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GENOMIC AND PHYSIOLOGICAL BIOREMEDIATION CHARACTERISTICS OF THE ACTINOBACTERIA FRANKIA

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GENOMIC AND PHYSIOLOGICAL BIOREMEDIATION CHARACTERISTICS OF THE ACTINOBACTERIA *FRANKIA*

BY

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DISSERTATION

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ABSTRACT

Introduction: *Frankia* is a genus of symbiotic, nitrogen fixing actinobacteria found in the soil and root tissue of actinorhizal plants throughout the world. Both *Frankia* and actinorhizal plants are resistant to a wide range of environmental and chemical stresses including heavy metals, high salinity, and drought. This makes *Frankia* and the actinorhizal symbiosis an interesting candidate for bioremediation applications. However, the microbial community found in the actinorhizal rhizosphere and surrounding soil has been implicated in some of the symbiotic and resistance traits attributed to *Frankia.* This necessitates thorough investigation of the genomic and genetic components of any bioremediation traits possessed by *Frankia*.

Aims: This work pursued three primary aims: 1). To expand the range of available whole genome sequences available for the genus *Frankia* and use them to assess the pan-genome characteristics of *Frankia,* 2). To determine the composition of the microbial communities associated with *Frankia* and actinorhizal plants*,* and 3). To assess the potential of *Frankia* to remediate dioxin-like compounds.

Results: Pan-genome analysis of 45 *Frankia* genomes revealed that the *Frankia* genus has small core genome made up of 44 genes with 9013 shell genes and over 62,000 cloud genes. Analysis also showed that *Frankia* has an open pan-genome structure with a Heap's alpha value of 0.86. Analysis of the 5 clades that form the *Frankia* genus indicated that each clade has a closed pan-genome structure with core genome sizes ranging from 383 to 3414. Metagenomic analysis of the microbiomes associated with *Coriaria myrtifolia*, *Casuarina glauca*, and New Hampshire lithic environments identified highly diverse communities that included *Frankia* strains not previously known to be associated with these specific actinorhizal hosts. NMDS analysis showed that each tissue type assessed had a unique microbial community structure. This work also found that microbial diversity was positively correlated with proximity to an actinorhizal host plant. Bioinformatic analysis identified 5 *Frankia* strains with a putative *bph* operon. Two strains were assessed further and exhibited resistance to dioxin-like compounds (biphenyl, 4-chlorobiphenyl, and dibenzofuran). The same two strains, EuI1c and EUN1f, were able to grow with dioxin-like compounds as a sole source of carbon in minimal media. RNA sequencing and qPCR showed that the putative *bph* operon was up-regulated in *Frankia* in response to dioxin-like compound exposure. Lastly, GC-FID analysis showed that *Frankia* is able to degrade biphenyl in liquid culture. These results advance the basic understanding of *Frankia* biology, and show that *Frankia* has the ability to be used as a bioremediation agent.

CHAPTER ONE

INTRODUCTION

Summary

Accelerating global change over the last century, including climate change, habitat loss, land-use change, pollution, and extinction, represents an existential threat to humanity and innumerable other species. These grand challenges are fundamentally interconnected which requires multidisciplinary solutions. The complex nature of environmental pollution makes novel, biologically sound, remediation strategies particularly vital.

Persistent organic pollutants (POPs) are ubiquitous environmental contaminants found throughout the world, and dioxin-like compounds are one of the most toxic and widespread classes of organic pollutants. Dioxin-like compounds are a functionally defined group of compounds that interfere with the aryl hydrocarbon receptor in vertebrates. The dioxin-aryl hydrocarbon receptor interaction leads to several chronic toxic effects including cancer, endocrine disruption, and teratogenesis. Dioxin-like compounds are also acutely toxic, causing contact dermatitis and tissue necrosis in vertebrates and invertebrates. Historic usage of dioxin-like compounds in a wide range of industrial applications including electrical transformers led to extensive contamination across the US and throughout the rest of the world, and dioxin-like compounds continue to be produced during the combustion of fossil fuels, waste materials, and improper electronics recycling. Current remediation efforts are very costly and disruptive, leaving remediated sites susceptible to erosion and colonization by exotic invasive species. Furthermore, many remediation methods fail to completely degrade dioxin-like compounds. Instead, dioxin-like compound-contaminated soil is often transported to toxic waste landfills, which become pollution risks themselves as they release toxic leachate. Therefore, new, more sustainable remediation solutions are needed to address dioxin-like compound contamination.

One of the most promising alternative remediation approaches is bioremediation, using biological organisms to degrade pollution *in situ*. Research on bioremediation has investigated the utility of plants, fungi, and bacteria as remediation agents, but it has proven difficult to identify candidates that combine two crucial traits necessary for effective bioremediation: the ability to degrade a target compound, and the ability to persist at the contaminated site. The *Frankia*-plant actinorhizal symbiosis is an intriguing system for bioremediation because both actinorhizal plants and *Frankia* bacteria are known to survive in harsh environments. The nature of the symbiosis means that actinorhizal plants could be used as source populations for remediating bacteria. Sequence data indicates that *Frankia* may have uncharacterized degradation pathways that could facilitate the remediation of dioxin-like compound-contaminated sites. However, these pathways must be experimentally confirmed, and the potential synergy represented by symbiotic communities must be explored in order to take full advantage of the natural remediation ability of the actinorhizal symbiosis. The declining cost of sequencing and growing availability of genomic information and analytic tools also provides the opportunity to identify new putative functions possessed by plant associated communities.

Background

Frankia biology

Frankia is a genus of gram positive, filamentous, nitrogen fixing actinobacteria that forms a facultative symbiosis with 8 families of actinorhizal plants (Benson and Silvester 1993, Chaia et al. 2010, Normand et al. 2014). *Frankia* has several morphological characteristics that develop depending on its environment. Free living and symbiotic *Frankia* are both able to produce sporangia that contain viable spores. Most strains of *Frankia* are also able to produce hopanoid-rich vesicles that facilitate nitrogen fixation by excluding oxygen and preserving oxygen-sensitive nitrogenase enzymes that catalyze the reduction of atmospheric N_2 to NH_3. *Frankia* also forms symbiotic nodules on compatible host plants that provide nitrogen to the actinorhizal plant which in turn provide carbon sources to *Frankia* (Benson and Silvester 1993, Berry et al. 1993, Chaia et al. 2010, Normand et al. 2014).

Based on 16S data and whole genome analyses, the *Frankia* genus is divided into 4 main clades. The largest clade, clade 1, is further divided into clade 1a and 1b. These 5 genetically distinct groups roughly correspond to the host range groups identified in numerous *Frankia* strains. Clades 1-3 each have a characteristic host range while clade 4 is atypical and rarely forms symbiotic nodules (Normand et al. 1996, Benson and Dawson 2007, Normand et al. 2007, Tisa et al. 2013).

Frankia Ecology

The *Frankia* symbiosis is thought to be initiated in a similar manner to the rhizobium-legume (RL) and arbuscular mycorrhizae (AM) symbioses with the host plant releasing a flavonoid signaling molecule that induces the production of a nodulation factor by *Frankia* (Wall 2000, Popovici et al. 2011, Schwencke and Caru 2010). However, unlike the RL and AM systems, the nodulation factors in the *Frankia*-actinorhizal symbiosis has yet to be conclusively determined. Recent work has narrowed key signaling chemicals to small hydrophilic molecules, but the exact structure remains unknown (Cissoko et al. 2018). Once the putative *Frankia* nodulation factor is detected by the actinorhizal host plant, the nodulation process is initiated by an extensive signaling pathway in the host plant. Nodulation can be either intercellular, or intracellular depending on whether *Frankia* penetrates the root hairs of its host, or between root cells (Wall 2000).

Individual strains of *Frankia* are necessary and sufficient to induce nodule formation, and pure cultures of *Frankia* are able to form fully functional, nitrogen fixing nodules. However, recent studies have shown that nodule occupancy appears to be more cosmopolitan than previously thought (D’Angelo 2016). Initial data suggest that nodulation can be enhanced by the presence of non-*Frankia* bacteria, and the diverse nodule communities that have been characterized by 16S sequencing suggest that other bacteria may play a role in the nodule community, rather than being “cheaters” and simpley taking advantage of the favorable nodule environment (D’Angelo 2016, Ghodhbane-Gtari et al. 2019). These characteristics are important when assessing the potential of the *Frankia*-actinorhizal symbiosis as a bioremediation tool. *Frankia* nodules harboring other bacteria capable of bioremediation would increase the number of potential applications for the actinorhizal symbiosis.

Nodule based nitrogen fixation is a critical aspect of the actinorhizal symbiosis and a major characteristic of most *Frankia* strains. Nitrogen fixation in *Frankia* takes place in vesicles produced to protect nitrogenase enzymes that are extremely oxygen sensitive. The vesicle wall has a high hopanoid content which excludes oxygen (Berry et al. 1993). All *Frankia* strains in clades 1-3 contain the *nif* regulon and are able to fix nitrogen as free living bacteria and during symbiosis. However, most clade 4 strains appear to have lost the nitrogen fixation function and no longer contain the *nif* regulon (Normand et al. 2007, Tisa et al. 2013).

Frankia genomic traits

Frankia and actinorhizal plants are globally distributed in environments ranging from harsh xeric conditions in Africa to arctic tundra conditions in Canada and Russia (Benson and Silvester 1993). Certain *Frankia* strains, especially strains in clade 1b, also tolerate high salinity levels (Ngom et al. 2016). Some *Frankia* strains are also resistant to a number of heavy metals (Richards et al. 2002). *Frankia* is also known to degrade several organic pollutants. Previous studies have confirmed that *Frankia* degrades atrazine and naphthalene in controlled aqueous conditions (Rehan et al. 2014, Baker et al. 2015). Growth assays show that *Frankia* QA3 resists naphthalene concentrations of at least 250 µM when supplemented with propionate, and is able to grow with naphthalene as the sole carbon source available (Baker et al 2015). qRT-PCR and proteomics data show that *Frankia* QA3 degrades naphthalene using the protocatechuate pathway (Baker et al 2015). The genes in the *atz* pathway (atrazine degradation pathway) enable at least two different *Frankia* strains, *Frankia* ACN14a and *inefficax*, to degrade atrazine. This ability was hypothesized based on bioinformatics, and confirmed using qRT-PCR and GC-MS analyses to identify upregulated genes and quantify the degradation of atrazine (Rehan et al. 2014).

Both of these compounds are toxins associated with many of the same industrial and agricultural applications as dioxin-like compounds. However, the genetic pathways for the initial degradation of atrazine and naphthalene are not able to degrade dioxin-like compounds based on *in silico* analysis (Swanson, unpublished data).

Frankia may also be able to degrade phenolic compounds, although direct evidence of this has not been published. Phenolic compounds are produced in relatively high concentrations by alders, one of the major host families of *Frankia* (Vogel and Dawson 1986). While some alder-derived phenolic compounds inhibit *Frankia,* at least one compound, o-hydroxyphenylacetic acid, promotes *Frankia* growth (Vogel and Dawson 1986). *Frankia* also produces phenolic compounds (Benson and Silvester 1993), which suggests that it may degrade them as well in order to scavenge carbon. This idea is supported by the presence of phenol catabolic enzymes in a number of *Frankia* genomes (Swanson, unpublished data).

There is also indirect evidence that *Frankia* is resistant to dioxin-like compound toxicity and may degrade some dioxin-like compound compounds (Roy et al. 2007, Lefrancois et al. 2009, Lefrancois et al. 2010). The actinorhizal symbiosis has been used to reclaim land degraded during oil extraction from Canadian tar sands. Sand oil extraction leaves land contaminated by many organic pollutants including polycyclic aromatic hydrocarbons (PAHs) which are structurally and chemically similar to dioxin-like compounds. Mineralization of PAHs was increased in field sites planted with the actinorhizal plant *Alnus glutinosa* after one year, compared to sites that were left barren. However, the mineralization rate at actinorhizal planted sites and control sites equalized after two years (Lefrancois et al 2010).

Several strains of *Frankia* have also been identified in PAH and dioxin-like compound polluted soils, suggesting that *Frankia* are at least resistant to dioxin-like compound toxicity. When *Alnus incana* seedlings were planted in PAH polluted soil collected from 8 locations in post-industrial Wolverhampton, *Frankia* clade 1a and 1b successfully nodulated plants in each condition tested (Ridgway et al. 2004). However, plants in soils with the highest PAH contamination had significantly reduced plant biomass, number of nodules, and nodule biomass compared to nodules and plants at less contaminated sites. Interestingly, the most polluted sites are also the only ones in which clade 3 *Frankia* nodulated *A. incana* plants, suggesting that environmental stress may play a role in *Frankia*-actinorhizal host specificity (Ridgway et al. 2004).

Additional evidence of that *Frankia* is resistant to dioxin-like compounds comes from a study on contaminated wastewater sludge in China. Isolation of clade 2 *Frankia* 16S RNA from sludge collected from facilities with significant PCB contamination indicates that *Frankia* is an active member of soil microbial communities that may degrade dioxin-like compounds. PCBs constituted up to 25% of the total available organic carbon in the sludge from which *Frankia* 16S RNA was isolated, suggesting that it was likely one of the carbon sources for active bacteria, including *Frankia* (Fang et al. 2013).

Frankia Metagenomics and Pan-genome

Advances in computing power and sequencing technologies in the past decade have dramatically increased access to genomic and metagenomic data. Since the first bacterial genome was completed in 1995 (Fleischmann et al. 1995), the cost of sequencing as deceased by orders and magnitude and the number of draft and completed genomes has increased exponentially yearly. NCBI now has over 20,000 complete bacterial genomes and over 500,000 bacterial draft genomes (NCBI). Besides the abundance of whole genome sequencing data, over 5,000 bacterial metagenomic studies have been published using both shotgun sequencing techniques and amplicon based approaches. Despite a lack of genetic tools, *Frankia* has not been left out of the sequencing age. 53 *Frankia* genomes have been sequenced to date, either with traditional isolation based techniques or metagenomic based sequencing and assembly. Previous analysis of *Frankia* genomic data has shown that members of genus have genomes that vary in size substantially, from 4.9 Mb to 11.2 Mb suggesting a high diversity between members of the genus (Normand et al. 2007).

Genome size is also an important factor in composition of the core and pan-genome of a species or genus. The core and pan-genome represent the essential and accessory genes of a specific taxa or set of genomes. The strict core-genome is estimated by identifying the genes or orthologous clusters that are present in every genome or strain of a given species, while the pan-genome is made up of every gene or ortholog identified in any of the analyzed genomes. Clearly, the composition of the core and pan-genome is dependent on the data set analyzed as well as the quality and completeness of the genomes analyzed. Despite these challenges, analyzing pan-genomes can give considerable insight into the dynamics of genome evolution. It is becoming increasingly clear that horizontal gene transfer and subsequent genome reduction is an important element of bacterial evolution (Gogarten and Townsend 2005, Syvanen 2012, Wolf and Koonin 2013, Soucy et al. 2015). On an evolutionary time scale, horizontal gene transfer can introduce genes from almost any organism to any other organism (Brown 2003, Almeida et al. 2008, Soucy et al. 2015). However, horizontal gene transfer is much more common between closely related species (Soucy et al. 2015). Therefore, assessing the pan-genome of closely related species such as strains that make up the genus *Frankia* is interesting and worthwhile. This is particularly relevant in the evolutionary dynamics of a specific trait, such as resistance to toxins, within a microbial community.

Previous bacterial community studies have assessed the phyllosphere and rhizosphere microbiome of numerous plants including rhizobium host plants (Roeland et al. 2012, Mendes et al. 2013, Singh et al. 2019, Parasuraman et al. 2019, Lui et al. 2020, Korenblum et al. 2020). In addition to assessing how community structures shift between phyllosphere and rhizosphere, valuable insight into community dynamics has been gained by assessing the difference between the epiphyte and endophyte communities within the phyllosphere (Bacon and White 2015). However, the *Frankia*-actinorhizal symbiosis has not been adequately investigated to date. *Coriaria myrtifolia* is one of the host plants of type 2 *Frankia* found throughout the eastern Mediterranean Ocean (Normand et al. 2007). *Coriaria myrtifolia* has been used in the dying and tanning industry in the Mediterranean since the tenth century CE (Cardon and Pinto 2007). However, all parts of the plant contain elevated concentrations of a sesquiterpene lactone called coriamyrtine that is hightly toxic to both humans and livestock (De Haro et al. 2005). The Toxicity of *C. myrtifolia* provides additional motivation to understand it’s ecology and the impact of plant toxins on phyllosphere microbiota.

Remediation Potential

Frankia as a Biodegrading Agent

Medhat Rehan, Erik Swanson and Louis S. Tisa

Abstract

The *Frankia* actinorhizal plant symbiosis plays an important role in colonization of soils contaminated with toxic aromatic hydrocarbons. Our understanding of the bacterial partner, *Frankia*, in the actinorhizal symbiosis has been greatly facilitated by the availability of sequenced genomes. The analysis of these *Frankia* genomes has suggested that these bacteria are metabolically diverse and have potential for toxic aromatic hydrocarbon degradation. In this chapter, we explore what is known about that metabolic potential.

Introduction

Frankia are filamentous nitrogen-fixing Gram-positive actinobacteria that are found as free-living microbes in the soil and in symbiotic associations with actinorhizal plants (Normand et al. 2014, Chaia et al. 2010, Benson and Silvester 1993, Schwencke and Caru 2010, Diagne et al. 2013). These bacteria fix nitrogen by converting atmospheric N_2 into biologically useful ammonia and supply the host plants with a source of reduced nitrogen. *Frankia* are developmentally complex and form three cell types: vegetative hyphae, spores located in sporangia, and vesicles. Hyphae are septate structures and form the growing state of this microbe. Under appropriate conditions, either terminal or intercalary multilocular sporangia are produced and contain many spores. When mature, the spores are released from the sporangia. The spores are presumed to aid in the survival and dispersal of *Frankia* in the environment. Vesicles are produced under nitrogen-limited conditions and consist of unique lipid-enveloped cellular structures that contain the enzymes responsible for nitrogen fixation. Thus, vesicles act as specialized structures for the nitrogen fixation process. *Frankia* are able to establish symbiotic nitrogen-fixing associations with over 220 species of woody dicotyledonous plants, termed actinorhizal plants, that are found in eight families of angiosperms (Normand et al. 2014, Benson and Silvester 1993, Schwencke and Caru 2001, Diagne et al. 2013, Benson and Dawson 2007). The symbiosis with *Frankia* allows these actinorhizal host plants to colonize nutrient-poor soil and harsh environments. Actinorhizal plants have been used to recolonize and reclaim industrial wastelands and environments contaminated with heavy metals and toxic aromatic hydrocarbon (Wheeler and Miller 1990, Lefrancois et al. 2010, Roy et al. 2007, Roy et al. 2005, Torri et al. 2010, Lorenc-Plucinska et al. 2013, Belanger et al. 2011, Sun et al. 2004, Ridgway et al. 2004). The metabolic potential of these bacteria has only recently been investigated in the context of bioremediation (Rehan et al. 2014a, Rehan et al. 2014b, Baker et al. 2015).

1.1. Frankia genomics and identification of metabolic potential

Based on phylogenetic analysis, *Frankia* strains have been classified into four main lineages (Normand et al. 1996, Ghodhbane-Gtari et al. 2010, Nouioui et al. 2011, Cournoyer and Lavire 1999, Gtari et al. 2014). Members of lineage 1 are found infective on host plants of the Betulaceae (Alnus), Myricaceae, and Casuariaraceae families, while lineage 2 represents strains that are infectiveon Rosaceae (Dryas, etc.), Coriariaceae (Coriaria), Datiscaceae (Datisca), and the genus Ceanothus (Rhamnaceae). Members of lineage 3 are the most promiscuous and are infective on Eleagnaceae, Rhamnaceae, Myricaceae, Gynmmostoma, and occasionally Alnus. The fourth *Frankia* lineage consists of the “atypical” strains which are unable to reinfect actinorhizal host plants or form ineffective root nodule structures that are unable to fix nitrogen. Our understanding of this genus has been greatly enhanced by the sequencing of several *Frankia* genomes from the different *Frankia* lineages (Normand et al. 2007, Ghodbhane-Gtari et al. 2013, Ghodbhane-Gtari et al. 2014, Hurst et al. 2014, Mansour et al. 2014, Nouioui et al. 2013, Sen et al. 2013, Tisa et al. 2013, Wall et al. 2013, Bagnarol et al. 2007). Analysis of *Frankia* genomes has revealed new potential with respect to metabolic diversity, natural product biosynthesis, and stress tolerance, which may help aid the cosmopolitan nature of the actinorhizal symbiosis (Tisa et al. 2013, Wall et al, 2013, Bagnarol et al. 2007, Udwary et al. 2011). In this chapter, we will describe what is known about the degradation properties of these bacteria.

2. Rhizodegradation

Among bacteria with bioremediation potential, *Frankia* are unique in that these bacteria form a symbiosis with actinorhizal plants. The implications of this trait for bioremediation efforts have only recently been explored. In the context of bioremediation, the most extensively studied system is the *Frankia*–Alnus association. Diverse assemblages of free-living *Frankia* strains are present in soils with polyaromatic hydrocarbon (PAH) contamination (Lefrancois et al. 2010, Roy et al. 2007, Roy et al. 2005, Ridgway et al. 2004, Fang et al. 2013, Diagne et al. 2015, Mallet and Roy 2014, Bissonnette et al. 2014). These *Frankia* strains readily form symbioses with alders, resulting in greatly increased alder fitness in harsh environments. The *Frankia*–alder symbiosis also increases the mineralization of representative organic pollutants in oil-sands reclamation sites. The *Frankia*–alder symbiosis has been used in reclamation projects because of these traits (Diagne et al. 2013, Lefrancois et al. 2010, Diagne et al. 2015, Mallet and Roy 2014, Bissonnette et al. 2014). Free-living *Frankia* also appears to be part of natural degradation communities. Specifically, *Frankia* has been found to be one of the most abundant genera in wastewater treatment communities (Fang et al. 2013). Based on these findings, *Frankia* appears to be an underutilized tool in holistic remediation approaches.

3. S- triazines degradation

3.1. Overview

Triazines are a class of herbicides composed of a heterocyclic six-membered ring with alternating carbon and nitrogen atoms joined by double bonds. These herbicides have been used extensively for control of broadleaf and grassy weeds in corn, sorghum, and sugarcane cultivation. Atrazine and simazine are the most ubiquitous members of the s-triazine family. Biodegradation of atrazine is a complex process and depends on the nature and amount of atrazine in soil or water (Mandelbaum et al 1995, Rousseaux et al. 2001, Singh et al. 2004). There are four major steps in atrazine degradation: hydrolysis, dealkylation, deamination, and ring cleavage. For the hydrolysis step, an amidohydrolase enzyme (AtzA) cleaves the carbon-chlorine (C-Cl) bond and thus dechlorinates atrazine to hydroxylatrazine. This intermediate is dealkylated and deaminated at the ethyl and isopropyl groups by the amidohydrolase enzymes, AtzB and AtzC, to produce cyanuric acid. This product is converted to ammonia and carbon dioxide by the AtzD, AtzE, and AtzF enzymes (Crawford et al. 1998, Govantes et al. 2009, Scott et al. 2009).

3.2. S-triazine degradation pathway in Frankia

In *Frankia*, the first two steps in atrazine degradation have been identified as well as the regulation of their gene expression (Rehan et al. 2014). The mineralization of atrazine to ammonia and carbon dioxide is generally initiated by hydrolytic dechlorination, catalyzed by the enzyme atrazine chlorohydrolase (AtzA). Alternatively, this reaction is catalyzed by another atrazine chlorohydrolase (TrzN), which is also able to use atrazine derivatives including desethyl-desisopropylatrazine as substrates. Analysis of the *Frankia* genomes identified candidate genes for the atrazine degradation pathway (Figure 1). The trzN gene was identified in *Frankia* alni ACN14a (FRAAL1474) and *Frankia* sp *inefficax* (Fra*inefficax*_5874) genomes and its amidohydrolase gene product is predicted to remove chlorine from s-triazine compounds to produce hydroxyatrazine or ammeline from atrazine and desethyl desisopropyl atrazine, respectively. Furthermore, a putative atzB gene was also identified in both *Frankia* genomes (FRAAL1473 and Fra*inefficax*_5875) whose predicted gene product, adenosine aminohydrolase 3, is involved in the dealkylation reaction of the N-ethyl group from hydroxyatrazine transforming it into N isopropylammelide. Physiological studies showed that *Frankia* ACN14a and *inefficax* cultures are able to break down atrazine and desethyl-desisopropylatrazine producing the end products hydroxyatrazine and N-isopropylammelide. Although the enzymes were not purified, these data clearly showed metabolism of atrazine. Analysis of gene expression in *Frankia* ACN14a found that the two genes, trzN (FRAAL1474) and atzB (FRAAL1473) are under control of the atzR (FRAAL1471) gene, which encodes a predicted LysR-type transcriptional regulator.

