosus(100);

T2 Indicators

	stat	p.value	
Otu0708	0.982	0.001 ***	p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(100);f__Montagnulaceae(100);g__unclassified_Montagnulaceae(100);s__Montagnulaceae_sp(100);
Otu0657	0.868	0.005 **	p__Basidiomycota(100);c__Agaricomycetes(100);o__Atheliales(100);f__unclassified_Atheliales(100);g__unclassified_Atheliales(100);s__Atheliales_sp(100);
Otu0134	0.816	0.003 **	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Hygrophoraceae(100);g__Humidicutis(100);s__Humidicutis_cf_marginata_MEN09_02(100);
Otu1333	0.816	0.003 **	p__Ascomycota(100);c__Orbiliomycetes(100);o__Orbiliales(100);f__Orbiliaceae(100);f__Orbiliaceae_unclassified(100);
Otu1981	0.816	0.011 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Cantharellales(100);f__Ceratobasidiaceae(100);g__Ceratobasidium(100);s__Ceratobasidium_sp(100);
Otu0848	0.808	0.003 **	p__Basidiomycota(100);c__Agaricomycetes(100);o__Cantharellales(100);o__Cantharellales_unclassified(60);o__Cantharellales_unclassified(60);
Otu0406	0.762	0.045 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Sebacinales(100);f__Sebacinales_Group_B(98);g__unclassified_Sebacinales_Group_B(98);s__Sebacinales_Group_B_sp(98);
Otu1214	0.760	0.040 *	p__Ascomycota(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);
Otu0940	0.733	0.037 *	p__Ascomycota(100);c__Dothideomycetes(100);o__Hysteriales(100);f__Gloniaceae(100);g__Cenococcum(100);
Otu1306	0.730	0.035 *	p__Ascomycota(100);c__Sordariomycetes(100);o__Sordariales(94);o__Sordariales_unclassified(94);o__Sordariales_unclassified(94);
Otu0829	0.723	0.036 *	p__Ascomycota(100);c__Sordariomycetes(100);o__Diaporthales(100);f__Schizoparmaceae(100);g__Pilidiella(100);s__Pilidiella_eucalyptorum(100);
Otu1566	0.713	0.050 *	p__Basidiomycota(100);p__Basidiomycota_unclassified(72);p__Basidiomycota_unclassified(72);p__Basidiomycota_unclassified(72);p__Basidiomycota_unclassified(72);

Otu0076	0.707	0.041 *	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__unclassified_Herpotrichiellaceae(100);s__Herpotrichiellaceae_sp(100);
Otu1281	0.707	0.031 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Polyporales(98);f__Meruliaceae(98);g__Hyphoderma(98);
Otu1308	0.707	0.041 *	p__Basidiomycota(100);c__Agaricomycetes(100);c__Agaricomycetes_unclassified(100);c__Agaricomycetes_unclassified(100);c__Agaricomycetes_unclassified(100);
Otu1582	0.707	0.043 *	p__Ascomycota(100);c__Sordariomycetes(100);o__Xylariales(100);f__Diatrypaceae(100);g__unclassified_Diatrypaceae(100);s__Diatrypaceae_sp(100);
Otu2314	0.707	0.043 *	p__Glomeromycota(100);c__Glomeromycetes(100);o__Glomerales(100);f__Glomeraceae(100);g__Glomus(100);
Otu2418	0.707	0.043 *	p__Ascomycota(100);c__Dothideomycetes(100);o__Capnodiales(100);f__Mycosphaerellaceae(100);g__Zasmidium(100);
Otu0377	0.697	0.028 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Thelephorales(100);f__Thelephoraceae(100);g__Tomentella(100);s__Tomentella_sublilacina(100);
Otu1029	0.692	0.043 *	p__Ascomycota(100);c__Leotiomycetes(100);o__Leotiomycetes_order_Incertae_sedis(100);f__Leotiomycetes_family_Incertae_sedis(100);g__Leohumicola(100);s__Leohumicola_verrucosa(83);
Otu2041	0.687	0.026 *	p__Basidiomycota(100);c__Agaricomycetes(100);c__Agaricomycetes_unclassified(100);c__Agaricomycetes_unclassified(100);c__Agaricomycetes_unclassified(100);
Otu1632	0.685	0.049 *	p__Ascomycota(100);c__Leotiomycetes(100);c__Leotiomycetes_unclassified(100);c__Leotiomycetes_unclassified(100);c__Leotiomycetes_unclassified(100);
Otu1952	0.685	0.044 *	p__Glomeromycota(100);c__Glomeromycetes(100);o__Diversisporales(100);f__Acaulosporaceae(100);g__Acaulospora(95);
Otu0511	0.674	0.036 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);o__Agaricales_unclassified(100);o__Agaricales_unclassified(100);

T4 Indicators

	stat	p.value	
Otu0992	0.816	0.008 **	p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);s__Mortierella_bainieri(100);
Otu1739	0.816	0.014 *	p__Ascomycota(100);c__Dothideomycetes(100);c__Dothideomycetes_unclassified(100);c__Dothideomycetes_unclassified(100);c__Dothideomycetes_unclassified(100);
Otu0982	0.810	0.020 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Mycenaceae(100);g__Mycena(100);
Otu0898	0.806	0.012 *	p__Basidiomycota(100);c__Agaricomycetes(100);c__Agaricomycetes_unclassified(100);c__Agaricomycetes_unclassified(100);c__Agaricomycetes_unclassified(100);
Otu0878	0.792	0.012 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Auriculariales(100);f__Auriculariales_family_Incertae_sedis(100);g__Basidiodendron(100);s__Basidiodendron_sp(100);
Otu1938	0.788	0.008 **	p__Ascomycota(100);c__Pezizomycetes(100);o__Pezizales(100);f__Pyronemataceae(100);g__Sphaerosporella(100);s__Sphaerosporella_sp(100);
Otu1424	0.787	0.012 *	p__Ascomycota(100);c__Dothideomycetes(100);c__Dothideomycetes_unclassified(100);c__Dothideomycetes_unclassified(100);c__Dothideomycetes_unclassified(100);
Otu1476	0.783	0.012 *	p__Basidiomycota(100);c__Agaricomycetes(100);c__Agaricomycetes_unclassified(100);c__Agaricomycetes_unclassified(100);c__Agaricomycetes_unclassified(100);
Otu1388	0.727	0.049 *	p__Basidiomycota(93);p__Basidiomycota_unclassified(93);p__Basidiomycota_unclassified(93);p__Basidiomycota_unclassified(93);p__Basidiomycota_unclassified(93);
Otu2072	0.710	0.040 *	p__Chytridiomycota(100);c__Chytridiomycetes(100);o__Rhizophydiales(100);f__Rhizophydiaceae(100);g__Rhizophydium(100);s__Rhizophydium_sp(100);
Otu1724	0.707	0.038 *	p__Ascomycota(100);c__Pezizomycetes(100);o__Pezizales(100);f__Pyronemataceae(100);g__Scutellinia(100);s__Scutellinia_sp(100);
Otu1644	0.679	0.042 *	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);

T60 Indicators

	stat	p.value	
Otu0345	0.996	0.002 **	p__Ascomycota(100);c__Ascomycota_class_Incertae_sedis(100);o__Ascomycota_order_Incertae_sedis(100);f__Ascomycota_family_Incertae_sedis(100);g__unclassified_Ascomycota(100);s__Ascon
Otu0290	0.990	0.001 ***	p__Basidiomycota(100);c__Agaricomycetes(100);o__Hymenochaetales(100);f__Hymenochaetaceae(100);g__Coltriciella(100);s__Coltriciella_sp(100);
Otu0430	0.979	0.002 **	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu0042	0.956	0.006 **	p__Basidiomycota(100);c__Agaricomycetes(100);o__Russulales(100);f__Russulaceae(100);f__Russulaceae_unclassified(99);
Otu1004	0.913	0.003 **	p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);f__Trichocomaceae_unclassified(100);
Otu1864	0.913	0.002 **	p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Penicillium(100);
Otu0503	0.899	0.001 ***	p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiales_family_Incertae_sedis(100);g__Hyphodiscus(100);s__Hyphodiscus_sp(100);
Otu0655	0.898	0.003 **	p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(99);g__Penicillium(99);
Otu0473	0.897	0.002 **	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu1162	0.883	0.002 **	p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Penicillium(100);s__Penicillium_sp(99);
Otu0510	0.877	0.008 **	p__Ascomycota(100);c__Sordariomycetes(100);o__Hypocreales(100);f__Hypocreales_family_Incertae_sedis(100);g__Acremonium(100);s__Acremonium_cavaraeanum(100);
Otu0729	0.868	0.002 **	p__Ascomycota(100);c__Sordariomycetes(100);o__Hypocreales(100);f__Ophiocordycipitaceae(100);g__Chaunopycnis(100);s__Chaunopycnis_alba(100);

Otu0784	0.845	0.011 *	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu0754	0.816	0.007 **	p__Ascomycota(100);c__Sordariomycetes(100);o__Hypocreales(100);f__unclassified_Hypocreales(100);g__unclassified_Hypocreales(100);s__Hypocreales_sp(100);
Otu0962	0.816	0.011 *	p__Ascomycota(100);c__Sordariomycetes(100);c__Sordariomycetes_unclassified(100);c__Sordariomycetes_unclassified(100);c__Sordariomycetes_unclassified(100);
Otu1441	0.816	0.008 **	p__Ascomycota(100);c__Dothideomycetes(100);o__Capnodiales(100);f__unclassified_Capnodiales(100);g__unclassified_Capnodiales(100);s__Capnodiales_sp(100);
Otu1483	0.816	0.007 **	p__Ascomycota(100);c__Sordariomycetes(100);o__Hypocreales(100);f__Cordycipitaceae(55);g__Beauveria(55);s__Beauveria_virella(55);
Otu1570	0.816	0.008 **	p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);
Otu1617	0.816	0.007 **	p__Basidiomycota(100);c__Agaricomycetes(100);c__Agaricomycetes_unclassified(100);c__Agaricomycetes_unclassified(100);c__Agaricomycetes_unclassified(100);
Otu1876	0.816	0.008 **	p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);s__Mortierella_sp(100);
Otu1953	0.816	0.003 **	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu0015	0.816	0.013 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Trechisporales(100);f__Hydnodontaceae(100);g__Trechispora(100);s__Trechispora_cohaerens(91);
Otu0055	0.816	0.003 **	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Amanitaceae(100);g__Amanita(100);s__Amanita_flavoconia(88);
Otu0301	0.805	0.011 *	p__Ascomycota(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);
Otu0495	0.800	0.023 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Cortinariaceae(100);g__Cortinarius(100);s__Cortinarius_stillatitius(96);
Otu0225	0.792	0.020 *	p__Ascomycota(100);c__Dothideomycetes(100);o__Hysteriales(100);f__Gloniaceae(100);g__Cenococcum(100);s__uncultured_Cenococcum(98);
Otu0393	0.767	0.025 *	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu1099	0.754	0.045 *	p__Ascomycota(100);c__Sordariomycetes(100);c__Sordariomycetes_unclassified(100);c__Sordariomycetes_unclassified(100);c__Sordariomycetes_unclassified(100);
Otu2145	0.736	0.026 *	p__Chytridiomycota(100);c__Monoblepharidomycetes(100);o__Monoblepharidales(69);o__Monoblepharidales_unclassified(69);o__Monoblepharidales_unclassified(69);
Otu1438	0.730	0.034 *	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu1295	0.707	0.039 *	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);f__Herpotrichiellaceae_unclassified(100);
Otu1462	0.707	0.044 *	p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Mucoraceae(100);g__Mucor(100);s__Mucor_moelleri(100);
Otu2429	0.707	0.039 *	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu0505	0.705	0.041 *	p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);o__Helotiales_unclassified(100);o__Helotiales_unclassified(100);
Otu1257	0.699	0.040 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Cortinariaceae(100);g__Cortinarius(100);s__Cortinarius_stillatitius(99);
Otu0637	0.698	0.036 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Trechisporales(100);f__Hydnodontaceae(100);g__Trechispora(100);
Otu0038	0.684	0.039 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Clavariaceae(100);g__unclassified_Clavariaceae(100);s__Clavariaceae_sp(100);

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T1 Indicators

	stat	p.value	
Otu0057	0.892	0.002 **	p__Basidiomycota(100);c__Agaricomycetes(100);o__Russulales(100);f__Russulaceae(100);g__Russula(100);s__Russula_rubellipes(100);
Otu0182	0.867	0.021 *	p__Ascomycota(100);c__Dothideomycetes(100);o__Capnodiales(100);f__Davidiellaceae(100);g__Davidiella(62);s__Davidiella_tassiana(62);
Otu0013	0.792	0.023 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Russulales(100);f__Russulaceae(100);g__Russula(100);
Otu0868	0.775	0.010 **	p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Rasamsonia(99);
Otu0912	0.775	0.005 **	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__unclassified_Chaetothyriales(100);g__unclassified_Chaetothyriales(100);s__Chaetothyriales_sp(100)
Otu0085	0.770	0.004 **	p__Ascomycota(100);c__Saccharomycetes(100);o__Saccharomycetales(100);f__Saccharomycetaceae(100);g__Saccharomyces(100);s__Saccharomyces_cerevisiae(100);
Otu0486	0.714	0.013 *	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__unclassified_Chaetothyriales(100);g__unclassified_Chaetothyriales(100);s__Chaetothyriales_sp(100)
Otu1559	0.696	0.019 *	p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(100);f__Pleosporales_family_Incertae_sedis(91);g__Massariosphaeria(91);s__Massariosphaeria_sp_FAEII23a(91);
Otu0761	0.661	0.031 *	p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(60);o__Pleosporales_unclassified(60);o__Pleosporales_unclassified(60);
Otu0646	0.632	0.039 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);o__Agaricales_unclassified(100);o__Agaricales_unclassified(100);
Otu0720	0.632	0.039 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);o__Agaricales_unclassified(100);o__Agaricales_unclassified(100);
Otu0743	0.632	0.041 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Thelephorales(100);f__Thelephoraceae(100);f__Thelephoraceae_unclassified(62);

Otu1083	0.632	0.037 *	p__Ascomycota(100);p__Ascomycota_unclassified(89);p__Ascomycota_unclassified(89);p__Ascomycota_unclassified(89);p__Ascomycota_unclassified(89);
Otu1428	0.632	0.048 *	p__Ascomycota(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);
Otu1669	0.632	0.048 *	p__Ascomycota(100);c__Sordariomycetes(100);o__Trichosphaeriales(100);f__Trichosphaeriales_family_Incertae_sedis(100);g__unclassified_Trichosphaeriales(100);s__Trichosphaeriales_sp(100);
Otu1725	0.632	0.039 *	p__Basidiomycota(100);c__Basidiomycota_class_Incertae_sedis(100);o__Malasseziales(100);f__unclassified_Malasseziales(100);g__unclassified_Malasseziales(100);s__Malasseziales_sp(100);
Otu1891	0.632	0.037 *	p__Ascomycota(100);c__Dothideomycetes(100);o__Hysteriales(100);f__unclassified_Hysteriales(100);g__unclassified_Hysteriales(100);s__Hysteriales_sp(100);
Otu1896	0.632	0.038 *	p__Ascomycota(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);
Otu2251	0.632	0.038 *	p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(100);f__Pleomassariaceae(100);g__unclassified_Pleomassariaceae(100);s__Pleomassariaceae_sp(100);
Otu0872	0.629	0.042 *	p__Basidiomycota(100);c__Agaricomycetes(100);c__Agaricomycetes_unclassified(100);c__Agaricomycetes_unclassified(100);c__Agaricomycetes_unclassified(100);

T2 Indicators

	stat	p.value	
Otu0601	0.655	0.046 *	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);o__Chaetothyriales_unclassified(100);o__Chaetothyriales_unclassified(100);
Otu0755	0.655	0.038 *	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu1903	0.655	0.043 *	p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);s__Mortierella_rishikesha(100);

T4 Indicators

	stat	p.value	
Otu0360	0.970	0.001 ***	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(87);g__unclassified_Herpotrichiellaceae(77);s__Herpotrichiellaceae_sp(77);
Otu0796	0.787	0.020 *	p__Glomeromycota(100);c__Glomeromycetes(100);o__Glomerales(100);f__Glomeraceae(100);g__unclassified_Glomeraceae(100);s__Glomeraceae_sp(100);
Otu0366	0.760	0.034 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Cantharellales(100);f__Botryobasidiaceae(100);g__Botryobasidium(100);s__Botryobasidium_subcoronatum(100);
Otu0728	0.755	0.023 *	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu0152	0.752	0.046 *	p__Ascomycota(100);c__Eurotiomycetes(100);c__Eurotiomycetes_unclassified(100);c__Eurotiomycetes_unclassified(100);c__Eurotiomycetes_unclassified(100);
Otu0533	0.735	0.048 *	p__Chytridiomycota(100);c__Chytridiomycetes(100);o__Spizellomycetales(100);f__Spizellomycetaceae(100);g__Powellomyces(100);s__Powellomyces_sp(100);
Otu0230	0.725	0.041 *	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__unclassified_Herpotrichiellaceae(100);s__Herpotrichiellaceae_sp(100);
Otu0485	0.707	0.032 *	p__Ascomycota(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);
Otu0992	0.707	0.025 *	p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);s__Mortierella_bainieri(100);
Otu1352	0.707	0.025 *	p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Endogonales(100);f__Endogonaceae(100);g__Endogone(100);s__Endogone_sp_1_RG_2012(100);

T60 Indicators

	stat	p.value	
Otu0301	1.000	0.001 ***	p__Ascomycota(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);
Otu0510	1.000	0.001 ***	p__Ascomycota(100);c__Sordariomycetes(100);o__Hypocreales(100);f__Hypocreales_family_Incertae_sedis(100);g__Acremonium(100);s__Acremonium_cavaraeanum(100);
Otu0607	0.996	0.001 ***	p__Ascomycota(100);c__Saccharomycetes(100);o__Saccharomycetales(100);f__Saccharomycetales_family_Incertae_sedis(100);g__Candida(100);s__Candida_sp_NCAIM_Y01936(100);
Otu0042	0.994	0.001 ***	p__Basidiomycota(100);c__Agaricomycetes(100);o__Russulales(100);f__Russulaceae(100);f__Russulaceae_unclassified(99);
Otu0655	0.983	0.001 ***	p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(99);g__Penicillium(99);
Otu0290	0.981	0.001 ***	p__Basidiomycota(100);c__Agaricomycetes(100);o__Hymenochaetales(100);f__Hymenochaetaceae(100);g__Coltriciella(100);s__Coltriciella_sp(100);
Otu0345	0.981	0.001 ***	p__Ascomycota(100);c__Ascomycota_class_Incertae_sedis(100);o__Ascomycota_order_Incertae_sedis(100);f__Ascomycota_family_Incertae_sedis(100);g__unclassified_Ascomycota
Otu0117	0.967	0.001 ***	p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Talaromyces(100);
Otu0157	0.924	0.003 **	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);o__Agaricales_unclassified(100);o__Agaricales_unclassified(100);
Otu0754	0.913	0.001 ***	p__Ascomycota(100);c__Sordariomycetes(100);o__Hypocreales(100);f__unclassified_Hypocreales(100);g__unclassified_Hypocreales(100);s__Hypocreales_sp(100);
Otu0729	0.904	0.001 ***	p__Ascomycota(100);c__Sordariomycetes(100);o__Hypocreales(100);f__Ophiocordycipitaceae(100);g__Chaunopycnis(100);s__Chaunopycnis_alba(100);
Otu0015	0.896	0.001 ***	p__Basidiomycota(100);c__Agaricomycetes(100);o__Trechisporales(100);f__Hydnodontaceae(100);g__Trechispora(100);s__Trechispora_cohaerens(91);

Otu1483	0.861	0.001 ***	p__Ascomycota(100);c__Sordariomycetes(100);o__Hypocreales(100);f__Cordycipitaceae(55);g__Beauveria(55);s__Beauveria_virella(55);
Otu0455	0.854	0.002 **	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu0744	0.823	0.006 **	p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);s__Umbelopsis_autotrophica(100);
Otu0430	0.816	0.007 **	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu1004	0.816	0.005 **	p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);f__Trichocomaceae_unclassified(100);
Otu1633	0.816	0.005 **	p__Basidiomycota(100);c__Agaricomycetes(100);o__Boletales(100);f__Boletaceae(100);f__Boletaceae_unclassified(100);
Otu0483	0.812	0.020 *	p__Ascomycota(100);c__Sordariomycetes(100);o__Xylariales(100);o__Xylariales_unclassified(100);o__Xylariales_unclassified(100);
Otu0055	0.812	0.007 **	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Amanitaceae(100);g__Amanita(100);s__Amanita_flavoconia(88);
Otu0393	0.807	0.008 **	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu0225	0.794	0.014 *	p__Ascomycota(100);c__Dothideomycetes(100);o__Hysteriales(100);f__Gloniaceae(100);g__Cenococcum(100);s__uncultured_Cenococcum(98);
Otu0784	0.778	0.002 **	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu0943	0.740	0.010 **	p__Ascomycota(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);
Otu0473	0.707	0.037 *	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu0503	0.707	0.020 *	p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiales_family_Incertae_sedis(100);g__Hyphodiscus(100);s__Hyphodiscus_sp(100);
Otu0902	0.707	0.030 *	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(97);f__Herpotrichiellaceae_unclassified(97);
Otu1079	0.707	0.025 *	p__Ascomycota(100);c__Dothideomycetes(100);o__Capnodiales(100);f__Davidiellaceae(100);g__Cladosporium(100);
Otu1162	0.707	0.022 *	p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Penicillium(100);s__Penicillium_sp(99);
Otu1383	0.707	0.029 *	p__Ascomycota(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);
Otu0431	0.705	0.033 *	p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);o__Helotiales_unclassified(100);o__Helotiales_unclassified(100);
Otu0038	0.701	0.040 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Clavariaceae(100);g__unclassified_Clavariaceae(100);s__Clavariaceae_sp(100);
Otu0504	0.698	0.031 *	p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);f__Trichocomaceae_unclassified(100);
Otu0793	0.648	0.042 *	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);

Fun B Horizon

T1 Indicators

	stat	p.value	
Otu0086	0.848	0.042 *	p__Ascomycota(100);c__Ascomycota_class_Incertae_sedis(63);o__Ascomycota_order_Incertae_sedis(63);f__Ascomycota_family_Incertae_sedis(63);g__Slimacomyces(63);s__Slimacomyces_isiola(6
Otu0168	0.816	0.009 **	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);o__Agaricales_unclassified(100);o__Agaricales_unclassified(100);
Otu0958	0.816	0.009 **	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__unclassified_Chaetothyriales(79);g__unclassified_Chaetothyriales(79);s__Chaetothyriales_sp(79);
Otu0022	0.801	0.004 **	p__Ascomycota(100);c__Saccharomycetes(100);o__Saccharomycetales(100);f__Trichomonascaceae(100);g__Sugiyamaella(100);s__Sugiyamaella_paludigena(100);
Otu0995	0.786	0.016 *	k__Fungi_unclassified(95);k__Fungi_unclassified(95);k__Fungi_unclassified(95);k__Fungi_unclassified(95);k__Fungi_unclassified(95);
Otu0013	0.782	0.021 *	k__Fungi_unclassified(95);k__Fungi_unclassified(95);k__Fungi_unclassified(95);k__Fungi_unclassified(95);k__Fungi_unclassified(95);
Otu0007	0.771	0.031 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Amanitaceae(100);g__Amanita(100);
Otu0050	0.754	0.032 *	p__Ascomycota(100);c__Leotiomycetes(100);o__Geoglossales(100);f__Geoglossaceae(100);g__Trichoglossum(100);s__Trichoglossum_walteri(100);
Otu0905	0.725	0.031 *	p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Vibrisseaceae(100);g__Phialocephala(100);s__Phialocephala_sp_CM16s1(100);
Otu0037	0.707	0.045 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Atheliales(100);f__Atheliaceae(100);g__Piloderma(100);s__Piloderma_sphaerosporum(100);
Otu0059	0.707	0.040 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Boletales(100);f__Boletaceae(100);f__Boletaceae_unclassified(95);
Otu0098	0.707	0.045 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Cortinariaceae(100);g__Cortinarius(100);
Otu0194	0.707	0.040 *	p__Basidiomycota(100);c__Agaricomycetes(100);o__unclassified_Agaricomycetes(100);f__unclassified_Agaricomycetes(100);g__unclassified_Agaricomycetes(100);s__Agaricomycetes_sp(100);
Otu0294	0.707	0.040 *	p__Ascomycota(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);
Otu0324	0.707	0.045 *	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu0361	0.707	0.045 *	p__Ascomycota(100);c__Saccharomycetes(100);o__Saccharomycetales(100);f__Saccharomycetales_family_Incertae_sedis(100);g__Debaryomyces(100);s__Debaryomyces_prosopidis(100);

Otu0408 0.707 0.045 * p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(100);f__Montagnulaceae(100);f__Montagnulaceae_unclassified(100);
Otu0443 0.707 0.045 * k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu0460 0.707 0.045 * p__Ascomycota(100);c__Sordariomycetes(100);o__Hypocreales(100);f__Cordycipitaceae(100);g__Cordyceps(100);s__Cordyceps_bassiana(100);
Otu0486 0.707 0.045 * p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__unclassified_Chaetothyriales(100);g__unclassified_Chaetothyriales(100);s__Chaetothyriales_sp(100);
Otu0497 0.707 0.045 * p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Agaricaceae(100);g__Agaricus(100);s__Agaricus_bisporus(100);
Otu0500 0.707 0.045 * p__Ascomycota(100);c__Dothideomycetes(100);o__Capnodiales(100);f__Capnodiales_family_Incertae_sedis(98);g__Rachicladosporium(84);
Otu0501 0.707 0.045 * p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__unclassified_Trichocomaceae(88);s__Trichocomaceae_sp(88);
Otu0519 0.707 0.045 * p__Ascomycota(100);c__Dothideomycetes(100);o__Capnodiales(100);f__Mycosphaerellaceae(100);g__Ramichloridium(100);s__Ramichloridium_indicum(76);
Otu0542 0.707 0.045 * p__Ascomycota(100);c__Ascomycota_class_Incertae_sedis(63);o__Ascomycota_order_Incertae_sedis(63);f__Ascomycota_family_Incertae_sedis(63);f__Ascomycota_family_Incertae_sedis_unclassi
Otu0564 0.707 0.043 * p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);o__Helotiales_unclassified(100);o__Helotiales_unclassified(100);
Otu0576 0.707 0.045 * p__Ascomycota(100);c__Sordariomycetes(100);o__Hypocreales(100);f__Bionectriaceae(100);g__Clonostachys(100);s__Clonostachys_rosea_f._catenulata(100);
Otu0585 0.707 0.045 * k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu0609 0.707 0.045 * p__Ascomycota(100);c__Dothideomycetes(100);o__Capnodiales(100);f__Teratosphaeriaceae(100);g__Teratosphaeria(89);
Otu0706 0.707 0.045 * p__Basidiomycota(53);p__Basidiomycota_unclassified(53);p__Basidiomycota_unclassified(53);p__Basidiomycota_unclassified(53);p__Basidiomycota_unclassified(53);
Otu0777 0.707 0.045 * p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Aspergillus(100);s__Aspergillus_niger(58);
Otu0792 0.707 0.045 * p__Ascomycota(100);c__Sordariomycetes(100);o__Trichosphaeriales(100);f__Trichosphaeriales_family_Incertae_sedis(100);g__unclassified_Trichosphaeriales(100);s__Trichosphaeriales_sp(100);
Otu0845 0.707 0.045 * p__Ascomycota(100);c__Dothideomycetes(100);o__Dothideales(100);f__Dothioraceae(100);g__Aureobasidium(100);s__Aureobasidium_pullulans_var._subglaciale(76);
Otu0936 0.707 0.045 * p__Ascomycota(100);c__Sordariomycetes(100);o__Sordariomycetes_order_Incertae_sedis(100);f__Glomerellaceae(100);g__Colletotrichum(100);
Otu0999 0.707 0.045 * p__Ascomycota(100);c__Sordariomycetes(100);o__Xylariales(100);f__Amphisphaeriaceae(100);g__Bartalinia(96);s__Bartalinia_robillardoides(96);
Otu1040 0.707 0.045 * p__Ascomycota(100);c__Sordariomycetes(100);o__Trichosphaeriales(100);f__Trichosphaeriales_family_Incertae_sedis(100);g__unclassified_Trichosphaeriales(100);s__Trichosphaeriales_sp(100);
Otu1224 0.707 0.040 * p__Basidiomycota(100);c__Agaricomycetes(100);o__Auriculariales(100);f__unclassified_Auriculariales(100);g__unclassified_Auriculariales(100);s__Auriculariales_sp(100);
Otu1271 0.707 0.045 * p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__unclassified_Chaetothyriales(94);g__unclassified_Chaetothyriales(94);s__Chaetothyriales_sp(94);
Otu1319 0.707 0.045 * p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(100);f__Sporormiaceae(100);f__Sporormiaceae_unclassified(94);
Otu1389 0.707 0.045 * p__Ascomycota(100);c__Sordariomycetes(100);o__Microascales(100);f__Microascaceae(100);g__Microascus(100);s__Microascus_manginii(100);
Otu1504 0.707 0.041 * p__Ascomycota(100);c__Sordariomycetes(100);o__Sordariomycetes_order_Incertae_sedis(100);f__Magnaporthaceae(100);g__unclassified_Magnaporthaceae(100);s__Magnaporthaceae_sp(100);
Otu1538 0.707 0.044 * p__Ascomycota(100);c__Sordariomycetes(100);o__Sordariales(100);o__Sordariales_unclassified(100);o__Sordariales_unclassified(100);
Otu1677 0.707 0.045 * p__Basidiomycota(100);p__Basidiomycota_unclassified(97);p__Basidiomycota_unclassified(97);p__Basidiomycota_unclassified(97);p__Basidiomycota_unclassified(97);
Otu1680 0.707 0.045 * p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(90);f__Montagnulaceae(86);f__Montagnulaceae_unclassified(86);
Otu0427 0.704 0.045 * p__Basidiomycota(100);c__Agaricomycetes(100);o__Hymenochaetales(100);f__unclassified_Hymenochaetales(100);g__unclassified_Hymenochaetales(100);s__Hymenochaetales_sp(100);
Otu0151 0.700 0.034 * p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__unclassified_Trichocomaceae(99);s__Trichocomaceae_sp(99);
Otu0502 0.693 0.038 * p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Penicillium(100);s__Penicillium_thomii(97);
Otu0745 0.676 0.040 * p__Glomeromycota(100);c__Glomeromycetes(100);o__Archaeosporales(100);f__Archaeosporaceae(100);g__unclassified_Archaeosporaceae(100);s__Archaeosporaceae_sp(100);
Otu0758 0.675 0.041 * p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(100);f__Montagnulaceae(100);f__Montagnulaceae_unclassified(91);
Otu0102 0.662 0.042 * p__Ascomycota(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);
Otu0247 0.655 0.049 * p__Basidiomycota(100);c__Agaricomycetes(100);o__Russulales(100);f__Russulaceae(100);g__Russula(100);s__Russula_vesca(100);

Group T2 #sps. 13
stat p.value
Otu1852 0.775 0.005 ** k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu0945 0.749 0.012 * k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu1745 0.748 0.018 * p__Ascomycota(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);p__Ascomycota_unclassified(100);
Otu0574 0.733 0.007 ** p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(100);o__Pleosporales_unclassified(100);o__Pleosporales_unclassified(100);

Otu1218	0.689	0.029	*	p__Ascomycota(100);c__Sordariomycetes(100);o__Hypocreales(100);o__Hypocreales_unclassified(100);o__Hypocreales_unclassified(100);
Otu0832	0.632	0.037	*	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu1263	0.632	0.035	*	p__Ascomycota(100);c__Sordariomycetes(100);c__Sordariomycetes_unclassified(100);c__Sordariomycetes_unclassified(100);c__Sordariomycetes_unclassified(100);
Otu1400	0.632	0.037	*	p__Basidiomycota(100);c__Agaricomycetes(100);o__Corticiales(100);f__Corticiaceae(100);g__Waitea(100);s__Rhizoctonia_oryzae(65);
Otu1435	0.632	0.043	*	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu1470	0.632	0.035	*	p__Glomeromycota(100);c__Glomeromycetes(100);o__Archaeosporales(100);f__unclassified_Archaeosporales(100);g__unclassified_Archaeosporales(100);s__Archaeosporales_sp(100);
Otu1568	0.632	0.047	*	p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Choanephoraceae(100);g__Poitrasia(100);s__Poitrasia_circinans(100);
Otu1683	0.632	0.035	*	p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Chaetothyriaceae(100);g__Cyphellophora(100);
Otu2546	0.632	0.043	*	k__Fungi_unclassified(91);k__Fungi_unclassified(91);k__Fungi_unclassified(91);k__Fungi_unclassified(91);k__Fungi_unclassified(91);

Group T4 #sps. 2

	stat	p.value		
Otu1624	0.745	0.016	*	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);
Otu0719	0.696	0.040	*	k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);k__Fungi_unclassified(100);

Group T60 #sps. 2

	stat	p.value		
Otu0588	0.803	0.023	*	p__Basidiomycota(100);c__Agaricomycetes(100);c__Agaricomycetes_unclassified(100);c__Agaricomycetes_unclassified(100);c__Agaricomycetes_unclassified(100);
Otu0117	0.707	0.043	*	p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Talaromyces(100);

Appendix C - Supplemental Materials for Chapter 4

Figure C 1 Bacterial community NMDS plot with both fire severities

Bacterial Non-Metric Multidimensional Scaling (NMDS) ordination of the five sampling years (T0, T1, T2, T4, and T6) within the two fire severities [stress=0.10]

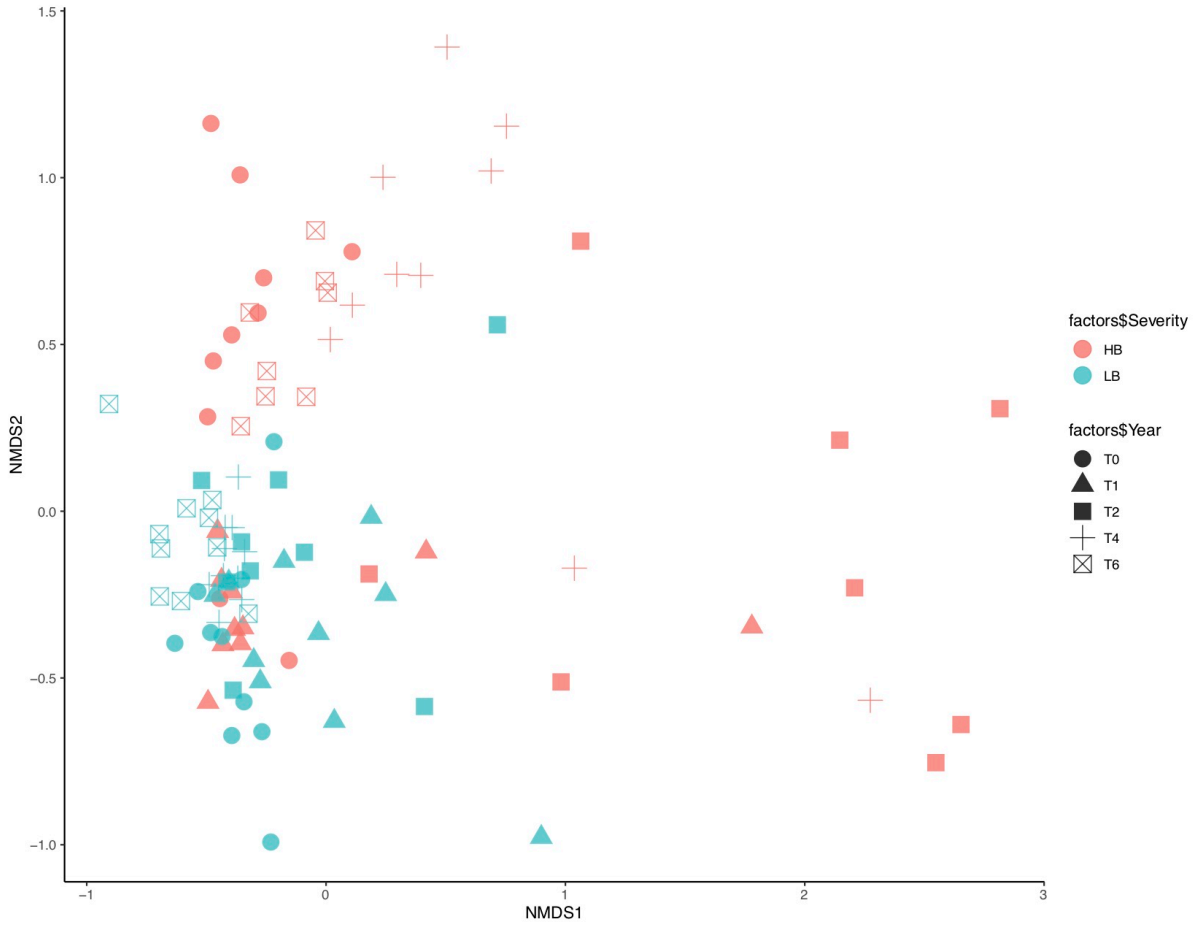

Figure C 2 Fungal community NMDS plot with both severities

Fungi Non-Metric Multidimensional Scaling (NMDS) ordination plots of the five sampling years (T0, T1, T2, T4, and T6) within the two fire severities [stress=0.19].

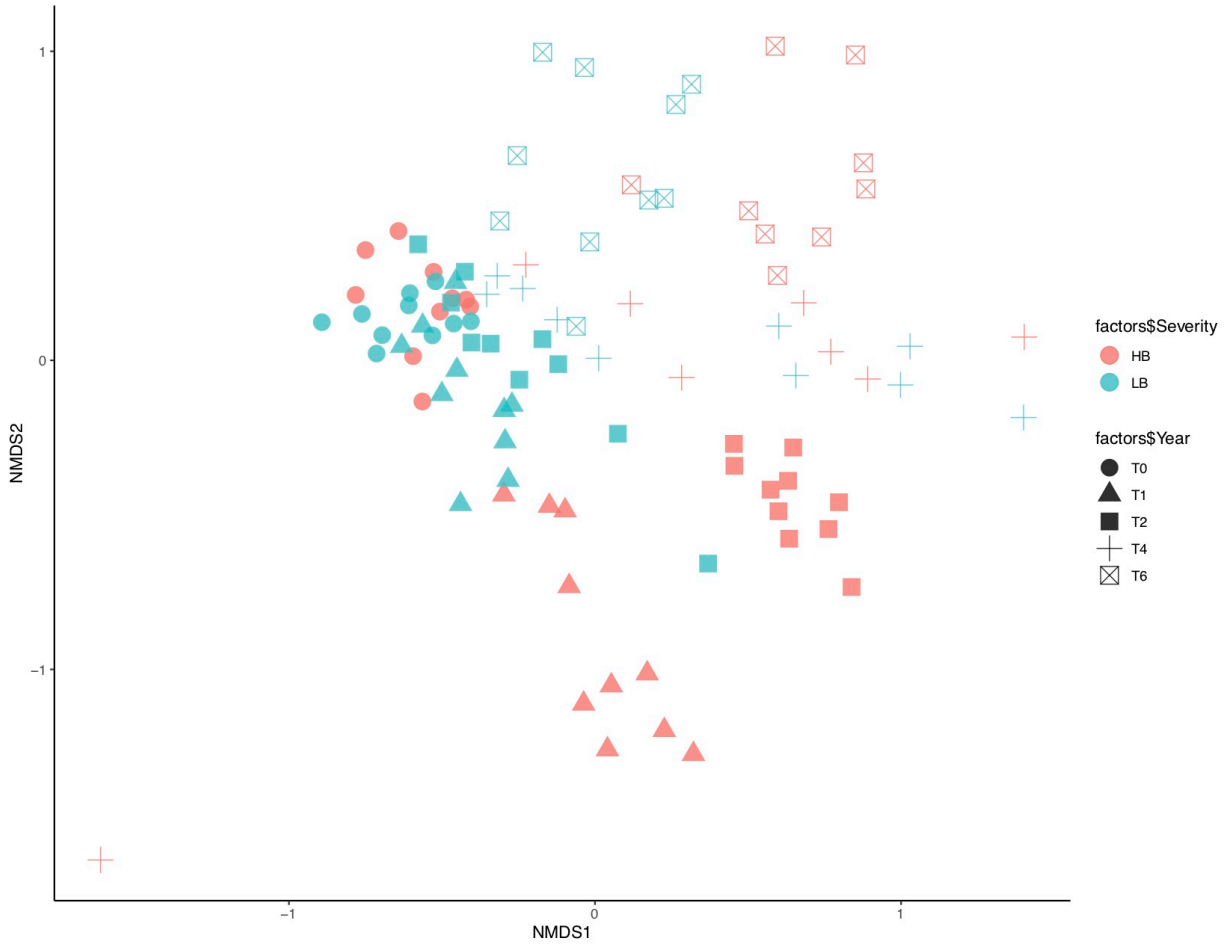

Figure C 3 Fungal Guild of all the guilds analyzed. Percentage of guild per each treatment.

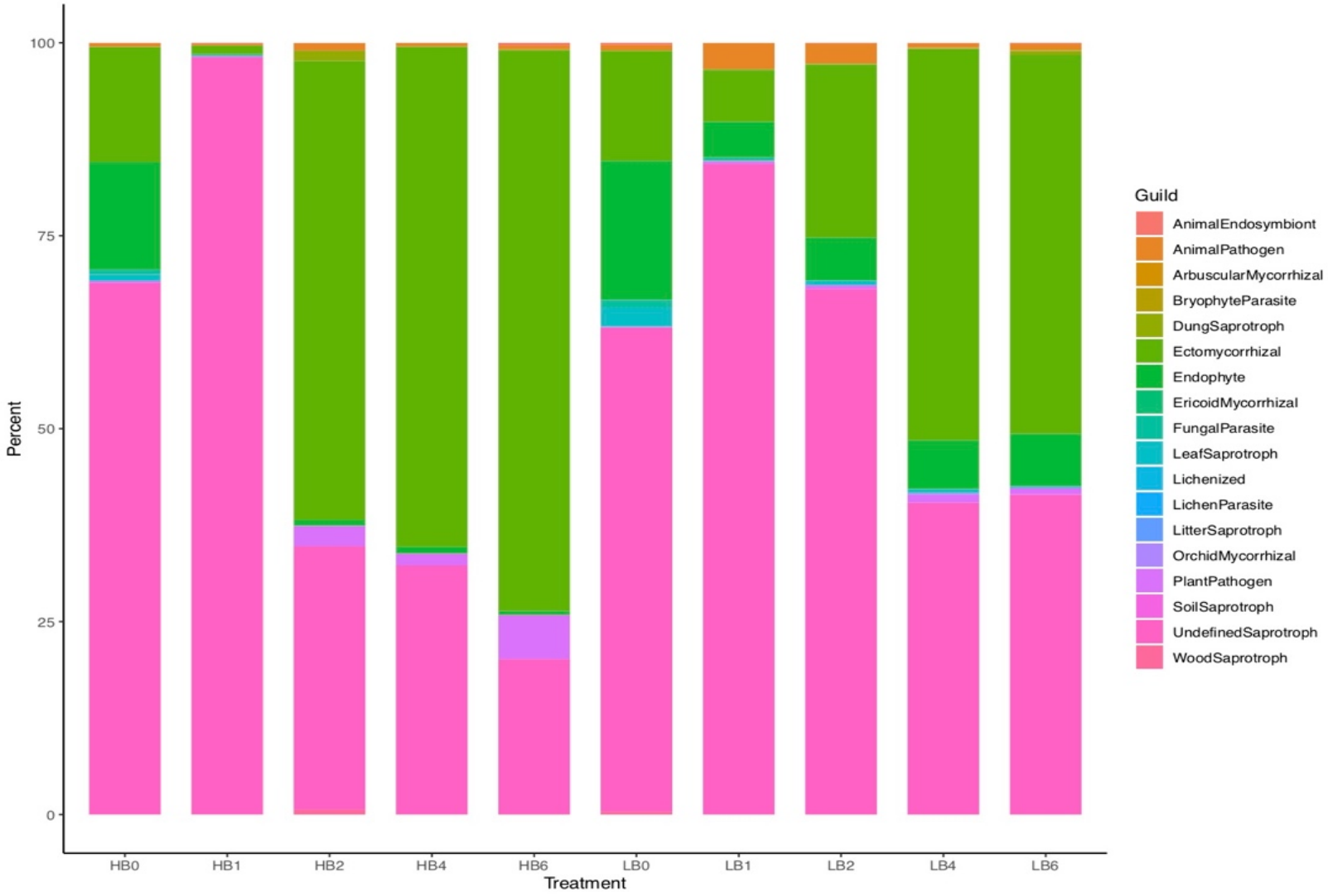

Figure C 4 Drought data

U.S. Drought data for Deschutes County, Oregon, USA. D0 – Abnormally dry; D1- Moderate drought; D2- Severe drought; D3- Extreme drought; Exceptional drought. Data and figure acquired from the National Integrated Drought Information System (NIDIS) www.drought.gov. (June of each year)

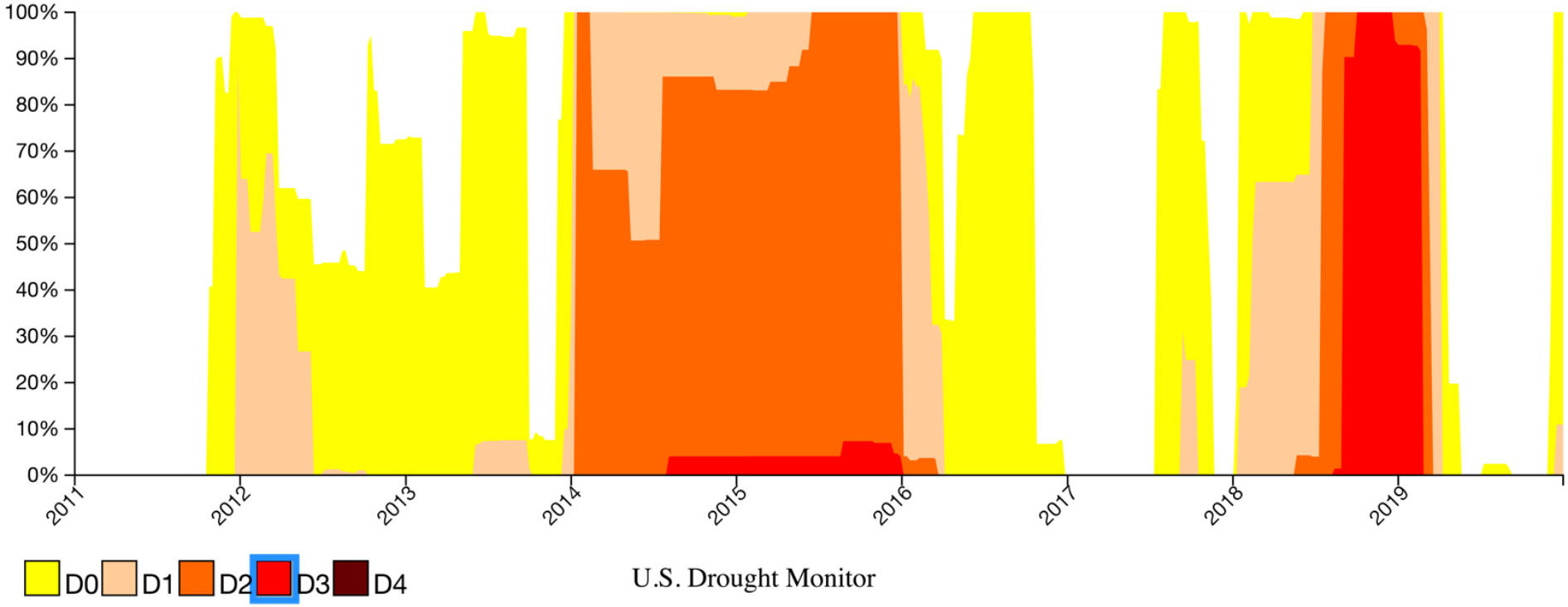

Table C 1 High burn bacterial indicator taxon analysis results

Group T0 #sps. 1277			
	stat	p.value	
Otu004718	0.532	0.044 *	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Actinomycetales_unclassified(98);
Otu000749	0.949	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Acidicapsa(100);Acidicapsa_unclassified(100);
Otu000823	0.548	0.034 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Acidipila(100);Acidipila_unclassified(100);
Otu000579	0.892	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Acidobacteria_Gp1_unclassified(100);Acidobacteria_Gp1_unclassified(100);
Otu000659	0.889	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Acidobacteria_Gp1_unclassified(100);Acidobacteria_Gp1_unclassified(100);
Otu000081	0.882	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Acidobacteria_Gp1_unclassified(100);Acidobacteria_Gp1_unclassified(100);
Otu000626	0.879	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Acidobacteria_Gp1_unclassified(100);Acidobacteria_Gp1_unclassified(100);
Otu000540	0.865	0.002 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Acidobacteria_Gp1_unclassified(100);Acidobacteria_Gp1_unclassified(100);
Otu000734	0.837	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Acidobacteria_Gp1_unclassified(100);Acidobacteria_Gp1_unclassified(100);
Otu002089	0.775	0.002 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Acidobacteria_Gp1_unclassified(100);Acidobacteria_Gp1_unclassified(100);
Otu003435	0.775	0.002 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Acidobacteria_Gp1_unclassified(100);Acidobacteria_Gp1_unclassified(100);
Otu000645	0.773	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Acidobacteria_Gp1_unclassified(100);Acidobacteria_Gp1_unclassified(100);
Otu001280	0.773	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Acidobacteria_Gp1_unclassified(100);Acidobacteria_Gp1_unclassified(100);
Otu002135	0.707	0.002 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Acidobacteria_Gp1_unclassified(100);Acidobacteria_Gp1_unclassified(100);
Otu003121	0.707	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Acidobacteria_Gp1_unclassified(100);Acidobacteria_Gp1_unclassified(100);
Otu002346	0.632	0.006 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Acidobacteria_Gp1_unclassified(100);Acidobacteria_Gp1_unclassified(100);
Otu002078	0.941	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Acidobacterium(100);Acidobacterium_unclassified(100);
Otu005622	0.548	0.027 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Candidatus_Koribacter(100);Candidatus_Koribacter_unclassified(100);
Otu003906	0.707	0.002 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Edaphobacter(100);Edaphobacter_unclassified(100);
Otu000220	0.881	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Gp1(100);Gp1_unclassified(100);
Otu000527	0.858	0.002 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Gp1(100);Gp1_unclassified(100);
Otu000320	0.793	0.002 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Gp1(100);Gp1_unclassified(100);
Otu000671	0.768	0.003 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Gp1(100);Gp1_unclassified(100);
Otu001255	0.749	0.005 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Gp1(100);Gp1_unclassified(100);
Otu004285	0.707	0.002 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Gp1(100);Gp1_unclassified(100);
Otu000457	0.700	0.006 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Gp1(100);Gp1_unclassified(100);