Bioinformatics analysis of the *Frankia* genomes revealed a potential full pathway for atrazine degradation in the *Frankia* sp *inefficax* genome (Figure 2). The atzC (Fra*inefficax*_4724) gene, which encodes a putative amidhydrolase enzyme, was identified and is predicted to be involved in the dealkylation of the N-isopropyl group from atrazine to produce cyanuric acid. With other bacterial systems, cyanuric acid is hydrolyzed to ammonium and carbon dioxide via the atzDEF operon (Govantes et al. 2009, Scott et al, 2009, Govantes et al. 2010). In *Frankia inefficax*, the atzD (Fra*inefficax*_3137) gene product is predicted

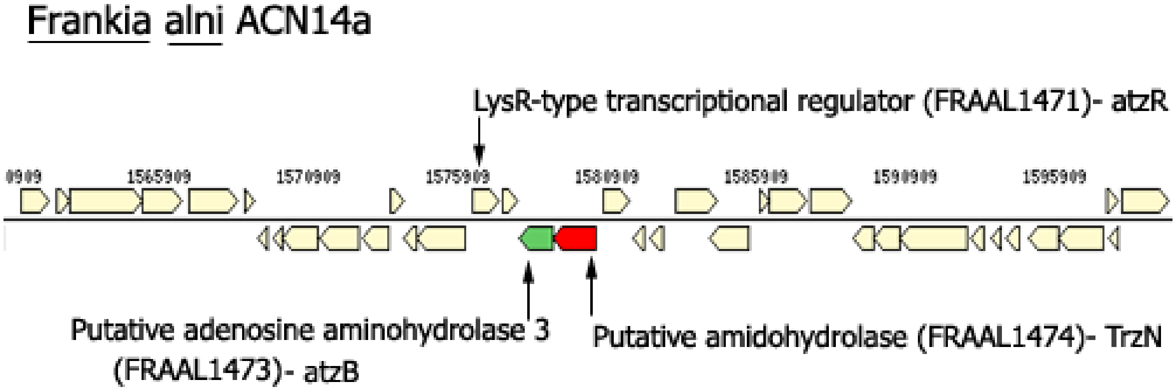


Figure 1. Gene cluster organization in Frankia alni ACN14a for atrazine degradation. The cluster contains a putativetrzN (FRAAL1474), putative atzB (FRAAL1473), and putative LysR-family transcriptional (atzR).

to transform cyanuric acid into carboxybiuret, which spontaneously decarboxylates to biuret. Putative atzE (Fra*inefficax*_1007 and 1008), and atzF (Fra*inefficax*_3831) genes were also identified in the *Frankia inefficax* genome and their gene products expected to complete s-triazine mineralization by converting biuret to allophanate and ammonia plus carbon dioxide. A trzR (Fra*inefficax*_3136) gene, which encodes a GntR family transcriptional regulator, is found before the atzD gene and is involved in the expression of that gene (Rehan unpublished).

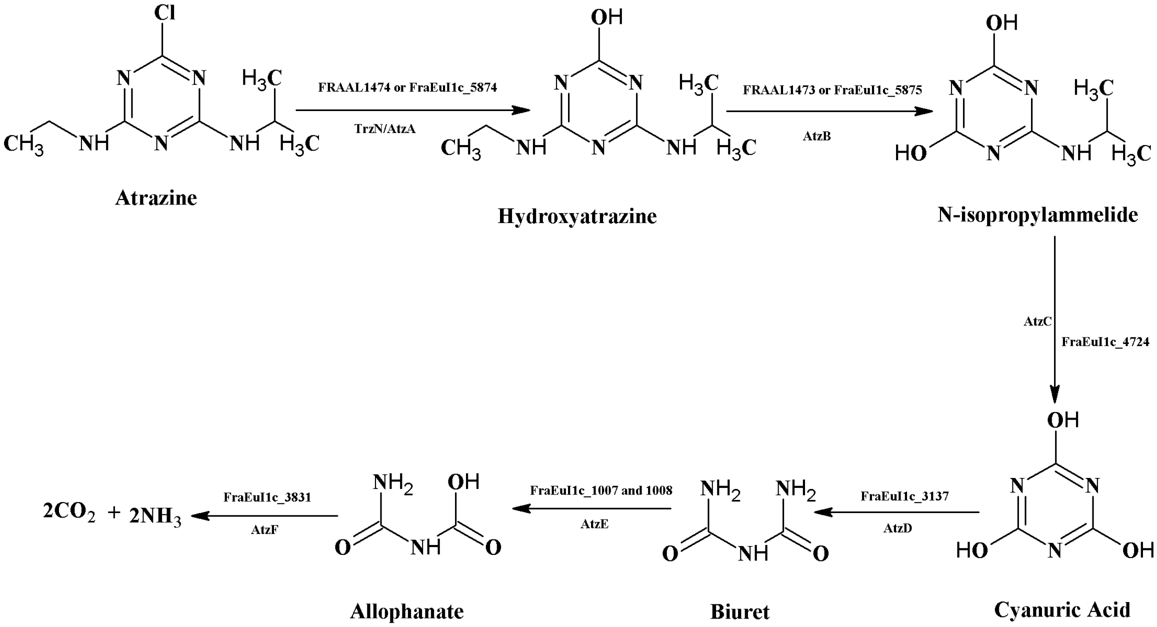


Figure 2. The atrazine degradation steps in Frankia strains inefficax and ACN14a include atrazine dechlorination and dealkylation and ring cleavage by TrzN, atzB, and atzD enzymes.

4. Aromatic compounds degradation

4.1. Biphenyl and polychlorinated biphenyl

Biphenyls and polychlorinated biphenyls (PCBs) are some of the most recalcitrant xenobiotics found in the environment. The degree of chlorination differs greatly among the PCBs, ranging *Frankia* as a Biodegrading Agent from 1 to 10, as does their position on the carbon atoms. Since the mid-1980s, the use of PCBs has been phased out in many countries. However, due to their toxicity, persistence in the environment, and potential carcinogenicity, they are still a major global environmental problem (Asturias et al. 1995, Fujihara and Furukawa 2008, Ang et al. 2005).

Bacteria degrade biphenyl and PCBs via the meta-cleavage pathway, which is encoded by the bph operon, and produces tricarboxylic acid and chlorobenzoate (CBA) as intermediates (Fuhihara and Furukawa 2008, Ang et al. 2005, Erickson and Mondello 1993, Furukawa et al. 1993). The first enzyme in this pathway is biphenyl dioxygenase, which is a multimeric complex consisting of the large α and small β subunits, and the ferredoxine and ferredoxine reductase subunits. The degradation process is initiated by biphenyl dioxygenase which incorporates two oxygen atoms at the 2 and 3 carbon positions of the aromatic ring (called 2,3-dioxygenation) to generate hydroxyl groups. For PCBs degradation, biphenyl dioxygenase catalyzes the initial 2,3-dioxygenation, and dihydrodiol dehydrogenase converts the product into 2,3-dihydroxybiphenyl. The enzyme, 2,3 dihydroxybiphenyl dioxygenase, cleaves the dihydroxylated ring to produce (chlorinated) 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoic acid (HOPDA). A hydrolase enzyme then hydrolyzes HOPDA to (chlorinated) benzoic acid and 2-hydroxypent a-2,4-dienoate.

4.1.1. Biphenyl degradation pathway in Frankia

At least four *Frankia* strains (ACN14a, CcI3, EUN1f, and *inefficax*) are resistant to biphenyl and polychlorinated biphenyl (PCB) at concentrations up to 5mM (Rehan 2012, Swanson unpublished results). Data mining for known organisms capable of biphenyl degradation (Asturias et al. 1995, Sylvester et al. 1996) and the availability of a *Frankia* genome database enabled the identification of genes potentially involved in biphenyl degradation in several of the *Frankia* strains listed above. Five genes were identified that encode enzymes involved in biphenyl degradation: the alpha and beta subunits of the aromatic-ring-hydroxylating dioxygenase, a Rieske (2Fe-2S) iron–sulfur domain protein, an alpha/beta hydrolase fold protein, and a short-chain dehydrogenase/reductase (SDR). These enzymes are putatively capable of oxidizing and hydroxylating benzene rings, and are also known as the upper meta-cleavage pathway. A lower pathway of aromatic ring degradation consisting of three genes (encoding the 2-hydroxypenta-2,4-dienoate hydratase; acylating acetaldehyde dehydrogenase; and 4-hydroxy-2-oxovalerate aldolase) is located downstream of this operon (Pieper et al. 2008, Swanson and Tisa unpublished data). Figure 3 shows the gene neighborhood of the Biphenyl degradation genes. These genes were also found in *Frankia* strain EUN1f and Dg1 genomes (Swanson and Tisa unpublished). Both the meta-cleavage upper and the lower pathways are commonly referred to as the bph operon in several other PCB-degrading bacteria. *Rhodococcus* RAH1, a species closely related to *Frankia*, utilizes bph genes homologous to those found in *Frankia* to metabolize PCBs as a sole carbon and energy source (Masai et al. 1995). Since at least two genes (Aromatic-ring-hydroxylating dioxygenase, subunit alpha-like protein (Fra*inefficax*_4097) and short-chain dehydrogenase/reductase (Fra*inefficax*_4101) in the bph operon in *Frankia* are upregulated in the presence of biphenyl, it is likely that *Frankia* also uses the bph operon to metabolize biphenyl and PCBs (Rehan and Tisa unpublished)

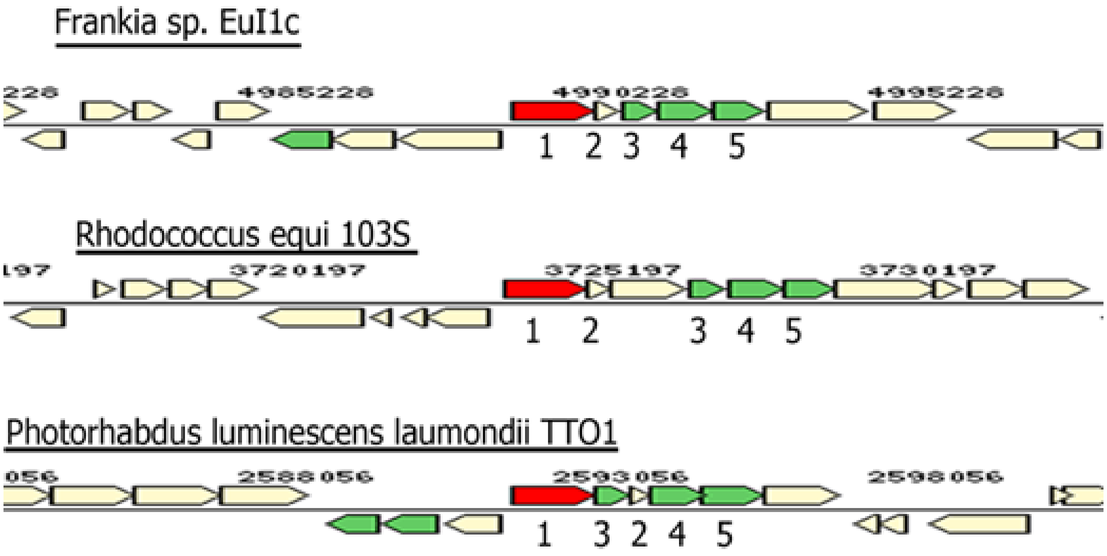


Figure 3. The gene neighborhood of bph operon in Frankia inefficax in comparison to Rhodococcus equi 103S and Photorhabdus luminescens laumondii TTO1 operon. (1) Aromatic-ring-hydroxylating dioxygenase, subunit alpha. (2) Rieske (2Fe-2S) iron–sulfur domain protein. (3) Aromatic-ring-hydroxylating dioxygenase, subunit beta. (4) Alpha/beta hydrolase fold protein. (5) Short-chain dehydrogenase/reductase SDR.

4.2. Phenol degradation

4.2.1. Overview

Phenol (or hydroxybenzene) consists of a benzene ring substituted with a hydroxyl group. Derivatives of this molecule are colloquially known as phenolic compounds. Phenolic compounds are ubiquitous chemicals with diverse properties and uses. The simplest phenolic compound, phenol, is widely used in oil and coal processing, tinctorial and metallurgic industries, and many other industrial applications. Phenol also enters the environment via vehicle exhaust and as the product of natural metabolic processes, and chlorophenols are widely used as biocides in agricultural applications (for a review see Michalowicz and Duda 2007). While anthropogenic phenolics are often hazardous, natural phenolic compounds are mostly harmless in the concentrations that are found in foods such as coffee and tea, and some are used as antibiotics (Belofsky et al. 2004, Naczk and Shahidi 2004). However, the toxicity of some phenolics, particularly phenol and chlorinated phenols, has prompted considerable research activity devoted to phenol remediation. Acute and chronic exposure to phenol and chlorophenol has serious health effects. Phenol and chlorophenol cause lipid peroxidation which ultimately leads to tissue necrosis, and liver and kidney damage (U.S. department of health and human services 2008). Additionally, chlorophenol exposure is associated with elevated risks of cancer, immune deficiencies, and teratogenic effects (Buckley et al. 2000, Moridani et al. 2004, Hooiveld et al. 1994).

4.2.2. General phenol degradation pathway

One of the most promising techniques for removing anthropogenic phenolics from the environment is bioremediation. As was the case for many compounds, the degradation pathway for phenol was first elucidated in a Pseudomonas strain (Shingler and Moore 1994). Most bacteria degrade phenolics using catechol catabolic enzymes, most importantly catechol-2,3-dioxygenase. Phenols are first hydroxylated to form catechol, and then catechol-2,3-dioxygenase cleaves the benzene ring at the meta position (Shingler and Moore 1994). Therefore, the degradation pathway that begins with catechol-2,3-dioxygenase is called the meta pathway (Figure 4). While the meta pathway is most prevalent, degradation can also begin with cleavage at the para or ortho position using catechol-1,2-oxygenase (Haggblom 1992, Ali et al. 1998, Jeong et al. 2003). After ring cleavage, 2-hydroxymuconic semialdehyde hydrolase catalyzes a decarboxylation reaction yielding 4-oxalocrotonate. 4-oxalocrotonate is hydrated by 2-oxopent-4-enoate hydratase to form 4-hydroxy-2-oxovalerate. 4-hydroxy-2-oxovalerate aldolase then splits 4-hydroxy-2-oxovalerate into pyruvate and acetaldehyde, which can then be incorporated into the central metabolic pathways (Shingler and Moore 1994).

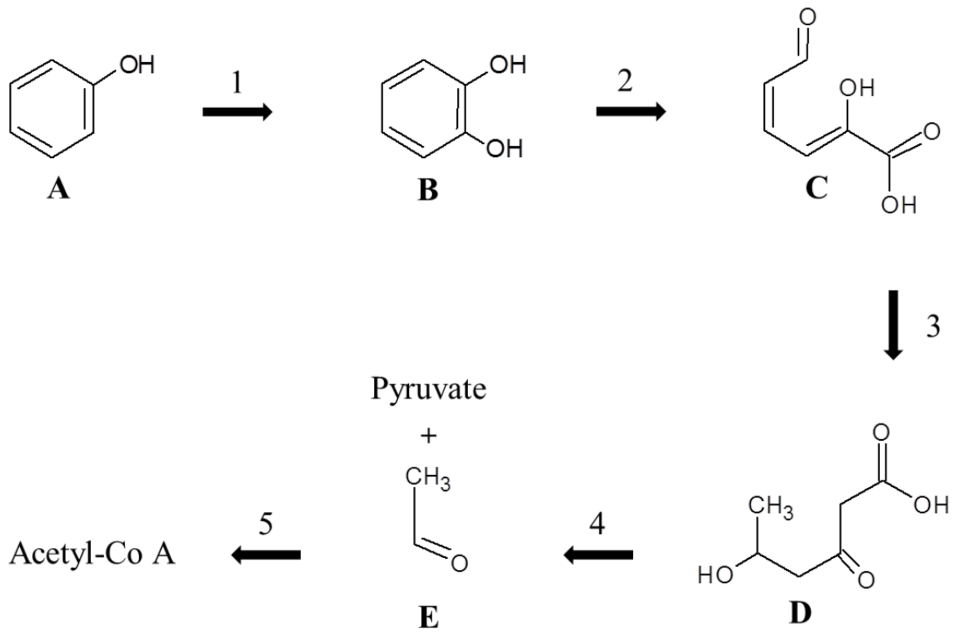


Figure 4. General phenol degradation pathway.

4.2.3. Phenolic compounds and Frankia

Frankia spp. both produce and are affected by phenolic compounds. However, it is unclear whether *Frankia* may degrade phenol and other phenolic compounds. The response of *Frankia* to phenolics was first studied in the context of plant–microbe interactions. Despite apparent functional and morphological similarities between *Frankia* nodules and leguminous nodules, the molecular and physiological mechanisms that control nodulation are distinct. Therefore, the unique process of nodulation by *Frankia* is still an area of intense research. Alnus spp. (Alders) plants are a major host plant for *Frankia*, and also have unusually high levels of phenolics in their root exudates, which affect the growth of *Frankia*. Most Alnus phenolics tested inhibit *Frankia* growth to varying degrees (Perradin et al. 1983, Vogel and Dawson 1986). Specifically, benzoic acids are less inhibitory than cinnamic acids such as caffeinic acid. However, one plant phenolic, o-hydroxyphenyl acetic acid, promoted *Frankia* growth, and both benzoic and cinnamic acids caused increased branching of *Frankia* hyphae. Low concentration plant phenolics also mediate a global shift in *Frankia* gene expression, while higher concentrations (above 30 mg L^{-1}) simply inhibit biosynthesis (Bagnarol et al. 2007). Interestingly, *Frankia* also increases phenolic expression of their host plant, causing them to produce more phenol, flavonoids, and hydroxycinnamic acid (Popovici et al. 2011). *Frankia* may promote excretion of phenolics as a way to increase available nutrients. However, this explanation depends on *Frankia* having the ability to degrade phenolic compounds. While no study has demonstrated that *Frankia* degrades phenolic compounds, there is genetic evidence that this bacterium may have the ability to degrade phenolics. First, some *Frankia* strains have genes coding for the production of catechol and other phenolic compounds (Udwary et al. 2011). Because bacteria often salvage the biomolecules they produce, the presence of an anabolic pathway suggests that a catabolic pathway is also present (Sekowsky et al. 2004). Furthermore, multiple *Frankia* strains contain catechol-2, 3-dioxygenase, the most important enzyme in the phenol degradation pathway (Swanson and Tisa unpublished data) (Ali et al. 1998). A closely related bacterium, *Rhodococcus* spp., uses the catechol-2,3-dioxygenase pathway to grow with phenol as its sole carbon source (Arif et al. 2013). The same species is also able to break down the more recalcitrant pentachlorophenol via the para pathway (Haggblom et al. 1988). This suggests that *Frankia* may break down phenol, a trait that could be applied in bioremediation efforts. Several *Frankia* strains are able to grow on phenol, quercetin, catechol, and other phenolic compounds (Furnholm, Greenleaf, and Tisa unpublished data), but the metabolism of their breakdown has not been studied.

4.3. Naphthalene degradation

4.3.1. Overview

Naphthalene is a ubiquitous polyaromatic hydrocarbon composed of two benzene rings joined at the 9 and 10 carbons (Figure 5). Naphthalene is produced by distilling and crystallizing coal tar, and also as by-product of fossil fuel combustion and cigarette smoke (Preuss et al. 2003). Naphthalene is used in a number of industrial applications including as feed stock for the production of plastics and resins, and as a component of creosote-based wood preservatives. Naphthalene is also used in tincture and leather tanning industries (Preuss et al. 2003). Unlike many organic pollutants, naphthalene does not bioaccumulate. Instead, naphthalene is metabolized and excreted in the urine of rats and humans (Preuss et al. 2003, Andreoli et al. 1999). Nonetheless, naphthalene is a problematic pollutant with numerous toxic effects. Acute exposure to naphthalene causes hemolytic anemia, and liver and neurological damage (U.S. Department of Health 2005). Chronic naphthalene exposure is associated with elevated cancer risk (Benigni 1997, Abdo et al. 2001). The toxicity of naphthalene and its prevalence as a pollutant has spurred research on remediation techniques, including bioremediation and biodegradation.

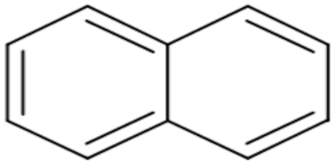


Figure 5. Structure of naphthalene.

4.3.2. Degradation pathway

The naphthalene biodegradation pathway was first studied in a strain of Pseudomonas which has two related naphthalene degradation pathways. The upper pathway catabolizes napathalene to produce salicylate and a molecule of pyruvate (Bosch et al. 1999). The lower pathway breaks salicylate down into acetyl-CoA and pyruvate (Bosch et al. 2000). The first step of the upper pathway is catalyzed by four proteins: naphthalene dioxygenase reductase, naphthalene dioxygenase ferredoxin, and naphthalene dioxygenase Fe-S protein small and large subunits. This collection of enzymes oxidizes naphthalene to produce cis-naphthalene dihydrodiol, which is subsequently dehydrogenated by naphthalene cis-dihyrdodiol dehydrogenase to form 1,2-dihydroxynaphthalene. 1,2-dihydronaphthalene dioxygenase then produces 2-hydroxychromene-2-carboxylate which is then cleaved by 2 hydroxychromene-2-carboxylate dehydrogenase to form cis-o-hydroxybenzylpyruvate. 1,2-dihydroxybenzylpyruvate aldolase then splits cis-o-hydroxybenzylpyruvate producing pyruvate and salicylaldehyde. Finally, salicylaldehyde dehydrogenase carboxylates salicylaldehyde to form salicylate (Bosch et al. 1999, Bosch et al. 2000). In the lower pathway, salicylate hydroxylase hydroxylates salicylate to produce catechol. The remaining benzene ring is then cleaved by catechol-2,3-dioxygenase to produce 2-hydroxymuconic semialdehyde (Bosch et al. 2000). Hydroxymuconic semialdehyde dehydrogenase then produces 2-hydroxyhexa-2,4-diene-1,6-dioate which is subsequently isomerized by 4-oxalocrotmate isomerase to produce 2-oxohexa-3-ene-1,6-dioate. This is then transformed into 2-oxopent-4-enoate by 4-oxalocrotomate decarboxylase. 2-oxopent-4-enole hydratase produces 4-hydroxy-2-oxovalerate, which is subsequently split into acetaldehyde and pyruvate by 2-oxo-4- hydroxypentanoate aldolase. Finally, acetaldehyde dehydrogenase converts acetaldehyde into acetyl Co-A (Bosch et al. 2000). Both of these pathways are also found in *Rhodococcus* spp, a close relative of *Frankia* (Grund et al. 1992).

4.3.3. Naphthalene degradation in Frankia

Not surprisingly, *Frankia* also metabolizes naphthalene as a sole carbon and energy source via a related pathway (Baker et al. 2015). Specifically, *Frankia* uses the protocatechuate pathway to convert naphthalene or a naphthalene derivative into acetyl Co-A and succinyl Co-A (Figure 6) (Baker et al. 2015). This finding confirms the role of *Frankia* in naphthalene degradation, which was suggested by earlier field studies (Lefrancois et al. 2010, Roy et al. 2007, Roy et al. 2005, Mallet and Roy 2014, Bissonette et al. 2014). In symbiosis with alders, *Frankia* increases polyaromatic hydrocarbon degradation in oil-sand tailings for the first 1.5 years (Lefrancois et al. 2010, Roy et al. 2005, Mallet and Roy 2014). However, after 2.5 years, alders without *Frankia* symbionts demonstrated naphthalene degradation equal to the degradation or *Frankia*-inoculated alders Lefrancois et al. 2010). The *Frankia*-alder symbiosis thrives in PAH-contaminated areas (Ridgway et al. 2004). Interestingly, alder plants found in these PAH-contaminated areas maintained a symbiosis with *Frankia* lineage III as opposed to the normal lineage I, suggesting that this pollutant affected nodulation and/or survival of the actinorhizal plants. Taken together, these findings indicate that *Frankia* could be a useful tool in naphthalene remediation.

4.4. Protocatechuate

4.4.1. Overview

Under oxic conditions, microbial degradation of many aromatic compounds occurs through the catechol or protocatechuate branch of the ß-ketoadipate pathway via either ortho cleavage by catechol 1,2-dioxygenase and protocatechuate 3,4-dioxygenase or meta-cleavage by catechol-2,3-dioxygenase and protocatechuate-4,5-dioxygenase.

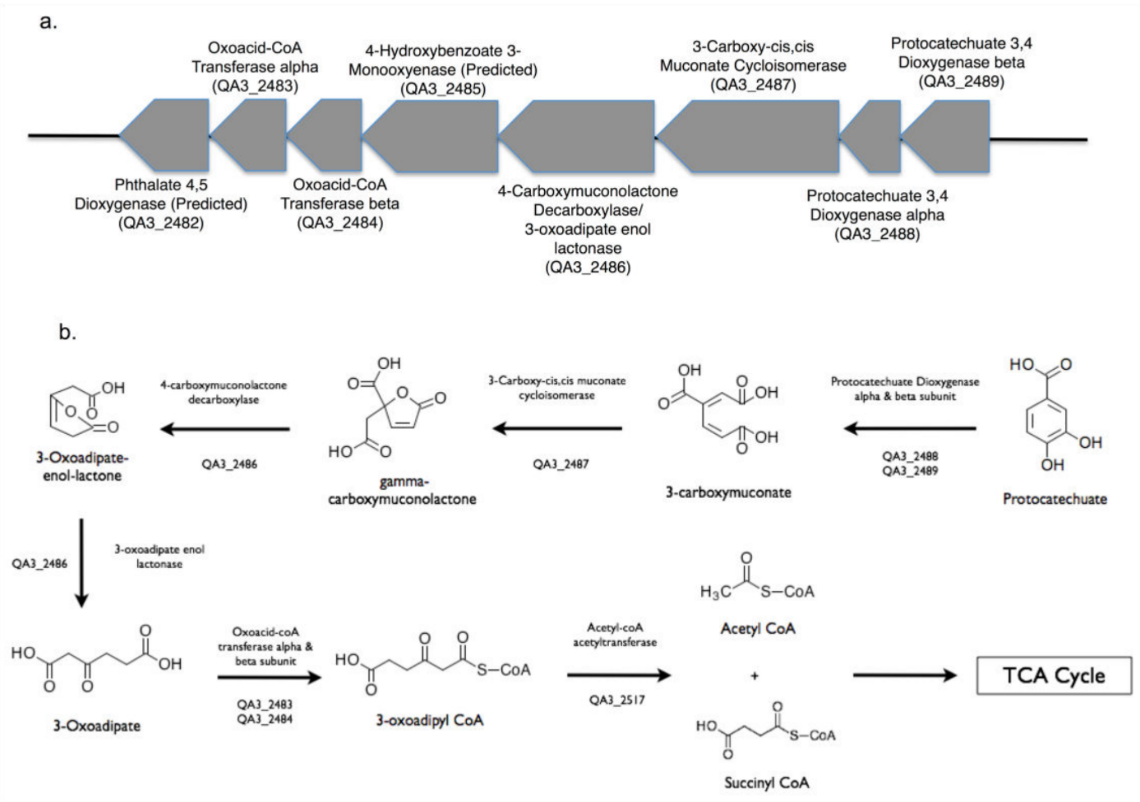


Figure 6. Putative naphthalene degradation pathway in Frankia [18]. (Figure is recopied with permission from Canadian Journal of Microbiology.)

4.4.2. Potential protocatechuate degradation pathway in Frankia

Besides the protochatechuate pathway found in *Frankia* QA3 (Baker et al. 2015), several other potential protocatechuate pathways have been identified from bioinformatics analysis of the available *Frankia* genomes. In *Frankia inefficax*, a potential operon (Fra*inefficax*_2560 -to- Fra*inefficax*_2564) for a putative protocatechuate pathway was identified (Figure 7). This operon encodes the predicted gene products involved in the putative pathway including protocatechuate 3,4-dioxygenase alpha and beta subunits, fumarate lyase, 3-oxoadipate enol-lactonase, and 4-hydroxybenzoate 3-monooxygenase. These gene products are similar to the protocatechuate degradation pathway found in *Rhodococcus* opacus 1CP (Eulberg et al. 1998, Perez-Pantoja et al. 2008). These results suggest that *Frankia* may use the protocatechuate degradation pathway to degrade many aromatic ring compounds after their conversion to protocatechuate.

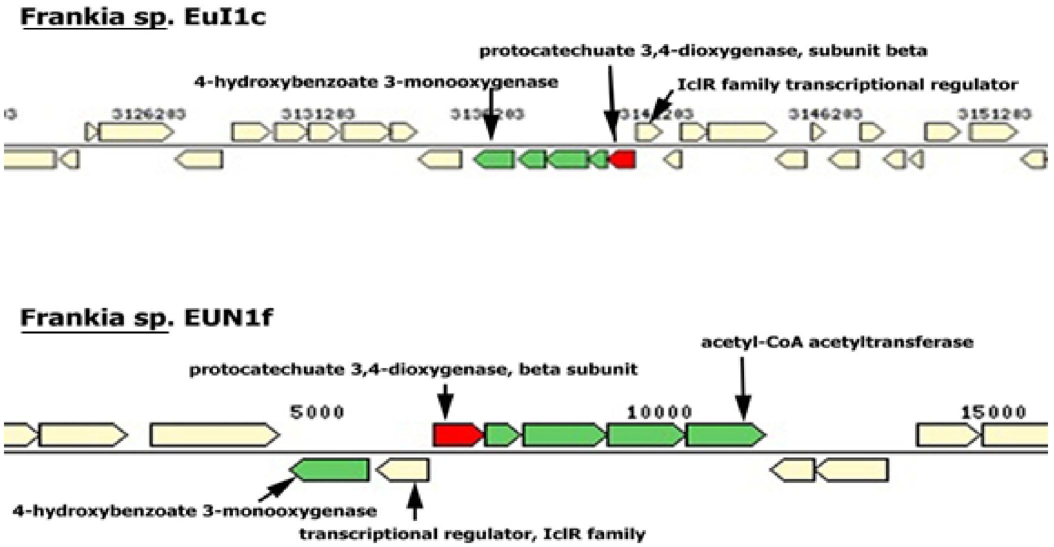


Figure 7. The proposed protocatechuate degradation pathway in Frankia strains inefficax and EUN1f.

5. Hydrocarbons

5.1. Overview

Petroleum-based energy and products are used extensively around the world. The pervasiveness of petroleum inevitably leads to serious environmental pollution. Petroleum is a complex mixture of hydrocarbons, cycloalkanes, aromatic hydrocarbons, and more complex chemicals like asphaltenes. These chemicals and their derivatives, which are termed petrogenic compounds, are released into the environment as a result of oil spills and combustion of petroleum-based products (Neff et al. 2005). Oil spills are one of the most serious sources of petroleum pollution and devastate aquatic and marine environments. Ongoing research to identify new methods for petroleum remediation is important because oil spills and other types of petroleum-derived pollution continue to pose environmental health risks. Hydrocarbon-degrading bacteria and fungi are widely distributed in marine and freshwater environments, as well as soil habitats (Okah and Trejo-Hernandez 2006, Lui et al. 2010). In Pseudomonas, the alkane hydroxylase (monooxygenase) system consists of three components: alkane hydroxylase (AlkB), rubredoxin, and rubredoxin reductase. This system is responsible for the first oxidation step in the utilization of n-alkanes (van Beilen et al. 1994). Similar alkane hydroxylase systems have been found in a variety of alkane-degrading bacteria (van Beilen et al. 2002). Alcanivorax sp. strain 2B5 will degrade C13–C30 n-alkanes and branched alkanes (pristine and phytane) from crude oil as the sole carbon source via a novel alkane hydroxylase gene (alkB). Other Acinetobacter are able to use n-alkanes with chain length C10–C40 as a sole source of carbon. In addition, the presence of multiple alkane hydroxylases in two *Rhodococcus* strains were characterized and both organisms contained at least four alkane monooxygenase gene homologs (alkB1, alkB2, alkB3, and alkB4) (Abdo et al. 2001, Whyte et al. 2002). A bioinformatics approach was used to identify these potential hydrocarbon degradation pathways among the sequenced *Frankia* strains. Functionally analyzed genes for the known hydrocarbon degradation pathways (Lui et al. 2010, Whyte et al. 2002) were used to probe the *Frankia* genome database and identify potential pathways. Our preliminary results (Rehan unpublished data) revealed that the F. alni ACN14a genome possesses a putative alkane-1 monooxygenase (Alkane omega- hydroxylase) gene (FRAAL1986), which is one of the known enzymes involved in the breakdown of n-alkanes (Figure 8). Furthermore, a similar gene (Franean1_2192) was also found in the *Frankia* sp. EAN1pec genome. These bioinformatics results support the hypothesis that *Frankia* may be able to degrade oil-spill-derived hydrocarbons. However, these preliminary results need further study.

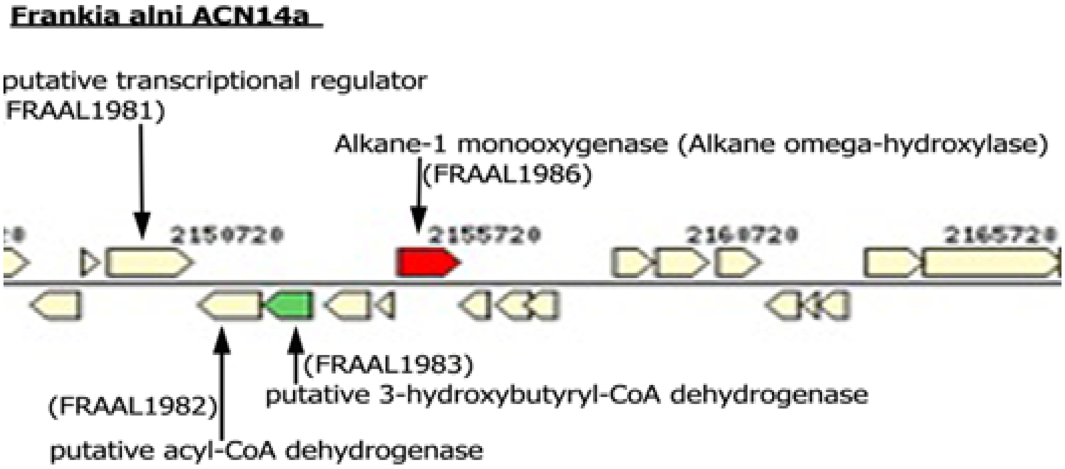


Figure 8. Potential alkane-1 monooxygenase identified in F. alni ACN14a.

6. Future aspects

Clearly, we have only begun to scratch the surface of the metabolism of *Frankia* and its biodegradative potential. These initial studies correlating metabolic capacity to gene function are the first step in exploiting the bacteria for their bioremediation ability. Further bioinformatics data mining are necessary to elucidate the unique metabolic potential of *Frankia*. However, these in silico studies require “wet lab” experiments to confirm these capabilities. From limited field studies, actinorhizal nodule occupancy seems to be under control by environmental conditions. The presence of *Frankia* lineage III strains inside alder nodules found under PAH-stressed soils suggests that this lineage may have a greater metabolic potential. The larger genome size of this lineage compared to the other infective strains also supports this hypothesis. However, further experiments are required to confirm this postulate.

***Frankia* and Dioxin-like compounds**

Dioxin-like compounds

The most widely accepted definition of dioxin-like compounds is closely tied to the concept of toxic equivalence factors (TEFs) (Barnes 1991, Safe 1992, Ahlborg and Hanberg 1994, Van den Berg et al. 1998, Van den Berg 2006). Based on early surveys of toxic organic compounds with similar chemistry to 2,3,7,8-tetrachlorodibenzodioxin (TCDD) that also interacted with the aryl hydrocarbon receptor, the toxicity and regulation of other compounds became defined in relation to 2,3,7,8-TCDD (Safe 1992). Early studies of dioxin-like compounds moved toward a consensus definition based on structural similarities to PCDDs or PCDFs, binding of the potential dioxin-like compound to the aryl hydrocarbon receptor, and documented activation of the aryl hydrocarbon receptor being linked to toxic effects. An additional criteria often attributed to dioxin-like compounds is high levels of recalcitrance and bioaccumulation (Van den Berg et al. 2006)

This ultimately means that dioxin-like compounds are a subset of PCDDs, PCDFs, and PCBs that induce a similar response mediated by the Aryl hydrocarbon receptor. Based on that definition, there are 17 laterally (i.e. 2,3,7,8) PCDD and PCDF congeners that are considered dioxin-like. Additionally, there are between 12 and 13 proposed polychlorinated biphenyl (PCB) congeners that are either mono-ortho or non-ortho substituted that are considered dioxin-like in function (Haws et al. 2005). The proposed PCB dioxin-like compound congener numbers are: Non-ortho (77, 126, 169), Mono-ortho (105, 114, 118, 123, 156, 157, 167, 189), Di-ortho (170, 180) (Haws et al. 2006). These have all been shown to have dioxin-like toxicity mediated through the aryl hydrocarbon receptor. However, many PCBs have also been shown to have additional toxicities unrelated to the classical aryl-mediated dioxin toxicity. In particular, non-dioxin-like PCBs have been associated with carcinogenesis (Van den Berg 1998).

Sources of Dioxin-like Compound Pollution

While there is some natural generation of dioxin-like compounds from forest fires and geological events, the majority of dioxin pollution is anthropogenic (EPA 1998). Dioxin-like compounds are primarily released into the environment as a result of low temperature, incomplete combustion of fossil fuels and plastics (Wang et al. 2003, Minh et al. 2003, Karstensen 2008, Zheng et al. 2008). This makes China and West Africa global hot spots for dioxin pollution do to the prevalence low tech combustion based processing of plastic and electronic waste, largely imported from Europe and North America (Minh et al. 2003, Chen et al. 2011, Leung et al, 2007). The recalcitrance of dioxins and their ability to disperse very long distances sorbed to dust particles and bioaccumulate means that these relatively moderate sources of pollution results in nearly ubiquitous exposure to low levels of dioxin-like compounds (Czuczwa et al. 1984, Eitzer and Hites 1989, Lohman and Seigneur 2001, Booth et al. 2013). Analysis of human adipose tissue samples from the general public by GC-MS typically yields a positive result on the 10 pg/g body weight order of magnitude (Alcock et al. 1998, Schuhmacher et al. 1999). The ubiquity of low level exposure makes it especially difficult to assess the chronic effects of minimal exposure levels. However, a handful of historical exposure events provide clear indications of the acute and chronic effects of moderate to severe exposure. The Seveso disaster exposed approximately 100,000 people in Seveso and nearby cities after an explosion at the ICMESA chemical plant in Meda released up to 34 kg of relatively pure TCDD into the atmosphere (Bertazzi et al. 1998). The long term health effects of this disaster are still being studied. Another significant exposure event happened when the defoliant Agent Orange was used during the Vietnam war. Agent orange had high levels of dioxin contamination resulting in a large group of affected people in Vietnam, Laos, and Cambodia (Schecter et al. 1995). Additional groups of high level exposure have been associated with contaminated rice oil in Japan, and contaminated fish in Japan and the Baltic states (Masuda 1994, Svensson et al. 1991). Studies involving those exposed in these incidents have contributed the majority of our understanding of dioxin-like compound toxicity in humans.

Health Effects of Dioxin-like Compound Pollution

Pathologies resulting from dioxin-like compound exposure are primarily mediated by misregulation of the aryl hydrocarbon receptor (Lucier et al. 1993, Mandal 2005, Sorg

2014). The toxic effects include chloroacne, cancer, teratogenesis, and endocrine disruption (Nouwen et al. 2001, White and Birnbaum 2017). Exposure has also been linked to increased risk of heart disease, liver failure, and diabetes (White and Birnbaum 2017). Studies show that dioxin-like compounds reversibly bind to the aryl hydrocarbon receptor protein which triggers a conformation change and activation. The activated form of the aryl hydrocarbon receptor is translocated to the nucleus where it regulates transcription of numerous genes, many of which are primarily active during fetal development (Sorg 2014, White and Birnbaum 2017). Misregulation of these genes is the putative cause of high rates of teratogenesis associated with dioxin exposure both in animal model systems and geographic locations with high levels of environmental pollution such as agent orange affected areas of Vietnam and Seveso, Italy (Schecter et al. 1995, Bertazzi et al. 1998). Studies have shown almost complete immunity to dioxin toxicity in mice with a aryl hydrocarbon receptor null mutation (Fernandez-Salguero et al. 1996). These lines of evidence support the assertion that even in instances were a mechanistic understanding of toxicity is lacking, the toxic effects of dioxin-like compounds are likely a result of aryl hydrocarbon activation.

Multiple national and international assessments of dioxin-like compounds have established maximum daily exposure limited between 10 and 100 pg/kg TCDD toxicity equivalents per day (van Leeuwen et al. 2000, World Health Organization). Following the Seveso disaster residents of the areas surrounding the ICMESA factory were exposed to initial dioxin concentrations of up to 580 μg/m^2 (Bertazzi et al. 1998). Blood and serum analysis of exposed individuals immediately after the explosion revealed dioxin concentrations between 1 and 56 µg/kg body weight. Dioxin concentrations were particularly high in children, and children also suffered higher rates of chloroacne, up to 48% of the population under the age of 18 in the most heavily contaminated zone. Widespread chloroacne was the primary acute effect of the Seveso accident observed in humans, but high death rates of up to 31% among small vertebrate populations were also reported. Liver, thymus, and lymphatic tissue necrosis in particularly susceptible populations was the primary toxic effect observed in the populations surrounding Seveso. However, there are a wide range of sensitivities to dioxin-like compounds, and subsequent long term studies have identified a number of chronic toxic effects in humans living in the Seveso region. Excess mortality analyses of Seveso survivors show higher incidence digestive cancers, heart disease, and diabetes (Bertazzi et al. 1998).

Remediation

Numerous remediation strategies have been developed for the removal of POPs. Common remediation strategies include chemical oxidation, subcritical water and steam extraction, photolysis, solvent and liquefied gas extraction, and mechanical shearing (Kulkarni et al. 2007). Modified versions of these methods can be used either *in situ* or *ex situ*. However, physical removal of contaminated soil for *ex situ* remediation has been the most common way of addressing POP pollution because POPs strongly adsorb to soil particles, making *in situ* removal and detoxification difficult. Once removed from a polluted site, contaminated soil is either buried in toxic waste landfills or treated off site to eliminate the POP contamination (Rabl et al. 2008, Vollmuth and Niessner 1995, Hermanson and Hites 1989).

This strategy has several drawbacks. First, removing all of the contaminated soil and sediment from a polluted site can be very costly. For example, efforts to remove PCBs contaminated sediment from the Hudson River have cost approximately $1.5 billion (Mann 2015). Another limitation of *ex situ* remediation is that the initial removal of the contaminated soil disrupts the surrounding community and leaves it prone to colonization by invasive species, making genuine remediation and restoration difficult to achieve. These degraded landscapes, particularly those that are colonized by non-native invasive species, have many adverse effects on surrounding populations, even after pollutants are successfully removed (Pejchar and Mooney 2009).

This means that effective and sustainable *in situ* remediation strategies are vitally needed to address the increasing amount of contaminated land around the world. Some of the remediation technologies listed above can be carried out *in situ*. However, most are difficult to scale at a contaminated site. The difficulties associated with conventional remediation strategies prompted the investigation of bioremediation as an alternative.

Considerable research has focused on bioremediation of dioxin-like compounds, particularly bioremediation of PCBs due to their abundance in the environment. The bioremediation of PCBs is broken down into two distinct processes: dehalogenation and transformation (Pieper 2005, Pieper and Seeger 2008). Dehalogenation is generally an anaerobic process that removes chlorines, bromines, and fluorines from PCBs and other dioxin-like compounds. The genus *Dehalococcoides* is the dominant taxonomic group of bacteria that carries out dehalogenation. Once the substitution of PCBs is reduced to 1 or 2 halogens (chlorine being by far the most common), aerobic bacteria are able to transform the PCBs into less toxic degradation products or molecules that can be incorporated into the central metabolism. There is some overlap between molecular pathways that transform dioxin-like compounds, but the most common pathway is encoded by the *bph* operon. This pathway is further broken up into the “upper pathway” and “lower pathway”. The upper pathway is initiated by a heterodimeric dioxygenase. The large α and small β dioxygenase subunits combine with a riske non-heme iron oxygen carrier to form a holoenzyme that catalyzes the addition of two oxygens to one of the dioxin-like compound rings. After oxygenation, the resulting cis-diol is hydrogenated in a NAD^+ dependent step to create a double bond between the new hydroxyl groups. A second dioxygenase cleaves the ring structure either between the hydroxyl groups generated by the first dioxygenase (ortho cleavage), or adjacent to either one of them (meta cleavage). After ring cleavage, a hydrolase splits the original molecule into a dieneoate and benzoate. The dieneoate is further metabolized by the lower pathway which produces one molecule of acetyl-CoA for each dieneoate. If the benzoate produced is still chlorinated, it is usually a dead-end product. However, if the benzoate is unsubstituted, it is can be mineralized in a separate benzoate degradation pathway (Pieper 2005, Pieper and Seeger 2008).

Knowledge gap

As detailed above, toxic organic pollution in general, and dioxin pollution in particular, pose a continued threat to humans and many other species. While some remediation projects have been successful, remediation methods remain costly and disruptive. The advent of widely available genomic data makes it possible to identify new microbial species with bioremediation potential. However, additional research is required to confirm putative remediation traits and elucidate the effects of symbiosis and community interactions on the remediation process. The focus of this work was to determine the function of a putative *bph* operon in *Frankia*, and begin to describe *Frankia* communities and genomics to better understand the role trans-species processes may play in remediation and resistance trait acquisition.

CHAPTER TWO

Phylogenetic and pan-genome analysis of the Frankia genus indicate divergent evolution and support the holobiont hypothesis

Introduction

Rationale

Soil health is a vital attribute of terrestrial ecosystems. Climate change, industrial agriculture, and changing land use trends such as urbanization threaten soil integrity and function (Ran et al. 2021, Chen et al. 2021, Pothula et al. 2019). Soil microbial communities are a key component of healthy soil ecosystems that greatly impact broader ecosystem and plant health (Sacca et al. 2017, Wei et al. 2020). In particular, the diverse communities that immediately surround root systems (the rhizosphere) exert a disproportional influence on soil health and resilience (Huang 2002). The rhizosphere surrounding actinorhizal plants is especially valuable because the actinorhizal symbiosis adds nitrogen to the soil via atmospheric nitrogen fixation carried out by *Frankia* spp. *Frankia* is a diverse genus of gram positive, filamentous, and symbiotic bacteria (Benson and Silvester 1993). In addition to fixing atmospheric nitrogen, members of the *Frankia* genus are resistant to many of the stresses associated with degraded and contaminated habitats. Strains in the *Frankia* genus have demonstrated resistance to heavy metals, high salt concentrations, and toxic xenobiotic hydrocarbons (Richards et al. 2002, Baker et al. 2015, Lefrancois et al. 2010, Rehan et al. 2014, Dawson and Gibson 1987).

Understanding the genetic diversity represented by *Frankia* is important in order to assess its full potential impact on soil health in both healthy and degraded soils.

Purpose

Significant effort has been devoted to exploring the genetics of *Frankia.* However, no systematic analysis of the core and pan-genome have had been completed to date. Furthermore, the complete breadth of the *Frankia* diversity represented by currently available sequence has not been explored. This study aimed to assess the diversity and evolutionary history of *Frankia*, with special emphasis on the development of resistance phenotypes.