Otu003981	0.632	0.006 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Gp1(100);Gp1_unclassified(100);
Otu000860	0.548	0.028 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Gp1(100);Gp1_unclassified(100);
Otu000465	0.961	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Granulicella(100);Granulicella_unclassified(100);
Otu000100	0.959	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Granulicella(100);Granulicella_unclassified(100);
Otu001573	0.946	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Granulicella(100);Granulicella_unclassified(100);
Otu003509	0.894	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Granulicella(100);Granulicella_unclassified(100);
Otu001116	0.875	0.003 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Granulicella(100);Granulicella_unclassified(100);
Otu001201	0.775	0.002 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Granulicella(100);Granulicella_unclassified(100);
Otu001972	0.739	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Granulicella(100);Granulicella_unclassified(100);
Otu001268	0.706	0.003 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Granulicella(100);Granulicella_unclassified(100);
Otu001492	0.680	0.005 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Granulicella(100);Granulicella_unclassified(100);
Otu003568	0.632	0.005 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Granulicella(100);Granulicella_unclassified(100);
Otu004456	0.632	0.009 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Granulicella(100);Granulicella_unclassified(100);
Otu002798	0.545	0.027 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Granulicella(100);Granulicella_unclassified(100);
Otu003089	0.541	0.031 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Granulicella(100);Granulicella_unclassified(100);
Otu003581	0.533	0.029 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Granulicella(100);Granulicella_unclassified(100);
Otu002833	0.532	0.049 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Granulicella(100);Granulicella_unclassified(100);
Otu000239	0.840	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Terriglobus(100);Terriglobus_unclassified(100);
Otu002858	0.912	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp10(100);Gp10(100);Gp10_unclassified(100);
Otu004157	0.624	0.009 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp10(100);Gp10(100);Gp10_unclassified(100);
Otu003759	0.837	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp12(100);Gp12(100);Gp12_unclassified(100);
Otu005011	0.632	0.004 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp12(100);Gp12(100);Gp12_unclassified(100);
Otu003822	0.940	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp13(100);Gp13(100);Gp13_unclassified(100);
Otu002351	0.867	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp13(100);Gp13(100);Gp13_unclassified(100);
Otu003460	0.745	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp16(100);Gp16(100);Gp16_unclassified(100);
Otu005479	0.673	0.007 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp17(100);Gp17(100);Gp17_unclassified(100);
Otu000114	0.918	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp2(100);Gp2(100);Gp2_unclassified(100);
Otu000590	0.892	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp2(100);Gp2(100);Gp2_unclassified(100);
Otu001322	0.872	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp2(100);Gp2(100);Gp2_unclassified(100);

Otu001770	0.823	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp2(100);Gp2(100);Gp2_unclassified(100);
Otu004483	0.798	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp2(100);Gp2(100);Gp2_unclassified(100);
Otu003541	0.775	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp2(100);Gp2(100);Gp2_unclassified(100);
Otu002485	0.763	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp2(100);Gp2(100);Gp2_unclassified(100);
Otu005040	0.688	0.002 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp2(100);Gp2(100);Gp2_unclassified(100);
Otu000889	0.632	0.005 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp2(100);Gp2(100);Gp2_unclassified(100);
Otu001325	0.632	0.004 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp2(100);Gp2(100);Gp2_unclassified(100);
Otu002602	0.632	0.006 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp2(100);Gp2(100);Gp2_unclassified(100);
Otu004685	0.614	0.007 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp2(100);Gp2(100);Gp2_unclassified(100);
Otu000267	0.479	0.046 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp2(100);Gp2(100);Gp2_unclassified(100);
Otu000654	0.894	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Acidobacteria_Gp3_unclassified(100);Acidobacteria_Gp3_unclassified(100);
Otu002270	0.894	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Acidobacteria_Gp3_unclassified(100);Acidobacteria_Gp3_unclassified(100);
Otu000782	0.865	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Acidobacteria_Gp3_unclassified(100);Acidobacteria_Gp3_unclassified(100);
Otu001618	0.739	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Acidobacteria_Gp3_unclassified(100);Acidobacteria_Gp3_unclassified(100);
Otu004587	0.707	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Acidobacteria_Gp3_unclassified(100);Acidobacteria_Gp3_unclassified(100);
Otu003142	0.629	0.011 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Acidobacteria_Gp3_unclassified(100);Acidobacteria_Gp3_unclassified(100);
Otu002283	0.606	0.025 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Acidobacteria_Gp3_unclassified(100);Acidobacteria_Gp3_unclassified(100);
Otu001999	0.849	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Candidatus_Solibacter(100);Candidatus_Solibacter_unclassified(100);
Otu003546	0.695	0.002 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Candidatus_Solibacter(100);Candidatus_Solibacter_unclassified(100);
Otu001704	0.632	0.006 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Candidatus_Solibacter(100);Candidatus_Solibacter_unclassified(100);
Otu001476	0.989	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu001828	0.969	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu001924	0.949	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu001613	0.946	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu001645	0.946	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu000154	0.944	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu001217	0.937	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu000799	0.930	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu000841	0.921	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);

Otu000704	0.908	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu001590	0.894	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu000072	0.893	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu000541	0.892	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu001964	0.891	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu000431	0.885	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu001553	0.878	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu000795	0.874	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu002747	0.872	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu004757	0.863	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu002236	0.858	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu001577	0.844	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu002069	0.837	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu001607	0.828	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu002203	0.816	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu003412	0.798	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu001219	0.794	0.002 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu004147	0.772	0.003 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu003551	0.768	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu001552	0.747	0.005 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu001130	0.707	0.003 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu004773	0.707	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu004030	0.679	0.002 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu003765	0.678	0.002 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu002755	0.632	0.006 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu003915	0.632	0.006 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu003983	0.632	0.005 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu004159	0.632	0.006 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu004545	0.632	0.004 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);

Otu004940	0.632	0.012 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu002401	0.624	0.009 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu004264	0.548	0.034 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu001825	0.830	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp4(100);Acidobacteria_Gp4_unclassified(100);Acidobacteria_Gp4_unclassified(100);
Otu004580	0.765	0.003 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp4(100);Acidobacteria_Gp4_unclassified(100);Acidobacteria_Gp4_unclassified(100);
Otu001399	0.725	0.004 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp4(100);Acidobacteria_Gp4_unclassified(100);Acidobacteria_Gp4_unclassified(100);
Otu002900	0.675	0.008 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp4(100);Acidobacteria_Gp4_unclassified(100);Acidobacteria_Gp4_unclassified(100);
Otu005248	0.775	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp4(100);Aridibacter(100);Aridibacter_unclassified(100);
Otu001231	0.724	0.005 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp4(100);Aridibacter(100);Aridibacter_unclassified(100);
Otu005081	0.681	0.006 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp4(100);Aridibacter(100);Aridibacter_unclassified(100);
Otu000727	0.962	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp4(100);Gp4(100);Gp4_unclassified(100);
Otu001246	0.845	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp4(100);Gp4(100);Gp4_unclassified(100);
Otu002043	0.812	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp4(100);Gp4(100);Gp4_unclassified(100);
Otu001052	0.676	0.017 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp4(100);Gp4(100);Gp4_unclassified(100);
Otu003512	0.632	0.005 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp4(100);Gp4(100);Gp4_unclassified(100);
Otu001938	0.548	0.043 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp4(100);Gp4(100);Gp4_unclassified(100);
Otu004945	0.548	0.034 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp4(100);Gp4(100);Gp4_unclassified(100);
Otu002684	0.566	0.013 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp6(100);Gp6(100);Gp6_unclassified(100);
Otu001224	0.923	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp7(100);Gp7(100);Gp7_unclassified(100);
Otu004186	0.783	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp7(100);Gp7(100);Gp7_unclassified(100);
Otu003804	0.741	0.003 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp7(100);Gp7(100);Gp7_unclassified(100);
Otu003201	0.707	0.002 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp7(100);Gp7(100);Gp7_unclassified(100);
Otu002424	0.630	0.010 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp7(100);Gp7(100);Gp7_unclassified(100);
Otu004714	0.615	0.008 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp7(100);Gp7(100);Gp7_unclassified(100);
Otu001617	0.767	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_unclassified(100);Acidobacteria_unclassified(100);Acidobacteria_unclassified(100);
Otu002890	0.867	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria_unclassified(100);Actinobacteria_unclassified(100);Actinobacteria_unclassified(100);
Otu005116	0.738	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Acidimicrobiales(100);Acidimicrobiales_unclassified(100);
Otu001365	0.710	0.005 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Acidimicrobiales(100);Acidimicrobiales_unclassified(100);
Otu001404	0.632	0.005 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Acidimicrobiales(100);Acidimicrobiales_unclassified(100);

Otu004349	0.632	0.005 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Acidimicrobiales(100);Acidimicrobiales_unclassified(100);
Otu001179	0.804	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Acidimicrobiales(100);Acidimicrobiales_unclassified(80);
Otu001370	0.707	0.002 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Acidimicrobiales(100);Acidimicrobineae_incertae_sedis(100);Aciditerrimonas(100);
Otu004633	0.667	0.009 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Acidimicrobiales(100);Acidimicrobineae_incertae_sedis(100);Aciditerrimonas(100);
Otu004382	0.804	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Acidimicrobiales(100);Acidimicrobineae_incertae_sedis(94);Aciditerrimonas(94);
Otu004735	0.689	0.004 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Acidimicrobiales(100);Acidimicrobineae_incertae_sedis(97);Aciditerrimonas(97);
Otu001294	0.849	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinobacteria_unclassified(100);Actinobacteria_unclassified(100);
Otu001481	0.788	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinobacteria_unclassified(100);Actinobacteria_unclassified(100);
Otu001046	0.775	0.002 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinobacteria_unclassified(100);Actinobacteria_unclassified(100);
Otu002182	0.707	0.003 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinobacteria_unclassified(100);Actinobacteria_unclassified(100);
Otu002339	0.655	0.011 *	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinobacteria_unclassified(100);Actinobacteria_unclassified(100);
Otu000830	0.859	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Acidothermaceae(100);Acidothermus(100);
Otu000461	0.871	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Actinomycetales_unclassified(100);
Otu001257	0.828	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Actinomycetales_unclassified(100);
Otu001729	0.761	0.002 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Actinomycetales_unclassified(100);
Otu002111	0.712	0.005 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Actinomycetales_unclassified(73);
Otu000759	0.865	0.002 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Actinomycetales_unclassified(86);
Otu001544	0.690	0.006 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Actinomycetales_unclassified(99);
Otu001621	0.805	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Catenulisporaceae(100);Catenulispora(100);
Otu002598	0.702	0.006 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Cryptosporangiaceae(100);Cryptosporangium(100);
Otu000769	0.819	0.002 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Cryptosporangiaceae(100);Jatrophihabitans(100);
Otu002134	0.703	0.008 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Cryptosporangiaceae(100);Jatrophihabitans(100);
Otu003287	0.541	0.037 *	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Geodermatophilaceae(100);Geodermatophilus(91);
Otu002481	0.599	0.043 *	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Geodermatophilaceae(100);Modestobacter(100);
Otu002826	0.713	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Micromonosporaceae(100);
Otu004151	0.703	0.003 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Micromonosporaceae(100);Virgisporangium(100);
Otu000119	0.974	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Mycobacteriaceae(100);Mycobacterium(100);
Otu001161	0.754	0.006 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Pseudonocardiaceae(100);
Otu001377	0.802	0.002 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Pseudonocardiaceae(100);Actinomycetospora(100);

Otu002477	0.707	0.017 *	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Pseudonocardiaceae(100);Actinophytocola(99);
Otu002759	0.580	0.031 *	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Streptomycetaceae(100);
Otu000550	0.745	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Thermomonosporaceae(100);Actinoallomurus(99);
Otu004196	0.630	0.025 *	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Gaiellales(100);Gaiellaceae(100);Gaiella(100);
Otu002246	0.707	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Rubrobacterales(100);Rubrobacteraceae(100);Rubrobacter(100);
Otu000898	0.927	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Solirubrobacterales(100);Conexibacteraceae(100);Conexibacter(100);
Otu002315	0.733	0.004 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Solirubrobacterales(100);Conexibacteraceae(100);Conexibacter(100);
Otu002677	0.717	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Solirubrobacterales(100);Conexibacteraceae(100);Conexibacter(100);
Otu003555	0.668	0.003 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Solirubrobacterales(100);Conexibacteraceae(72);Conexibacter(72);
Otu002198	0.677	0.005 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Solirubrobacterales(100);Conexibacteraceae(94);Conexibacter(94);
Otu001996	0.840	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Solirubrobacterales(100);Conexibacteraceae(98);Conexibacter(98);
Otu002523	0.548	0.038 *	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Solirubrobacterales(100);Solirubrobacterales_unclassified(97);
Otu001106	0.927	0.001 ***	Bacteria(100);Armatimonadetes(100);Armatimonadetes_gp5(100);Armatimonadetes_gp5_unclassified(100);Armatimonadetes_gp5_unclassified(100);
Otu001902	0.921	0.001 ***	Bacteria(100);Armatimonadetes(100);Armatimonadetes_gp5(100);Armatimonadetes_gp5_unclassified(100);Armatimonadetes_gp5_unclassified(100);
Otu002176	0.748	0.002 **	Bacteria(100);Armatimonadetes(100);Armatimonadetes_gp5(100);Armatimonadetes_gp5_unclassified(100);Armatimonadetes_gp5_unclassified(100);
Otu004123	0.707	0.002 **	Bacteria(100);Armatimonadetes(100);Armatimonadetes_gp5(100);Armatimonadetes_gp5_unclassified(100);Armatimonadetes_gp5_unclassified(100);
Otu002954	0.683	0.002 **	Bacteria(100);Armatimonadetes(100);Armatimonadetes_gp5(100);Armatimonadetes_gp5_unclassified(100);Armatimonadetes_gp5_unclassified(100);
Otu002715	0.632	0.006 **	Bacteria(100);Armatimonadetes(100);Armatimonadetes_gp5(100);Armatimonadetes_gp5_unclassified(100);Armatimonadetes_gp5_unclassified(100);
Otu004004	0.632	0.006 **	Bacteria(100);Armatimonadetes(100);Armatimonadetes_gp5(100);Armatimonadetes_gp5_unclassified(100);Armatimonadetes_gp5_unclassified(100);
Otu002997	0.898	0.001 ***	Bacteria(100);Armatimonadetes(100);Armatimonadia(100);Armatimonadales(100);Armatimonadaceae(100);Armatimonas/Armatimonadetes_gp1(100);
Otu002130	0.855	0.001 ***	Bacteria(100);Armatimonadetes(100);Armatimonadia(100);Armatimonadales(100);Armatimonadaceae(100);Armatimonas/Armatimonadetes_gp1(100);
Otu003214	0.828	0.002 **	Bacteria(100);Armatimonadetes(100);Armatimonadia(100);Armatimonadales(100);Armatimonadaceae(100);Armatimonas/Armatimonadetes_gp1(100);
Otu005132	0.707	0.001 ***	Bacteria(100);Armatimonadetes(100);Armatimonadia(100);Armatimonadales(100);Armatimonadaceae(100);Armatimonas/Armatimonadetes_gp1(100);
Otu004758	0.682	0.006 **	Bacteria(100);Armatimonadetes(100);Armatimonadia(100);Armatimonadales(100);Armatimonadaceae(100);Armatimonas/Armatimonadetes_gp1(100);
Otu003143	0.651	0.004 **	Bacteria(100);Armatimonadetes(100);Armatimonadia(100);Armatimonadales(100);Armatimonadaceae(100);Armatimonas/Armatimonadetes_gp1(100);
Otu003872	0.632	0.002 **	Bacteria(100);Armatimonadetes(100);Armatimonadia(100);Armatimonadales(100);Armatimonadaceae(100);Armatimonas/Armatimonadetes_gp1(100);

Otu002764	0.894	0.001 ***	Bacteria(100);Armatimonadetes(100);Chthonomonadetes(100);Chthonomonadales(100);Chthonomonadaceae(100);Chthonomonas/Armatimonadetes_gp3(100);
Otu005216	0.894	0.001 ***	Bacteria(100);Armatimonadetes(100);Chthonomonadetes(100);Chthonomonadales(100);Chthonomonadaceae(100);Chthonomonas/Armatimonadetes_gp3(100);
Otu002195	0.845	0.002 **	Bacteria(100);Armatimonadetes(100);Chthonomonadetes(100);Chthonomonadales(100);Chthonomonadaceae(100);Chthonomonas/Armatimonadetes_gp3(100);
Otu002732	0.831	0.002 **	Bacteria(100);Armatimonadetes(100);Chthonomonadetes(100);Chthonomonadales(100);Chthonomonadaceae(100);Chthonomonas/Armatimonadetes_gp3(100);
Otu004209	0.764	0.001 ***	Bacteria(100);Armatimonadetes(100);Chthonomonadetes(100);Chthonomonadales(100);Chthonomonadaceae(100);Chthonomonas/Armatimonadetes_gp3(100);
Otu005127	0.711	0.003 **	Bacteria(100);Armatimonadetes(100);Chthonomonadetes(100);Chthonomonadales(100);Chthonomonadaceae(100);Chthonomonas/Armatimonadetes_gp3(100);
Otu002917	0.681	0.007 **	Bacteria(100);Armatimonadetes(100);Chthonomonadetes(100);Chthonomonadales(100);Chthonomonadaceae(100);Chthonomonas/Armatimonadetes_gp3(100);
Otu000157	0.987	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001124	0.979	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu000130	0.977	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003137	0.971	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001271	0.949	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003158	0.949	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004886	0.949	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004974	0.949	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001711	0.942	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002730	0.940	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003594	0.940	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003184	0.940	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002513	0.938	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001834	0.937	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001548	0.937	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001002	0.934	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001436	0.932	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu000691	0.926	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001175	0.925	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003383	0.925	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);

Otu001011	0.923	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu000836	0.918	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001914	0.916	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001640	0.904	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001135	0.900	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003710	0.900	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002617	0.894	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004357	0.894	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001586	0.891	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002367	0.887	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001917	0.885	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003270	0.883	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004051	0.882	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002530	0.881	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004348	0.880	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004225	0.875	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003182	0.875	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001858	0.874	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004018	0.870	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001333	0.870	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003018	0.864	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005617	0.861	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001676	0.859	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001146	0.854	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002453	0.852	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001879	0.848	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001469	0.844	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002435	0.843	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001234	0.843	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);

Otu002191	0.840	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001128	0.837	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001209	0.837	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001239	0.837	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002599	0.837	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002726	0.837	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002963	0.837	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003168	0.837	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003537	0.837	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005279	0.837	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001180	0.836	0.012 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002635	0.833	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003787	0.833	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001881	0.829	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003917	0.826	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003005	0.826	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003711	0.823	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002253	0.822	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001930	0.817	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005425	0.817	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002795	0.816	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001912	0.815	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003597	0.813	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu000657	0.812	0.007 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003032	0.809	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003060	0.807	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003065	0.803	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005582	0.799	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002304	0.791	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);

Otu001846	0.786	0.003 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001841	0.775	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002655	0.775	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003626	0.775	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003703	0.775	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003960	0.775	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004215	0.775	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004294	0.775	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004317	0.775	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004477	0.775	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004598	0.775	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004754	0.775	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005242	0.775	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005245	0.775	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005286	0.775	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005550	0.775	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002943	0.772	0.005 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001954	0.770	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004439	0.770	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004720	0.768	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003366	0.762	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002212	0.762	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004627	0.762	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005027	0.762	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001042	0.762	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004956	0.761	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004679	0.761	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001125	0.761	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003726	0.756	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);

Otu002619	0.756	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005142	0.754	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002552	0.753	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002786	0.752	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004819	0.751	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002916	0.751	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004041	0.748	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002840	0.745	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004943	0.744	0.004 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004178	0.742	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005472	0.739	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005393	0.737	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002248	0.735	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003607	0.733	0.004 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003237	0.730	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002669	0.730	0.003 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003527	0.723	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003953	0.723	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004586	0.719	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003414	0.718	0.004 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002443	0.716	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004702	0.716	0.004 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002012	0.715	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004234	0.712	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005427	0.711	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002760	0.709	0.006 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001867	0.707	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001940	0.707	0.003 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002386	0.707	0.003 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);

Otu003190	0.707	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004005	0.707	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004083	0.707	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004645	0.707	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005067	0.707	0.003 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005112	0.707	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005408	0.707	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004398	0.704	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002661	0.701	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004925	0.699	0.004 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002818	0.698	0.006 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005205	0.696	0.003 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005046	0.695	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004763	0.695	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001058	0.693	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002610	0.692	0.004 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001222	0.691	0.016 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004286	0.691	0.007 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004788	0.691	0.004 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003567	0.688	0.003 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003059	0.686	0.006 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001599	0.685	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003977	0.685	0.003 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004101	0.684	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005483	0.681	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003390	0.678	0.004 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004177	0.674	0.004 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002929	0.673	0.011 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003976	0.671	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);

Otu003820	0.668	0.007 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003197	0.667	0.004 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003565	0.667	0.003 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004424	0.665	0.005 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002219	0.664	0.037 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005522	0.663	0.005 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004579	0.660	0.011 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002205	0.660	0.009 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002258	0.656	0.012 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003286	0.655	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002672	0.643	0.019 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004379	0.643	0.014 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005371	0.636	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003490	0.634	0.021 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001876	0.632	0.003 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002228	0.632	0.004 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002388	0.632	0.006 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003483	0.632	0.004 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003573	0.632	0.007 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003912	0.632	0.031 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004104	0.632	0.009 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004316	0.632	0.007 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004387	0.632	0.005 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004440	0.632	0.010 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004644	0.632	0.008 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004843	0.632	0.005 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005073	0.632	0.006 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005258	0.632	0.006 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005507	0.632	0.006 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);

Otu005581	0.632	0.005 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003454	0.629	0.011 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003367	0.626	0.022 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003434	0.626	0.004 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003350	0.626	0.013 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003781	0.625	0.005 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005442	0.623	0.010 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004862	0.614	0.006 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004734	0.611	0.007 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004881	0.609	0.009 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004436	0.606	0.009 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004854	0.606	0.006 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005606	0.606	0.011 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003869	0.598	0.019 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002868	0.595	0.013 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004638	0.593	0.006 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003651	0.592	0.019 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005206	0.591	0.014 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005496	0.584	0.013 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005139	0.583	0.013 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003354	0.580	0.007 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004505	0.577	0.033 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004955	0.575	0.028 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003665	0.574	0.040 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003041	0.574	0.029 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004521	0.572	0.035 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005536	0.563	0.017 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003842	0.561	0.032 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002355	0.548	0.026 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);

Otu003004	0.548	0.038 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003188	0.548	0.029 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003692	0.548	0.028 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003974	0.548	0.032 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004553	0.548	0.034 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005030	0.548	0.023 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005195	0.548	0.036 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005328	0.548	0.023 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005351	0.548	0.035 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005471	0.548	0.028 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003498	0.541	0.021 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004179	0.535	0.036 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002299	0.532	0.040 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005539	0.528	0.031 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003979	0.512	0.047 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005187	0.507	0.046 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001081	0.859	0.002 **	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu002287	0.829	0.001 ***	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu002385	0.797	0.001 ***	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu003882	0.781	0.003 **	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu001911	0.775	0.002 **	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu003834	0.775	0.001 ***	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu003353	0.771	0.002 **	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu002645	0.771	0.001 ***	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu003641	0.770	0.001 ***	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu002836	0.758	0.001 ***	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu002725	0.746	0.001 ***	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu003393	0.743	0.022 *	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu002405	0.740	0.002 **	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);