Methods

Pan-genome analysis

Forty five genomes were included in the *Frankia* pan genome analysis (Appendix A1). Thirty nine genomes were used in the *Bradyrhizobium* pan-genome, and 67 genomes were used for the *Rhizobium* pan-genome. Reference sequence genome assembly data for previously sequenced strains was obtained from the NCBI database as gff3 files. All genome assemblies were annotated with PROKKA (Seemann 2014) for consistency and compatibility with Panaroo (Tonkin-Hill et al. 2020). Panaroo was used to determine the the core and pan-genome size and content of the *Frankia* genus as a whole, and for each of the 4 established clades individually. Pan-genomes were also calculated for clade 1a and clade 1c individually. Python (Van Rossum and Drake 2009) scripting was used to process the pan genome results and generate sets of unique genes for each genome relative to the *Frankia* genus as a whole, and each clade individually. Core-gene FASTA files were imported into Blast2Go (Gotz et al. 2008) to annotate each gene set with gene ontology information. A custom BLAST database was generated in Blast2GO using the same 45 *Frankia* genomes from the core genome analysis to determine initial gene identities. Functional characterization to was completed using 14 InterPro member databases (CDD, HAMAP, HMMPanther, HMMPfam, HMMPIR, FprintScan. Phohius, SuperFamily, Gene3D, SFLD, Pattern Scan, HMMTigr, HMMSmart, ProfileScan) to identify protein families, functional domains, and repeats. After InterPro analysis, functional analysis and previous annotations from PROKKA and BLAST results were merged and augmented using ANNEX. Gene ontology based enzyme mapping was completed using the Blast2GO tool GO-EnzymeCode.

The R package micropan (Snipen and Liland 2015) was used to determine structure of each genus and clade level pan-genome. The Heap's Law function was calculated using 1000 permutations on each pan-genome matrix and the intercept and alpha decay values were recorded.

The alignment of the full *Frankia* genus level core-genome was imported into CLC workbench (CLC Genomics Workshop, digitalinsights.qiagen.com) and used to generate a phylogeny using neighbor-joining and Jukes Cantor. Phylogeny strength was assessed using bootstrapping with 1000 replicates.

Results

Based on the 45 genomes selected, the genus level pan-genome of *Frankia* consists of 44 core genes and 71,438 accessory genes. The *Frankia* genus has an open pan-genome structure as indicated by the a Heap's law alpha decay value below 1.0. The Heap's Law decay value for the *Frankia* genus level pan-genome is 0.86 (Table 2.1). The biological processes of each gene cluster in the core genome based on InterPro gene ontology assignments showed that 2% of the core genome is involved in cyclic organic compound biosynthesis processes, 2% is involved in RNA metabolism, 6% is involved in purine metabolism, 42% is involved in ribosome biogenesis, and 49% is involved in translation.

Table 2.1: Pan-genome characteristics of Frankia, Rhizobium, and Bradyrhizobium genera.

Thresholds	**99-100%**	**95-99%**	**15-95%**	**0-15%**	**0-100%**			
Pan-Genome	**Core**	**Soft Core**	**Shell**	**Cloud**	**Total**	**Heap's Intercept**	**Heap's Alpha**	**Open vs Closed**
Rhizobium	31	7	8026	123823	131887	1777.37	0.66	Open
Bradyrhizobium	198	26	9307	72488	82019	4709.46	1.05	Closed
Frankia	26	18	9013	62425	71482	2580.18	0.86	Open
***Frankia* Clade 1A**	2920	0	9704	0	12624	1475.94	2.00	Closed
***Frankia* Clade 1C**	3414	0	2202	2114	7730	1186.71	1.92	Closed
***Frankia* Clade 1**	977	0	8862	9366	19205	2087.03	1.43	Closed
***Frankia* Clade 2**	383	0	8992	14086	23461	3390.12	1.89	Closed
***Frankia* Clade 3**	1058	0	13545	25540	40143	3040.32	1.53	Closed
***Frankia* Clade 4**	568	0	28179	0	28747	1847.16	2.00	Closed

Molecular Function assignments showed showed that 2% of *Frankia* core genes have hydrolase activity, 2% are nucleotide transferases, 3% have purine ribonucleotide binding activity, 4% have purine nucleoside triphosphate binding activity, 10% have DNA binding activity, 29% have RNA binding activity, and 50% are structural components of ribosomes.

Frankia clade level pan-genomes were calculated with clade 1 which included 18 genomes, clade 1A with 5 genomes, clade 1C with 13 genomes, clade 2 with 10 genomes, clade 3 with 11 genomes, and clade 4 with 6 genomes (Table 2.2). The *Frankia* clade 1 pan-genome contains 19,205 gene clusters. 977 of those genes are core genes, while 18,228 are accessory genes. Analyzed on their own, *Frankia* clade 1 genomes have a closed pan-genome structure with a Heap's alpha decay value of 1.43. The *Frankia* clade 1A pan-genome contains 12,624 total gene clusters of which 2920 are core genes. Clade 1A has a closed pan-genome structure with a Heap's alpha decay value of 2.00. The *Frankia* clade 1C pan-genome contains 7730 gene clusters and has a core genome consisting of 3,414 genes. Frankia clade 1C genomes have an Heap's alpha decay value of 1.92 indicating a closed pan-genome structure. The *Frankia* clade 2 pan-genome contains 23,461 gene clusters of which 383 represent the core genome. *Frankia* clade 2 genomes have a Heap's alpha decay value of closed pan-genome structure (Table 2.1)

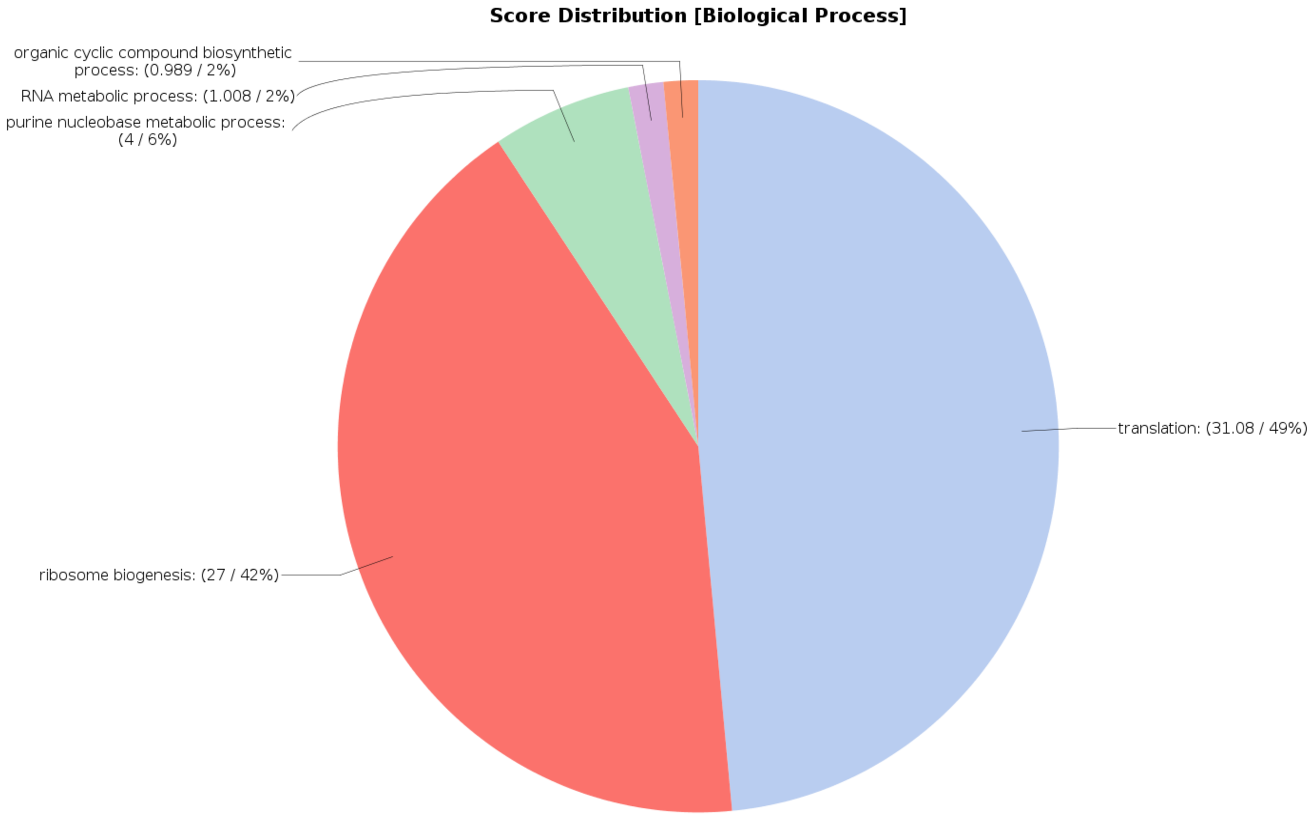


Figure 2.1: Biological process gene ontology annotation distribution of the Frankia genus level core-genome

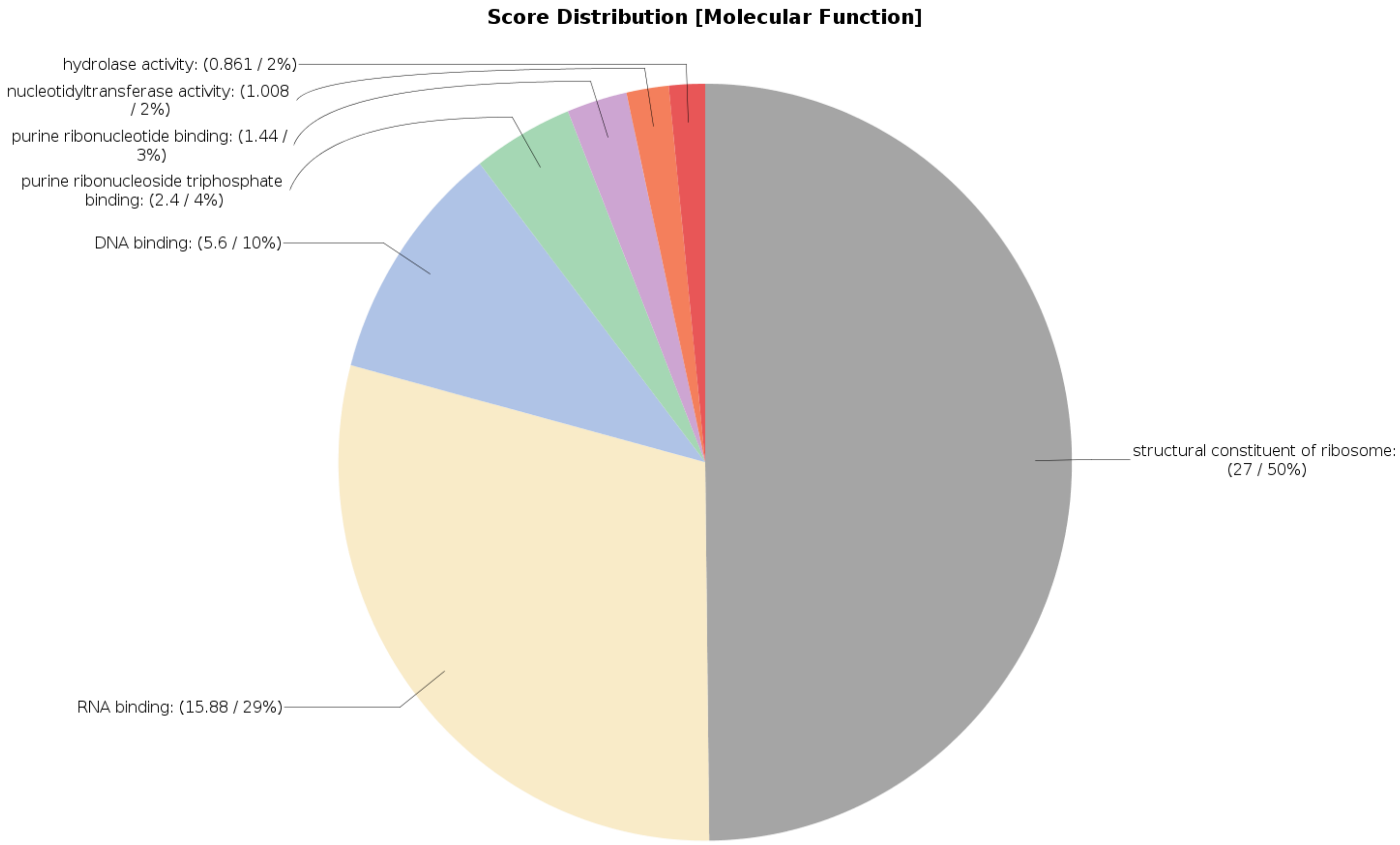


Figure 2.2: Molecular process gene ontology annotation distribution of the Frankia genus level core-genome.

Frankia clade 3 has a pan-genome size of 40,143 gene clusters of which 1058 represent the core genome. Clade 3 genomes have a closed pan-genome structure with a Heap's alpha decay value of 1.53. The *Frankia* clade 4 pan-genome is made up of 28,747 gene clusters with 568 core genes. *Frankia* clade 4 genomes have closed pan-genome structure with a Heap's alpha decay value of 2.00. Clade level core genomes were annotated with genes ontology assignments are grouped based on molecular function and biological process. The percentages of gene clusters in each clade core genome that belong to a given gene ontology category are summarized in figures 2.3-2.13.

Based on the 39 genomes selected, the *Rhizobium* pan-genome consists of 38 core genes and 131,849 accessory genes. The *Rhizobium* pan-genome has an Heap's alpha decay value of 0.66 which indicates an open pan-genome. InterPro biological process gene ontology assignments showed that 1% of the genes in the *Rhizobium* core-genome are involved in cellular component biogenesis, 2% are involved in primary metabolic process regulation, 2% are involved in the regulation of nitrogen compound metabolism, 2% are involved in cofactor metabolism, 2% are involved in carboxylic acid biosynthesis, 2% are stimuli response genes, 2% are amide biosynthesis genes, 3% are involved in regulation of cellular metabolism, 3% are involved in cellular protein metabolism, 4% are involved in nucleobase-containing compount biosynthesis, 4% are involved in drug metabolism, 5% are involved in the regulation of macromolecule metabolism, 6% are alpha-amino acid metabolism genes, 6% are oragnonitrogen compound biosynthesis genes, 7% are transmembrane transport genes, 8% are cellular

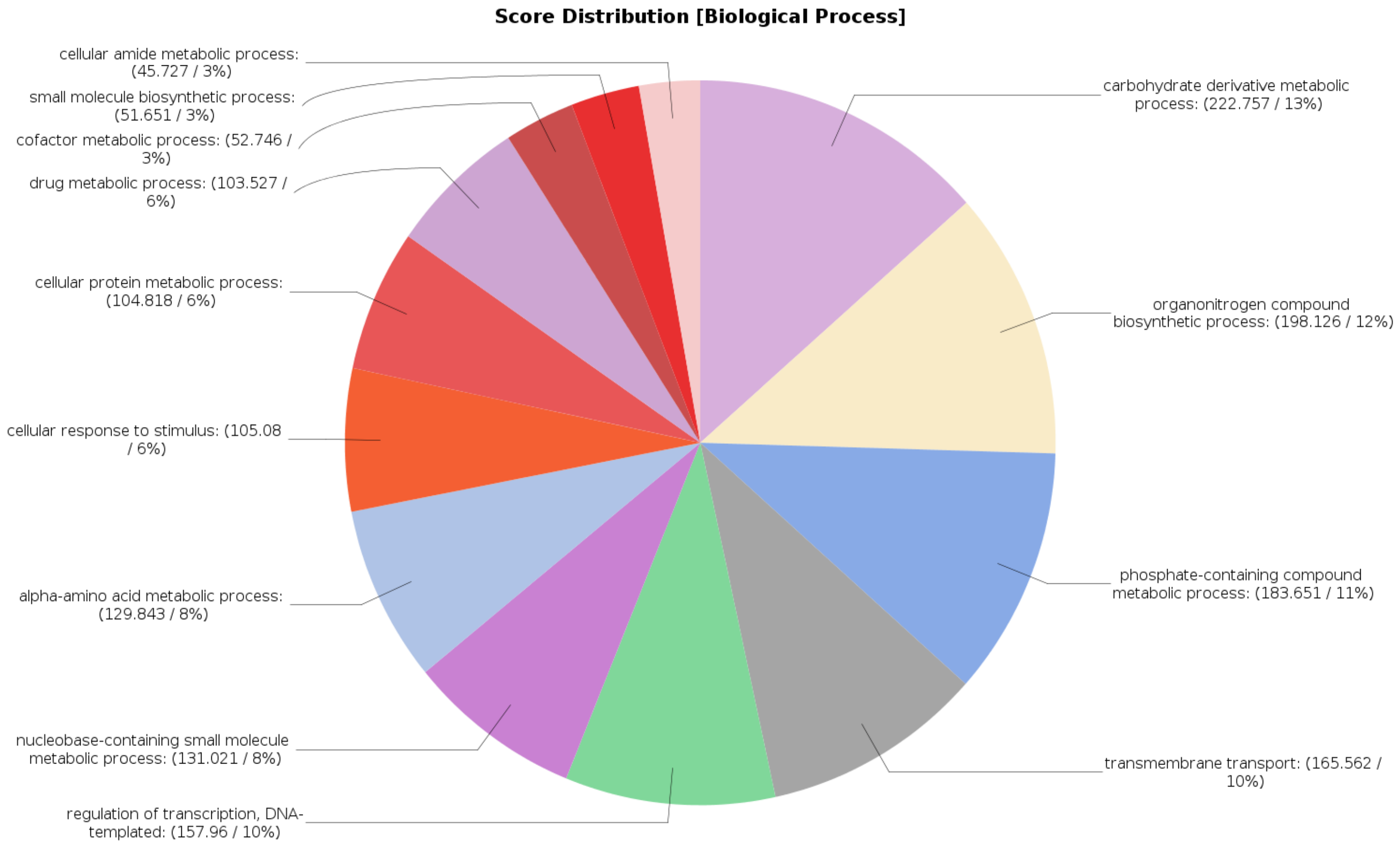


Figure 2.3: Biological process gene ontology annotation distribution of the Frankia clade 1A core-genome

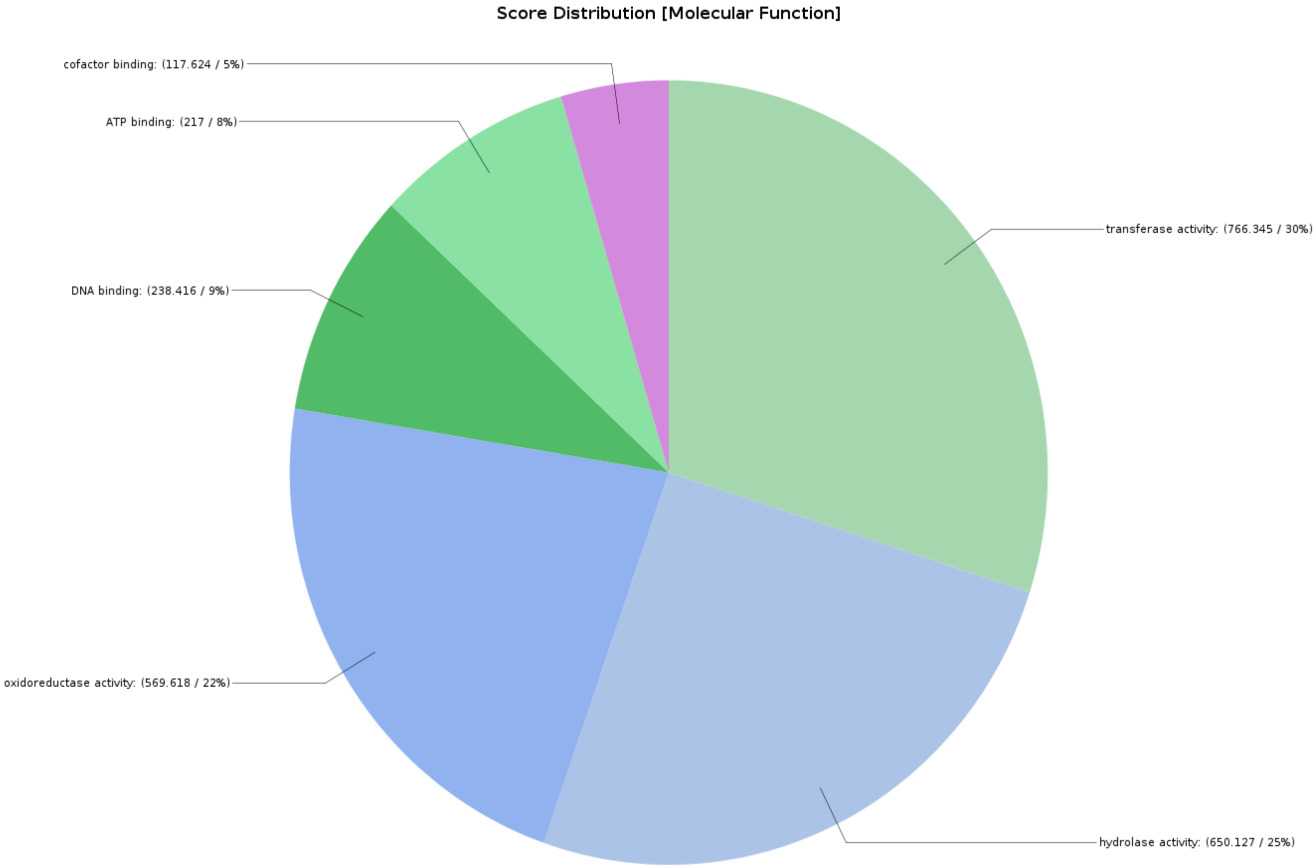


Figure 2.4: Molecular process gene ontology annotation distribution of the Frankia clade 1A core-genome.

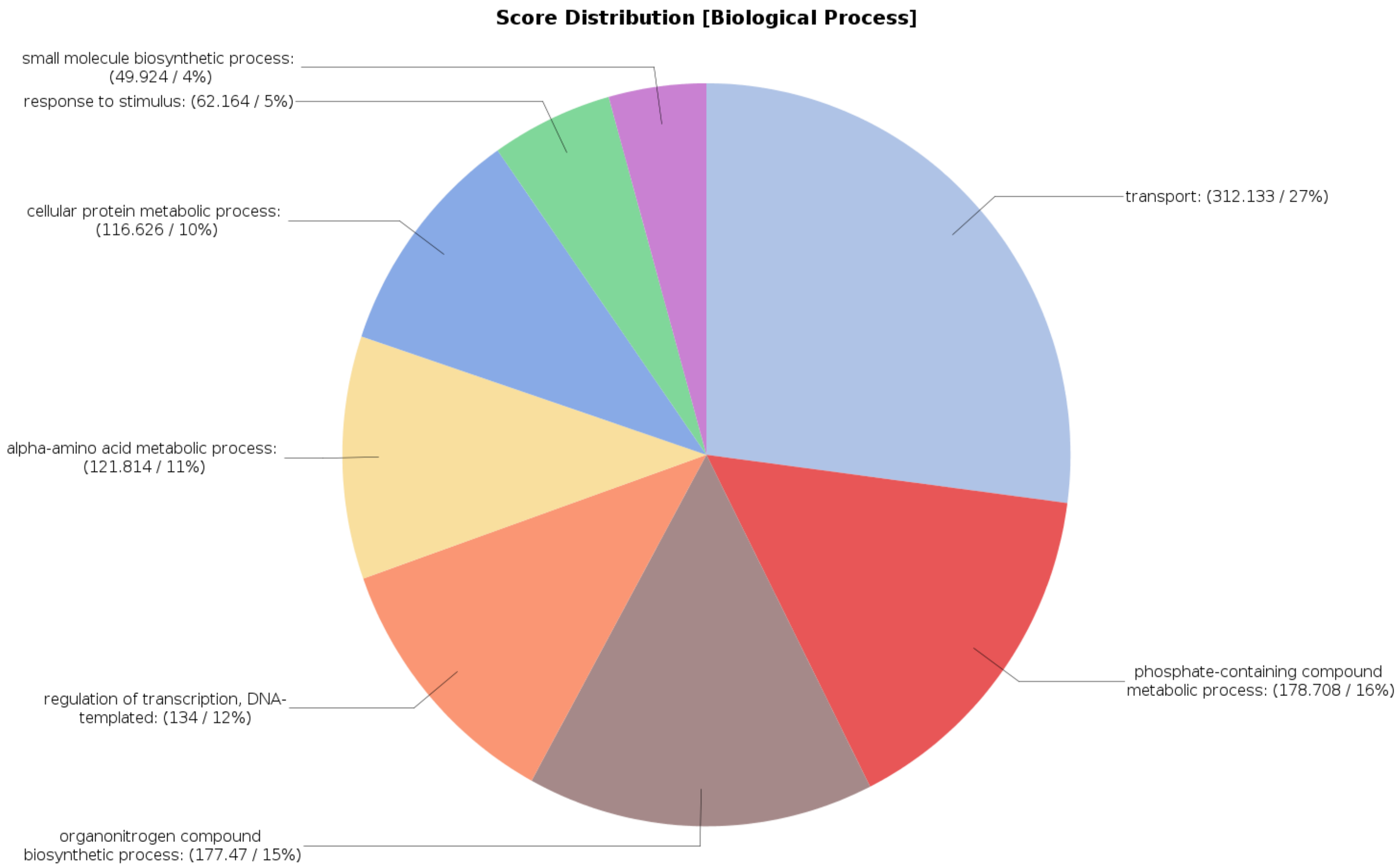


Figure 2.5: Biological process gene ontology annotation distribution of the Frankia clade 1C core-genome

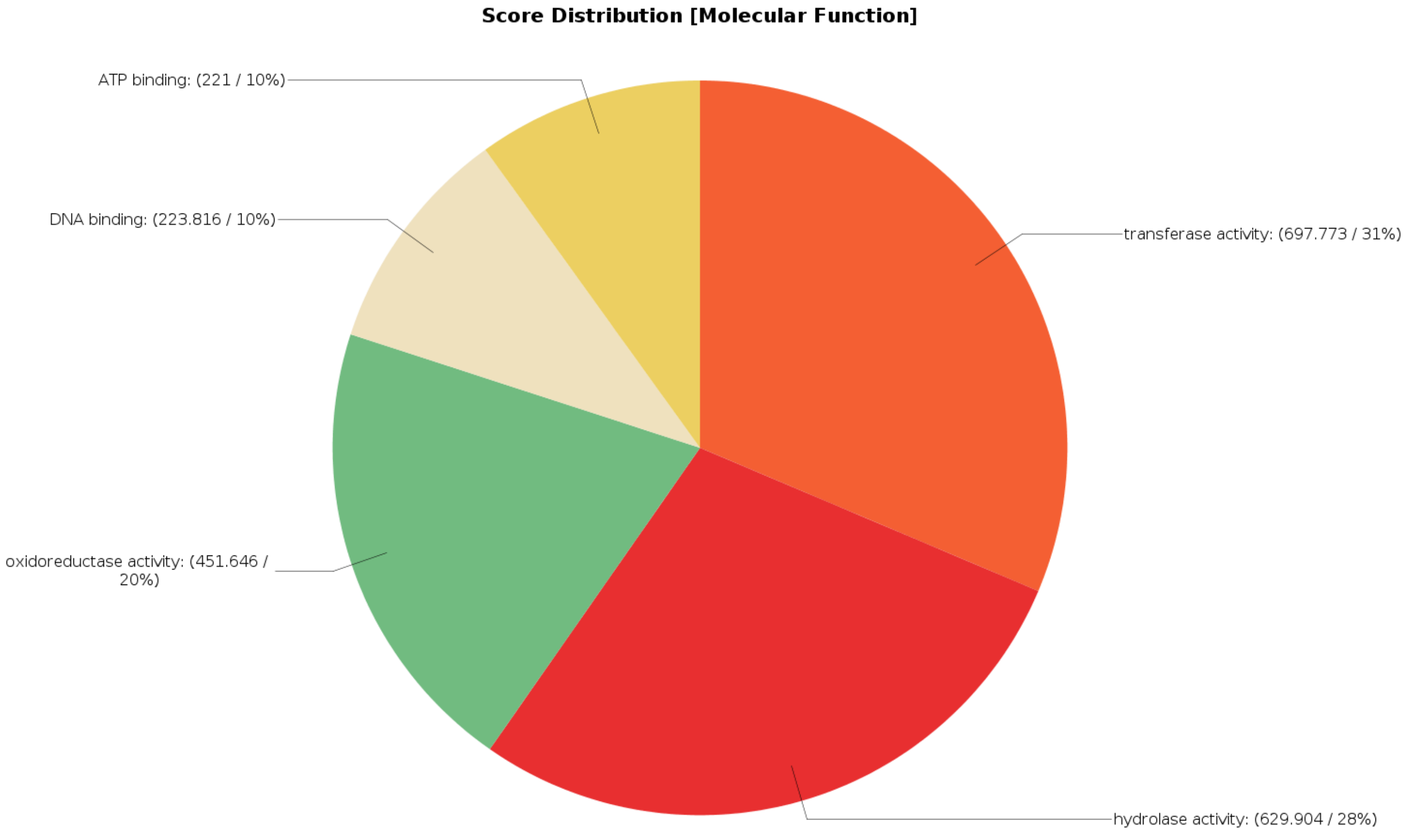


Figure 2.6: Molecular process gene ontology annotation distribution of the Frankia clade 1C core-genome.

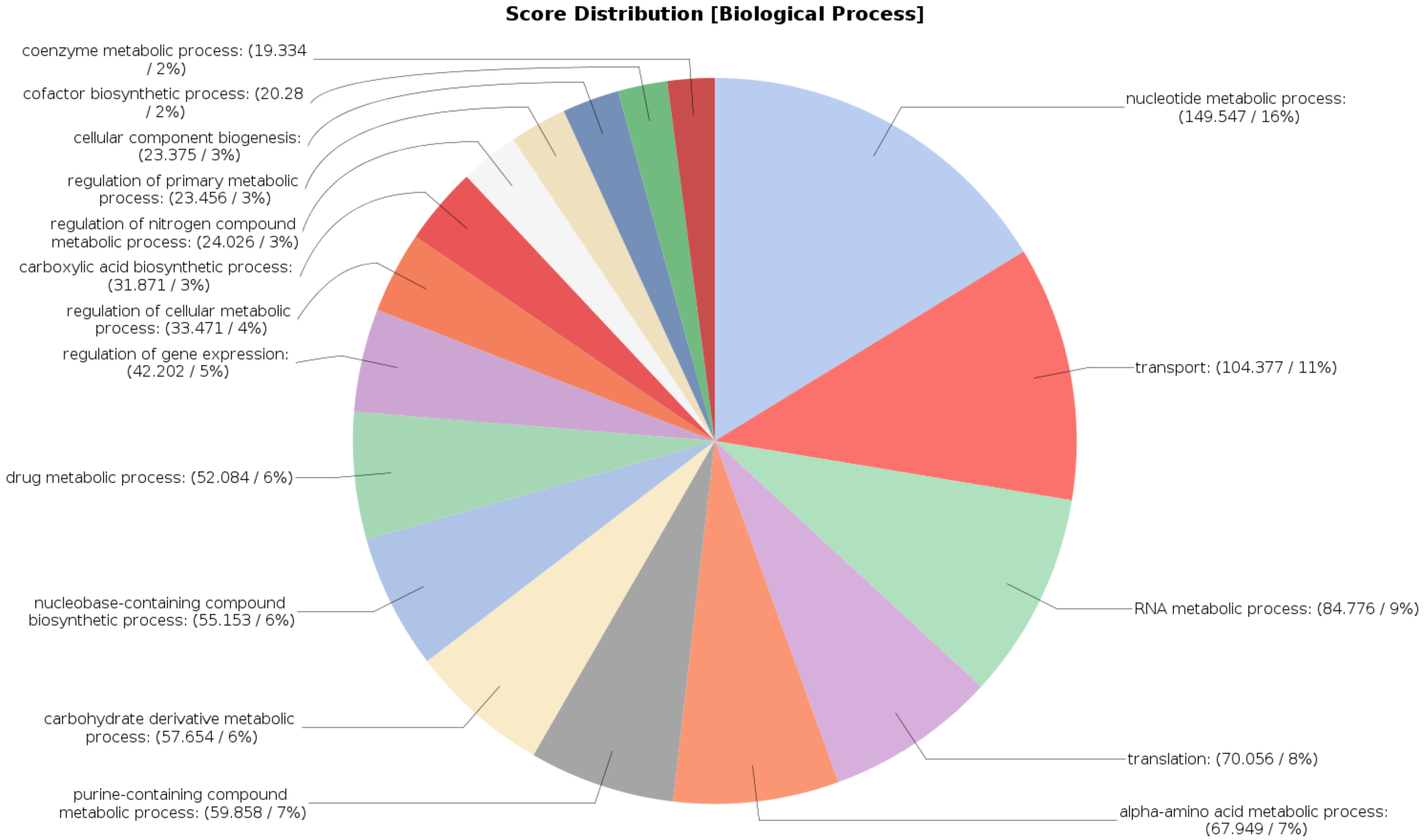


Figure 2.7: Biological process gene ontology annotation distribution of the Frankia clade 1 core-genome

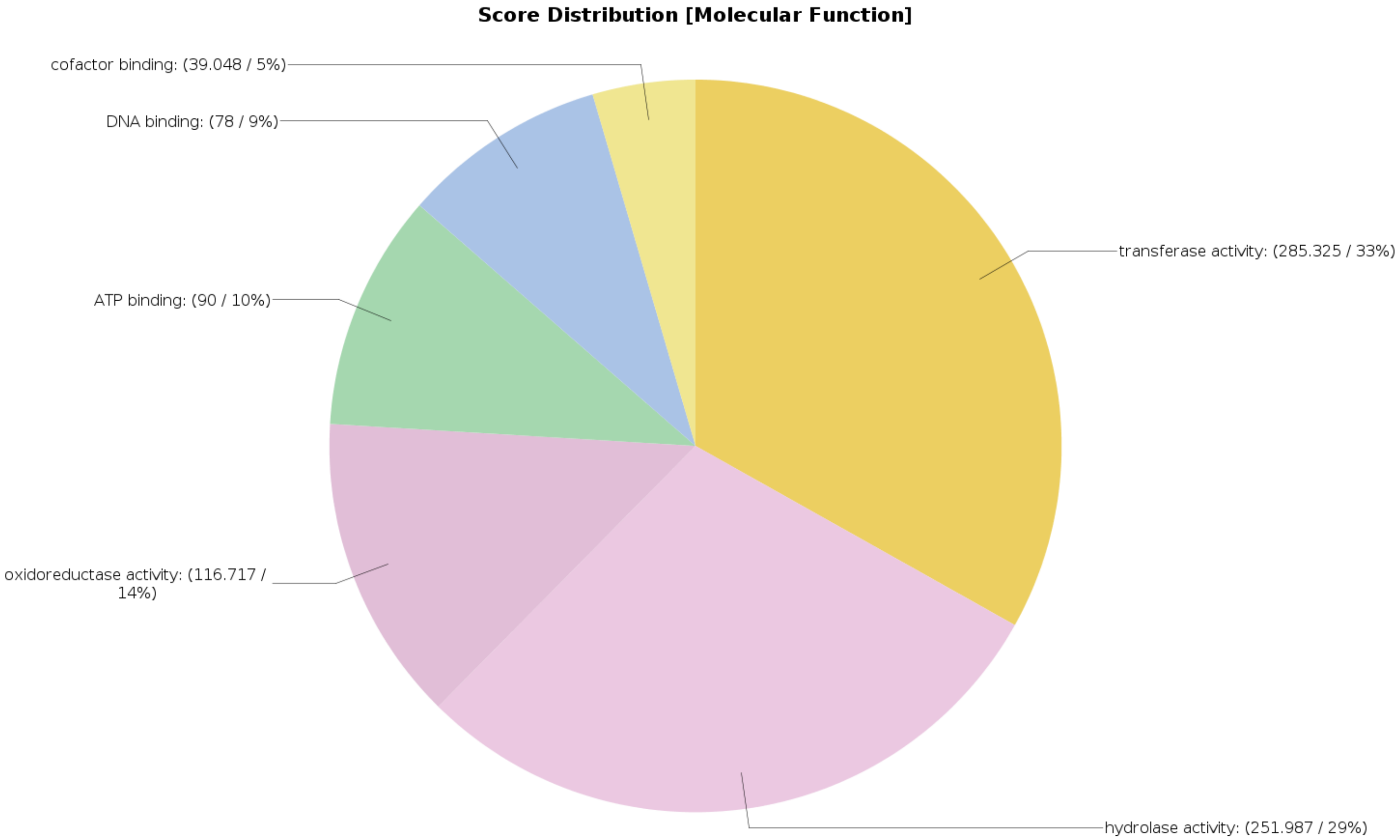


Figure 2.8: Molecular process gene ontology annotation distribution of the Frankia clade 1 core-genome.

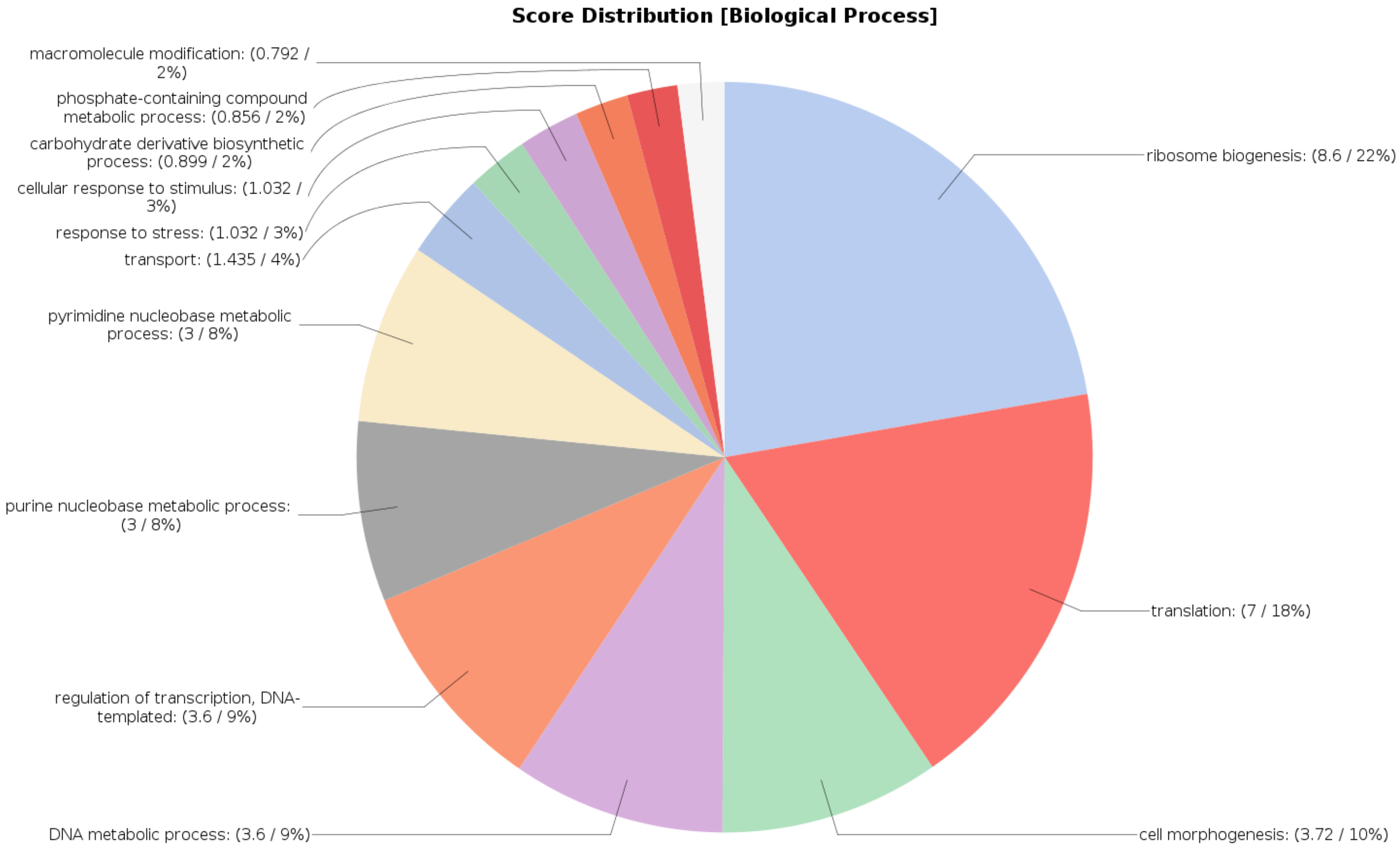


Figure 2.9: Biological process gene ontology annotation distribution of the Frankia clade 2 core-genome

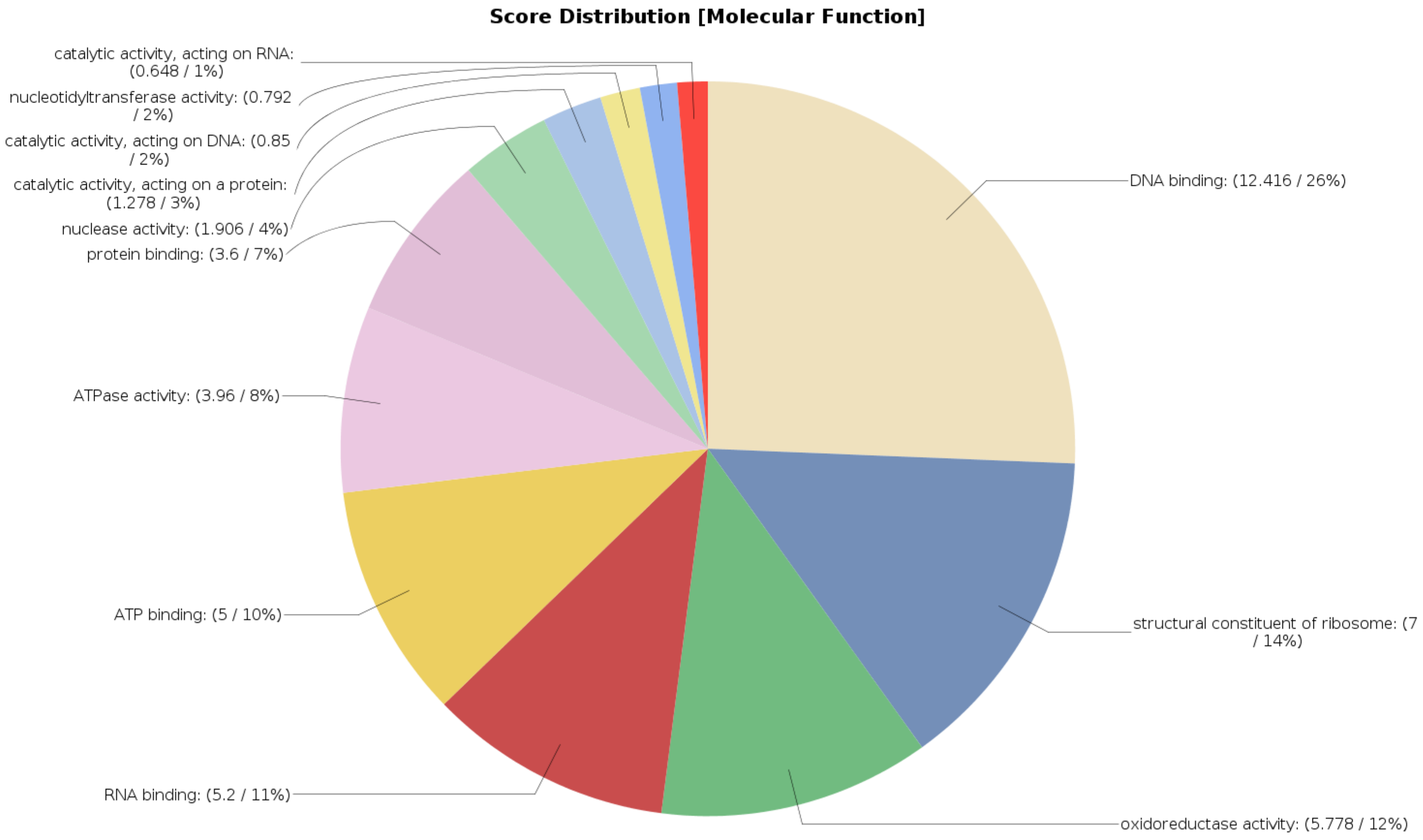


Figure 2.10: Molecular process gene ontology annotation distribution of the Frankia clade 2 core-genome.