Otu003251	0.736	0.006 **	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu002289	0.712	0.003 **	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu002613	0.707	0.003 **	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu002810	0.707	0.003 **	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu002950	0.707	0.002 **	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu003002	0.707	0.002 **	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu003877	0.707	0.003 **	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu003991	0.671	0.008 **	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu004291	0.651	0.009 **	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu005099	0.632	0.002 **	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu005202	0.632	0.007 **	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu000998	0.631	0.018 *	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu004503	0.610	0.019 *	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu002028	0.548	0.032 *	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu003239	0.548	0.034 *	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu003232	0.767	0.001 ***	Bacteria(100);Bacteroidetes(100);Bacteroidia(100);Bacteroidales(100);Bacteroidales_unclassified(100);
Otu000147	0.962	0.001 ***	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Chryseolinea(100);
Otu001870	0.834	0.001 ***	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Chryseolinea(100);
Otu000809	0.705	0.001 ***	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Chryseolinea(100);
Otu005304	0.632	0.004 **	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Chryseolinea(100);
Otu001169	0.630	0.023 *	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Chryseolinea(100);
Otu003505	0.614	0.005 **	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Chryseolinea(100);
Otu001866	0.548	0.035 *	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Chryseolinea(100);
Otu001012	0.830	0.001 ***	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Chryseolinea(98);
Otu001683	0.707	0.002 **	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Cytophagaceae(100);Cytophaga(100);
Otu003118	0.613	0.034 *	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Cytophagaceae(100);Cytophaga(100);
Otu000439	0.946	0.001 ***	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Cytophagaceae(88);
Otu001831	0.622	0.019 *	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Cytophagales_unclassified(100);
Otu002144	0.548	0.029 *	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Cytophagales_unclassified(100);

Otu005252	0.620	0.018 *	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Cytophagales_unclassified(92);
Otu000507	0.804	0.003 **	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Cytophagales_unclassified(98);
Otu000416	0.906	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu003652	0.824	0.002 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu005085	0.822	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu000910	0.791	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu003446	0.775	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu003472	0.741	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu004323	0.707	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu000685	0.707	0.013 *	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu000930	0.705	0.006 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu002221	0.703	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu004634	0.689	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu003316	0.670	0.009 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu005368	0.670	0.003 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu003234	0.663	0.009 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu005567	0.635	0.028 *	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu001033	0.623	0.015 *	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu003818	0.617	0.013 *	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu001494	0.546	0.036 *	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu003559	0.894	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Ferruginibacter(100);
Otu003379	0.855	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Ferruginibacter(100);
Otu002167	0.817	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Ferruginibacter(100);
Otu001454	0.687	0.002 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Ferruginibacter(100);
Otu003728	0.632	0.004 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Ferruginibacter(100);
Otu005022	0.616	0.012 *	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Ferruginibacter(100);
Otu002138	0.548	0.028 *	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Ferruginibacter(100);
Otu000363	0.977	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Flavihumibacter(100);
Otu002517	0.650	0.006 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Flavisolibacter(100);

Otu001594	0.632	0.008 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Flavisolibacter(61);
Otu000600	0.999	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Flavitalea(70);
Otu000660	0.820	0.002 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Flavitalea(70);
Otu002856	0.768	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Parafilimonas(100);
Otu002459	0.626	0.015 *	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Parafilimonas(100);
Otu004501	0.665	0.009 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Segetibacter(100);
Otu003695	0.588	0.023 *	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(65);
Otu004494	0.683	0.003 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(92);
Otu001730	0.676	0.006 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);
Otu001990	0.763	0.002 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Mucilaginibacter(100);
Otu004600	0.733	0.003 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Mucilaginibacter(100);
Otu001974	0.731	0.027 *	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Mucilaginibacter(100);
Otu001151	0.696	0.006 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Mucilaginibacter(100);
Otu002076	0.632	0.006 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Mucilaginibacter(100);
Otu004081	0.548	0.031 *	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Mucilaginibacter(100);
Otu005289	0.514	0.050 *	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Mucilaginibacter(100);
Otu005530	0.827	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriales_unclassified(100);
Otu000474	0.834	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriales_unclassified(77);
Otu004434	0.795	0.002 **	Bacteria(100);BRC1(100);BRC1_unclassified(100);BRC1_unclassified(100);BRC1_unclassified(100);
Otu000744	0.936	0.001 ***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu001609	0.933	0.001 ***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu000625	0.932	0.001 ***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu002605	0.919	0.001 ***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu001485	0.888	0.001 ***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu002934	0.885	0.001 ***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu000714	0.864	0.001 ***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu000344	0.862	0.001 ***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);

Otu001191	0.835	0.001	***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu001085	0.832	0.002	**	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu001029	0.823	0.001	***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu000949	0.818	0.001	***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu002296	0.816	0.001	***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu002243	0.803	0.001	***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu003675	0.798	0.001	***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu001215	0.792	0.001	***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu002026	0.790	0.001	***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu002970	0.778	0.003	**	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu002504	0.775	0.001	***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu004951	0.775	0.001	***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu003655	0.767	0.001	***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu002370	0.763	0.001	***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu001620	0.762	0.003	**	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu004088	0.760	0.001	***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu002867	0.756	0.001	***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu003933	0.738	0.003	**	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu001796	0.713	0.008	**	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu002781	0.707	0.002	**	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu004750	0.707	0.003	**	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu005476	0.707	0.002	**	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu005570	0.707	0.003	**	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);

Otu003668	0.661	0.012 *	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu005287	0.657	0.003 **	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu002332	0.632	0.008 **	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu003886	0.632	0.004 **	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu005149	0.618	0.009 **	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu004138	0.616	0.007 **	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu003683	0.548	0.028 *	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu004506	0.548	0.043 *	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu005499	0.548	0.033 *	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu002347	0.536	0.036 *	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu001722	0.784	0.006 **	Bacteria(100);candidate_division_WPS-2(100);candidate_division_WPS-2_unclassified(100);candidate_division_WPS-2_unclassified(100);candidate_division_WPS-2_unclassified(100);
Otu000293	0.770	0.004 **	Bacteria(100);candidate_division_WPS-2(100);candidate_division_WPS-2_unclassified(100);candidate_division_WPS-2_unclassified(100);candidate_division_WPS-2_unclassified(100);
Otu000672	0.717	0.007 **	Bacteria(100);candidate_division_WPS-2(100);candidate_division_WPS-2_unclassified(100);candidate_division_WPS-2_unclassified(100);candidate_division_WPS-2_unclassified(100);
Otu004669	0.632	0.006 **	Bacteria(100);candidate_division_WPS-2(100);candidate_division_WPS-2_unclassified(100);candidate_division_WPS-2_unclassified(100);candidate_division_WPS-2_unclassified(100);
Otu003133	0.592	0.016 *	Bacteria(100);candidate_division_WPS-2(100);candidate_division_WPS-2_unclassified(100);candidate_division_WPS-2_unclassified(100);candidate_division_WPS-2_unclassified(100);
Otu002853	1.000	0.001 ***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu001688	0.894	0.001 ***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu001851	0.894	0.001 ***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu001728	0.889	0.001 ***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu000961	0.881	0.001 ***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu001578	0.866	0.001 ***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu002428	0.837	0.001 ***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004090	0.837	0.001 ***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);

Otu005047	0.837	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu001922	0.834	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004162	0.825	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu003324	0.818	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu002907	0.806	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004909	0.793	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu003815	0.793	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004787	0.791	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu003130	0.787	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu003921	0.775	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004028	0.775	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004303	0.775	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu005128	0.775	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu005243	0.772	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu002588	0.767	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu001850	0.762	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu002662	0.762	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu002568	0.755	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu003497	0.755	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004902	0.751	0.004	**	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004801	0.747	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu003506	0.746	0.002	**	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004044	0.744	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);

Otu002414	0.742	0.003	**	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu002426	0.736	0.002	**	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu001992	0.736	0.002	**	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu003716	0.734	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu003432	0.719	0.003	**	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu005404	0.709	0.002	**	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu001326	0.707	0.002	**	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu003484	0.707	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004665	0.707	0.003	**	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004700	0.707	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004715	0.707	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu005323	0.707	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004404	0.701	0.004	**	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004614	0.698	0.003	**	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu002181	0.698	0.005	**	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu001826	0.690	0.003	**	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu002295	0.689	0.002	**	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu005435	0.687	0.001	***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004628	0.685	0.003	**	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004265	0.684	0.006	**	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu002829	0.684	0.004	**	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004775	0.679	0.003	**	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu003955	0.663	0.002	**	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);

Otu002109	0.652	0.011	* Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu001214	0.632	0.005	** Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004009	0.632	0.004	** Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004425	0.632	0.006	** Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004550	0.632	0.004	** Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004939	0.632	0.008	** Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu005517	0.632	0.005	** Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004510	0.623	0.010	** Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu002123	0.622	0.022	* Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu003566	0.621	0.013	* Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu001827	0.620	0.040	* Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004573	0.616	0.010	** Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu003175	0.604	0.003	** Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu001686	0.594	0.012	* Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004056	0.573	0.033	* Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004059	0.566	0.021	* Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu001988	0.548	0.033	* Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu002905	0.548	0.033	* Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu003255	0.548	0.034	* Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu003526	0.548	0.031	* Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu002507	0.621	0.012	* Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Chlamydiales_unclassified(100);
Otu003107	0.610	0.033	* Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Chlamydiales_unclassified(100);
Otu000835	0.742	0.013	* Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Chlamydiales_unclassified(76);
Otu002641	0.749	0.018	* Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Chlamydiales_unclassified(89);

Otu003914	0.632	0.005 **	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Chlamydiales_unclassified(97);
Otu003186	0.548	0.031 *	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Chlamydiales_unclassified(99);
Otu004304	0.764	0.001 ***	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);
Otu002603	0.735	0.003 **	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);
Otu005086	0.707	0.002 **	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);
Otu004698	0.675	0.007 **	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);
Otu003585	0.613	0.011 *	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);
Otu004677	0.576	0.040 *	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);
Otu004378	0.548	0.027 *	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);
Otu004487	0.537	0.034 *	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);
Otu004243	0.775	0.001 ***	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);Neochlamydia(100);
Otu002016	0.748	0.007 **	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);Neochlamydia(100);
Otu002959	0.561	0.028 *	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);Neochlamydia(100);
Otu003428	0.520	0.048 *	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);Neochlamydia(100);
Otu003889	0.552	0.032 *	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);Neochlamydia(85);
Otu004741	0.582	0.017 *	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);Neochlamydia(98);
Otu003257	0.748	0.001 ***	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);Parachlamydia(100);
Otu005473	0.689	0.002 **	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);Parachlamydia(100);
Otu003318	0.632	0.010 **	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);Parachlamydia(100);
Otu004799	0.666	0.007 **	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);Parachlamydia(80);
Otu001802	0.842	0.002 **	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);Parachlamydia(87);
Otu002579	0.689	0.006 **	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(100);Parachlamydia(92);
Otu000350	0.888	0.001 ***	Bacteria(100);Chloroflexi(100);Anaerolineae(100);Anaerolineales(100);Anaerolineaceae(100);
Otu001747	0.771	0.003 **	Bacteria(100);Chloroflexi(100);Anaerolineae(100);Anaerolineales(100);Anaerolineaceae(100);
Otu002539	0.661	0.010 **	Bacteria(100);Chloroflexi(100);Anaerolineae(100);Anaerolineales(100);Anaerolineaceae(100);
Otu003426	0.650	0.001 ***	Bacteria(100);Chloroflexi(100);Anaerolineae(100);Anaerolineales(100);Anaerolineaceae(100);
Otu002273	0.548	0.031 *	Bacteria(100);Chloroflexi(100);Anaerolineae(100);Anaerolineales(100);Anaerolineaceae(100);
Otu002652	0.542	0.030 *	Bacteria(100);Chloroflexi(100);Anaerolineae(100);Anaerolineales(100);Anaerolineaceae(100);
Otu001378	0.857	0.001 ***	Bacteria(100);Chloroflexi(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);

Otu003363	0.775	0.001 ***	Bacteria(100);Chloroflexi(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);
Otu001753	0.765	0.003 **	Bacteria(100);Chloroflexi(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);
Otu000490	0.725	0.010 **	Bacteria(100);Chloroflexi(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);
Otu003082	0.704	0.001 ***	Bacteria(100);Chloroflexi(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);
Otu002819	0.696	0.002 **	Bacteria(100);Chloroflexi(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);
Otu001718	0.686	0.007 **	Bacteria(100);Chloroflexi(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);
Otu003766	0.613	0.018 *	Bacteria(100);Chloroflexi(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);
Otu003624	0.548	0.024 *	Bacteria(100);Chloroflexi(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);
Otu001139	0.949	0.001 ***	Bacteria(100);Chloroflexi(100);Ktedonobacteria(100);Ktedonobacterales(100);Ktedonobacteraceae(100);Ktedonobacter(100);
Otu002091	0.949	0.001 ***	Bacteria(100);Chloroflexi(100);Ktedonobacteria(100);Ktedonobacterales(100);Ktedonobacteraceae(100);Ktedonobacter(100);
Otu000278	0.765	0.002 **	Bacteria(100);Chloroflexi(100);Ktedonobacteria(100);Ktedonobacterales(100);Ktedonobacteraceae(100);Ktedonobacter(100);
Otu002420	0.569	0.040 *	Bacteria(100);Chloroflexi(100);Ktedonobacteria(100);Ktedonobacterales(100);Ktedonobacteraceae(100);Ktedonobacter(100);
Otu001950	0.758	0.003 **	Bacteria(100);Chloroflexi(100);Ktedonobacteria(100);Ktedonobacterales(100);Ktedonobacteraceae(99);Ktedonobacter(99);
Otu000661	0.716	0.007 **	Bacteria(100);Firmicutes(100);Clostridia(100);Clostridia_unclassified(100);Clostridia_unclassified(100);
Otu001786	0.807	0.004 **	Bacteria(100);Firmicutes(100);Clostridia(100);Clostridiales(100);Clostridiaceae_1(100);Clostridium_sensu_stricto(100);
Otu002516	0.798	0.001 ***	Bacteria(100);Firmicutes(100);Clostridia(100);Clostridiales(100);Peptococcaceae_1(100);Desulfosporosinus(100);
Otu002550	0.719	0.001 ***	Bacteria(100);Firmicutes(100);Firmicutes_unclassified(100);Firmicutes_unclassified(100);Firmicutes_unclassified(100);
Otu004173	0.632	0.005 **	Bacteria(100);Firmicutes(100);Firmicutes_unclassified(100);Firmicutes_unclassified(100);Firmicutes_unclassified(100);
Otu004191	0.548	0.031 *	Bacteria(100);Firmicutes(100);Firmicutes_unclassified(100);Firmicutes_unclassified(100);Firmicutes_unclassified(100);
Otu005448	0.548	0.034 *	Bacteria(100);Firmicutes(100);Firmicutes_unclassified(100);Firmicutes_unclassified(100);Firmicutes_unclassified(100);
Otu000651	0.929	0.001 ***	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu001884	0.862	0.001 ***	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu003709	0.837	0.001 ***	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu003905	0.837	0.001 ***	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu004066	0.837	0.001 ***	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu000874	0.825	0.001 ***	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu004027	0.824	0.001 ***	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu004292	0.814	0.001 ***	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu005059	0.800	0.001 ***	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);

Otu003747	0.775	0.001 ***	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu001685	0.734	0.005 **	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu001669	0.707	0.001 ***	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu005101	0.707	0.002 **	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu004471	0.698	0.003 **	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu001583	0.680	0.032 *	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu003147	0.658	0.007 **	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu005044	0.632	0.003 **	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu005054	0.632	0.005 **	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu004014	0.625	0.013 *	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu004524	0.624	0.006 **	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu005063	0.583	0.008 **	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu004963	0.548	0.023 *	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu004190	0.530	0.038 *	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu005244	0.512	0.043 *	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu004333	0.624	0.014 *	Bacteria(100);Latescibacteria(100);Latescibacteria_unclassified(100);Latescibacteria_unclassified(100);Latescibacteria_unclassified(100);
Otu005144	0.526	0.027 *	Bacteria(100);Latescibacteria(100);Latescibacteria_unclassified(100);Latescibacteria_unclassified(100);Latescibacteria_unclassified(100);
Otu004978	0.775	0.001 ***	Bacteria(100);Microgenomates(100);Microgenomates_unclassified(100);Microgenomates_unclassified(100);Microgenomates_unclassified(100);
Otu001090	0.976	0.001 ***	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu003752	0.921	0.001 ***	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu001381	0.897	0.001 ***	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu001909	0.879	0.001 ***	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu001806	0.837	0.001 ***	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu003735	0.837	0.001 ***	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu003346	0.820	0.001 ***	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu004045	0.727	0.002 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu003577	0.708	0.001 ***	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu003531	0.707	0.001 ***	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu003794	0.707	0.002 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);

Otu004976	0.707	0.001 ***	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu003171	0.705	0.002 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu003773	0.702	0.002 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu004080	0.695	0.013 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu002873	0.694	0.005 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu005327	0.686	0.004 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu001889	0.684	0.002 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu005133	0.649	0.008 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu004618	0.634	0.021 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu002883	0.632	0.005 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu002946	0.632	0.010 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu004797	0.632	0.006 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu004811	0.632	0.005 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu004927	0.632	0.004 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu004989	0.632	0.005 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu005326	0.632	0.006 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu005380	0.632	0.005 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu004164	0.629	0.013 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu003016	0.628	0.007 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu003530	0.628	0.008 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu005621	0.620	0.012 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu003783	0.616	0.015 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu004278	0.615	0.006 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu005219	0.601	0.016 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu002989	0.587	0.011 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu005343	0.585	0.025 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu003952	0.577	0.023 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu004167	0.576	0.027 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu003925	0.568	0.029 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);

Otu005090	0.548	0.027 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu005400	0.548	0.034 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu005573	0.548	0.026 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu005500	0.820	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Candidatus_Brocadiales(100);Candidatus_Brocadiaceae(100);
Otu004447	0.622	0.005 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Candidatus_Brocadiales(100);Candidatus_Brocadiaceae(100);
Otu003078	0.959	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu002461	0.914	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu003560	0.906	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu002062	0.903	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu003263	0.876	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu001041	0.856	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu001358	0.854	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu003155	0.839	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu002623	0.837	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu002269	0.835	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu004657	0.821	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu002261	0.807	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu001001	0.802	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu001022	0.791	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu003119	0.775	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu003253	0.775	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu003385	0.775	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu004458	0.775	0.002 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu005271	0.775	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu002452	0.765	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu002894	0.755	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu002004	0.754	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu003647	0.738	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu005523	0.735	0.002 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);

Otu004479	0.727	0.002 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu002700	0.725	0.006 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu002402	0.721	0.004 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu005362	0.714	0.002 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu004344	0.707	0.003 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu004468	0.707	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu004649	0.707	0.002 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu004154	0.707	0.008 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu003077	0.701	0.002 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu004903	0.693	0.003 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu002494	0.691	0.024 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu001805	0.685	0.026 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu002823	0.684	0.003 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu002978	0.684	0.002 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu003144	0.683	0.003 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu005337	0.671	0.004 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu004680	0.670	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu005401	0.654	0.023 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu003151	0.650	0.027 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu002220	0.642	0.007 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu004727	0.632	0.007 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu005106	0.632	0.021 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu004827	0.629	0.008 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu003322	0.619	0.013 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu003592	0.595	0.008 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu005208	0.593	0.020 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu003507	0.588	0.020 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu004391	0.587	0.022 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu004413	0.572	0.024 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);

Otu002825	0.548	0.034 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu004144	0.530	0.033 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu004491	0.526	0.028 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu004820	0.775	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Aquisphaera(100);
Otu003543	0.770	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Aquisphaera(100);
Otu004643	0.882	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Aquisphaera(55);
Otu001589	0.872	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Blastopirellula(100);
Otu002284	0.930	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Blastopirellula(88);
Otu003686	0.704	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Gemmata(100);
Otu004810	0.687	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Gemmata(100);
Otu004888	0.640	0.010 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Gemmata(100);
Otu004946	0.548	0.028 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Gemmata(100);
Otu003538	0.729	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Gemmata(57);
Otu003998	0.707	0.003 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Gemmata(66);
Otu003628	0.632	0.007 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Gemmata(92);
Otu003303	0.784	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Pirellula(100);
Otu005616	0.650	0.009 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Pirellula(100);
Otu001240	0.948	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Pirellula(99);
Otu001642	0.826	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Schlesneria(100);
Otu001260	0.887	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Singulisphaera(100);
Otu001603	0.829	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Singulisphaera(100);
Otu004595	0.707	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Singulisphaera(100);
Otu003406	0.696	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Singulisphaera(100);
Otu004500	0.690	0.003 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Singulisphaera(100);
Otu005451	0.635	0.006 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Singulisphaera(100);
Otu003625	0.700	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Singulisphaera(90);
Otu005347	0.632	0.006 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Singulisphaera(90);
Otu000929	0.912	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Singulisphaera(95);
Otu002857	0.631	0.011 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Singulisphaera(95);

Otu003349	0.790	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Singulisphaera(96);
Otu002611	0.743	0.002 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Singulisphaera(96);
Otu002353	0.710	0.002 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Thermogutta(100);
Otu002696	0.931	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Zavarzinella(100);
Otu001307	0.828	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Zavarzinella(100);
Otu003685	0.775	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Zavarzinella(100);
Otu004915	0.775	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Zavarzinella(100);
Otu002003	0.727	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Zavarzinella(100);
Otu004849	0.707	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Zavarzinella(100);
Otu004938	0.693	0.002 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Zavarzinella(100);
Otu002634	0.647	0.005 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Zavarzinella(100);
Otu005069	0.701	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Zavarzinella(69);
Otu004125	0.548	0.024 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Zavarzinella(82);
Otu002813	0.687	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Zavarzinella(83);
Otu001659	0.886	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Zavarzinella(89);
Otu002821	0.930	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Zavarzinella(90);
Otu005178	0.588	0.013 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Zavarzinella(96);
Otu003751	0.767	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Zavarzinella(99);
Otu005200	0.673	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Zavarzinella(99);
Otu001206	0.854	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetia_unclassified(100);Planctomycetia_unclassified(100);
Otu005121	0.632	0.005 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetia_unclassified(100);Planctomycetia_unclassified(100);
Otu004408	0.626	0.003 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetia_unclassified(100);Planctomycetia_unclassified(100);
Otu003851	0.632	0.007 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_incertae_sedis(100);Rhizomicrobium(100);
Otu003250	0.548	0.033 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_incertae_sedis(100);Rhizomicrobium(100);
Otu003812	0.949	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu000460	0.877	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu004748	0.874	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu001829	0.873	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu002841	0.864	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);

Otu004046	0.858	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu003544	0.845	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu002002	0.837	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu003108	0.837	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu002430	0.819	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu003473	0.811	0.003 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu004463	0.807	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu002961	0.789	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu003010	0.786	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu005064	0.714	0.004 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu003090	0.712	0.011 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu001556	0.707	0.002 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu003622	0.707	0.003 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu003589	0.705	0.005 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu004402	0.693	0.002 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu001421	0.683	0.004 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu003874	0.678	0.004 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu003689	0.632	0.002 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu005552	0.632	0.003 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu004571	0.622	0.004 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu002449	0.618	0.011 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu002589	0.611	0.035 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu004015	0.548	0.037 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Caulobacterales(100);Caulobacteraceae(100);
Otu004367	0.757	0.002 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Caulobacterales(100);Caulobacteraceae(100);Brevundimonas(91);
Otu003301	0.934	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Caulobacterales(100);Caulobacteraceae(100);Phenylobacterium(99);
Otu005043	0.541	0.030 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Caulobacterales(100);Caulobacteraceae(100);Phenylobacterium(99);
Otu001942	0.917	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Hyphomicrobiaceae(100);Pedomicrobium(100);
Otu005487	0.760	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Hyphomicrobiaceae(100);Pedomicrobium(100);
Otu003590	0.748	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Hyphomicrobiaceae(100);Rhodoplanes(100);