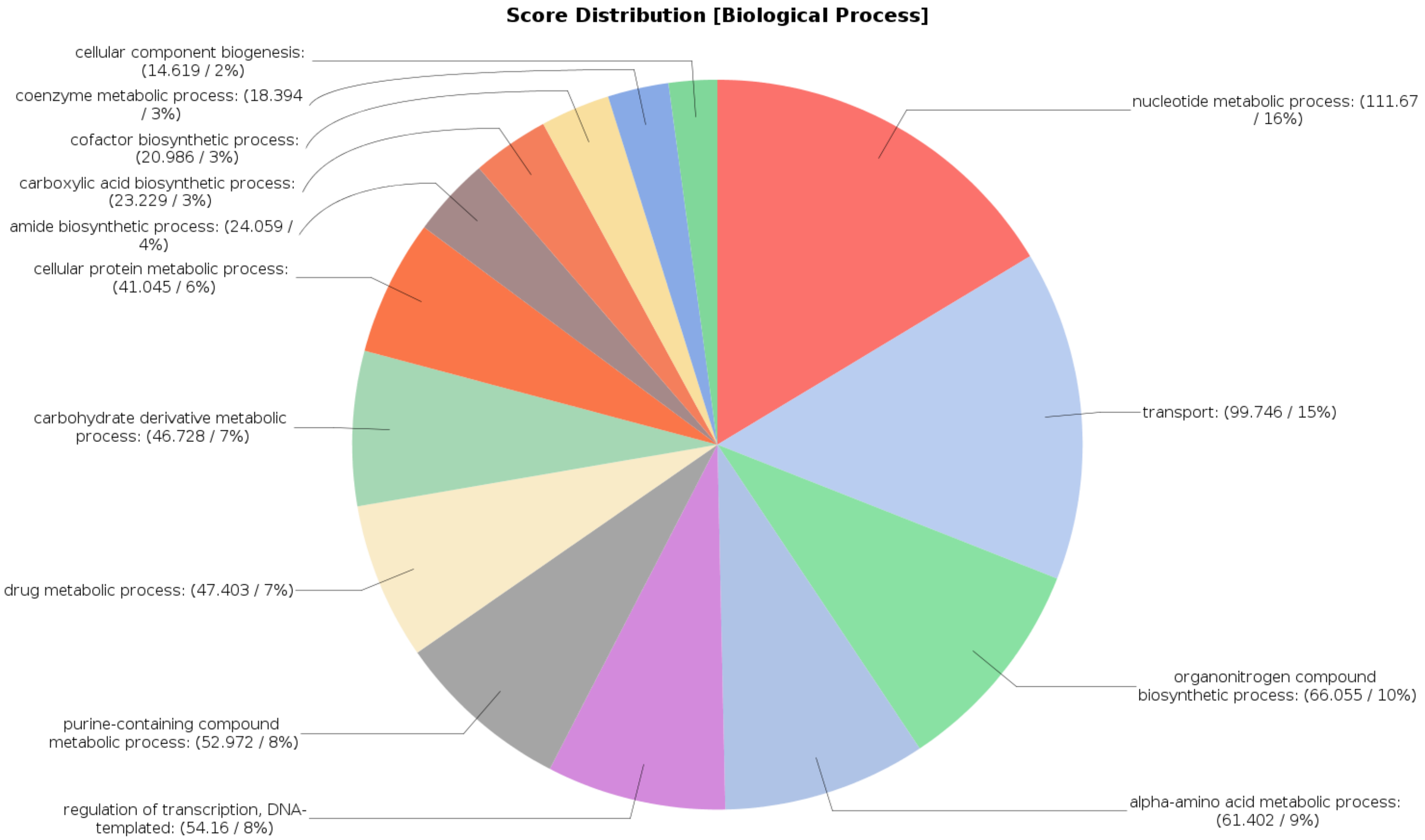


Figure 2.11 Biological process gene ontology annotation distribution of the Frankia clade 3 core-genome

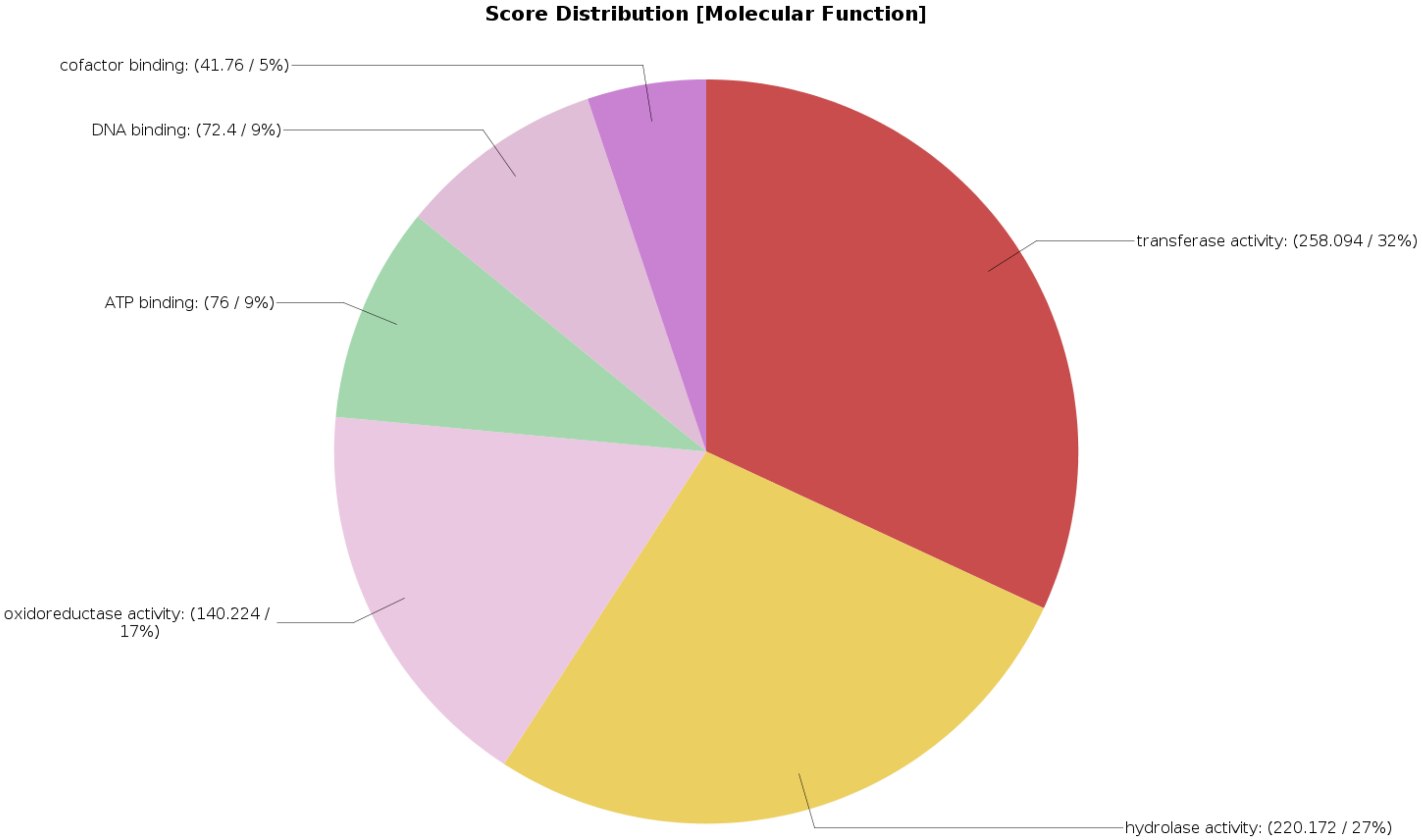


Figure 2.12: Molecular process gene ontology annotation distribution of the Frankia clade 3 core-genome.

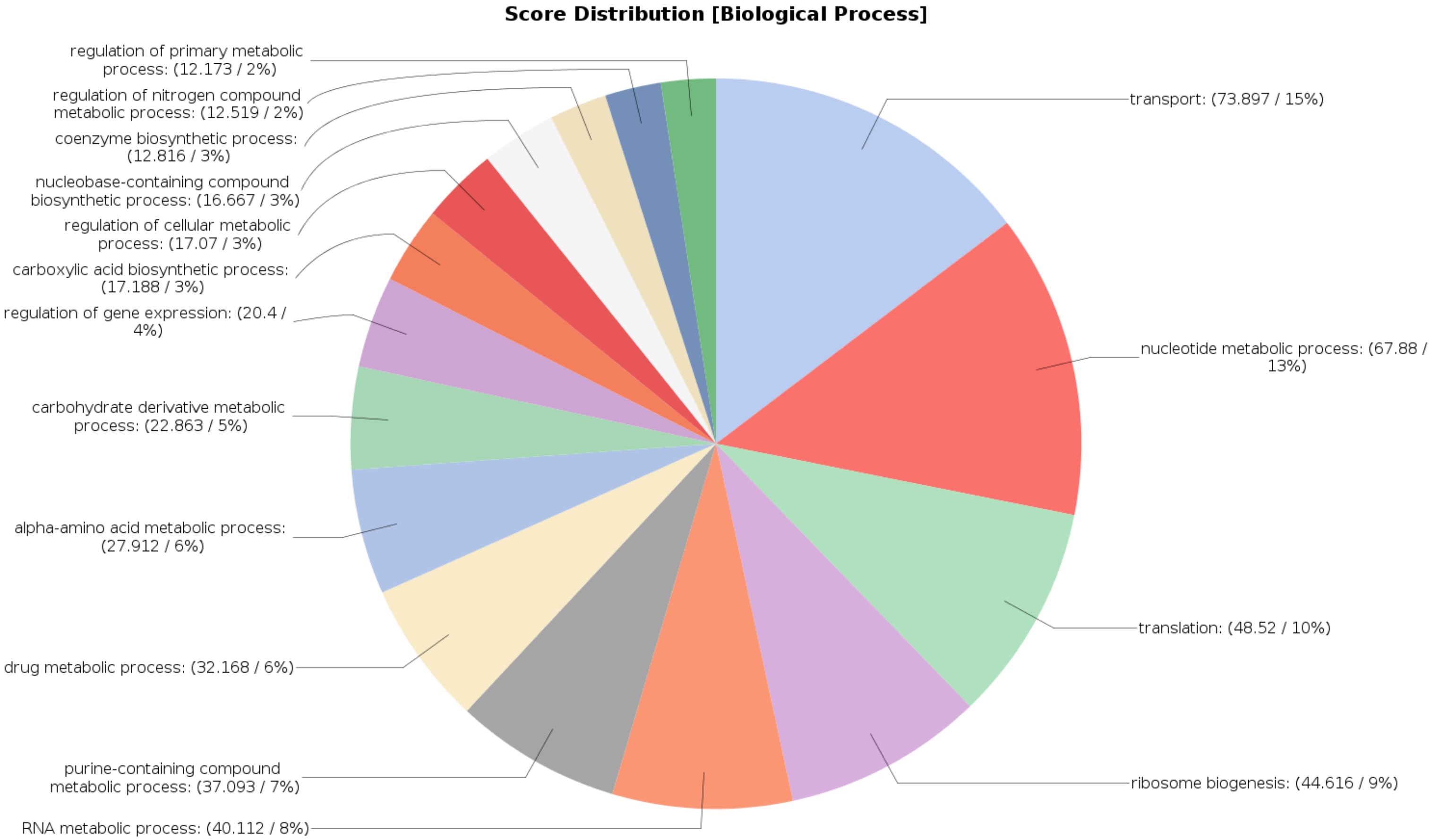


Figure 2.13: Biological process gene ontology annotation distribution of the Frankia clade 4 core-genome

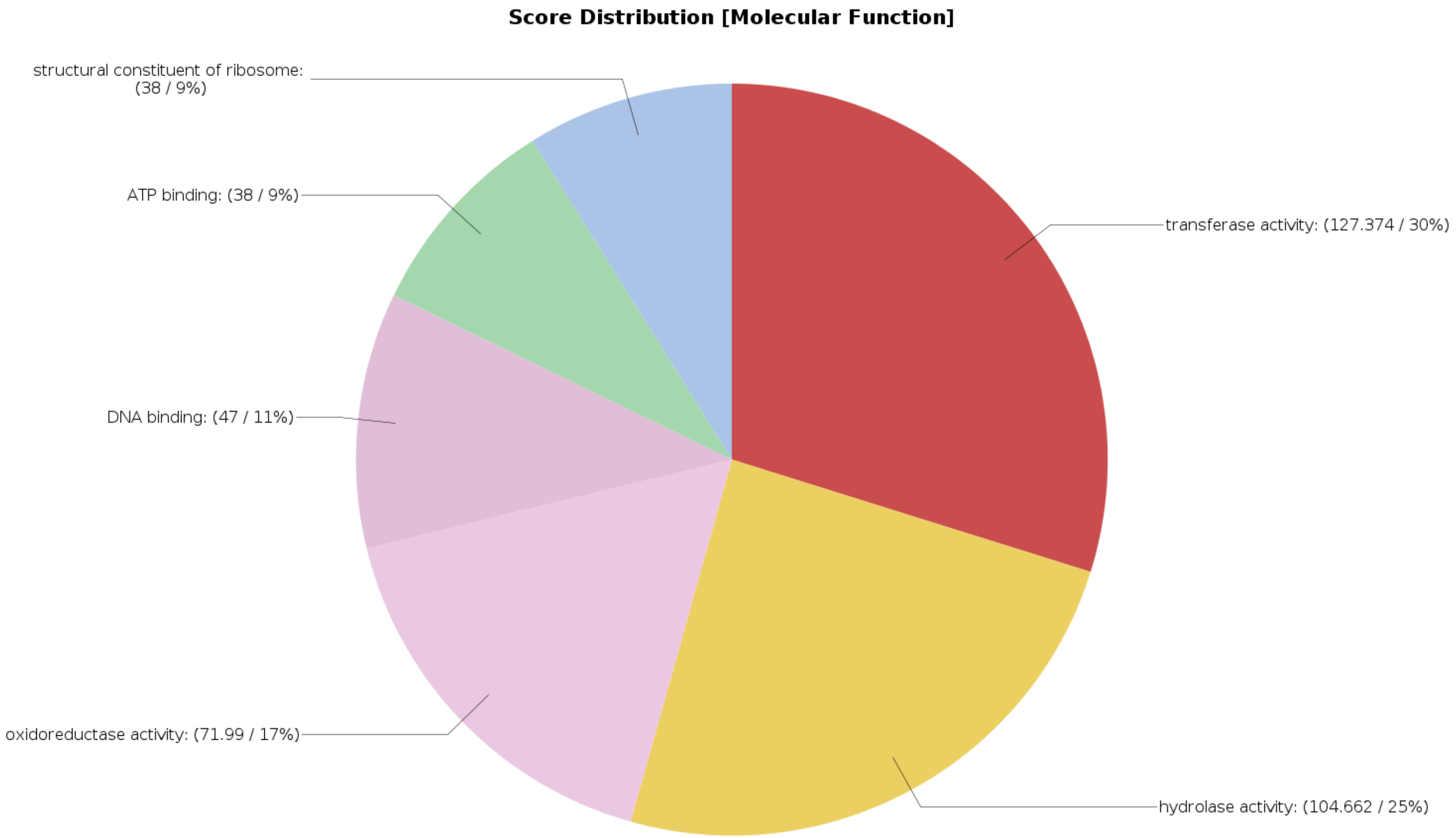


Figure 2.14: Molecular process gene ontology annotation distribution of the Frankia clade 4 core-genome.

macromolecule biosynthesis genes, 8% are carbohydrate derivative metabolism genes, 9% are involved in gene expression, 10% are involved in nucleotide metabolism, and 13% are involved in RNA metabolic processes.

Grouping the *Rhizobium* core genes by IntroPro molecular function annotations showed that 4% of genes are involved in cofactor binding, 7% are involved in ATP binding, 10% are involved in transmembrane transport, 14% are involved in oxidoreductase activity, 17% are involved in nucleic acid binding, 23% are involved in hydrolase activity, and 25% are involved in transferase activity.

Based on the 67 genomes selected, the *Bradyrhizobium* pan-genome consists of 224 core genes and 83,795 accessory genes. The Heap's alpha decay value for Bradyrhizobium is 1.05, indicating a closed pan-genome structure. IntroPro biological process gene ontology assignments showed that 2% of Bradyrhizobium core genome homologue clusters are involved in biological process regulation, 2% are involved in nucleoside triphosphate metabolism, 3% are involved in carxoylic acid biosynthesis, 3% are involved in coenzyme biosynthesis, 6% are involved in purine ribonucleoside metabolism, 7% are involved in purine ribonucleotide metabolism, 7% are drug metabolic process genes, 7% are RNA metabolic process genes, 12% are transmembrane transport genes, 23% are ribosome biogenesis genes, and 25% are involved in translation.

Grouping the *Bradyrhizobium* core-genome gene clusters based on molecular function showed that 3% the core genome is involved in purine ribonucleotide binding, 4% is involved in purine ribonucleotide binding, 6% is involved in cofactor binding, 7%

is involved in pyrophosphatase activity, 9% is involved in DNA binding, 15% is involved in RNA binding, 15% is involved in transferase activity, 18% codes for structural components of ribosomes, and 24% is involved in oxidoreductase activity.

Phylogenetic analysis of the *Frankia* genus produced 5 well supported clades. Each of the major clade branches are supported by a bootstrapping value of 100 based on 1000 iterations.

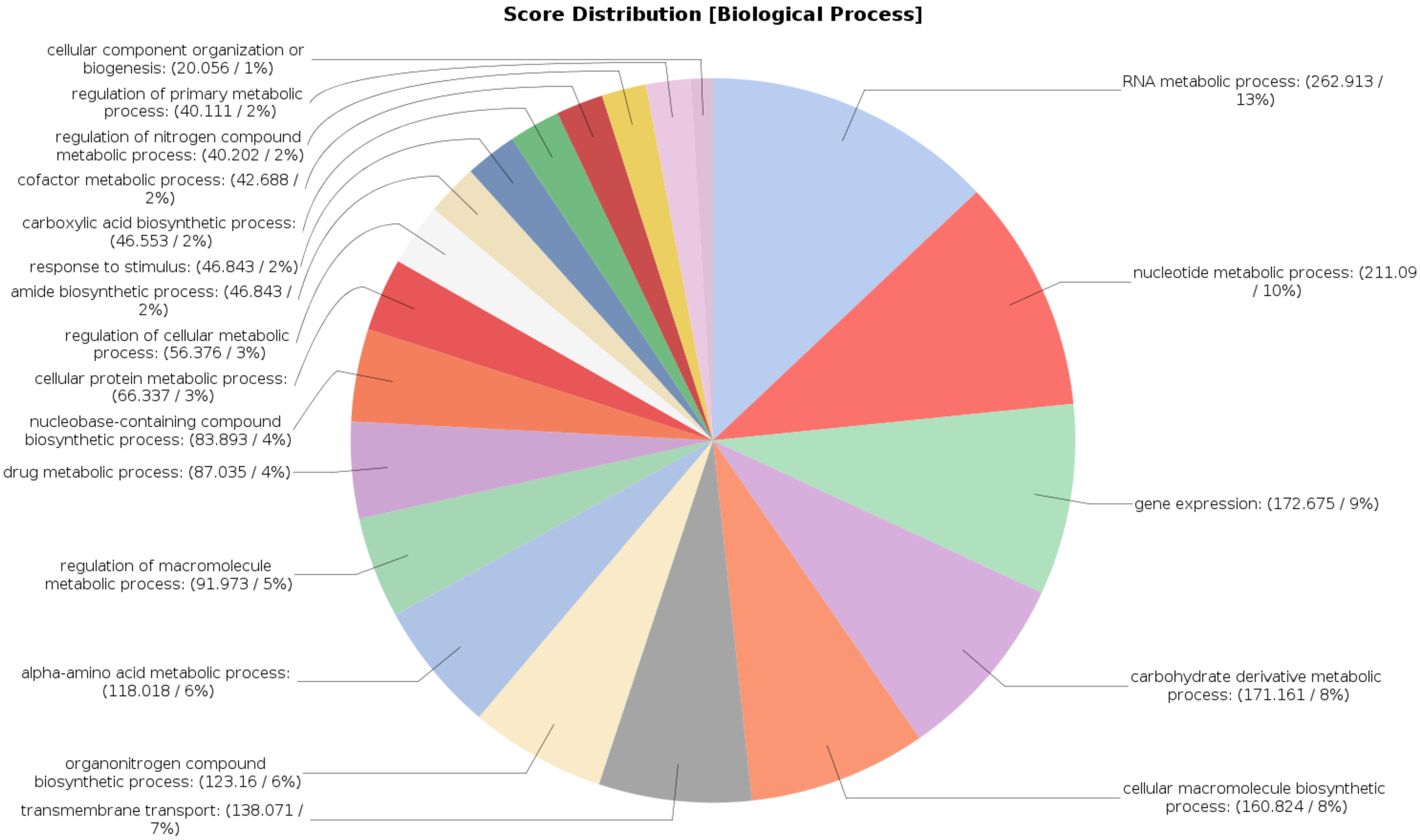


Figure 2.15 Biological process gene ontology annotation distribution of Rhizobium genus level core-genome

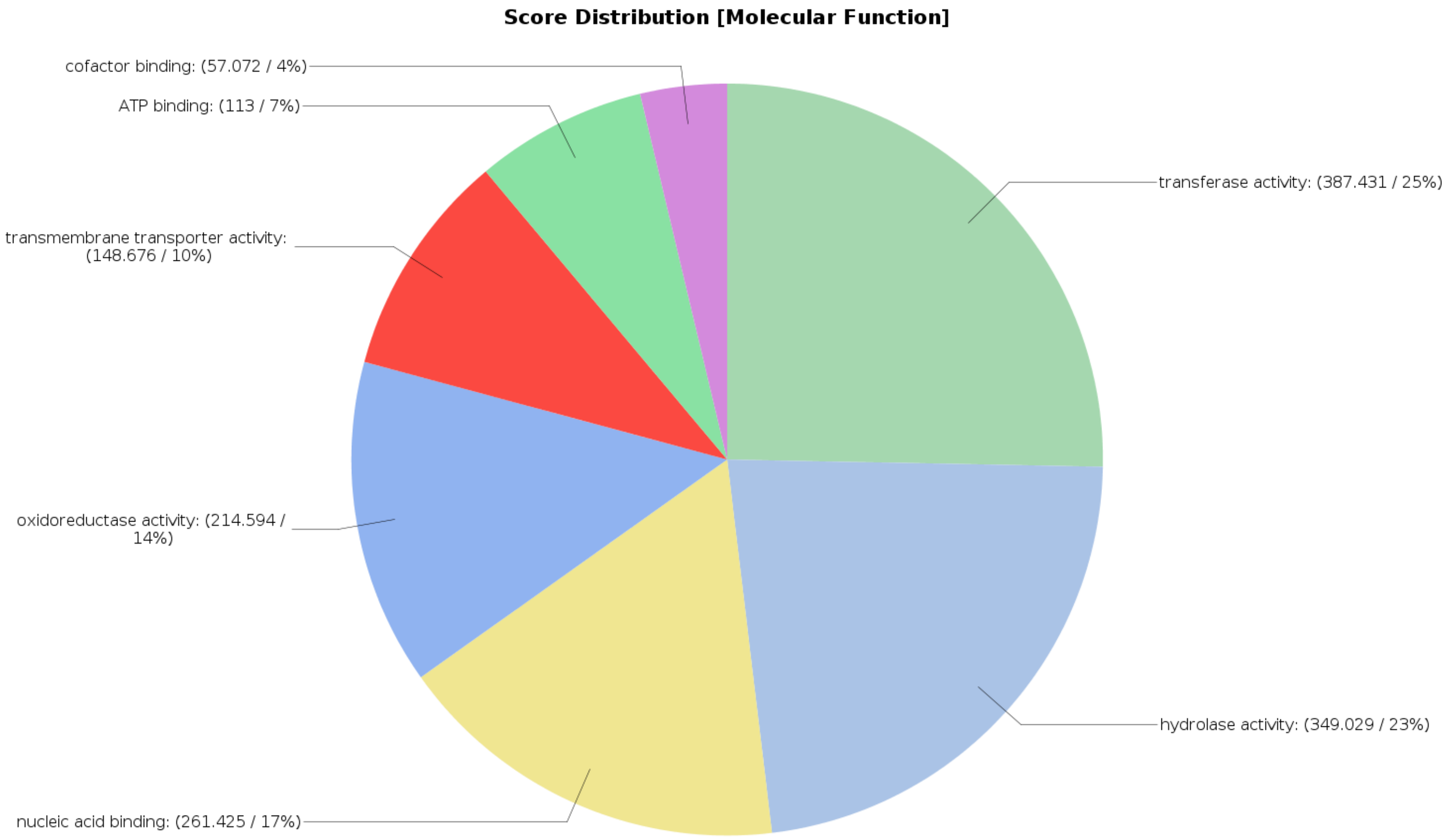


Figure 2.16: Molecular process gene ontology annotation distribution of the Rhizobium genus level core-genome.