Otu005185	0.548	0.028 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Methylocystaceae(93);
Otu003489	0.534	0.040 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiaceae(100);Rhizobium(100);
Otu001877	0.729	0.023 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiaceae(63);Ciceribacter(63);
Otu003596	0.773	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_incertae_sedis(99);Bauldia(97);
Otu001890	0.961	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(100);
Otu002487	0.879	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(100);
Otu000300	0.872	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(100);
Otu000699	0.846	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(100);
Otu002862	0.832	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(100);
Otu001799	0.784	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(100);
Otu001648	0.783	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(100);
Otu004531	0.721	0.002 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(100);
Otu003310	0.707	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(100);
Otu000264	0.706	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(100);
Otu005221	0.691	0.004 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(100);
Otu005005	0.632	0.006 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(100);
Otu005325	0.581	0.015 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(58);
Otu003942	0.765	0.002 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(95);
Otu005096	0.677	0.002 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(97);
Otu003833	0.676	0.014 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(98);
Otu004082	0.827	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(99);
Otu001661	0.660	0.036 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(99);
Otu001368	0.837	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Roseiarcaceae(100);Roseiarcus(100);
Otu003736	0.823	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Roseiarcaceae(100);Roseiarcus(100);
Otu002094	0.764	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Roseiarcaceae(99);Roseiarcus(99);
Otu002693	0.733	0.006 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Xanthobacteraceae(100);Pseudolabrys(100);
Otu003887	0.807	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Xanthobacteraceae(70);Pseudolabrys(70);
Otu004435	0.804	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Xanthobacteraceae(97);Pseudolabrys(96);
Otu003047	0.865	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Xanthobacteraceae(99);Pseudolabrys(99);

Otu000161	0.967	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);
Otu001369	0.936	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);
Otu001705	0.924	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);
Otu000292	0.919	0.002 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);
Otu003846	0.871	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);
Otu001131	0.823	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);
Otu001182	0.802	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);
Otu002702	0.632	0.006 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);
Otu003528	0.632	0.006 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);
Otu003739	0.632	0.007 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);
Otu002216	0.548	0.028 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);
Otu003807	0.548	0.026 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);
Otu004796	0.548	0.034 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);
Otu004995	0.548	0.034 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);
Otu004990	0.509	0.040 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);
Otu000834	0.850	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);Acidisoma(100);
Otu004183	0.763	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);Acidisoma(100);
Otu002974	0.632	0.006 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);Acidisoma(100);
Otu004288	0.548	0.024 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);Acidisoma(100);
Otu000233	0.852	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);Acidisoma(51);
Otu002404	0.548	0.034 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);Acidisoma(98);
Otu002909	0.837	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);Acidisoma(99);
Otu002438	0.671	0.024 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Reyranella(100);
Otu001727	0.915	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillaceae(100);
Otu000971	0.888	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillaceae(100);
Otu000819	0.887	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillaceae(100);
Otu001519	0.853	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillaceae(100);
Otu001074	0.817	0.003 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillaceae(100);
Otu001479	0.743	0.010 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillaceae(100);

Otu003035	0.707	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillaceae(100);
Otu001778	0.693	0.002 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillaceae(100);
Otu004272	0.646	0.011 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillaceae(100);
Otu005240	0.632	0.007 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillaceae(100);
Otu005515	0.541	0.040 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillaceae(100);
Otu005231	0.527	0.047 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillaceae(100);
Otu005452	0.753	0.003 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillaceae(65);
Otu002984	0.671	0.006 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillaceae(75);
Otu001460	0.894	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillaceae(81);
Otu001332	0.834	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillaceae(91);
Otu005414	0.707	0.002 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillaceae(97);
Otu002612	0.621	0.005 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillaceae(97);
Otu000839	0.991	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillales_unclassified(100);
Otu000873	0.862	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillales_unclassified(100);
Otu000534	0.800	0.002 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillales_unclassified(100);
Otu001830	0.776	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillales_unclassified(100);
Otu002811	0.710	0.011 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillales_unclassified(100);
Otu004143	0.716	0.002 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillales_unclassified(58);
Otu005468	0.707	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillales_unclassified(85);
Otu002802	0.828	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillales_unclassified(92);
Otu004035	0.710	0.015 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Sphingomonadales(100);Sphingomonadaceae(100);Novosphingobium(98);
Otu000117	0.967	0.001 ***	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu001306	0.948	0.001 ***	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu000888	0.927	0.001 ***	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu001506	0.852	0.001 ***	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu001651	0.816	0.001 ***	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu001852	0.816	0.001 ***	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu002165	0.815	0.001 ***	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu000740	0.808	0.001 ***	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);

Otu002597	0.786	0.002 **	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu005291	0.775	0.001 ***	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu000410	0.745	0.008 **	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu002968	0.717	0.002 **	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu004133	0.682	0.002 **	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu002471	0.701	0.003 **	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Burkholderiales(100);Burkholderiaceae(100);Burkholderia(100);
Otu003105	0.632	0.007 **	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Burkholderiales(100);Burkholderiaceae(98);Burkholderia(98);
Otu002178	0.700	0.004 **	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Burkholderiales(100);Burkholderiales_unclassified(100);
Otu000608	0.885	0.001 ***	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Burkholderiales(100);Burkholderiales_unclassified(99);
Otu004340	0.694	0.005 **	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Burkholderiales(100);Oxalobacteraceae(100);
Otu003661	0.616	0.012 *	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Burkholderiales(100);Oxalobacteraceae(100);Collimonas(93);
Otu003603	0.920	0.001 ***	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Rhodocyclales(100);Rhodocyclaceae(100);
Otu001376	0.836	0.003 **	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Rhodocyclales(100);Rhodocyclaceae(100);
Otu003447	0.746	0.001 ***	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Rhodocyclales(100);Rhodocyclaceae(100);
Otu000735	0.745	0.006 **	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Rhodocyclales(100);Rhodocyclaceae(100);
Otu001795	0.630	0.019 *	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Rhodocyclales(100);Rhodocyclaceae(100);
Otu000907	0.986	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Bdellovibrionales(100);Bdellovibrionaceae(100);Vampirovibrio(100);
Otu001615	0.890	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Bdellovibrionales(100);Bdellovibrionaceae(100);Vampirovibrio(100);
Otu000743	0.854	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Bdellovibrionales(100);Bdellovibrionaceae(100);Vampirovibrio(100);
Otu001741	0.837	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Bdellovibrionales(100);Bdellovibrionaceae(100);Vampirovibrio(100);
Otu002609	0.766	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Bdellovibrionales(100);Bdellovibrionaceae(100);Vampirovibrio(100);
Otu001195	0.726	0.004 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Bdellovibrionales(100);Bdellovibrionaceae(100);Vampirovibrio(100);
Otu004973	0.548	0.033 *	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Bdellovibrionales(100);Bdellovibrionaceae(100);Vampirovibrio(100);
Otu003800	0.886	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Deltaproteobacteria_unclassified(100);Deltaproteobacteria_unclassified(100);
Otu001539	0.808	0.002 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Deltaproteobacteria_unclassified(100);Deltaproteobacteria_unclassified(100);
Otu004765	0.804	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Deltaproteobacteria_unclassified(100);Deltaproteobacteria_unclassified(100);
Otu001373	0.799	0.005 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Deltaproteobacteria_unclassified(100);Deltaproteobacteria_unclassified(100);
Otu001388	0.757	0.004 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Deltaproteobacteria_unclassified(100);Deltaproteobacteria_unclassified(100);
Otu004850	0.701	0.002 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Deltaproteobacteria_unclassified(100);Deltaproteobacteria_unclassified(100);

Otu002541	0.629	0.007 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Deltaproteobacteria_unclassified(100);Deltaproteobacteria_unclassified(100);
Otu002846	0.548	0.022 *	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Deltaproteobacteria_unclassified(100);Deltaproteobacteria_unclassified(100);
Otu002988	0.707	0.003 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Cystobacteraceae(100);
Otu000663	0.894	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Cystobacteraceae(100);Anaeromyxobacter(100);
Otu005335	0.591	0.020 *	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Cystobacteraceae(100);Anaeromyxobacter(100);
Otu003571	0.928	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Cystobacteraceae(90);Anaeromyxobacter(90);
Otu005598	0.540	0.031 *	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Cystobacteraceae(98);Anaeromyxobacter(98);
Otu005061	0.632	0.006 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Haliangiaceae(97);Haliangium(97);
Otu005098	0.615	0.013 *	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Kofleriaceae(100);Kofleria(100);
Otu001874	0.783	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Labilitrichaceae(100);Labilithrix(100);
Otu005033	0.680	0.006 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Labilitrichaceae(100);Labilithrix(100);
Otu002083	0.632	0.006 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Labilitrichaceae(100);Labilithrix(100);
Otu004671	0.632	0.012 *	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Labilitrichaceae(100);Labilithrix(100);
Otu005450	0.707	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcaceae(99);Myxococcus(71);
Otu001937	0.924	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu003922	0.894	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu001185	0.892	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu004131	0.876	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu003219	0.876	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu002488	0.858	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu004135	0.822	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu002991	0.796	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu004236	0.775	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu003391	0.765	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu003725	0.746	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu001453	0.734	0.004 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu001196	0.733	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu003397	0.732	0.004 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu002448	0.708	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);

Otu002774	0.689	0.005 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu002581	0.671	0.002 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu002335	0.656	0.020 *	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu003347	0.632	0.006 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu004394	0.632	0.007 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu005109	0.632	0.005 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu001692	0.614	0.006 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu001339	0.564	0.023 *	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu004403	0.562	0.025 *	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu002593	0.907	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(78);
Otu002604	0.819	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(90);
Otu002902	0.773	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(95);
Otu004369	0.786	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(96);
Otu003640	0.786	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(96);
Otu003236	0.789	0.003 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(97);
Otu003549	0.815	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(99);
Otu003748	0.537	0.046 *	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(99);
Otu001703	0.894	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Polyangiaceae(100);
Otu002913	0.837	0.002 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Polyangiaceae(100);
Otu003732	0.804	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Polyangiaceae(100);
Otu001663	0.797	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Polyangiaceae(100);
Otu003062	0.731	0.002 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Polyangiaceae(100);
Otu005107	0.688	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Polyangiaceae(100);
Otu002286	0.636	0.006 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Polyangiaceae(100);
Otu004794	0.632	0.003 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Polyangiaceae(100);
Otu005058	0.575	0.017 *	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Polyangiaceae(100);
Otu004950	0.548	0.029 *	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Polyangiaceae(100);
Otu005296	0.632	0.005 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Polyangiaceae(100);Chondromyces(97);
Otu003750	0.720	0.003 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Polyangiaceae(70);

Otu003208	0.654	0.010 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Polyangiaceae(98);
Otu001908	0.801	0.003 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Polyangiaceae(99);
Otu003387	0.586	0.008 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_incertae_sedis(100);Candidatus_Carsonella(100);
Otu000256	0.959	0.001 ***	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu004315	0.849	0.001 ***	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu000286	0.838	0.003 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu002785	0.828	0.001 ***	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu001475	0.825	0.001 ***	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu005352	0.804	0.001 ***	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu002131	0.775	0.002 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu002660	0.775	0.002 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu001968	0.768	0.001 ***	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu002703	0.743	0.002 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu004866	0.709	0.008 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu003081	0.708	0.014 *	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu003706	0.707	0.001 ***	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu004642	0.707	0.003 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu003634	0.696	0.002 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu004150	0.689	0.004 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu002720	0.688	0.007 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu003857	0.632	0.004 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu003927	0.632	0.005 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu004010	0.574	0.019 *	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu001814	0.548	0.036 *	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);

Otu005001	0.548	0.042 *	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu005475	0.548	0.035 *	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu005533	0.548	0.024 *	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu004747	0.544	0.040 *	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu005210	0.530	0.037 *	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu003180	0.709	0.006 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Legionellales(100);Coxiellaceae(100);Aquicella(100);
Otu003160	0.625	0.017 *	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Legionellales(100);Coxiellaceae(100);Aquicella(100);
Otu003510	0.596	0.015 *	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Legionellales(100);Coxiellaceae(100);Aquicella(100);
Otu004012	0.548	0.029 *	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Legionellales(100);Legionellaceae(100);Legionella(100);
Otu000991	0.715	0.006 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Xanthomonadales(100);Sinobacteraceae(100);
Otu005331	0.618	0.007 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Xanthomonadales(100);Sinobacteraceae(100);
Otu000951	0.904	0.001 ***	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Xanthomonadales(100);Sinobacteraceae(100);Nevskia(100);
Otu000906	0.594	0.012 *	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Xanthomonadales(100);Sinobacteraceae(100);Povalibacter(100);
Otu002521	0.868	0.001 ***	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Xanthomonadales(100);Sinobacteraceae(100);Povalibacter(59);
Otu005283	0.696	0.002 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Xanthomonadales(100);Sinobacteraceae(100);Povalibacter(69);
Otu001980	0.837	0.001 ***	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Xanthomonadales(100);Sinobacteraceae(100);Solimonas(74);
Otu003141	0.894	0.001 ***	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Xanthomonadales(100);Sinobacteraceae(100);Steroidobacter(100);
Otu004118	0.745	0.001 ***	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Xanthomonadales(100);Sinobacteraceae(100);Steroidobacter(100);
Otu005355	0.707	0.003 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Xanthomonadales(100);Sinobacteraceae(100);Steroidobacter(100);
Otu000912	0.824	0.001 ***	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Xanthomonadales(100);Sinobacteraceae(98);
Otu000097	0.989	0.001 ***	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Xanthomonadales(100);Xanthomonadales_unclassified(84);
Otu000592	0.988	0.001 ***	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu002027	0.984	0.001 ***	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu000602	0.919	0.001 ***	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu001163	0.908	0.001 ***	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu004293	0.894	0.001 ***	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu002483	0.889	0.001 ***	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu001273	0.874	0.001 ***	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);

Otu003370	0.869	0.001 ***	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu001497	0.834	0.001 ***	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu004900	0.830	0.001 ***	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu002529	0.812	0.001 ***	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu005545	0.812	0.001 ***	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu000402	0.797	0.002 **	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu004499	0.775	0.002 **	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu004894	0.775	0.001 ***	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu003411	0.772	0.001 ***	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu005396	0.765	0.001 ***	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu004052	0.742	0.001 ***	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu004884	0.742	0.001 ***	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu003178	0.719	0.005 **	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu002375	0.707	0.001 ***	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu003480	0.707	0.002 **	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu005588	0.707	0.002 **	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu003007	0.694	0.008 **	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu005164	0.691	0.001 ***	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu004260	0.685	0.002 **	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu005564	0.674	0.005 **	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu003561	0.662	0.007 **	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu005490	0.645	0.005 **	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu004911	0.632	0.004 **	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu005498	0.632	0.005 **	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu004119	0.612	0.033 *	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu004872	0.607	0.014 *	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu005512	0.590	0.024 *	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu004975	0.571	0.026 *	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu004932	0.548	0.033 *	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);

Otu005071	0.548	0.031 *	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu005395	0.548	0.035 *	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu005613	0.548	0.035 *	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu005312	0.543	0.040 *	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu004770	0.679	0.001 ***	Bacteria(100);Verrucomicrobia(100);Opitutae(100);Opitutales(100);Opitutaceae(100);Alterococcus(100);
Otu003892	0.620	0.013 *	Bacteria(100);Verrucomicrobia(100);Opitutae(100);Opitutales(100);Opitutaceae(100);Alterococcus(100);
Otu001493	0.856	0.001 ***	Bacteria(100);Verrucomicrobia(100);Opitutae(100);Opitutales(100);Opitutaceae(100);Opitutus(100);
Otu003112	0.779	0.014 *	Bacteria(100);Verrucomicrobia(100);Opitutae(100);Opitutales(100);Opitutaceae(100);Opitutus(100);
Otu004852	0.711	0.001 ***	Bacteria(100);Verrucomicrobia(100);Opitutae(100);Opitutales(100);Opitutaceae(100);Opitutus(100);
Otu002390	0.702	0.004 **	Bacteria(100);Verrucomicrobia(100);Opitutae(100);Opitutales(100);Opitutaceae(100);Opitutus(100);
Otu002255	0.695	0.008 **	Bacteria(100);Verrucomicrobia(100);Opitutae(100);Opitutales(100);Opitutaceae(100);Opitutus(100);
Otu003817	0.686	0.011 *	Bacteria(100);Verrucomicrobia(100);Opitutae(100);Opitutales(100);Opitutaceae(100);Opitutus(100);
Otu001448	0.632	0.006 **	Bacteria(100);Verrucomicrobia(100);Opitutae(100);Opitutales(100);Opitutaceae(100);Opitutus(100);
Otu005029	0.618	0.006 **	Bacteria(100);Verrucomicrobia(100);Opitutae(100);Opitutales(100);Opitutaceae(100);Opitutus(100);
Otu000469	0.981	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu000181	0.979	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu000302	0.960	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu000519	0.960	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu003176	0.947	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu001097	0.939	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu001174	0.935	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu001111	0.932	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu002030	0.928	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu001123	0.919	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu001065	0.872	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu001409	0.840	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu000484	0.835	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu001354	0.835	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu000849	0.821	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);

Otu001773	0.815	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu001439	0.807	0.002 **	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu000585	0.806	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu001637	0.802	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu003272	0.798	0.002 **	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu000781	0.789	0.002 **	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu000255	0.787	0.013 *	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu004021	0.786	0.003 **	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu004589	0.775	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu001207	0.766	0.007 **	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu001982	0.762	0.002 **	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu001120	0.740	0.002 **	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu004648	0.740	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu003365	0.707	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu002573	0.698	0.003 **	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu004306	0.684	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu004445	0.683	0.004 **	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu003327	0.632	0.006 **	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu004779	0.632	0.006 **	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu003893	0.600	0.008 **	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu002896	0.548	0.031 *	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu004511	0.545	0.048 *	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu003378	0.536	0.044 *	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu000184	0.811	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Terrimicrobium(100);Terrimicrobium_unclassified(100);
Otu001302	0.563	0.017 *	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Terrimicrobium(100);Terrimicrobium_unclassified(100);
Otu004227	0.548	0.031 *	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Terrimicrobium(100);Terrimicrobium_unclassified(100);
Otu001021	0.935	0.001 ***	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu002939	0.927	0.001 ***	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu001929	0.914	0.001 ***	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);

Otu002679	0.905	0.001 ***	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu001351	0.894	0.001 ***	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu000532	0.881	0.002 **	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu001451	0.844	0.001 ***	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu001456	0.837	0.001 ***	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu003126	0.837	0.001 ***	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu001282	0.827	0.001 ***	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu002964	0.824	0.002 **	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu000549	0.821	0.001 ***	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu003306	0.815	0.001 ***	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu000872	0.811	0.002 **	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu003437	0.803	0.001 ***	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu005372	0.800	0.001 ***	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu001457	0.783	0.003 **	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu005397	0.775	0.001 ***	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu001746	0.770	0.003 **	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu003861	0.739	0.003 **	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu002499	0.716	0.015 *	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu005481	0.707	0.001 ***	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu003314	0.703	0.003 **	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu004525	0.694	0.005 **	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu005386	0.693	0.003 **	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu003100	0.685	0.006 **	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu005377	0.667	0.004 **	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu002870	0.665	0.005 **	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu002213	0.664	0.008 **	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu004732	0.651	0.025 *	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu002177	0.636	0.006 **	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu005542	0.632	0.003 **	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);

Otu003542	0.607	0.012 *	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu002627	0.598	0.019 *	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu001587	0.548	0.036 *	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu005025	0.548	0.034 *	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu004130	0.507	0.045 *	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu000999	0.874	0.001 ***	Bacteria(100);Verrucomicrobia(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);
Otu001316	0.827	0.006 **	Bacteria(100);Verrucomicrobia(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);
Otu003083	0.761	0.001 ***	Bacteria(100);Verrucomicrobia(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);
Otu002379	0.760	0.002 **	Bacteria(100);Verrucomicrobia(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);
Otu001048	0.740	0.008 **	Bacteria(100);Verrucomicrobia(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);
Otu002754	0.730	0.002 **	Bacteria(100);Verrucomicrobia(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);
Otu005366	0.686	0.002 **	Bacteria(100);Verrucomicrobia(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);
Otu005374	0.607	0.022 *	Bacteria(100);Verrucomicrobia(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);
Otu004637	0.520	0.042 *	Bacteria(100);Verrucomicrobia(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);
Otu004226	0.728	0.004 **	Bacteria(100);Verrucomicrobia(100);Verrucomicrobiae(100);Verrucomicrobiales(100);Verrucomicrobiaceae(100);
Otu002093	0.548	0.037 *	Bacteria(100);Verrucomicrobia(100);Verrucomicrobiae(100);Verrucomicrobiales(100);Verrucomicrobiaceae(100);Luteolibacter(100);
Otu001978	0.876	0.001 ***	Bacteria(100);Verrucomicrobia(100);Verrucomicrobiae(100);Verrucomicrobiales(100);Verrucomicrobiaceae(100);Roseimicrobium(81);

Group T1 #sps. 10

	stat	p.value	
Otu001565	0.823	0.004 **	Bacteria(100);Firmicutes(100);Clostridia(100);Clostridia_unclassified(100);Clostridia_unclassified(100);
Otu000274	0.817	0.011 *	Bacteria(100);Firmicutes(100);Clostridia(100);Clostridiales(100);Clostridiales_unclassified(100);
Otu003909	0.812	0.001 ***	Bacteria(100);Firmicutes(100);Firmicutes_unclassified(100);Firmicutes_unclassified(100);Firmicutes_unclassified(100);
Otu004611	0.803	0.001 ***	Bacteria(100);Firmicutes(100);Bacilli(100);Bacillales(100);Paenibacillaceae_1(57);
Otu000512	0.771	0.021 *	Bacteria(100);Firmicutes(100);Bacilli(100);Bacillales(100);Paenibacillaceae_1(100);Paenibacillus(100);
Otu000611	0.765	0.044 *	Bacteria(100);Firmicutes(100);Clostridia(100);Clostridia_unclassified(100);Clostridia_unclassified(100);
Otu003578	0.755	0.001 ***	Bacteria(100);Firmicutes(100);Bacilli(100);Bacillales(100);Paenibacillaceae_1(97);
Otu004443	0.728	0.004 **	Bacteria(100);Firmicutes(100);Clostridia(100);Clostridia_unclassified(100);Clostridia_unclassified(100);
Otu003988	0.696	0.023 *	Bacteria(100);Firmicutes(100);Firmicutes_unclassified(100);Firmicutes_unclassified(100);Firmicutes_unclassified(100);

Otu002162	0.667	0.046 *	Bacteria(100);Firmicutes(100);Bacilli(100);Bacillales(100);Bacillales_unclassified(65);

Group T2 #sps. 98

	stat	p.value	
Otu002958	0.888	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp6(100);Gp6(100);Gp6_unclassified(100);
Otu005454	0.608	0.017 *	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Acidimicrobiales(100);Iamiaceae(100);Iamia(100);
Otu004384	0.870	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinobacteria_unclassified(100);Actinobacteria_unclassified(100);
Otu002750	0.763	0.032 *	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinobacteria_unclassified(100);Actinobacteria_unclassified(100);
Otu004238	0.691	0.004 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinobacteria_unclassified(100);Actinobacteria_unclassified(100);
Otu001121	0.948	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Actinomycetales_unclassified(98);
Otu001803	0.936	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Geodermatophilaceae(100);Blastococcus(100);
Otu002633	0.996	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Geodermatophilaceae(100);Geodermatophilus(100);
Otu003170	0.927	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Nocardioidaceae(100);Nocardioides(100);
Otu003173	0.647	0.006 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Nocardioidaceae(100);Nocardioides(100);
Otu005065	0.864	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Solirubrobacterales(100);Conexibacteraceae(100);Conexibacter(100);
Otu003819	0.855	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Solirubrobacterales(100);Conexibacteraceae(100);Conexibacter(100);
Otu001391	0.828	0.003 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Solirubrobacterales(100);Solirubrobacteraceae(100);Solirubrobacter(100);
Otu005432	0.812	0.001 ***	Bacteria(100);Armatimonadetes(100);Armatimonadia(100);Armatimonadales(100);Armatimonadaceae(100);Armatimonas/Armatimonadetes_gp1(100);
Otu001608	0.916	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005419	0.908	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002267	0.903	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu000903	0.849	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003684	0.819	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003903	0.694	0.007 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005088	0.685	0.035 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004522	0.583	0.043 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002766	0.847	0.001 ***	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Cytophagaceae(100);Adhaeribacter(100);
Otu002169	0.972	0.001 ***	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Cytophagaceae(100);Siphonobacter(100);
Otu002624	0.844	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Flavisolibacter(100);

Otu003254	0.817	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Flavisolibacter(100);
Otu005140	0.737	0.003 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Parasegetibacter(100);
Otu001309	0.963	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Pedobacter(100);
Otu000305	0.953	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Pedobacter(100);
Otu000940	0.884	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Pedobacter(100);
Otu003442	0.858	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Pedobacter(100);
Otu000882	0.836	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Pedobacter(100);
Otu002680	0.791	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Pedobacter(100);
Otu005168	0.700	0.007 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Pedobacter(100);
Otu003891	0.787	0.002 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Pedobacter(95);
Otu002532	0.847	0.001 ***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu000764	0.887	0.004 **	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu005169	0.824	0.002 **	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu002482	0.795	0.007 **	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu000665	0.734	0.037 *	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004809	0.686	0.017 *	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004795	0.826	0.001 ***	Bacteria(100);Chloroflexi(100);Thermomicrobia(100);Sphaerobacterales(100);Sphaerobacteraceae(100);
Otu003529	0.855	0.001 ***	Bacteria(100);Firmicutes(100);Bacilli(100);Bacillales(100);Bacillales_unclassified(100);
Otu003677	0.827	0.001 ***	Bacteria(100);Firmicutes(100);Bacilli(100);Bacillales(100);Bacillales_unclassified(100);
Otu005278	0.752	0.002 **	Bacteria(100);Firmicutes(100);Bacilli(100);Bacillales(100);Bacillales_unclassified(100);
Otu003290	0.756	0.002 **	Bacteria(100);Firmicutes(100);Bacilli(100);Bacillales(100);Paenibacillaceae_1(100);Paenibacillus(100);
Otu005367	0.820	0.001 ***	Bacteria(100);Firmicutes(100);Bacilli(100);Bacillales(100);Paenibacillaceae_1(99);
Otu001480	0.905	0.001 ***	Bacteria(100);Firmicutes(100);Clostridia(100);Clostridia_unclassified(100);Clostridia_unclassified(100);
Otu002365	0.927	0.001 ***	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu003371	0.716	0.006 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu005170	0.577	0.029 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu004812	0.558	0.030 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);