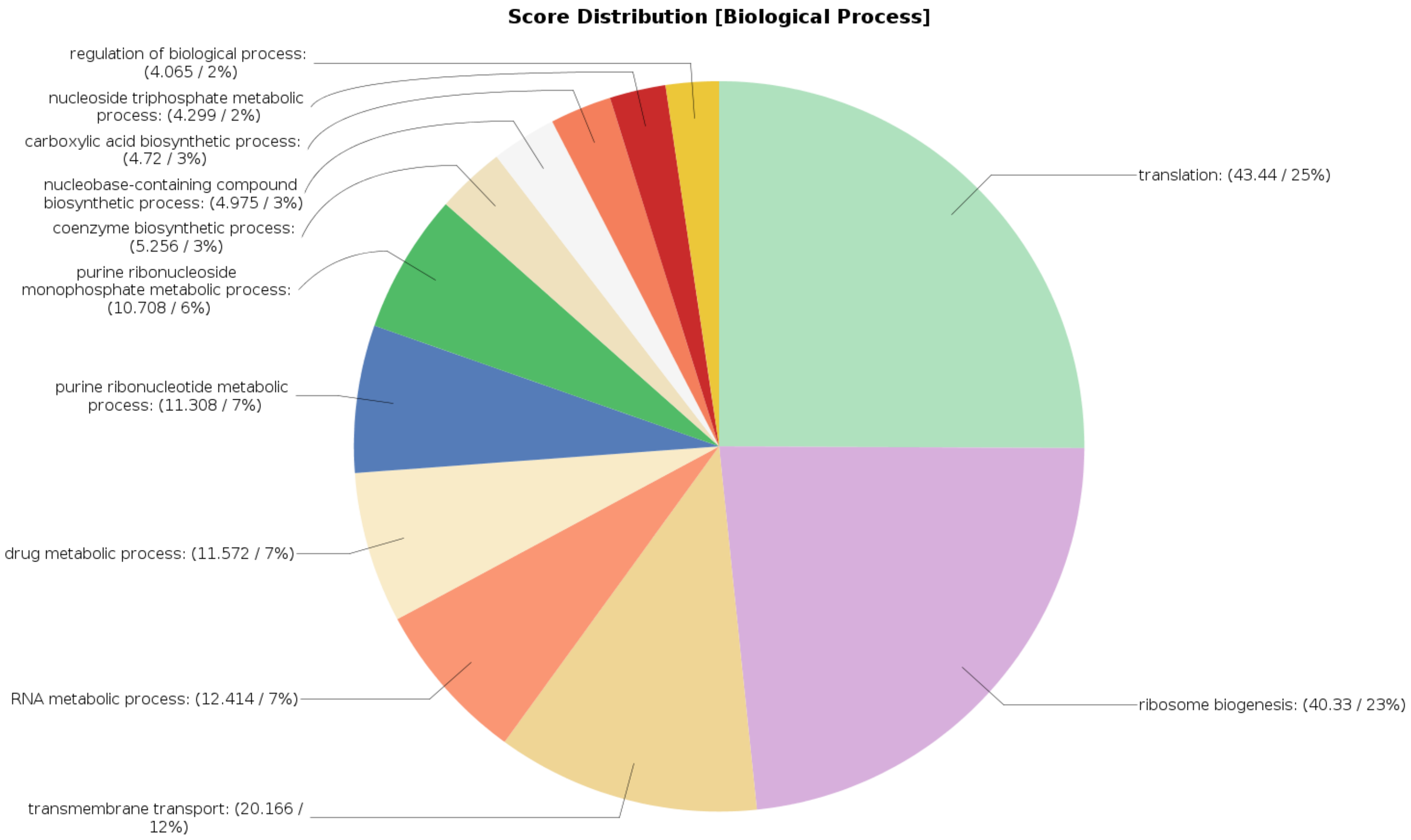


Figure 2.17: Biological process gene ontology annotation distribution of Bradyrhizobium genus level core-genome

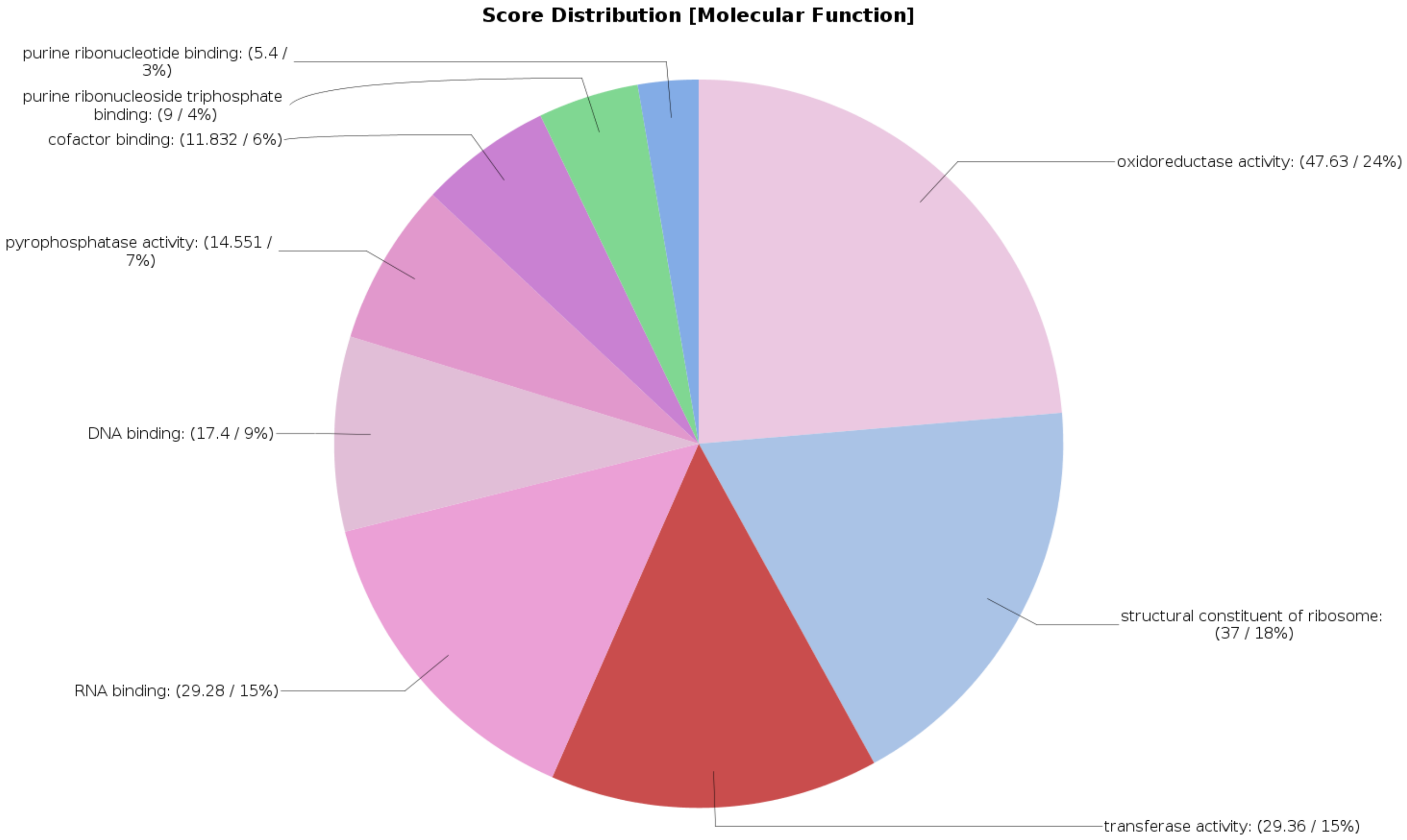


Figure 2.18: Molecular process gene ontology annotation distribution of the Bradyrhizobium genus level core-genome

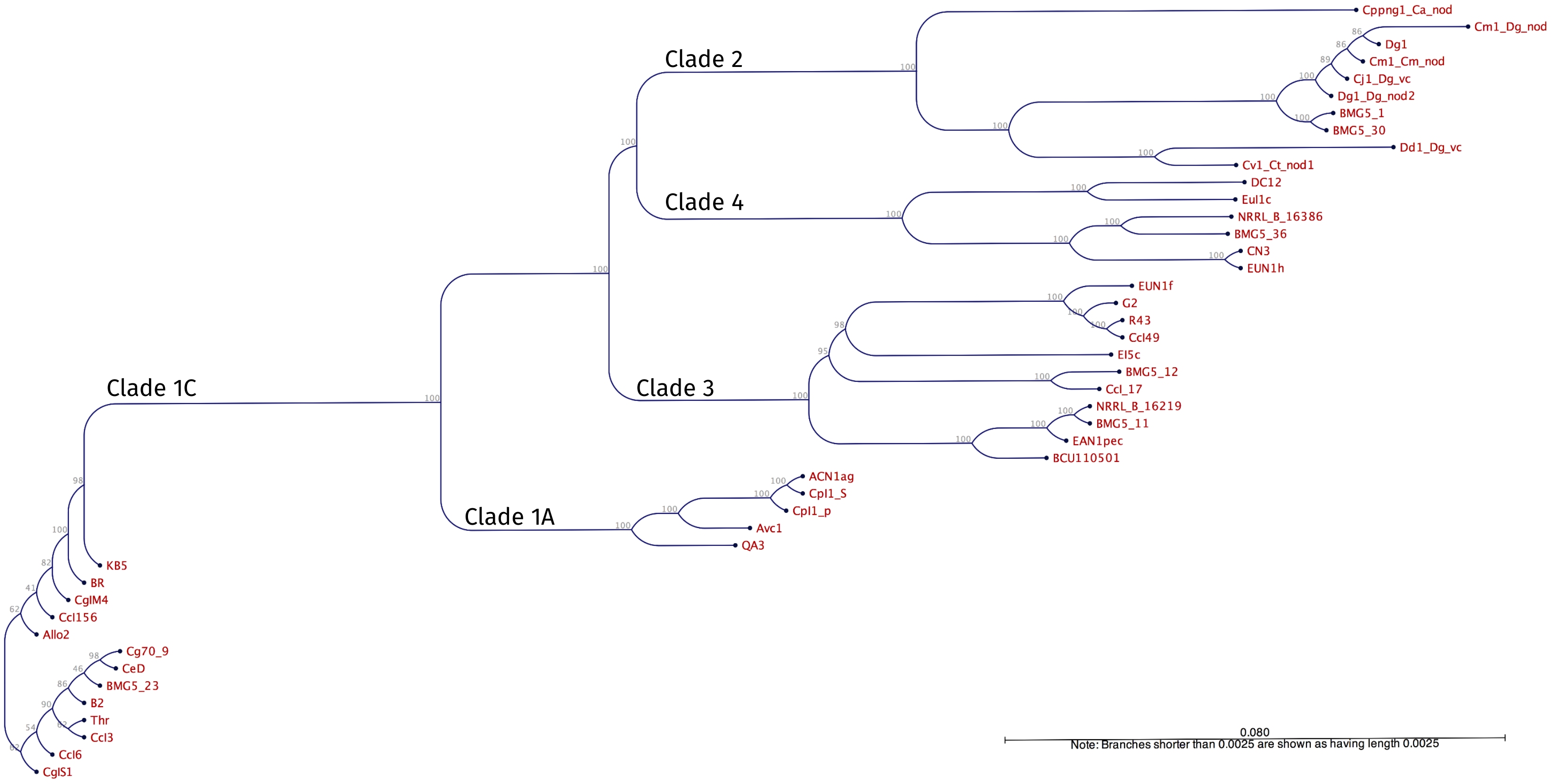


Figure 2.19: Frankia phylogeny of 45 strains based on 44 core genes identified in this analysis. Node support values were calculated using bootstrapping with 1000 replicates.

Discussion

The evolution of microorganisms is primarily characterized by classical darwinian selection. Even the high rates of horizontal gene transfer and high phenotypic stochasticity observed in many microbes can be described as a selection based trait. Additionally, most organisms are dominated by purifying selection (low K_a/K_s) and gene reduction. This has resulted in relatively small genome sizes in bacteria and an ecological restriction to stable niche spaces over evolutionary time (Wolf and Koonin 2013). Purifying selection and small genome size are most evident in obligate symbionts due to the long-term stability of the host niche space. Extreme examples of this phenomenon include mitosomes, mitochondria, and chloroplasts (Wolf and Koonin 2013, McCutcheon and Moran 2011). The evolutionary history of microbes is dominated by genome reduction punctuated by spikes in the incorporation of novel genetic information through horizontal gene transfer. These spikes or peaks in genetic information are theorized to occur during dramatic environmental changes or exposure to organisms or microbial communities that contain effective horizontal gene transfer mechanisms such as phage, Hfr cells, or virus-like horizontal gene transfer mechanisms like those found in *Rhodobacter capsulatus* (McDaniel *et al.* 2010). After an infusion of genetic information, sub-populations of microbes isolated in new and relatively stable niche space begins gene reduction once again, sometimes referred to as a valley. This shows how the core and accessory genome of microorganisms are maintained in an equilibrium by both adaptive mutation and random gene gain and loss events depending on the time frame considered.

Rickettsia spp. exemplifies this well. Comparative genomics of *Rickettsia spp*. suggests that the genus is approaching a low point in the peaks-and-valley process of genome evolution, consistent with its typically strictly obligate parasitic lifestyle. Nevertheless, there are still *Rickettsia* strains that survive as facultative symbionts (Blanc *et al.* 2007, Merhej and Raoult 2011, Sakurai *et al.* 2005). This shows that while many *Rickettsia* lineages have become obligate parasites with reduced genomes, some lineages have maintained enough genome diversity to function as free living organisms and exemplify the plasticity of the pan-genome.

Similarly, *Buchnera aphidicola* is at the bottom of a genome reduction valley (McCutcheon and Moran 2011). *Buchnera aphidicola* strains are obligate intracellular symbionts of aphids (Brinza *et al.* 2009). The *B. aphidicola*-aphid symbiosis originated approximately 150 mya, and *B. aphidicola* and their aphid hosts are now reciprocally dependent on each other for reproduction (van Ham *et al.* 2003). *Buchnera aphidicola* replicates in specialized bacteriocytes within the aphid and is vertically transmitted during aphid embryogenesis. Generally, only a single *B. aphidicola* cell is transferred to each embryonic aphid. Aphids now depend on *B. aphidicola* for some amino acid synthesis and nitrogen conversion (glutamine to glutamate). Similarly, *Buchnera aphidicola* are now dependent on the bacteriocyte environment and an aphid-provided supply of phloem. Isolation from other microbes in the bacteriocyte niche drastically limits exposure of *B. aphidicola* to potential horizontal gene transfer. The stability of the bacteriocyte niche creates additional selective pressure to eliminate nonessential genes. These factors have resulted in a 70% reduction in genome size since the last common symbiotic ancestor of *B. aphidicola. Buchnera aphidicola* genomes are now between 420 and 600 kb and are characterized by an extremely closed pan-genome. The pan-genome reaches saturation after only 3-4 genomes with a Heap's alpha decay values near 2 and stable gene content and arrangement (Medini *et al.* 2005, Brinza *et al.* 2009). Approximately 50 million years has passed since the last major genome rearrangement in *B. aphidicola*. The estimated core and pan-genome size for *B. aphidicola* is approximately 150 and 2500 orthologous clusters respectively (Mira *et al.* 2010, Snipen *et al.* 2009). A pan-genome of 2500 is very small. *Escherichia coli* has an estimated pan-genome of approximately 45000 orthologous clusters. The genome of *B. aphidicola* has been significantly reduced as a product of a stable symbiotic niche and the associated selective pressure. However, a small N_e is often associated with genetic drift, and *B. aphidicola* is not an exception (Kuo *et al.* 2009). The minimal changes that occur in the pan-genome of *B. aphidicola* are generally a product of the extreme bottle-necking that occurs with each generation of aphids. However, the genomic effects of these bottle-necks are attenuated by the high selective pressure to maintain all the functions necessary to persist in the obligate symbiosis. Therefore, the current pan-genome is under tight selective pressure to maintain or increase the fitness of *B. aphidicola* in its host environment.

Contrasting *B. aphidicola*, *Prochlorococcus spp.* has one of the largest, most diverse, and most unstable pan-genomes studied (Kettler *et al.* 2007, Biller *et al.* 2015). *Prochlorococcus* is the smallest known oxygenic phototroph and occupies diverse aquatic niches around the world, especially in warm oligotrophic environments down to depths of

200m or more. *Prochlorococcus* is characterized by a small genome of between 1.7 – 2.4Mb and individual isolates have relatively simple metabolisms. At the core genome level, the strains cluster into two groups adapted to relatively high or low light levels. The low light strains occupy the deep water niches and the high light strains occupy the shallow niches. Initial genomic studies concluded that most of the diversity contained by *Prochlorococcus* was an artifact of the divergence of the two clades. However, additional genome sequencing revealed that while the core genome estimate stayed close to 1000 orthologous clusters, each new strain contained a considerable amount of unique genetic information. The current estimate for the pan-genome of *Prochlorococcus* is almost 90000 orthologous clusters. Horizontal gene transfer likely explains the majority of this genetic diversity (Biller *et al.* 2015). The community of microbes that *Prochlorococcus* interacts with could help explain how *Prochlorococcus* has developed such high collective diversity. The niche space of *Prochlorococcus* overlaps with *Rhodobacter capsulatus* (Sun *et al.* 2014). *Rhodobacter capsulatus* is a species of non-sulfur purple bacteria that inhabit marine and freshwater environments (Weaver *et al.* 1975). *Rhodobacter capsulatus* are metabolically diverse and can perform facultative anaerobiosis, nitrogen fixation, xenobiotic metabolism, and photosynthesis (Weaver *et al.* 1975). They also contain an unusual mechanism for gene exchange, the virus-like gene transfer agent (GTA) system (McDaniel *et al.* 2010). Exposure to this mechanism combined with the stochastic nature of marine environments, including currents and mixing that move organisms from one geographical niche space to another very quickly, could drive the pan-genome expansion of *Prochlorococcus.* Thus, the group of organisms labeled *Prochlorococcus* in the literature seems to be reaching a peak in its genomic evolution. This makes sense in light of other studies suggesting that genetic diversity based phenotypic switching (also called bet-hedging) is more effective in stochastic environments than sensing and responding to changes (Balaban *et al.* 2004, Rainey *et al.* 2011, Kussell and Leibler 2005). As subpopulations of *Prochlorococcus* become isolated in more stable conditions, they will likely begin speciation by eliminating unnecessary genes that currently populate the pan-genome. It is important to note that the results of pan-genome analyses are dependent the number of genomes considered. If a diverse group of organisms is considered a species or genera, it will likely have a large pan-genome and small core genome with a high rate of change because the populations that make up the species experience different selective pressures and are exposed to different levels of potential horizontal gene transfer.

Based on the previous pan-genome analyses discussed above, both *Frankia* and *Rhizobium* appear to have had recent or ongoing periods of rapid horizontal gene transfer and to be in a stage of genome rearrangement and reduction. The *Frankia* genus level pan-genome has an open structure (Heap's alpha decay 0.86) while each of the clade level pan-genomes have closed pan-genome structures with Heap's alpha decay between 1.43 and 2.00. The *Rhizobium* genus has a open pan-genome with a Heap's alpha value of 0.66 while *Bradyrhizobium* has a closed pan-genome with a Heap's alpha value of 1.05. These values indicate that Rhizobium strains and species have relatively high rates of horizontal gene transfer, while *Bradyrhizobium* species are relatively stable.

The wide range of pan-genome structures observed in *Frankia* provides an interesting case study into the dynamics of gene gain and loss in a symbiotic context. Nodulation initiation and nitrogen fixation represent evolutionary constraints and appear to be causing *Frankia* strains to diverge into lineages with three distinct characteristics. Clades 1A, 1C, and 2 are comparatively selective in host range, have relatively small genome sizes, and are likely undergoing genome contraction according their pan-genomic characteristics. Nevertheless, clades 1A, 1C and 2 all retain the ability to fix nitrogen and initiate nodulation. Compared to clades 1 and 2, clade three has a broad host range and large genome size. Furthermore, the pan-genome structure of clade three indicates that strains in clade three are experiencing genome expansion, likely through gene gain from horizontal gene transfer. Despite this, clade three genomes have maintained the Nif regulon and genes necessary to initiate nodulation. In contrast, *Frankia* clade 4 strains have either lost the ability to initiate nodulation on their own, or have lost elements of the Nif regulon. *Frankia* clade 4 strains also have reduced and irregular genome sizes. This suggests that *Frankia* clade 4 strains could become obligate co-infecting symbionts.

CHAPTER THREE

Microbiome analysis of Coriaria myrtifolia, Casuarina glauca, and New Hampshire lithic environments

Introduction

Rationale

Microbial diversity is a key determinant of the health and function of nearly every biological system and higher organism. Modern sequencing technology has made 16S meta-amplicon data a powerful tool to explore the taxonomic profiles that define specific human health conditions, ecological system disruptions, and advantageous environmental community functions. Over the last decade numerous studies have illustrated the utility of 16S amplicon analyses in a wide range of applications. Amplicon sequencing was used to determine a diagnostic taxonomic profile of the colon microbiome of cancer patients (Flemer et al. 2017), and to find species-specific assemblages of microbes in sub-tropical sponges (Schmitt et al. 2011). 16S amplicon analysis was also used to elucidate the dominate taxa in the 150 years-long Park Grass Experiment in Hertfordshire UK in an effort to understand how long-term land use impacts soil health (Zhalnina et al. 2014). They found that soil carbon and nitrogen levels, microbial diversity, and plant diversity were all interdependent and significantly impacted by human intervention. A similar interdependence of soil nutrients, microbes, and plants has been demonstrated in a number of other studies (Hester et al. 2018, Ouyang and Norton 2020, Schmidt et al. 2019).

Understanding how these interactions affect overall ecosystem health and resilience during and after disturbances such as climate change, invasive species introduction, and nitrogen pollution is key to addressing many of the problems facing humankind in the coming decades. Elucidation of plant-microbial interactions is particularly important because of the mitigating role that many plants play in human-impacted landscapes including urbanized and agricultural land (Hamilton et al. 2016, Hoch et al. 2019). Determining how specific plants-microbe interactions influence community structures is an essential first step toward the larger goal of understanding and appropriately utilizing the potential remediating functions and ecosystem services provided by microbial communities.

This study assessed two plants with economic and ecological significance: *Coriaria myrtifolia* and *Casuarina glauca. Coriaria myrtifolia* is an actinorhizal plant species primarily distributed around the Mediterranean region. As actinorhizal plants, the *C. myrtifolia* and the *Frankia* symbiosis fixes atmospheric nitrogen and helps stabilize and enrich degraded and contaminated soils. *Coriaria myrtifolia* plants were historically used in the dying and tanning industries and have more recently received interest because they contain sesquiterpene lactones such as picrotoxin. In relatively high doses, picrotoxin can be fatal to livestock and humans, but the psychoactive properties of some sesquiterpenes has made *C. myrtifolia* a drug discovery candidate.

Casuarina glauca is also an actinorhizal host species which forms a nitrogen fixing symbiosis with *Frankia* sp. While *C. glauca* is native to Australia, is has be transplanted to northern Africa and North America. *Casuarina glauca* is extensively used to stabilize soil and to serve as a windbreak. *Casuarina glauca* is also used as a firewood source and has been adopted in silviculture to supply wood for a number of industrial purposes. Understanding the microbiomes of these plants and the soil they inhabit is an important step toward gaining a better understanding of their ecological role and maximizing their economic usefulness.

Similarly, assessing microbial community interactions within soil and lithic environments is a crucial step toward understanding the role they play in numerous ecological processes. Soil microbial diversity is associated with positive effects on human and environmental health, and is an important component of biogeochemical cycles.

Futhermore, understanding how anthropogenic perturbations impact soil microbial communities and by extension soil-microbial interactions is important in mitigation the continuing effects of industrialization on ecosystem services. Metagenomic and meta-amplicon based analyses are powerful tools which provide an initial overview of the taxa present in these important communities and how they change in response to human influences.

Purpose

This work surveyed microbial communities inhabiting environmental spaces representative of three important interactions: plant-microbe interactions, soil-microbe interactions, lithic-microbe interactions. The aims of these analyses were to 1.) determine the composition and structure of the phyllosphere (both endophyte and epiphyte), rhizosphere, and soil microbial communities of *Coriaria myrtifolia* in Algeria and 2.) determine composition of the soil and nodule microbiomes associated with *Casuarina* *glauca* at a industial site in Tunisia and 3.) determine the community composition of microbes associated with lithic decomposition in New Hampshire. We also sought to determine the effect non-*Frankia* bacterial occupants of *C. myrtifolia* nodules might have on nodulation, nitrogen cycling, and remediation and investigated the role toxic plant secondary compounds in the picrotoxane famliy may play in structuring the microbiome of *C. myrtifolia.*

Methods

Community Sampling

Tissue samples were collected in triplicate from wild *C. myrtifolia* plants growing at Les Gorges de Kharrata in Bejaia, Algeria. *Coriaria myrtifolia* was chosen based on its unique combination of economic value in the leather and dyeing industries, ecological value as a pioneer species and symbiotic host for *Frankia,* and its production of the toxic sesquiterpene coriamyrtin. Wild plants in Bejaia were chosen over cultivated *C. myrtifolia* to better assess the natural phytomicrobiome and it's influences on the soil microbial community. Fruit, leaf, stem, root, and nodule tissues were samples from each plant. Rhizosphere and soil samples from the same location were also collected in triplicate starting with rhizosphere samples collected from the same *C. myrtifolia* plants from which tissue was collected and including soil samples 30, 100, and 1000 meters distant from each plant. The exact GPS coordinate of each sampling location was recorded and mapped.

Plant tissue (5g fresh weight) was collected from *C. myrtifolia* leaves, fruit, stems, roots, and nodules and in sterile collection bags and immediately transported on ice to a laboratory at the Abbas University (Sétif, Algeria) for DNA extraction. Soil and rhizosphere samples (10 g) were collected in sterile collection bags and transported to Abbas University (Sétif, Algeria) for processing.