Otu001013	0.898	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Caulobacterales(100);Caulobacteraceae(100);
Otu001820	0.945	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Caulobacterales(100);Caulobacteraceae(100);Brevundimonas(100);
Otu003164	0.842	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Caulobacterales(100);Caulobacteraceae(100);Phenylobacterium(100);
Otu004462	0.664	0.014 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Caulobacterales(100);Caulobacteraceae(100);Phenylobacterium(100);
Otu002595	0.905	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Bradyrhizobiaceae(100);
Otu000832	0.975	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Bradyrhizobiaceae(100);Rhodopseudomonas(100);
Otu001087	0.992	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Hyphomicrobiaceae(100);Devosia(100);
Otu002522	0.909	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Methylobacteriaceae(100);Microvirga(100);
Otu005282	0.779	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiaceae(100);Shinella(68);
Otu002185	0.927	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_incertae_sedis(100);Vasilyevaea(100);
Otu001025	0.985	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(100);
Otu004261	0.924	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(100);
Otu004904	0.959	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(82);
Otu001771	0.981	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodobacterales(100);Rhodobacteraceae(100);Rubellimicrobium(100);
Otu003948	0.943	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodobacterales(100);Rhodobacteraceae(100);Rubellimicrobium(100);
Otu000788	0.949	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);Roseomonas(100);
Otu003333	0.900	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);Roseomonas(100);
Otu004554	0.815	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Sphingomonadales(100);Erythrobacteraceae(100);
Otu000436	0.979	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Sphingomonadales(100);Sphingomonadaceae(100);
Otu005204	0.888	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Sphingomonadales(100);Sphingomonadaceae(100);
Otu003206	0.969	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Sphingomonadales(100);Sphingomonadaceae(100);Novosphingobium(100);
Otu000868	0.947	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Sphingomonadales(100);Sphingomonadaceae(100);Parablastomonas(100);
Otu001410	0.938	0.001 ***	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu001935	0.858	0.001 ***	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu005556	0.674	0.004 **	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu002722	0.935	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Bdellovibrionales(100);Bacteriovoracaceae(100);Bacteriovorax(100);
Otu004684	0.849	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Bdellovibrionales(100);Bacteriovoracaceae(100);Peredibacter(100);
Otu002658	0.846	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Bdellovibrionales(100);Bacteriovoracaceae(100);Peredibacter(100);
Otu003793	0.853	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Bdellovibrionales(100);Bdellovibrionaceae(100);Bdellovibrio(100);

Otu005010	0.680	0.020 *	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Bdellovibrionales(100);Bdellovibrionaceae(100);Bdellovibrio(100);
Otu004076	0.812	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Deltaproteobacteria_unclassified(100);Deltaproteobacteria_unclassified(100);
Otu001756	0.841	0.005 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Legionellales(100);Legionellaceae(100);Legionella(100);
Otu002792	0.764	0.003 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Legionellales(100);Legionellaceae(100);Legionella(100);
Otu002262	0.804	0.001 ***	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Pseudomonadales(100);Pseudomonadaceae(100);Cellvibrio(100);
Otu003956	0.920	0.001 ***	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu004893	0.687	0.007 **	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu003006	0.656	0.050 *	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu004244	0.770	0.001 ***	Bacteria(100);Verrucomicrobia(100);Opitutae(100);Opitutales(100);Opitutaceae(100);Opitutus(100);
Otu000960	0.782	0.006 **	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu004847	0.772	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu002431	0.737	0.007 **	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu002326	0.717	0.012 *	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu004569	0.660	0.011 *	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu003867	0.900	0.001 ***	Bacteria(100);Verrucomicrobia(100);Verrucomicrobiae(100);Verrucomicrobiales(100);Verrucomicrobiaceae(100);
Otu004613	0.741	0.012 *	Bacteria(100);Verrucomicrobia(100);Verrucomicrobiae(100);Verrucomicrobiales(100);Verrucomicrobiaceae(100);Luteolibacter(100);
Otu004305	0.799	0.003 **	Bacteria(100);Verrucomicrobia(100);Verrucomicrobiae(100);Verrucomicrobiales(100);Verrucomicrobiaceae(100);Prosthecobacter(100);

Group T4 #sps. 23

	stat	p.value	
Otu000644	0.918	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002478	0.834	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005189	0.792	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004115	0.738	0.030 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003410	0.720	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001633	0.701	0.004 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005072	0.675	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005146	0.645	0.012 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001694	0.792	0.007 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Parasegetibacter(100);

Otu000811	0.735	0.009 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriales_unclassified(100);
Otu001344	0.799	0.001 ***	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu004220	0.628	0.012 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu003177	0.614	0.044 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu001733	0.546	0.042 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu001975	0.924	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu002569	0.723	0.043 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Gemmata(100);
Otu001393	0.840	0.003 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Schlesneria(100);
Otu003729	0.780	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu004203	0.810	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(100);
Otu002571	0.805	0.005 **	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu001389	0.775	0.007 **	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu003838	0.803	0.002 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Legionellales(100);Coxiellaceae(100);Aquicella(100);
Otu001995	0.795	0.022 *	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);

Group T6 #sps. 64

	stat	p.value	
Otu004581	0.700	0.006 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp6(100);Gp6(100);Gp6_unclassified(100);
Otu002864	0.666	0.017 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp6(100);Gp6(100);Gp6_unclassified(100);
Otu004516	0.605	0.047 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp7(100);Gp7(100);Gp7_unclassified(100);
Otu003396	0.748	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Acidimicrobiales(100);Acidimicrobiales_unclassified(100);
Otu001426	0.886	0.002 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Solirubrobacterales(100);Conexibacteraceae(100);Conexibacter(100);
Otu004863	0.583	0.023 *	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Solirubrobacterales(100);Solirubrobacterales_unclassified(97);
Otu004185	0.500	0.043 *	Bacteria(100);Armatimonadetes(100);Armatimonadetes_gp4(100);Armatimonadetes_gp4_unclassified(100);Armatimonadetes_gp4_unclassified(100);
Otu004592	0.856	0.001 ***	Bacteria(100);Armatimonadetes(100);Armatimonadetes_gp5(100);Armatimonadetes_gp5_unclassified(100);Armatimonadetes_gp5_unclassified(100);
Otu003637	0.856	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003384	0.820	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003312	0.784	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);

Otu004172	0.781	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005259	0.751	0.003 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004551	0.741	0.004 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003269	0.722	0.011 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004002	0.715	0.013 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002400	0.707	0.014 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005274	0.707	0.006 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004696	0.705	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003046	0.697	0.020 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004374	0.689	0.014 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002342	0.677	0.007 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002762	0.659	0.010 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002281	0.612	0.013 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003660	0.500	0.048 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002297	0.749	0.006 **	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Cytophagaceae(100);
Otu003218	0.858	0.001 ***	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Ohtaekwangia(100);
Otu004335	0.609	0.024 *	Bacteria(100);Bacteroidetes(100);Flavobacteriia(100);Flavobacteriales(100);Flavobacteriaceae(100);Flavobacterium(100);
Otu005390	0.707	0.002 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Pedobacter(100);
Otu005441	0.759	0.003 **	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu004102	0.500	0.049 *	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu002116	0.735	0.006 **	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu003281	0.648	0.049 *	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu005226	0.612	0.011 *	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu005241	0.585	0.028 *	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu004774	0.568	0.019 *	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu003663	0.756	0.002 **	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Chlamydiales_unclassified(100);
Otu004800	0.612	0.006 **	Bacteria(100);Chloroflexi(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);Chloroflexi_unclassified(100);

Otu003954	0.801	0.001 ***	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu005359	0.793	0.002 **	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu003797	0.780	0.001 ***	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu002957	0.748	0.005 **	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu004127	0.721	0.009 **	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu003129	0.708	0.005 **	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu001017	0.795	0.004 **	Bacteria(100);Ignavibacteriae(100);Ignavibacteria(100);Ignavibacteriales(100);Ignavibacteriaceae(100);
Otu003734	0.676	0.032 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu003172	0.500	0.048 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu003037	0.639	0.004 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu002872	0.729	0.007 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(100);
Otu004991	0.727	0.002 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Sphingomonadales(100);Sphingomonadaceae(100);Sphingomonas(100);
Otu005276	0.667	0.040 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Sphingomonadales(100);Sphingomonadaceae(100);Sphingomonas(96);
Otu003701	0.756	0.010 **	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu004760	0.700	0.004 **	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Rhodocyclales(100);Rhodocyclaceae(100);
Otu004766	0.642	0.049 *	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Haliangiaceae(68);Haliangium(68);
Otu003017	0.848	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu003138	0.774	0.001 ***	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu004518	0.772	0.004 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu003618	0.612	0.007 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu003669	0.742	0.021 *	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_incertae_sedis(100);Candidatus_Carsonella(100);
Otu004839	0.674	0.007 **	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu004668	0.668	0.006 **	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu005277	0.609	0.012 *	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu002923	0.845	0.002 **	Bacteria(100);Verrucomicrobia(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);Verrucomicrobia_unclassified(100);
Otu005529	0.588	0.024 *	Bacteria(100);Verrucomicrobia(100);Verrucomicrobiae(100);Verrucomicrobiales(100);Verrucomicrobiaceae(100);

Table C 2 Low burn bacterial indicator taxon analysis results

Group T1 #sps. 16			
	stat	p.value	
Otu001251	0.806	0.027 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Sphingomonadales(100);Sphingomonadaceae(100);
Otu000788	0.752	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);Roseomonas(100);
Otu000578	0.750	0.009 **	Bacteria(100);Firmicutes(100);Bacilli(100);Bacillales(100);Planococcaceae(100);Lysinibacillus(89);
Otu000265	0.727	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp4(100);Aridibacter(100);Aridibacter_unclassified(100);
Otu004871	0.719	0.002 **	Bacteria(100);Bacteroidetes(100);Flavobacteriia(100);Flavobacteriales(100);Flavobacteriaceae(100);Flavobacterium(100);
Otu000960	0.659	0.010 **	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu002408	0.647	0.020 *	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Mucilaginibacter(100);
Otu002544	0.632	0.004 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu001691	0.631	0.012 *	Bacteria(100);Firmicutes(100);Bacilli(100);Bacillales(100);Planococcaceae(100);Sporosarcina(100);
Otu005591	0.620	0.017 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004490	0.610	0.040 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Acetobacteraceae(100);
Otu003170	0.563	0.025 *	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Nocardioidaceae(100);Nocardioides(100);
Otu003399	0.558	0.016 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Caulobacterales(100);Caulobacteraceae(100);
Otu003330	0.548	0.033 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004476	0.548	0.030 *	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Nocardioidaceae(100);Nocardioides(100);
Otu001769	0.526	0.029 *	Bacteria(100);Firmicutes(100);Bacilli(100);Bacillales(100);Paenibacillaceae_1(68);
Group T2 #sps. 58			
	stat	p.value	
Otu002401	0.863	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu001749	0.845	0.001 ***	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu002823	0.834	0.009 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu003533	0.823	0.001 ***	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu005178	0.816	0.002 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Zavarzinella(96);
Otu002198	0.809	0.005 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Solirubrobacterales(100);Conexibacteraceae(94);Conexibacter(94);

Otu005503	0.802	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu003401	0.793	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002328	0.787	0.006 **	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu004030	0.784	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu004493	0.783	0.003 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp7(100);Gp7(100);Gp7_unclassified(100);
Otu001266	0.773	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Acidimicrobiales(100);Acidimicrobiaceae(87);
Otu005200	0.769	0.002 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Zavarzinella(99);
Otu005234	0.758	0.004 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu003146	0.755	0.022 *	Bacteria(100);Armatimonadetes(100);Armatimonadetes_gp5(100);Armatimonadetes_gp5_unclassified(100);Armatimonadetes_gp5_unclassified(100);
Otu003607	0.752	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004903	0.748	0.012 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu004233	0.747	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001863	0.743	0.005 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu005471	0.740	0.011 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003238	0.732	0.001 ***	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Zavarzinella(100);
Otu004017	0.732	0.007 **	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu003798	0.728	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp4(100);Aridibacter(100);Aridibacter_unclassified(100);
Otu003015	0.722	0.007 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu002312	0.716	0.009 **	Bacteria(100);Actinobacteria(100);Actinobacteria_unclassified(100);Actinobacteria_unclassified(100);Actinobacteria_unclassified(100);
Otu004380	0.713	0.006 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu002070	0.710	0.002 **	Bacteria(100);Microgenomates(100);Microgenomates_unclassified(100);Microgenomates_unclassified(100);Microgenomates_unclassified(100);
Otu004938	0.703	0.027 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);Zavarzinella(100);
Otu004322	0.699	0.005 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu005536	0.698	0.009 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002762	0.679	0.039 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001656	0.679	0.002 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillales_unclassified(100);
Otu003915	0.676	0.004 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu005559	0.671	0.003 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu004267	0.667	0.006 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);

Otu002663	0.667	0.001 ***	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004316	0.652	0.012 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005161	0.649	0.017 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004386	0.632	0.010 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005050	0.619	0.010 **	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu004158	0.607	0.006 **	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu004060	0.606	0.010 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Legionellales(100);Coxiellaceae(100);Aquicella(100);
Otu004351	0.602	0.019 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu003359	0.593	0.050 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu005447	0.592	0.019 *	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu001483	0.575	0.013 *	Bacteria(100);Armatimonadetes(100);Armatimonadetes_gp5(100);Armatimonadetes_gp5_unclassified(100);Armatimonadetes_gp5_unclassified(100);
Otu003477	0.569	0.040 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003791	0.564	0.037 *	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Burkholderiales(100);Burkholderiales_unclassified(100);
Otu005180	0.563	0.013 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001329	0.563	0.045 *	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Acidimicrobiales(100);Iamiaceae(99);Iamia(99);
Otu000394	0.550	0.037 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004696	0.530	0.021 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu001906	0.506	0.041 *	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu003741	0.471	0.039 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004203	0.471	0.040 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhizobiales(100);Rhizobiales_unclassified(100);
Otu004212	0.471	0.032 *	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu005177	0.471	0.030 *	Bacteria(100);Bacteroidetes(100);Flavobacteriia(100);Flavobacteriales(100);Cryomorphaceae(100);Fluviicola(100);
Otu005316	0.471	0.028 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);

Group T4 #sps. 7

	stat	p.value	
Otu001072	0.819	0.010 **	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu002242	0.777	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003129	0.766	0.003 **	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);

Otu002948	0.732	0.005 **	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Actinomycetales_unclassified(57);
Otu002042	0.691	0.034 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu004626	0.644	0.028 *	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Betaproteobacteria_unclassified(100);Betaproteobacteria_unclassified(100);
Otu005224	0.629	0.034 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);

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	stat	p.value	
Otu001151	0.907	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Mucilaginibacter(100);
Otu002085	0.875	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillales_unclassified(85);
Otu000663	0.875	0.006 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Cystobacteraceae(100);Anaeromyxobacter(100);
Otu002950	0.867	0.001 ***	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu000998	0.865	0.001 ***	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu001002	0.859	0.014 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004014	0.851	0.001 ***	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu001912	0.836	0.039 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu000654	0.831	0.005 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Acidobacteria_Gp3_unclassified(100);Acidobacteria_Gp3_unclassified(100);
Otu001492	0.819	0.002 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Granulicella(100);Granulicella_unclassified(100);
Otu001082	0.805	0.027 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu001448	0.805	0.002 **	Bacteria(100);Verrucomicrobia(100);Opitutae(100);Opitutales(100);Opitutaceae(100);Opitutus(100);
Otu002135	0.803	0.005 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Acidobacteria_Gp1_unclassified(100);Acidobacteria_Gp1_unclassified(100);
Otu002138	0.802	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Ferruginibacter(100);
Otu001758	0.801	0.003 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Gp1(100);Gp1_unclassified(100);
Otu004600	0.800	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Mucilaginibacter(100);
Otu003255	0.794	0.006 **	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu003848	0.791	0.002 **	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu004779	0.784	0.001 ***	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu002660	0.777	0.002 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu003089	0.777	0.015 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Granulicella(100);Granulicella_unclassified(100);
Otu003369	0.776	0.003 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);Ferruginibacter(100);

Otu000889	0.775	0.010 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp2(100);Gp2(100);Gp2_unclassified(100);
Otu003629	0.772	0.004 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillaceae(100);
Otu005289	0.771	0.001 ***	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Mucilaginibacter(100);
Otu003435	0.771	0.008 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Acidobacteria_Gp1_unclassified(100);Acidobacteria_Gp1_unclassified(100);
Otu003484	0.770	0.006 **	Bacteria(100);Candidatus_Saccharibacteria(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);Candidatus_Saccharibacteria_unclassified(100);
Otu005114	0.768	0.001 ***	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Rhodospirillales(100);Rhodospirillaceae(60);
Otu001730	0.767	0.050 *	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);
Otu005339	0.765	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinomycetales(100);Thermomonosporaceae(61);
Otu001587	0.762	0.014 *	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu005184	0.762	0.001 ***	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Acidimicrobiales(100);Acidimicrobiales_unclassified(100);
Otu004455	0.760	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Acidobacteria_Gp1_unclassified(100);Acidobacteria_Gp1_unclassified(100);
Otu002896	0.757	0.007 **	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu002920	0.753	0.036 *	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);
Otu005063	0.749	0.002 **	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu004846	0.749	0.007 **	Bacteria(100);Proteobacteria(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);Proteobacteria_unclassified(100);
Otu004107	0.747	0.002 **	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriales_unclassified(100);
Otu002405	0.745	0.004 **	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu003581	0.745	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Granulicella(100);Granulicella_unclassified(100);
Otu004540	0.742	0.001 ***	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Xanthomonadales(100);Xanthomonadaceae(100);Rhodanobacter(100);
Otu001683	0.739	0.016 *	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Cytophagaceae(100);Cytophaga(100);
Otu001401	0.739	0.016 *	Bacteria(100);Chlamydiae(100);Chlamydiia(100);Chlamydiales(100);Parachlamydiaceae(86);Parachlamydia(86);
Otu002504	0.736	0.013 *	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu002206	0.732	0.001 ***	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Granulicella(100);Granulicella_unclassified(100);
Otu003851	0.729	0.007 **	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_incertae_sedis(100);Rhizomicrobium(100);
Otu004506	0.703	0.004 **	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu003886	0.700	0.013 *	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu003723	0.700	0.019 *	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(88);
Otu004168	0.695	0.004 **	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Bdellovibrionales(100);Bdellovibrionaceae(100);Vampirovibrio(100);

Otu004130	0.689	0.005 **	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu002915	0.688	0.002 **	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu003927	0.686	0.005 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu004940	0.686	0.016 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu004057	0.680	0.016 *	Bacteria(100);Planctomycetes(100);Planctomycetia(100);Planctomycetales(100);Planctomycetaceae(100);
Otu004171	0.678	0.006 **	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu004790	0.678	0.038 *	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu003782	0.676	0.049 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu002717	0.674	0.012 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Gp1(100);Gp1_unclassified(100);
Otu004701	0.670	0.033 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003229	0.669	0.003 **	Bacteria(100);Proteobacteria(100);Gammaproteobacteria(100);Gammaproteobacteria_unclassified(100);Gammaproteobacteria_unclassified(100);
Otu003872	0.669	0.022 *	Bacteria(100);Armatimonadetes(100);Armatimonadia(100);Armatimonadales(100);Armatimonadaceae(100);Armatimonas/Armatimonadetes_gp1(100);
Otu005549	0.667	0.011 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003036	0.667	0.030 *	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu003989	0.666	0.006 **	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu005113	0.652	0.010 **	Bacteria(100);Verrucomicrobia(100);Opitutae(100);Opitutales(100);Opitutaceae(100);Opitutus(100);
Otu004259	0.648	0.022 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Caulobacterales(100);Caulobacteraceae(100);
Otu004097	0.648	0.019 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu003458	0.648	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004081	0.647	0.027 *	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Sphingobacteriaceae(100);Mucilaginibacter(100);
Otu004159	0.643	0.038 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu004308	0.639	0.050 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Caulobacterales(100);Caulobacteraceae(100);Phenylobacterium(100);
Otu005504	0.637	0.009 **	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu004204	0.637	0.026 *	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinobacteria_unclassified(100);Actinobacteria_unclassified(100);
Otu004311	0.632	0.002 **	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu002543	0.632	0.035 *	Bacteria(100);Actinobacteria(100);Actinobacteria(100);Actinobacteria_unclassified(100);Actinobacteria_unclassified(100);
Otu004227	0.630	0.017 *	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Terrimicrobium(100);Terrimicrobium_unclassified(100);
Otu002260	0.630	0.020 *	Bacteria(100);Bacteroidetes(100);Sphingobacteriia(100);Sphingobacteriales(100);Chitinophagaceae(100);

Otu001795	0.629	0.014 *	Bacteria(100);Proteobacteria(100);Betaproteobacteria(100);Rhodocyclales(100);Rhodocyclaceae(100);
Otu001813	0.628	0.043 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu004864	0.627	0.012 *	Bacteria(100);Bacteroidetes(100);Cytophagia(100);Cytophagales(100);Flammeovirgaceae(97);
Otu005244	0.625	0.019 *	Bacteria(100);Gemmatimonadetes(100);Gemmatimonadetes(100);Gemmatimonadales(100);Gemmatimonadaceae(100);Gemmatimonas(100);
Otu005080	0.624	0.010 **	Bacteria(100);candidate_division_WPS-1(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);candidate_division_WPS-1_unclassified(100);
Otu003016	0.624	0.036 *	Bacteria(100);Parcubacteria(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);Parcubacteria_unclassified(100);
Otu004823	0.616	0.025 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Candidatus_Solibacter(100);Candidatus_Solibacter_unclassified(100);
Otu003817	0.614	0.022 *	Bacteria(100);Verrucomicrobia(100);Opitutae(100);Opitutales(100);Opitutaceae(100);Opitutus(100);
Otu003847	0.613	0.026 *	Bacteria(100);Verrucomicrobia(100);Spartobacteria(100);Spartobacteria_unclassified(100);Spartobacteria_unclassified(100);
Otu004954	0.612	0.047 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp3(100);Gp3(100);Gp3_unclassified(100);
Otu003729	0.602	0.037 *	Bacteria(100);Proteobacteria(100);Alphaproteobacteria(100);Alphaproteobacteria_unclassified(100);Alphaproteobacteria_unclassified(100);
Otu002241	0.601	0.046 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp1(100);Gp1(100);Gp1_unclassified(100);
Otu003882	0.598	0.033 *	Bacteria(100);Bacteroidetes(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);Bacteroidetes_unclassified(100);
Otu004559	0.550	0.035 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp2(100);Gp2(100);Gp2_unclassified(100);
Otu003315	0.548	0.029 *	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Myxococcales(100);Myxococcales_unclassified(100);
Otu003713	0.548	0.027 *	Bacteria(100);Verrucomicrobia(100);Subdivision3(100);Subdivision3_unclassified(100);Subdivision3_unclassified(100);
Otu004708	0.548	0.038 *	Bacteria(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);Bacteria_unclassified(100);
Otu005137	0.548	0.036 *	Bacteria(100);Proteobacteria(100);Deltaproteobacteria(100);Bdellovibrionales(100);Bdellovibrionaceae(100);Vampirovibrio(100);
Otu004877	0.545	0.041 *	Bacteria(100);Acidobacteria(100);Acidobacteria_Gp4(100);Aridibacter(100);Aridibacter_unclassified(100);
Otu003496	0.544	0.048 *	Bacteria(100);Verrucomicrobia(100);Opitutae(100);Opitutales(100);Opitutaceae(100);Opitutus(100);

Table C 3 High burn fungal indicator taxon analysis results

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	stat	p.value	
Otu0374	0.623	0.006 **	k__Fungi(100);p__Ascomycota(100);c__Ascomycota_class_Incertae_sedis(100);o__Ascomycota_order_Incertae_sedis(100);f__Ascomycota_family_Incertae_sedis(100);g__Slimacomyces(100);s__Slimacomyces_isiola(100);
Otu0441	0.548	0.038 *	k__Fungi(100);p__Ascomycota(100);c__Ascomycota_class_Incertae_sedis(100);o__Ascomycota_order_Incertae_sedis(100);f__Ascomycota_family_Incertae_sedis(100);g__Xenochalara(100);s__Xenochalara_sp(100);
Otu0519	0.548	0.033 *	k__Fungi(100);p__Ascomycota(100);c__Ascomycota_class_Incertae_sedis(100);o__Ascomycota_order_Incertae_sedis(100);f__Ascomycota_family_Incertae_sedis(100);g__Xenochalara(100);s__Xenochalara_sp(100);
Otu0404	0.870	0.001 ***	k__Fungi(100);p__Ascomycota(100);c__Dothideomycetes(100);o__Dothideomycetes_order_Incertae_sedis(100);f__Myxotrichaceae(100);g__Oidiodendron(100);s__Oidiodendron_chlamydosporicum(100);
Otu0300	0.702	0.002 **	k__Fungi(100);p__Ascomycota(100);c__Dothideomycetes(100);o__Dothideomycetes_order_Incertae_sedis(100);f__Myxotrichaceae(100);g__Oidiodendron(100);s__Oidiodendron_maius(100);
Otu0331	0.698	0.010 **	k__Fungi(100);p__Ascomycota(100);c__Dothideomycetes(100);o__Dothideomycetes_order_Incertae_sedis(100);f__Pseudeurotiaceae(100);g__Pseudeurotium(100);
Otu0237	0.665	0.011 *	k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Capronia(100);s__Capronia_peltigerae(97);
Otu0155	0.843	0.001 ***	k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Capronia(100);s__Capronia_sp_94003b(100);
Otu0150	0.796	0.005 **	k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Capronia(100);s__Capronia_sp_94003b(100);
Otu0335	0.607	0.047 *	k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Capronia(100);s__Capronia_sp_94003b(100);
Otu0036	0.891	0.001 ***	k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Cladophialophora(100);
Otu0105	0.830	0.001 ***	k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Cladophialophora(100);
Otu0211	0.820	0.001 ***	k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Cladophialophora(100);
Otu0153	0.669	0.006 **	k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Cladophialophora(100);
Otu0263	0.629	0.005 **	k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Cladophialophora(100);
Otu0488	0.540	0.035 *	k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Cladophialophora(100);
Otu0110	0.945	0.001 ***	k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Cladophialophora(100);s__Cladophialophora_chaetospira(100);
Otu0440	0.707	0.002 **	k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Cladophialophora(100);s__Cladophialophora_chaetospira(100);
Otu0391	0.632	0.003 **	k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Cladophialophora(100);s__Cladophialophora_sp_olrim407(97);
Otu0215	0.805	0.001 ***	k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Cladophialophora(100);s__Cladophialophora_sp_TRN488(100);
Otu0039	0.965	0.001 ***	k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Cladophialophora(100);s__Cladophialophora_sp(83);
Otu0101	0.631	0.012 *	k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Cladophialophora(100);s__Cladophialophora_sp(94);

Otu0383 0.632
0.007 ** k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Exophiala(100);s__Exophiala_sp(100);
Otu0547 0.632
0.005 ** k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Rhinocladiella(100);s__Rhinocladiella_sp_VL271(100);
Otu0194 0.650
0.002 ** k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Penicillium(100);s__Penicillium_nodositatum(100);
Otu0378 0.775
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Rasamsonia(100);s__Rasamsonia_sp(100);
Otu0290 0.548
0.026 * k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Rasamsonia(100);s__Rasamsonia_sp(100);
Otu0542 0.707
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Sagenomella(100);s__Sagenomella_diversispora(100);
Otu0753 0.632
0.006 ** k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Sagenomella(100);s__Sagenomella_diversispora(100);
Otu0798 0.548
0.044 * k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Sagenomella(100);s__Sagenomella_diversispora(100);
Otu0245 0.704
0.006 ** k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Talaromyces(100);
Otu0875 0.548
0.038 * k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Talaromyces(100);s__Talaromyces_purpureus(100);
Otu0320 0.548
0.029 * k__Fungi(100);p__Ascomycota(100);c__Lecanoromycetes(100);o__Pertusariales(100);f__Megasporaceae(100);g__Aspicilia(100);s__Aspicilia_sp(100);
Otu0130 0.833
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiales_family_Incertae_sedis(100);g__Ascocoryne(100);s__Ascocoryne_sp(100);
Otu0024 0.937
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiales_family_Incertae_sedis(100);g__Cadophora(100);s__Cadophora_finlandica(100);
Otu0258 0.548
0.033 * k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiales_family_Incertae_sedis(100);g__Hyphodiscus(100);s__Hyphodiscus_hymeniophilus(100);
Otu0092 0.632
0.003 ** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiales_family_Incertae_sedis(100);g__Hyphodiscus(100);s__Hyphodiscus_sp(100);
Otu0121 0.936
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiales_family_Incertae_sedis(100);g__Infundichalara(100);s__Infundichalara_sp(100);
Otu0095 0.924
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiales_family_Incertae_sedis(100);g__Infundichalara(100);s__Infundichalara_sp(100);
Otu0191 0.879
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiales_family_Incertae_sedis(100);g__Leptodontidium(100);s__Leptodontidium_sp(100);
Otu0085 0.917
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiales_family_Incertae_sedis(100);g__Xenopolyscytalum(100);s__Xenopolyscytalum_sp(100);
Otu0081 0.882
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiales_family_Incertae_sedis(100);g__Xenopolyscytalum(100);s__Xenopolyscytalum_sp(100);
Otu0266 0.790
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiales_family_Incertae_sedis(100);g__Xenopolyscytalum(100);s__Xenopolyscytalum_sp(100);
Otu0279 0.632
0.007 ** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Hyaloscyphaceae(100);g__Lachnellula(100);
Otu0138 0.771
0.004 ** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Vibrisseaceae(100);g__Phialocephala(100);s__Phialocephala_fortinii(100);
Otu0906 0.548
0.030 * k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Vibrisseaceae(100);g__Phialocephala(100);s__Phialocephala_fortinii(100);
Otu0724 0.494
0.049 * k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Vibrisseaceae(100);g__Phialocephala(100);s__Phialocephala_fortinii(100);

Otu0177 0.888 0.001 *** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Leotiomycetes_order_Incertae_sedis(100);f__Leotiomycetes_family_Incertae_sedis(100);g__Collophora(100);s__Collophora_sp(100);
Otu0239 0.577 0.036 * k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Leotiomycetes_order_Incertae_sedis(100);f__Leotiomycetes_family_Incertae_sedis(100);g__Geomyces(100);
Otu0132 0.939 0.001 *** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Leotiomycetes_order_Incertae_sedis(100);f__Leotiomycetes_family_Incertae_sedis(100);g__Leohumicola(100);
Otu0238 0.749 0.001 *** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Leotiomycetes_order_Incertae_sedis(100);f__Leotiomycetes_family_Incertae_sedis(100);g__Leohumicola(100);
Otu0161 0.903 0.001 *** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Leotiomycetes_order_Incertae_sedis(100);f__Leotiomycetes_family_Incertae_sedis(100);g__Meliniomyces(100);s__Meliniomyces_bicolor(92);
Otu0151 0.894 0.001 *** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Leotiomycetes_order_Incertae_sedis(100);f__Leotiomycetes_family_Incertae_sedis(100);g__Meliniomyces(100);s__Meliniomyces_sp(100);
Otu0224 0.707 0.001 *** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Leotiomycetes_order_Incertae_sedis(100);f__Leotiomycetes_family_Incertae_sedis(100);g__Meliniomyces(100);s__Meliniomyces_sp(99);
Otu0240 0.548 0.041 * k__Fungi(100);p__Ascomycota(100);c__Sordariomycetes(100);o__Hypocreales(100);f__Hypocreaceae(100);g__Trichoderma(100);s__Trichoderma_viride(100);
Otu0196 0.678 0.006 ** k__Fungi(100);p__Ascomycota(100);c__Sordariomycetes(100);o__Sordariales(100);f__Chaetomiaceae(100);g__Humicola(100);s__Humicola_grisea_var._grisea(100);
Otu0070 0.691 0.018 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Agaricaceae(100);g__Lycoperdon(100);s__Lycoperdon_subumbrinum(67);
Otu0203 0.548 0.034 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Cortinariaceae(100);g__Cortinarius(100);
Otu0045 0.707 0.001 *** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Inocybaceae(100);g__Inocybe(100);
Otu0087 0.548 0.041 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Inocybaceae(100);g__Inocybe(100);s__Inocybe_nematoloma(100);
Otu0386 0.655 0.006 ** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Inocybaceae(100);g__Inocybe(100);s__Inocybe_sp_OTU301(100);
Otu0086 0.547 0.036 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Mycenaceae(100);g__Mycena(100);
Otu0091 0.623 0.035 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Mycenaceae(100);g__Mycena(100);s__Mycena_cinerella(100);
Otu0031 0.710 0.013 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Atheliales(100);f__Atheliaceae(100);g__Byssocorticium(100);s__Byssocorticium_sp(100);
Otu0061 0.948 0.001 *** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Boletales(100);f__Rhizopogonaceae(100);g__Rhizopogon(100);
Otu0128 0.919 0.001 *** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Boletales(100);f__Rhizopogonaceae(100);g__Rhizopogon(100);
Otu0169 0.856 0.002 ** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Boletales(100);f__Rhizopogonaceae(100);g__Rhizopogon(100);s__Rhizopogon_evadens(100);
Otu0301 0.548 0.028 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Cantharellales(100);f__Clavulinaceae(100);g__Clavulina(100);s__Clavulina_sp(100);
Otu0074 0.632 0.005 ** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Cantharellales(100);f__Hydnaceae(100);g__Sistotrema(100);
Otu0147 0.547 0.037 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Cantharellales(100);f__Hydnaceae(100);g__Sistotrema(100);
Otu0030 0.886 0.001 *** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Gomphales(100);f__Gomphaceae(100);g__Gautieria(100);s__Gautieria_sp_StumpMdws2278CA(80);
Otu0324 0.632 0.002 ** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Russulales(100);f__Albatrellaceae(100);g__Leucogaster(100);s__Leucogaster_citrinus(100);

Otu0228 0.548
0.027 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Thelephorales(100);f__Bankeraceae(100);g__Boletopsis(100);s__Boletopsis_grisea(100);
Otu0053 0.614
0.008 ** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Thelephorales(100);f__Bankeraceae(100);g__Hydnellum(100);s__Hydnellum_peckii(100);
Otu0184 0.548
0.035 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Trechisporales(100);f__Hydnodontaceae(100);g__Trechispora(100);s__Trechispora_sp(100);
Otu0323 0.632
0.005 ** k__Fungi(100);p__Basidiomycota(100);c__Dacrymycetes(100);o__Dacrymycetales(100);f__Dacrymycetaceae(100);g__Cerinosterus(100);s__Cerinosterus_sp(100);
Otu0629 0.548
0.031 * k__Fungi(100);p__Basidiomycota(100);c__Microbotryomycetes(100);o__Sporidiobolales(100);f__Sporidiobolales_family_Incertae_sedis(100);g__Rhodotorula(100);
Otu0479 0.548 k__Fungi(100);p__Basidiomycota(100);c__Microbotryomycetes(100);o__Sporidiobolales(100);f__Sporidiobolales_family_Incertae_sedis(100);g__Rhodotorula(100);s__Rhodotorula_lignoph
0.033 * ila(100);
Otu0201 0.775 k__Fungi(100);p__Basidiomycota(100);c__Tremellomycetes(100);o__Cystofilobasidiales(100);f__Cystofilobasidiales_family_Incertae_sedis(100);g__Syzygospora(100);s__Syzygospora_sp(10
0.001 *** 0);
Otu0127 0.883
0.001 *** k__Fungi(100);p__Basidiomycota(100);c__Tremellomycetes(100);o__Filobasidiales(100);f__Filobasidiaceae(100);g__Cryptococcus(100);s__Cryptococcus_terricola(100);
Otu0677 0.548
0.029 * k__Fungi(100);p__Basidiomycota(100);c__Tremellomycetes(100);o__Tremellales(100);f__Tremellales_family_Incertae_sedis(100);g__Cryptococcus(100);s__Cryptococcus_aerius(100);
Otu0634 0.548
0.022 * k__Fungi(100);p__Basidiomycota(100);c__Tremellomycetes(100);o__Tremellales(100);f__Tremellales_family_Incertae_sedis(100);g__Cryptococcus(100);s__Cryptococcus_podzolicus(74);
Otu0636 0.548
0.026 * k__Fungi(100);p__Basidiomycota(100);c__Tremellomycetes(100);o__Tremellales(78);f__Tremellales_family_Incertae_sedis(78);g__Tremella(78);s__Tremella_foliacea(78);
Otu0131 0.879 k__Fungi(100);p__Basidiomycota(100);c__Tritirachiomycetes(100);o__Tritirachiomycetes_order_Incertae_sedis(100);f__Tritirachiomycetes_family_Incertae_sedis(100);g__Paratritirachium
0.002 ** (100);s__Paratritirachium_sp(100);
Otu0409 0.635 k__Fungi(100);p__Basidiomycota(100);c__Tritirachiomycetes(100);o__Tritirachiomycetes_order_Incertae_sedis(100);f__Tritirachiomycetes_family_Incertae_sedis(100);g__Paratritirachium
0.007 ** (100);s__Paratritirachium_sp(100);
Otu0295 0.733 k__Fungi(100);p__Basidiomycota(100);c__Tritirachiomycetes(100);o__Tritirachiomycetes_order_Incertae_sedis(100);f__Tritirachiomycetes_family_Incertae_sedis(100);g__Paratritirachium
0.001 *** (100);s__Paratritirachium_sp(98);
Otu0598 0.775
0.001 *** k__Fungi(100);p__Basidiomycota(100);c__Wallemiomycetes(100);o__Geminibasidiales(100);f__Geminibasidiaceae(100);g__Geminibasidium(100);s__Geminibasidium_sp(100);
Otu0080 0.774
0.004 ** k__Fungi(100);p__Basidiomycota(100);c__Wallemiomycetes(100);o__Geminibasidiales(100);f__Geminibasidiaceae(100);g__Geminibasidium(100);s__Geminibasidium_sp(100);
Otu0518 0.738
0.001 *** k__Fungi(100);p__Basidiomycota(100);c__Wallemiomycetes(100);o__Geminibasidiales(100);f__Geminibasidiaceae(100);g__Geminibasidium(100);s__Geminibasidium_sp(100);
Otu0807 0.632
0.005 ** k__Fungi(100);p__Basidiomycota(100);c__Wallemiomycetes(100);o__Geminibasidiales(100);f__Geminibasidiaceae(100);g__Geminibasidium(100);s__Geminibasidium_sp(100);
Otu0778 0.577
0.017 * k__Fungi(100);p__Basidiomycota(100);c__Wallemiomycetes(100);o__Geminibasidiales(100);f__Geminibasidiaceae(100);g__Geminibasidium(100);s__Geminibasidium_sp(100);
Otu0892 0.548
0.029 * k__Fungi(100);p__Basidiomycota(100);c__Wallemiomycetes(100);o__Geminibasidiales(100);f__Geminibasidiaceae(100);g__Geminibasidium(100);s__Geminibasidium_sp(100);
Otu0694 0.548 k__Fungi(100);p__Chytridiomycota(100);c__Monoblepharidomycetes(100);o__Monoblepharidales(100);f__Oedogoniomycetaceae(100);g__Oedogoniomyces(100);s__Oedogoniomyces_sp
0.038 * _CR90(100);
Otu0471 0.548
0.034 * k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Endogonales(100);f__Endogonaceae(100);g__Endogone(100);s__Endogone_sp_1_RG_2012(100);
Otu0492 0.548
0.034 * k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Endogonales(100);f__Endogonaceae(100);g__Endogone(100);s__Endogone_sp_1_RG_2012(100);
Otu0223 0.769
0.001 *** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);
Otu0075 0.787
0.006 ** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);s__Mortierella_alpina(60);

Otu0112 0.775
0.001 *** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);s__Mortierella_gemmifera(95);
Otu0014 0.774
0.008 ** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);s__Mortierella_humilis(100);
Otu0094 0.753
0.001 *** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);s__Mortierella_sp_04M_158(100);
Otu0051 0.705
0.013 * k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);s__Mortierella_sp_WD32A(99);
Otu0253 0.697
0.002 ** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);s__Mortierella_sp(100);
Otu0504 0.548
0.029 * k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Lentamycetaceae(100);g__Lentamyces(100);s__Lentamyces_zychae(55);
Otu0366 0.628
0.006 ** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Mucoraceae(100);g__Mucor(100);s__Mucor_brunneogriseus(100);
Otu0219 0.707
0.003 ** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);
Otu0861 0.548
0.044 * k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);
Otu0009 0.987 k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);s__Umbelopis_ramanniana_var_angulis
0.001 *** pora(100);
Otu0093 0.939 k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);s__Umbelopis_ramanniana_var_angulis
0.001 *** pora(100);
Otu0007 0.943
0.020 * k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);s__Umbelopsis_dimorpha(100);
Otu0317 0.706
0.001 *** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);s__Umbelopsis_dimorpha(100);
Otu0351 0.548
0.023 * k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);s__Umbelopsis_ramanniana(100);
Otu0003 0.940
0.006 ** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);s__Umbelopsis_sp(100);
Otu0025 0.931
0.001 *** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);s__Umbelopsis_sp(100);
Otu0096 0.893
0.001 *** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);s__Umbelopsis_sp(100);
Otu0632 0.548
0.033 * k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);s__Umbelopsis_sp(100);
Otu0918 0.548
0.024 * k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);s__Umbelopsis_sp(85);
Otu0114 0.947
0.001 *** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);s__Umbelopsis_sp(96);
Otu0043 0.942
0.001 *** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);s__Umbelopsis_sp(99);

Group T1 #sps. 16

stat p.value
Otu0684 0.533
0.049 * k__Fungi(100);p__Ascomycota(100);c__Dothideomycetes(100);o__Capnodiales(100);f__Mycosphaerellaceae(100);g__Mycosphaerella(100);s__Mycosphaerella_nyssicola(95);

Otu0608 0.632 k__Fungi(100);p__Ascomycota(100);c__Dothideomycetes(100);o__Dothideomycetes_order_Incertae_sedis(100);f__Myxotrichaceae(100);g__Oidiodendron(100);s__Oidiodendron_chlamydosporicum(100);
0.006 **

Otu0058 0.566 k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Leotiomycetes_order_Incertae_sedis(100);f__Leotiomycetes_family_Incertae_sedis(100);g__Meliniomyces(100);s__Meliniomyces_bicolor(100);
0.014 *

Otu0029 0.948
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Pezizomycetes(100);o__Pezizales(100);f__Morchellaceae(100);g__Morchella(100);

Otu0042 0.835
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Pezizomycetes(100);o__Pezizales(100);f__Morchellaceae(100);g__Morchella(100);

Otu0149 0.548
0.034 * k__Fungi(100);p__Ascomycota(100);c__Pezizomycetes(100);o__Pezizales(100);f__Morchellaceae(100);g__Morchella(100);s__Morchella_septimelata(100);

Otu0016 0.791
0.008 ** k__Fungi(100);p__Ascomycota(100);c__Pezizomycetes(100);o__Pezizales(100);f__Pyronemataceae(100);g__Scutellinia(100);

Otu0818 0.548
0.030 * k__Fungi(100);p__Ascomycota(100);c__Pezizomycetes(100);o__Pezizales(100);f__Pyronemataceae(100);g__Scutellinia(100);

Otu0010 0.894
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Pezizomycetes(100);o__Pezizales(100);f__Pyronemataceae(100);g__Scutellinia(100);s__Scutellinia_sp(100);

Otu0027 0.837
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Pezizomycetes(100);o__Pezizales(100);f__Pyronemataceae(100);g__Tricharina(100);s__Tricharina_praecox_var._praecox(100);

Otu0582 0.548
0.025 * k__Fungi(100);p__Ascomycota(100);c__Sordariomycetes(100);o__Xylariales(100);f__Xylariales_family_Incertae_sedis(100);g__Microdochium(100);s__Microdochium_sp(100);

Otu0907 0.548
0.036 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Clavariaceae(100);g__Clavaria(100);s__Clavaria_acuta(100);

Otu0779 0.548
0.033 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Entolomataceae(100);g__Clitopilus(100);

Otu0628 0.548
0.026 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Strophariaceae(100);g__Stropharia(100);

Otu0468 0.945
0.001 *** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Cantharellales(100);f__Cantharellales_family_Incertae_sedis(100);g__Minimedusa(100);s__Minimedusa_sp(100);

Otu0575 0.707
0.001 *** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Polyporales(100);f__Meruliaceae(100);g__Irpex(100);s__Irpex_sp_JSL_2009a(100);

Group T2 #sps. 32

stat p.value

Otu0589 0.548
0.041 * k__Fungi(100);p__Ascomycota(100);c__Dothideomycetes(100);o__Capnodiales(100);f__Capnodiales_family_Incertae_sedis(100);g__Phaeotheca(100);s__Phaeotheca_sp(100);

Otu0357 0.668
0.005 ** k__Fungi(100);p__Ascomycota(100);c__Dothideomycetes(100);o__Dothideales(100);f__Dothideaceae(100);g__Endoconidioma(100);s__Endoconidioma_populi(100);

Otu0316 0.611
0.044 * k__Fungi(100);p__Ascomycota(100);c__Dothideomycetes(100);o__Dothideales(100);f__Dothioraceae(100);g__Aureobasidium(100);

Otu0137 0.823
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Dothideomycetes(100);o__Dothideales(100);f__Dothioraceae(100);g__Hormonema(100);s__Hormonema_sp(100);

Otu0524 0.632 k__Fungi(100);p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(100);f__Pleosporales_family_Incertae_sedis(100);g__Ochrocladosporium(100);s__Ochrocladosporium_elatum(100);
0.003 **

Otu0292 0.714
0.006 ** k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Phaeococcomyces(100);s__Phaeococcomyces_sp(100);

Otu0283 0.548
0.024 * k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Phaeomoniella(100);s__Phaeomoniella_sp(100);

Otu0531 0.632 0.005 ** k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiomycetes_order_Incertae_sedis(100);f__Eurotiomycetes_family_Incertae_sedis(100);g__Sarcinomyces(100);s__Sarcinomyces_crustaceus(100);
Otu0703 0.632 0.003 ** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Leotiomycetes_order_Incertae_sedis(69);f__Leotiomycetes_family_Incertae_sedis(69);g__Collophora(69);
Otu0034 0.948 0.001 *** k__Fungi(100);p__Ascomycota(100);c__Pezizomycetes(100);o__Pezizales(100);f__Pezizaceae(100);g__Chromelosporium(100);s__Chromelosporium_sp(100);
Otu0123 0.932 0.001 *** k__Fungi(100);p__Ascomycota(100);c__Sordariomycetes(100);o__Sordariales(100);f__Lasiosphaeriaceae(100);g__Apiosordaria(100);s__Apiosordaria_sp(100);
Otu0895 0.548 0.019 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Cortinariaceae(100);g__Cortinarius(100);
Otu0033 0.956 0.001 *** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Lyophyllaceae(100);g__Lyophyllum(100);s__Lyophyllum_semitale(100);
Otu0285 0.707 0.001 *** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Psathyrellaceae(100);g__Coprinellus(100);
Otu0588 0.548 0.028 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Strophariaceae(100);g__Hypholoma(100);s__Hypholoma_capnoides(100);
Otu0392 0.580 0.038 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Strophariaceae(100);g__Hypholoma(100);s__Hypholoma_fasciculare(100);
Otu0044 0.896 0.001 *** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Strophariaceae(100);g__Pholiota(100);s__Pholiota_highlandensis(100);
Otu0017 0.837 0.006 ** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Strophariaceae(100);g__Pholiota(100);s__Pholiota_highlandensis(100);
Otu0656 0.548 0.041 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Strophariaceae(100);g__Pholiota(100);s__Pholiota_highlandensis(100);
Otu0071 0.704 0.002 ** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricomycetes_order_Incertae_sedis(100);f__Agaricomycetes_family_Incertae_sedis(100);g__Cotylidia(100);s__Cotylidia_undulata(100);
Otu0844 0.632 0.003 ** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Boletales(100);f__Suillaceae(100);g__Suillus(100);s__Suillus_lakei(100);
Otu0376 0.831 0.001 *** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Boletales(100);f__Suillaceae(100);g__Suillus(100);s__Suillus_sp(100);
Otu0041 0.742 0.008 ** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Boletales(100);f__Suillaceae(100);g__Suillus(100);s__Suillus_variegatus(100);
Otu0222 0.893 0.001 *** k__Fungi(100);p__Basidiomycota(100);c__Agaricostilbomycetes(100);o__Agaricostilbales(100);f__Chionosphaeraceae(100);g__Kurtzmanomyces(100);s__Kurtzmanomyces_nectairei(100);
Otu0505 0.632 0.005 ** k__Fungi(100);p__Basidiomycota(100);c__Microbotryomycetes(100);o__Sporidiobolales(100);f__Sporidiobolales_family_Incertae_sedis(100);g__Rhodotorula(100);s__Rhodotorula_sonckii(100);
Otu0705 0.548 0.038 * k__Fungi(100);p__Basidiomycota(100);c__Tremellomycetes(100);o__Tremellales(100);f__Tremellales_family_Incertae_sedis(100);g__Cryptococcus(100);
Otu0244 0.850 0.001 *** k__Fungi(100);p__Chytridiomycota(100);c__Chytridiomycetes(100);o__Spizellomycetales(100);f__Spizellomycetaceae(100);g__Powellomyces(100);s__Powellomyces_hirtus(100);
Otu0048 0.949 0.001 *** k__Fungi(100);p__Chytridiomycota(100);c__Chytridiomycetes(100);o__Spizellomycetales(100);f__Spizellomycetaceae(100);g__Spizellomyces(100);
Otu0205 0.729 0.003 ** k__Fungi(100);p__Chytridiomycota(100);c__Chytridiomycetes(100);o__Spizellomycetales(100);f__Spizellomycetaceae(100);g__Spizellomyces(100);
Otu0455 0.632 0.003 ** k__Fungi(100);p__Chytridiomycota(100);c__Chytridiomycetes(100);o__Spizellomycetales(100);f__Spizellomycetaceae(100);g__Spizellomyces(100);s__Spizellomyces_pseudodichotomus(100);
Otu0212 0.693 0.002 ** k__Fungi(100);p__Chytridiomycota(100);c__Chytridiomycetes(100);o__Spizellomycetales(100);f__Spizellomycetaceae(100);g__Spizellomyces(100);s__Spizellomyces_sp(100);
Otu0516 0.845 0.001 *** k__Fungi(100);p__Chytridiomycota(100);c__Monoblepharidomycetes(100);o__Monoblepharidales(100);f__Oedogoniomycetaceae(100);g__Oedogoniomyces(100);s__Oedogoniomyces_sp_CR90(100);

Group T4 #sps. 9

	stat	p.value	
Otu0221	0.677		
	0.046	*	k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Sagenomella(100);s__Sagenomella_diversispora(100);
Otu0990	0.500		
	0.029	*	k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Sagenomella(100);s__Sagenomella_diversispora(100);
Otu0816	0.500		
	0.028	*	k__Fungi(100);p__Ascomycota(100);c__Sordariomycetes(100);o__Sordariales(100);f__Lasiosphaeriaceae(100);g__Podospora(100);s__Podospora_sp_CDJL_2009a(100);
Otu0879	0.500		
	0.028	*	k__Fungi(100);p__Ascomycota(100);c__Sordariomycetes(100);o__Sordariales(100);f__Lasiosphaeriaceae(100);g__Zopfiella(100);s__Zopfiella_sp(100);
Otu0477	0.500		
	0.025	*	k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Auriculariales(100);f__Auriculariales_family_Incertae_sedis(100);g__Auricularia(100);s__Auricularia_sp(100);
Otu0871	0.500		
	0.028	*	k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Corticiales(100);f__Corticiaceae(100);g__Laetisaria(100);s__Laetisaria_arvalis(100);
Otu0711	0.491		
	0.043	*	k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Polyporales(100);f__Meripilaceae(100);g__Rigidoporus(100);s__Rigidoporus_corticola(100);
Otu0942	0.500		
	0.025	*	k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Thelephorales(100);f__Thelephoraceae(100);g__Tomentella(100);s__Tomentella_sublilacina(100);
Otu0553	0.572		k__Fungi(100);p__Chytridiomycota(100);c__Monoblepharidomycetes(100);o__Monoblepharidales(100);f__Oedogoniomycetaceae(100);g__Oedogoniomyces(100);s__Oedogoniomyces_sp
	0.025	*	_CR90(100);

Group T6 #sps. 13

	stat	p.value	
Otu0119	0.978		
	0.001	***	k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Eurotiales(100);f__Trichocomaceae(100);g__Penicillium(100);s__Penicillium_novae-zeelandiae(98);
Otu0415	0.577		
	0.011	*	k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiales_family_Incertae_sedis(100);g__Tetracladium(100);s__Tetracladium_sp(73);
Otu0100	0.814		
	0.001	***	k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Leotiales(100);f__Leotiaceae(100);g__Microglossum(100);s__Microglossum_griseoviride(94);
Otu0497	0.667		
	0.001	***	k__Fungi(100);p__Ascomycota(100);c__Sordariomycetes(100);o__Chaetosphaeriales(100);f__Chaetosphaeriaceae(100);g__Codinaeopsis(100);s__Codinaeopsis_sp(100);
Otu0475	0.577		k__Fungi(100);p__Ascomycota(100);c__Sordariomycetes(100);o__Sordariomycetes_order_Incertae_sedis(100);f__Magnaporthaceae(100);g__Gaeumannomyces(100);s__Gaeumannomyce
	0.007	**	s_incrustans(100);
Otu0297	0.816		
	0.001	***	k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Marasmiaceae(100);g__Hydropus(100);s__Hydropus_marginellus(100);
Otu0183	0.816		
	0.001	***	k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Psathyrellaceae(100);g__Coprinopsis(100);s__Coprinopsis_calospora(100);
Otu0185	0.577		
	0.014	*	k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Atheliales(100);f__Atheliaceae(100);g__Amphinema(100);s__Amphinema_sp(100);
Otu0160	0.582		
	0.038	*	k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Hymenochaetales(100);f__Hymenochaetaceae(100);g__Coltricia(100);s__Coltricia_sp_1_RG_2012(100);
Otu0821	0.692		
	0.001	***	k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Thelephorales(100);f__Thelephoraceae(100);g__Tomentella(100);s__Tomentella_sublilacina(95);
Otu0227	0.916		
	0.001	***	k__Fungi(100);p__Basidiomycota(100);c__Wallemiomycetes(100);o__Wallemiales(100);f__Wallemiaceae(100);g__Wallemia(100);s__Wallemia_muriae(100);

Otu0186 0.646 k__Fungi(100);p__Chytridiomycota(100);c__Chytridiomycetes(100);o__Spizellomycetales(100);f__Spizellomycetaceae(100);g__Spizellomyces(100);s__Spizellomyces_pseudodichotomus(10
0.009 ** 0);
Otu0443 0.577
0.014 * k__Fungi(100);p__Chytridiomycota(100);c__Chytridiomycetes(100);o__Spizellomycetales(100);f__Spizellomycetaceae(100);g__Spizellomyces(100);s__Spizellomyces_sp_PL_078(100);

Table C 4 Low burn fungal indicator taxon analysis results

Group T0 #sps. 54

stat p.value
Otu0570 0.548 k__Fungi(100);p__Ascomycota(100);c__Ascomycota_class_Incertae_sedis(100);o__Ascomycota_order_Incertae_sedis(100);f__Ascomycota_family_Incertae_sedis(100);g__Gyoerffyella(100)
0.030 * ;s__Gyoerffyella_entomobryoides(100);
Otu0441 0.679 k__Fungi(100);p__Ascomycota(100);c__Ascomycota_class_Incertae_sedis(100);o__Ascomycota_order_Incertae_sedis(100);f__Ascomycota_family_Incertae_sedis(100);g__Xenochalara(100)
0.002 ** ;s__Xenochalara_sp(100);
Otu0528 0.548
0.031 * k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Capronia(100);s__Capronia_sp_94003b(100);
Otu0105 0.984
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Cladophialophora(100);
Otu0036 0.933
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Cladophialophora(100);
Otu0153 0.859
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Cladophialophora(100);
Otu0069 0.849
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Cladophialophora(100);
Otu0234 0.819
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Cladophialophora(100);
Otu0440 0.556
0.034 * k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Cladophialophora(100);s__Cladophialophora_chaetospira(100);
Otu0377 0.707
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Cladophialophora(100);s__Cladophialophora_minutissima(100);
Otu0101 0.623
0.032 * k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Cladophialophora(100);s__Cladophialophora_sp(94);
Otu0454 0.704
0.006 ** k__Fungi(100);p__Ascomycota(100);c__Eurotiomycetes(100);o__Chaetothyriales(100);f__Herpotrichiellaceae(100);g__Exophiala(100);s__Exophiala_moniliae(100);
Otu0453 0.733
0.002 ** k__Fungi(100);p__Ascomycota(100);c__Lecanoromycetes(100);o__Pertusariales(100);f__Megasporaceae(100);g__Aspicilia(100);s__Aspicilia_sp(100);
Otu0430 0.737
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiaceae(100);g__Crocicreas(100);
Otu0423 0.693
0.002 ** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiaceae(100);g__Hymenoscyphus(100);s__Hymenoscyphus_sp_aurim710(100);
Otu0330 0.615
0.007 ** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiaceae(100);g__Rhizoscyphus(100);s__Rhizoscyphus_sp(100);

Otu0414 0.762
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiales_family_Incertae_sedis(100);g__Catenulifera(100);s__Catenulifera_sp(100);
Otu0371 0.548
0.032 * k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiales_family_Incertae_sedis(100);g__Hyphodiscus(100);
Otu0258 0.759
0.002 ** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiales_family_Incertae_sedis(100);g__Hyphodiscus(100);s__Hyphodiscus_hymeniophilus(100);
Otu0607 0.632
0.006 ** k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiales_family_Incertae_sedis(100);g__Scleropezicula(100);s__Scleropezicula_sp(100);
Otu0279 0.624
0.031 * k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Hyaloscyphaceae(100);g__Lachnellula(100);
Otu0620 0.506
0.042 * k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Phacidiaceae(100);g__Phacidium(100);s__Phacidium_lacerum(100);
Otu0239 0.670
0.024 * k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Leotiomycetes_order_Incertae_sedis(100);f__Leotiomycetes_family_Incertae_sedis(100);g__Geomyces(100);
Otu0276 0.548
0.038 * k__Fungi(100);p__Ascomycota(100);c__Pezizomycetes(100);o__Pezizales(100);f__Sarcosomataceae(100);g__Pseudoplectania(100);s__Pseudoplectania_sp(100);
Otu0240 0.677
0.046 * k__Fungi(100);p__Ascomycota(100);c__Sordariomycetes(100);o__Hypocreales(100);f__Hypocreaceae(100);g__Trichoderma(100);s__Trichoderma_viride(100);
Otu0806 0.598
0.012 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Cortinariaceae(100);g__Cortinarius(100);
Otu0144 0.678
0.045 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Mycenaceae(100);g__Mycena(100);
Otu0078 0.692
0.027 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Mycenaceae(100);g__Mycena(100);s__Mycena_sp(100);
Otu0061 0.817
0.010 ** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Boletales(100);f__Rhizopogonaceae(100);g__Rhizopogon(100);
Otu0218 0.680
0.043 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Cantharellales(100);f__Botryobasidiaceae(100);g__Botryobasidium(100);s__Botryobasidium_subcoronatum(100);
Otu0030 0.976
0.003 ** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Gomphales(100);f__Gomphaceae(100);g__Gautieria(100);s__Gautieria_sp_StumpMdws2278CA(80);
Otu0187 0.703
0.018 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Thelephorales(100);f__Bankeraceae(100);g__Sarcodon(100);s__Sarcodon_imbricatus(100);
Otu0189 0.616
0.025 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Thelephorales(100);f__Thelephoraceae(100);g__Tomentella(100);
Otu0184 0.820
0.001 *** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Trechisporales(100);f__Hydnodontaceae(100);g__Trechispora(100);s__Trechispora_sp(100);
Otu0369 0.612
0.038 * k__Fungi(100);p__Basidiomycota(100);c__Microbotryomycetes(100);o__Leucosporidiales(100);f__Leucosporidiaceae(100);g__Mastigobasidium(100);s__Mastigobasidium_sp(100);
Otu0646 0.667
0.004 ** k__Fungi(100);p__Basidiomycota(100);c__Microbotryomycetes(100);o__Sporidiobolales(100);f__Sporidiobolales_family_Incertae_sedis(100);g__Rhodotorula(100);
Otu0204 0.802 k__Fungi(100);p__Basidiomycota(100);c__Microbotryomycetes(100);o__Sporidiobolales(100);f__Sporidiobolales_family_Incertae_sedis(100);g__Rhodotorula(100);s__Rhodotorula_nothofa
0.006 ** gi(100);
Otu0725 0.526
0.047 * k__Fungi(100);p__Basidiomycota(100);c__Microbotryomycetes(100);o__Sporidiobolales(100);f__Sporidiobolales_family_Incertae_sedis(100);g__Sporobolomyces(100);
Otu0413 0.594
0.040 * k__Fungi(100);p__Basidiomycota(100);c__Tremellomycetes(100);o__Cystofilobasidiales(100);f__Cystofilobasidiaceae(100);g__Guehomyces(100);s__Guehomyces_pullulans(100);
Otu0201 0.899 k__Fungi(100);p__Basidiomycota(100);c__Tremellomycetes(100);o__Cystofilobasidiales(100);f__Cystofilobasidiales_family_Incertae_sedis(100);g__Syzygospora(100);s__Syzygospora_sp(10
0.001 *** 0);
Otu0548 0.544
0.044 * k__Fungi(100);p__Basidiomycota(100);c__Tremellomycetes(100);o__Filobasidiales(100);f__Filobasidiaceae(100);g__Cryptococcus(100);s__Cryptococcus_sp(100);

Otu0566 0.548
0.023 * k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);s__Mortierella_globulifera(100);
Otu0750 0.582
0.018 * k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);s__Mortierella_humilis(100);
Otu0229 0.705
0.002 ** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);s__Mortierella_macrocystis(100);
Otu0823 0.516
0.038 * k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);s__Mortierella_macrocystis(100);
Otu0282 0.706
0.002 ** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);s__Mortierella_parvispora(100);
Otu0410 0.688
0.001 *** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);s__Mortierella_pulchella(100);
Otu0094 0.902
0.001 *** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);s__Mortierella_sp_04M_158(100);
Otu0506 0.740
0.001 *** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);s__Mortierella_sp_04M_158(100);
Otu0219 0.861
0.001 *** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);
Otu0411 0.585
0.008 ** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);
Otu0172 0.720
0.008 ** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);s__Umbelopsis_autotrophica(100);
Otu0180 0.750
0.001 *** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);s__Umbelopsis_isabellina(60);
Otu0207 0.813
0.001 *** k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);s__Umbelopsis_ramanniana(100);

Group T1 #sps. 9

stat p.value
Otu0029 0.891
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Pezizomycetes(100);o__Pezizales(100);f__Morchellaceae(100);g__Morchella(100);
Otu0042 0.632
0.007 ** k__Fungi(100);p__Ascomycota(100);c__Pezizomycetes(100);o__Pezizales(100);f__Morchellaceae(100);g__Morchella(100);
Otu0010 1.000
0.001 *** k__Fungi(100);p__Ascomycota(100);c__Pezizomycetes(100);o__Pezizales(100);f__Pyronemataceae(100);g__Scutellinia(100);s__Scutellinia_sp(100);
Otu0493 0.541
0.043 * k__Fungi(100);p__Ascomycota(100);c__Pezizomycetes(100);o__Pezizales(100);f__Pyronemataceae(100);g__Sphaerosporella(100);s__Sphaerosporella_sp(100);
Otu0023 0.835
0.002 ** k__Fungi(100);p__Ascomycota(100);c__Sordariomycetes(100);o__Sordariales(100);f__Sordariaceae(100);g__Neurospora(100);s__Neurospora_terricola(100);
Otu0592 0.542
0.034 * k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Clavariaceae(100);g__Clavaria(100);s__Clavaria_californica(100);
Otu0044 0.758
0.002 ** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Strophariaceae(100);g__Pholiota(100);s__Pholiota_highlandensis(100);
Otu0337 0.798
0.002 ** k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Tricholomataceae(100);g__Tricholoma(100);s__Tricholoma_saponaceum(100);
Otu0869 0.548
0.030 * k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mortierellales(100);f__Mortierellaceae(100);g__Mortierella(100);s__Mortierella_cystojenkinii(100);

Group T2 #sps. 15

	stat	p.value	
Otu0090	0.877	0.001 ***	k__Fungi(100);p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(100);f__Pleosporales_family_Incertae_sedis(100);g__Ochrocladosporium(100);s__Ochrocladosporium_elatum(96);
Otu0275	0.613	0.049 *	k__Fungi(100);p__Ascomycota(100);c__Pezizomycetes(100);o__Pezizales(100);f__Pyronemataceae(100);g__Geopora(100);s__Geopora_sp_BS_2010(100);
Otu0033	0.680	0.014 *	k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Lyophyllaceae(100);g__Lyophyllum(100);s__Lyophyllum_semitale(100);
Otu0017	0.773	0.003 **	k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Strophariaceae(100);g__Pholiota(100);s__Pholiota_highlandensis(100);
Otu0762	0.548	0.033 *	k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Tricholomataceae(100);g__Tricholoma(100);s__Tricholoma_magnivelare(100);
Otu0376	0.645	0.004 **	k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Boletales(100);f__Suillaceae(100);g__Suillus(100);s__Suillus_sp(100);
Otu0222	0.620	0.048 *	k__Fungi(100);p__Basidiomycota(100);c__Agaricostilbomycetes(100);o__Agaricostilbales(100);f__Chionosphaeraceae(100);g__Kurtzmanomyces(100);s__Kurtzmanomyces_nectairei(100);
Otu0379	0.568	0.017 *	k__Fungi(100);p__Basidiomycota(100);c__Microbotryomycetes(100);o__Sporidiobolales(100);f__Sporidiobolales_family_Incertae_sedis(100);g__Rhodosporidium(100);s__Rhodosporidium_sp_MAC_2011b(100);
Otu0432	0.632	0.009 **	k__Fungi(100);p__Basidiomycota(100);c__Microbotryomycetes(100);o__Sporidiobolales(100);f__Sporidiobolales_family_Incertae_sedis(100);g__Rhodotorula(100);
Otu0505	0.632	0.004 **	k__Fungi(100);p__Basidiomycota(100);c__Microbotryomycetes(100);o__Sporidiobolales(100);f__Sporidiobolales_family_Incertae_sedis(100);g__Rhodotorula(100);s__Rhodotorula_sonckii(100);
Otu0953	0.548	0.041 *	k__Fungi(100);p__Basidiomycota(100);c__Microbotryomycetes(100);o__Sporidiobolales(100);f__Sporidiobolales_family_Incertae_sedis(100);g__Rhodotorula(100);s__Rhodotorula_sonckii(100);
Otu0695	0.548	0.034 *	k__Fungi(100);p__Basidiomycota(100);c__Microbotryomycetes(100);o__Sporidiobolales(100);f__Sporidiobolales_family_Incertae_sedis(100);g__Sporobolomyces(100);s__Sporobolomyces_griseoflavus(100);
Otu0677	0.601	0.012 *	k__Fungi(100);p__Basidiomycota(100);c__Tremellomycetes(100);o__Tremellales(100);f__Tremellales_family_Incertae_sedis(100);g__Cryptococcus(100);s__Cryptococcus_aerius(100);
Otu0489	0.542	0.047 *	k__Fungi(100);p__Chytridiomycota(100);c__Chytridiomycetes(100);o__Spizellomycetales(100);f__Spizellomycetaceae(100);g__Kochiomyces(100);s__Kochiomyces_dichotomus(100);
Otu0554	0.533	0.049 *	k__Fungi(100);p__Chytridiomycota(100);c__Chytridiomycetes(100);o__Spizellomycetales(100);f__Spizellomycetaceae(100);g__Kochiomyces(100);s__Kochiomyces_sp(99);

Group T4 #sps. 5

	stat	p.value	
Otu0553	0.775	0.001 ***	k__Fungi(100);p__Chytridiomycota(100);c__Monoblepharidomycetes(100);o__Monoblepharidales(100);f__Oedogoniomycetaceae(100);g__Oedogoniomyces(100);s__Oedogoniomyces_sp_CR90(100);
Otu0048	0.694	0.012 *	k__Fungi(100);p__Chytridiomycota(100);c__Chytridiomycetes(100);o__Spizellomycetales(100);f__Spizellomycetaceae(100);g__Spizellomyces(100);
Otu0050	0.691	0.002 **	k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Hydnangiaceae(100);g__Laccaria(100);
Otu0444	0.599	0.016 *	k__Fungi(100);p__Ascomycota(100);c__Sordariomycetes(100);o__Coniochaetales(100);f__Coniochaetaceae(100);g__Coniochaeta(100);s__Coniochaeta_sp(100);
Otu0463	0.535	0.028 *	k__Fungi(100);p__Ascomycota(100);c__Dothideomycetes(100);o__Capnodiales(100);f__Davidiellaceae(100);g__Davidiella(66);s__Davidiella_tassiana(66);

Group T6 #sps. 19

	stat	p.value	
Otu0451	0.632		
0.002	**		k__Fungi(100);p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(100);f__Pleosporales_family_Incertae_sedis(100);g__Berkleasmium(100);
Otu0344	0.707		k__Fungi(100);p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(100);f__Pleosporales_family_Incertae_sedis(100);g__Massariosphaeria(100);s__Massariosphaeria_sp_FAEII
0.002	**		23a(100);
Otu0304	0.621		
0.014	*		k__Fungi(100);p__Ascomycota(100);c__Dothideomycetes(100);o__Pleosporales(100);f__Venturiaceae(100);g__Venturia(100);
Otu0426	0.548		
0.029	*		k__Fungi(100);p__Ascomycota(100);c__Leotiomycetes(100);o__Helotiales(100);f__Helotiales_family_Incertae_sedis(100);g__Glarea(100);
Otu0497	0.632		
0.003	**		k__Fungi(100);p__Ascomycota(100);c__Sordariomycetes(100);o__Chaetosphaeriales(100);f__Chaetosphaeriaceae(100);g__Codinaeopsis(100);s__Codinaeopsis_sp(100);
Otu0893	0.528		
0.029	*		k__Fungi(100);p__Ascomycota(100);c__Sordariomycetes(100);o__Hypocreales(100);f__Hypocreaceae(100);g__Sphaerostilbella(100);s__Sphaerostilbella_novae_zelandiae(100);
Otu0365	0.548		
0.036	*		k__Fungi(100);p__Ascomycota(100);c__Sordariomycetes(100);o__Sordariales(100);f__Chaetomiaceae(100);g__Chaetomium(100);
Otu0475	0.632		k__Fungi(100);p__Ascomycota(100);c__Sordariomycetes(100);o__Sordariomycetes_order_Incertae_sedis(100);f__Magnaporthaceae(100);g__Gaeumannomyces(100);s__Gaeumannomyces
0.004	**		_incrustans(100);
Otu0297	0.837		
0.001	***		k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Marasmiaceae(100);g__Hydropus(100);s__Hydropus_marginellus(100);
Otu0183	0.894		
0.001	***		k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Agaricales(100);f__Psathyrellaceae(100);g__Coprinopsis(100);s__Coprinopsis_calospora(100);
Otu0590	0.548		
0.031	*		k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Russulales(100);f__Russulaceae(100);g__Lactarius(100);s__Lactarius_cf_gerardii_AVerbeken05_283(100);
Otu0660	0.632		
0.002	**		k__Fungi(100);p__Basidiomycota(100);c__Agaricomycetes(100);o__Thelephorales(100);f__Thelephoraceae(100);g__Pseudotomentella(100);s__Pseudotomentella_atrofusca(100);
Otu0507	0.549		
0.017	*		k__Fungi(100);p__Basidiomycota(100);c__Tremellomycetes(100);o__Cystofilobasidiales(100);f__Cystofilobasidiaceae(100);g__Mrakia(100);s__Mrakia_frigida(100);
Otu0845	0.548		
0.027	*		k__Fungi(100);p__Basidiomycota(100);c__Wallemiomycetes(100);o__Geminibasidiales(100);f__Geminibasidiaceae(100);g__Geminibasidium(100);s__Geminibasidium_sp(100);
Otu0227	0.945		
0.001	***		k__Fungi(100);p__Basidiomycota(100);c__Wallemiomycetes(100);o__Wallemiales(100);f__Wallemiaceae(100);g__Wallemia(100);s__Wallemia_muriae(100);
Otu0394	0.670		k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Kickxellales(100);f__Kickxellaceae(100);g__Ramicandelaber(100);s__Ramicandelaber_sp_HMH_2010b(75)
0.005	**		;
Otu0416	0.536		
0.038	*		k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Rhizopodaceae(100);g__Rhizopus(100);s__Rhizopus_arrhizus_var._arrhizus(100);
Otu0881	0.577		k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);s__Umbelopis_ramanniana_var_angulisp
0.036	*		ora(100);
Otu0926	0.548		
0.040	*		k__Fungi(100);p__Zygomycota(100);c__Zygomycota_class_Incertae_sedis(100);o__Mucorales(100);f__Umbelopsidaceae(100);g__Umbelopsis(100);s__Umbelopsis_dimorpha(100);