The effect of industrial hydrocarbon and heavy metal pollution on soil and *C. glauca* nodule microbes was also addressed with community profiling. Soil, rhizosphere, nodule, and pseudonodule samples were collected the Almes agro-industrial complex in Bizerte, Tunisia, and transported to the University of Tunis for processing and DNA extraction. The Bizete site was chosen based on previous long-term contamination with heavy metals and industrial solvents. Soil, rhizosphere, and nodules samples were collected from both an area with historical wastewater contamination, and a control site without contamination. Pseudonodules were only present in the contaminated area. Four,

Sample	GPS Coordinate	Elevation (m)
Rhizosphere A	N 36° 31' 9.379" E 5° 16' 45.616"	314
Rhizosphere B	N 36° 31' 9.516" E 5° 16' 46.474"	320
Rhizosphere C	N 36° 31' 9.818" E 5° 16' 44.209"	294
30m A	N 36° 31' 10.211" E 5° 16' 46.225"	288
30m B	N 36° 31' 10.448" E 5° 16' 46.894"	303
30m C	N 36° 31' 10.344" E 5° 16' 45.415"	296
100m A	N 36° 31' 12.004" E 5° 16' 48"	288
100m B	N 36° 31' 14.725” E 5° 16' 46.624"	277
100m C	N 36° 31' 11.665” E 5° 16' 47.845"	282
1000m A	N 36° 31' 36.095" E 5° 17' 7.746"	235
1000m B	N 36° 31' 30.551” E 5° 17' 2.72"	238
1000m C	N 36° 31' 35.98” E 5° 17' 8.833"	222

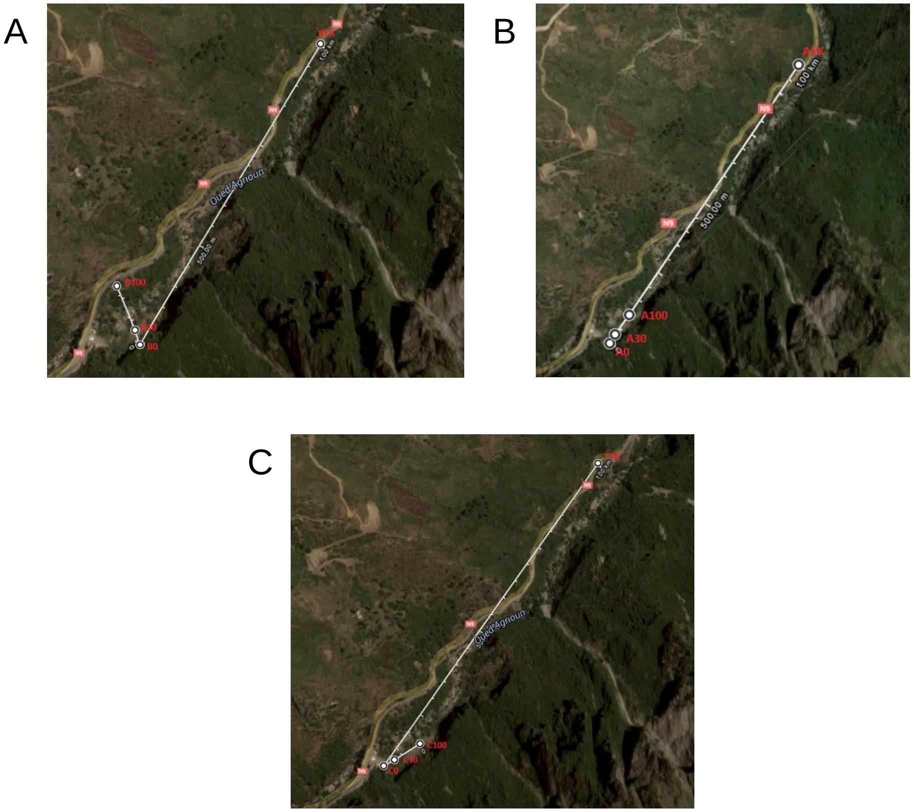


Figure 3.1: Location and geographic information for Algerian phytomicrobiome, soil, and rhizosphere samples. Map insets A, B, and C correspond to the three C. myrtifolia plant replicates.

1 g samples of nodules and pseudonodules were collected and 10g soil and rhizosphere samples were collected in triplicate at a depth of approximately 20 cm. All samples were collected in sterile plastic collection bags and stored at 4 °C until DNA extraction.

Sample preparation

DNA was extracted from the epiphytic and endophytic communities from each plant tissue sample. Prior to DNA extraction, the samples were divided into sub-samples, and the first sub-sample of each tissue was used as the epiphyte sample. DNA from these samples was extracted by macerating 1 g of tissue in 500 ml of a sterile, isotonic solution containing 0.01% Tween-80 and subsequently shaking the macerated tissue at 150 rpms for 2 hours. This crude extract was filtered using 0.22 μm filters prior to final DNA extraction. DNA was purification using the Qiagen Plant DNA extraction kit per manufacturer's instructions.

The second sub-sample of each tissue sample was used to characterize the endophytic community. These samples were surface sterilized by shaking in 30% (v/v) H_2O_2 for 30 minutes and subsequently rinsed aseptically 3x with molecular grade water. Successful surface sterilization was checked by spread plating a 300 μl aliquot of the last rinse on nutrient agar. After successful sterilization, each tissue sub-sample was aseptically powdered in liquid nitrogen. DNA was extracted and purified from these powdered tissue samples using the Qiagen Plant DNeasy extraction kit per manufacturer's instructions (Qiagen, Hilden, Germany).

DNA from the soil and rhizosphere samples from Algeria and Tunisia were extracted using Qiagen DNeasy PowerSoil kits according to the manufacturer's instructions (Qiagen, Valencia, California). All samples were treated with RNAse A for 30 minutes at 37 °C and subsequently dried and shipped to the University of New Hampshire for 16S DNA sequencing.

Microbial interaction with lithography *– adapted from Remiszewski, Kiley, "NUTRIENT CYCLING ALONG MICROBIAL AND LITHOLOGIC GRADIENTS AND FOSTERING STUDENT SELF CONFIDENCE IN SCIENCE" (2020). Doctoral Dissertations. 2534.*

Experimental design and sample collection

Mesh bags (50 µm pore size) designed to exclude plant roots but allow hyphae and bacteria to enter were filled with crushed granite or tonalite and were buried at two sites: Hubbard Brook Experimental Forest (HBEF; 43.9490 N, 71.7852 W) and a willow farm in Fairfield, VT (44.7687N, 72.9251W) following procedures adapted from Wallander et al. (2001) (Remiszewski et al., 2016). Granite or tonalite samples were chipped, crushed, and sieved to include only particles between 250 and 500 µm. All rock samples were acid-washed for 24 hours in 1 N nitric acid and rinsed with purified deionized water (18MΩ DI water) before burial. Approximately10 g of crushed rock was added to each mesh bag. Control bags with each rock type were reserved and stored at -20 °C.

Hubbard Brook Experimental Forest contains hardwoods and conifer species and receives an average of 1395 mm of precipitation per year with a mean annual temperature of 5.5 °C. Soils at HBEF are spodosols (Bailey et al., 2014) developed in glacial drift of primarily granitic origin (S. Bailey et al. 2003) with a pH ranging between 3.5-4.5

(Bourgault et al., 2015). Soils are thin on upper slopes with bedrock exposed in stream channels and along ridgelines (Bailey et al., 2014). The willow farm was selected due to the presence of *Salix repens*, a host species for both AM and EcM fungi (van der Heijden, 2001). Fairfield VT receives between 1016 and 1270mm of annual precipitation (NOAA National Weather Service, 2019). The soil at the site is a fine sand-loam spodosol with 8-15% slopes (USDA Natural Resources Conservation Service, 2019). The Fairfield Pond Formation, comprised of quartz-sericite-chlorite, phyllite and foliated quartzite, underlies the site (Ratcliffe et al., 2011).

Site selection was made to test *in situ* microbial community development on weathering soils with suspected EcM or AM fungal symbioses. The sites at Hubbard brook contain young soils with shallow depth to bedrock and confirmed AM and EcM host plants (Schwarz et al., 2003; vanDoorn et al., 2011). Hubbard Brook site 206 is dominated by beech (*Fagus grandifolia*) and birch (*Betula sp*.), which are known to associate with EcM fungi. Sugar maple (*Acer saccharum*), which associates with AM fungi, is dominant at site 237. Mesh bags were buried near individual trees selected based on maturity and proximity to non-dominant vegetation likely to host the opposite fungal type of the selected tree. Maple trees were selected in site 237 and either beech or birch trees were selected in site 206. The bags were buried in Hubbard Brook Experimental Forest in August 2018 at the base of each selected tree in both site 206 and site 237. In September 2018 ,the mesh bags were buried in the same manner an area planted with *S. repens* specimens at the willow farm in Fairfield VT. The bags at both sites were buried in the organic horizon at 10 cm depth or where the Organic Horizon met the mineral A

Horizon, whichever occurred first. Soil samples from the base of representative trees of each species were collected with sterile trowel at same time the mesh bags were buried and stored at -80 0 C for microbial community analyses. The mesh bags were retrieved from Hubbard Brook sites 206 and 237 in June 2019 and from the VT site in July 2019. Soil samples were also collected from all three sites at time of retrieval with a sterile trowel and stored along with the mesh in-growth bags at -80 0 C for community composition analysis.

Immediately after retrieval, all rock samples were stored at -80°C prior to processing for sequencing. Aliquots of crushed rock were remove from the bags and DNA was extracted separately from the soil surrounding the mesh bags and the crushed rock samples contained within the bags using the DNeasy PowerSoil DNA Isolation Kit according the manufacturer's instructions (Qiagen, Valencia, California).

DNA Sequencing

All DNA samples were submitted to the Hubbard Genome Center at the University of New Hampshire for sequencing of the v4 hyper-variable region of the 16S ribosomal gene according to the Earth Microbiome Project (EMP) protocol. Briefly, the v4 hyper-variable region of the 16S ribosomal gene was amplified using EMP 515F/806R universal PCR primers and sequenced using a 250bp paired-end approach with Nextera library preparation using the Illumina HiSeq 2000 platform (Illumina, San Diego, California) as previously described (Louati et al. 2020). Reads were demulitplexed by the Hubbard Genome Center prior to analysis.

Data Analysis

QIMME2: Demultiplexed reads were received from the Hubbard Genome Center and imported to the Quantitative Insights into Microbial Ecolgy 2 (QIIME2) software suite for processing. Despite repeated sequencing and read pooling, poor quality at the 5' end of reverse reads resulted in decreased pairing and a significant loss of sequencing depth. Therefore, a single-end analysis using only the forward reads was selected. The forward reads were trimmed and error-corrected with DADA2 removing chimeric reads and truncating reads at 240bp to exclude reads with a Phred quality below 35. Phylogenetic diversity of the resulting features was determined with MAFFT (Multiple Alignment using Fast Fourier Transformation) and fasttree using the Qiime2 phylogeny plugin. Taxonomic assignment of the sequence variants in the feature table was accomplished using the Qiime2 feature-classifier plugin. A feature classifier was trained using native-Bayes and the full length SILVA 99% identity 16S database (release 138). The resulting classifier was used with the classify-sklearn method to assign taxonomy to the feature table. Genus and phyla level tables were exported from QIIME2 for diversity analysis in R.

Alpha diversity in each of the four data sets was determined based on observed operational taxonomic units (OTUs) with taxonomies assigned at both the phylum and genus level. Python scripting was used to process and format QIIME2 feature table data which was plotted in R using ggplot2. Non-metric Multidimensional Scaling (NMDS) analysis was carried out in R using separate exported QIMME2 feature tables collapsed to genus level taxonomic OTUs. The metaMDS function in the vegan package of R was used for the NMDS analyses with Bray-Curtis distance, a trymax of 50 and K of 2. Before NDMS analysis, all feature counts in each sample were relativized by the total number of features in the sample to control for extraction and amplification error. The veganCovEllipse function (Torondel et al. 2016) was used to generate 95% confidence intervals within the ordination space. Ellipses were plotted to represent the confidence interval information and the NMDS data plotted in the sample figure. NDMS figures were generated with ggplo2 in R. Relative abundance taxonomic bar plots were generated with ggplot2 using using QIIME2 feature tables with taxa collapsed to OTUs at the phyum and genus level. Pairwise PERMANOVA (Permutational Multivariate Analysis of Variance) analyses were carried out in R using the adonis function in the vegan package to test the significance of between group differences observed in the NMDS analyses. Bray-Curtis distance and Bonferroni correction was used in each PERMANOVA analysis. Simper analysis was carried out to assess the contribution individual features had on the observed differences between samples. Simper analyses were out using the vegan package in R with the default parameters gain insight into the taxa driving differences between groups observed in NMDS and PERMANOVA.

Endolithic community beta diversity was assessed using the Principal Coordinates Analysis (PCoA) implemented in QIMME2. PCoA was calculated based on a Bray-Curtis distance matrix of sequence variants transformed to per sample relative abundance.

After taxonomic assignment at the genus level (QIIME2 taxa L6) was completed in QIIME2, reads assigned to the genus *Frankia* in samples from the roots, rhizosphere, and all three bulk soil types were exported and reassigned to *Frankia* clade level bins with a custom python script. Specifically, a BLAST database was made using the v4 region of the 45 previously sequenced *Frankia* strains. The the average expect value for alignments between each read and the all the *Frankia* strain v4 sequences in a given clade was calculated. All reads were then assigned to a bin corresponding to the clade with the lowest average expect value for that read. The number of reads in each clade bin was normalized by total reads per sample and used to generate a heat map.

Results

Sequencing Results

The 16S meta-amplicon data from 4 sites was analyzed to determine their community composition and assess the ability of community sequencing data sets to provide insight into the remediation and land reclamation potential specific microbial assemblages. Sequencing of the *C. myrtifolia* phytomicrobiome resulted in 1,080,585 total reads in the 30 individual samples after quality filtering and 4,289 unique features. Features per sample ranged from 1,219 to 130,272 with a median of 14,577.5 feature per sample and a 3rd quartile frequency of 52,549.8. The frequency of features ranged from 2 to 291,203 with a mean frequency of 251.9 and a 3rd quartile frequency of 63. Alpha rarefaction curves indicate that the sequencing depth was adequate to capture most of the observable diversity.

Sequencing of the *C. myrtifolia* rhizosphere and nearby soil samples resulted in 129,045 total reads after quality filtering and 4,551 unique features in 12 samples.

Table 3.1: Summary of sequencing results for the C. myrtifolia phytomicrobiome.

Sample ID	***Total reads***	***Average Reads***	***Average OTUs/Sample***
All Plant Samples	1,075,722.00	35,857.40	91.7
Endophyte Samples	664,416.00	44,294.40	71.6
Leaf	36,553.00	12,184.30	15.7
Fruit	24,452.00	8,150.70	56
Stem	60,669.00	20,223.00	29.67
Root	194,431.00	64,810.30	88.67
Nodule	348,311.00	116,103.70	168
Epiphyte Samples	411,306.00	27,420.40	111.9
Leaf	54,075.00	18,025.00	12.3
Fruit	25,625.00	8,541.70	76.33
Stem	16,017.00	5,339.00	32.33
Root	190,677.00	63,559.00	133.67
Nodule	124,912.00	41,637.30	304.67
Soil Samples	129,135.00	10,761.30	187.0
Rhizosphere	83,749.00	27,916.30	350.0
30 m away	18,181.00	6,060.30	168.0
100 m away	13,616.00	4,538.70	116.0
1,000 m away	13,589.00	4,529.70	114.0

Features per sample ranged from 203 in rhizosphere sample B to 62,808. Alpha rarefaction curves indicate that sequencing depth of the soil and rhizosphere samples was adequate to capture most of the diversity present at the sites.

Sequencing of *Casuarina* rhizosphere and nearby soil at the Almes industrial in Tunisia resulted in 325,465 total reads in the 24 samples with 6,791 total unique features. The number of features per sample varied from 290 to 33,407 with a median frequency of 12,072. The frequency of feature ranged from 2 to 21,216 with a median frequency of 6 and 3rd quartile frequency of 24. The alpha rarefaction curves generated from the samples indicated that sequencing depth was adequate to capture the majority of available diversity.

Sequencing of endolithic samples from Hubbard Brook Experimental Forest and a Vermont willow farm resulted in 1,854,496 total reads and 31,546 unique features in 79 samples. Frequency per sample ranged from 6 to 43,383 features per sample with a mean of 23,474.6 features per sample. The 1st quartile frequency was 13,738.5 features per sample and 3rd quartile frequency was 34,037.0 features per sample. Total feature frequency ranged from 2 to 47,255 with a mean frequency of 58.8 and a 3rd quartile frequency of 10. Rarefaction plots indicate adequate sequencing depth to capture the available microbial diversity.

Alpha Diversity and Taxonomy

Alpha diversity was determined for each sample based on Operational Taxonomic Units assigned at multiple taxonomic levels. Phylum and Genus level OTUs features were chosen as the best representations of the diversity data. Nodule samples had the

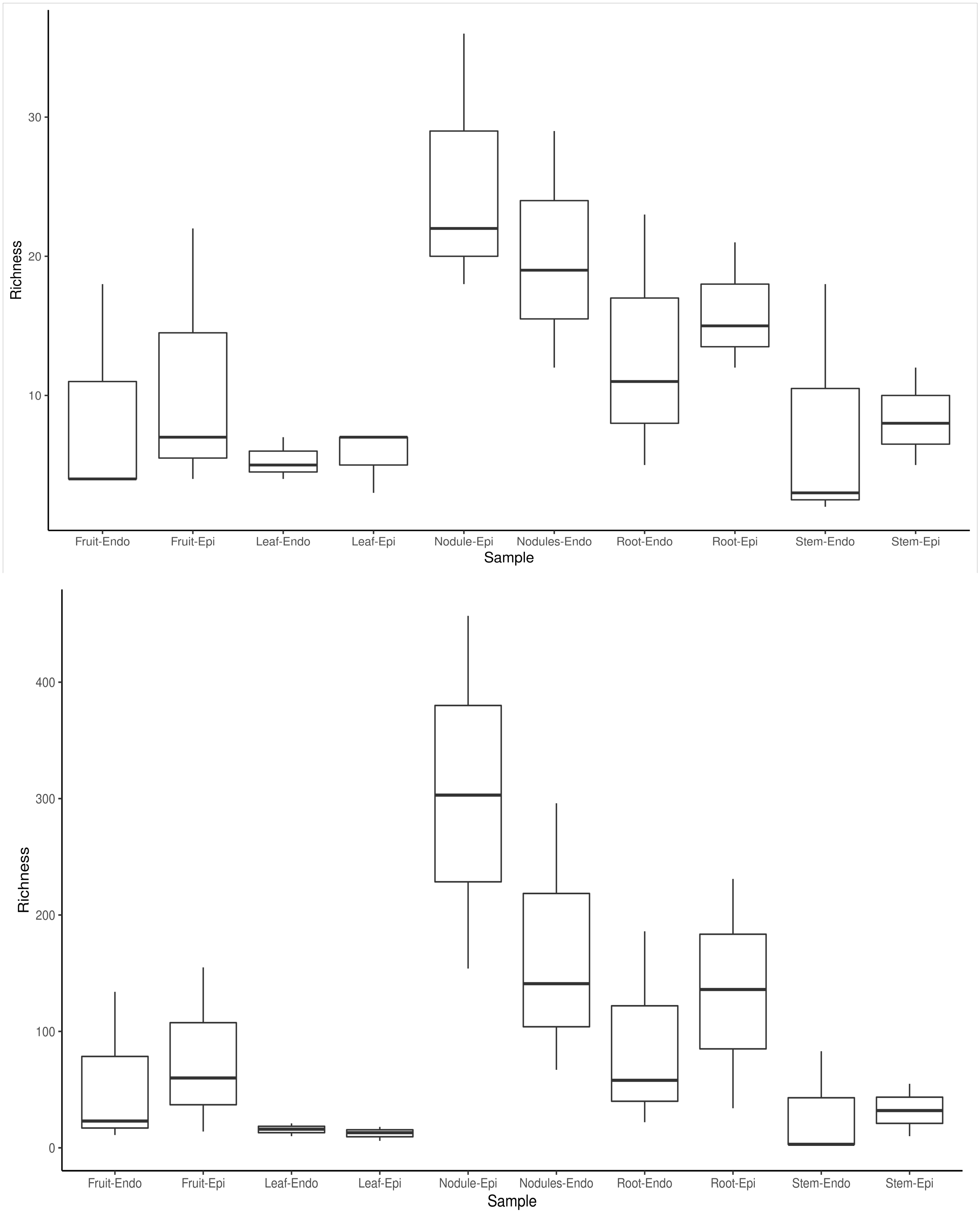


Figure 3.2: Phylum (upper) and genus (lower) level alpha diversity of the C. myrtifolia phytomicrobiome. Boxes represent 25th to 75th percentile variance around the mean. Whiskers represent 1.5 interval quartile ranges. Data points outside of the whiskers are considered outliers and are plotted separately.

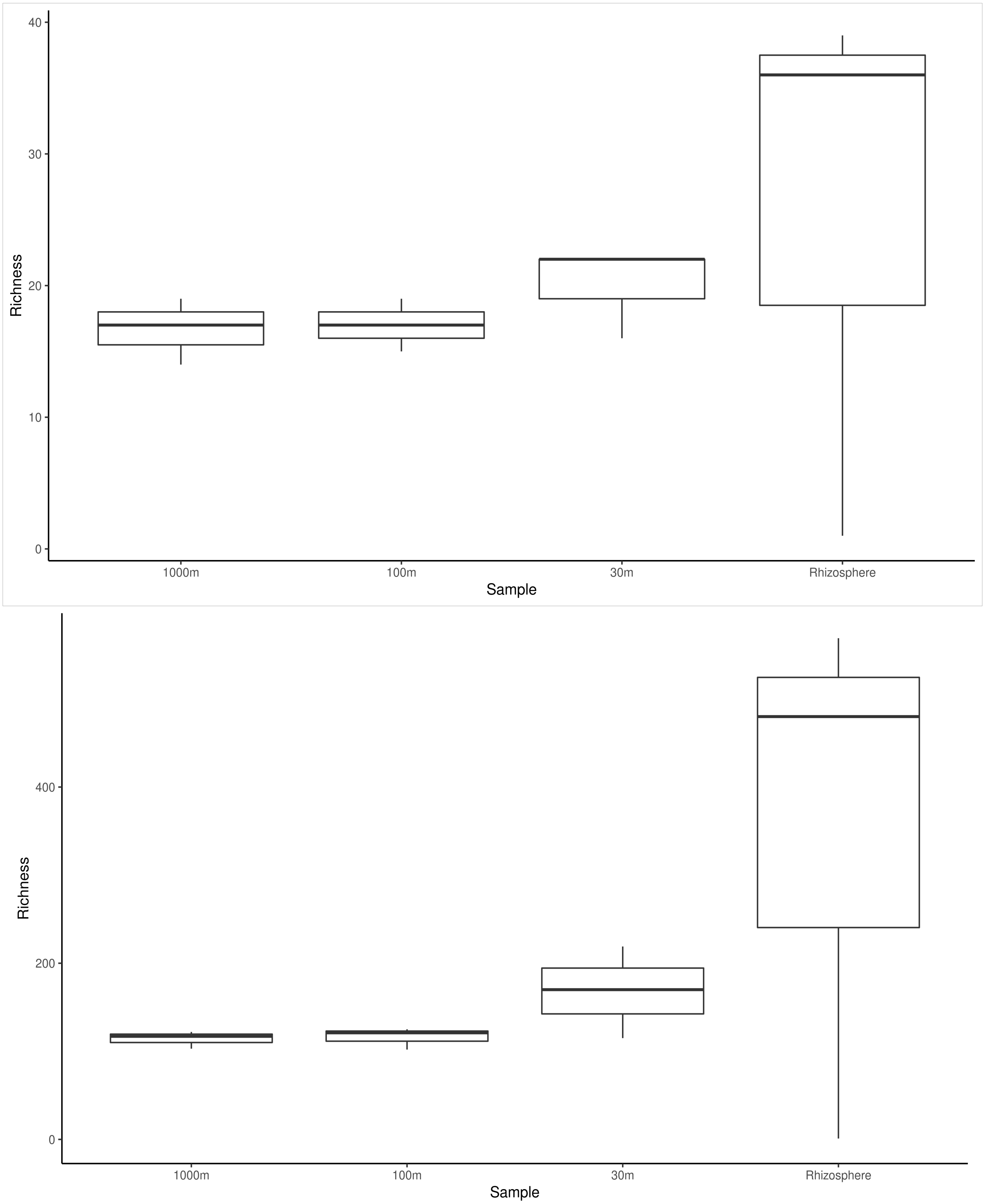


Figure 3.3: Phylum (upper) and genus (lower) level alpha diversity of C. myrtifolia soil and rhizosphere microbiomes. Boxes represent 25th to 75th percentile variance around the mean. Whiskers represent 1.5 interval quartile ranges. Data points outside of the whiskers are considered outliers and are plotted separately.

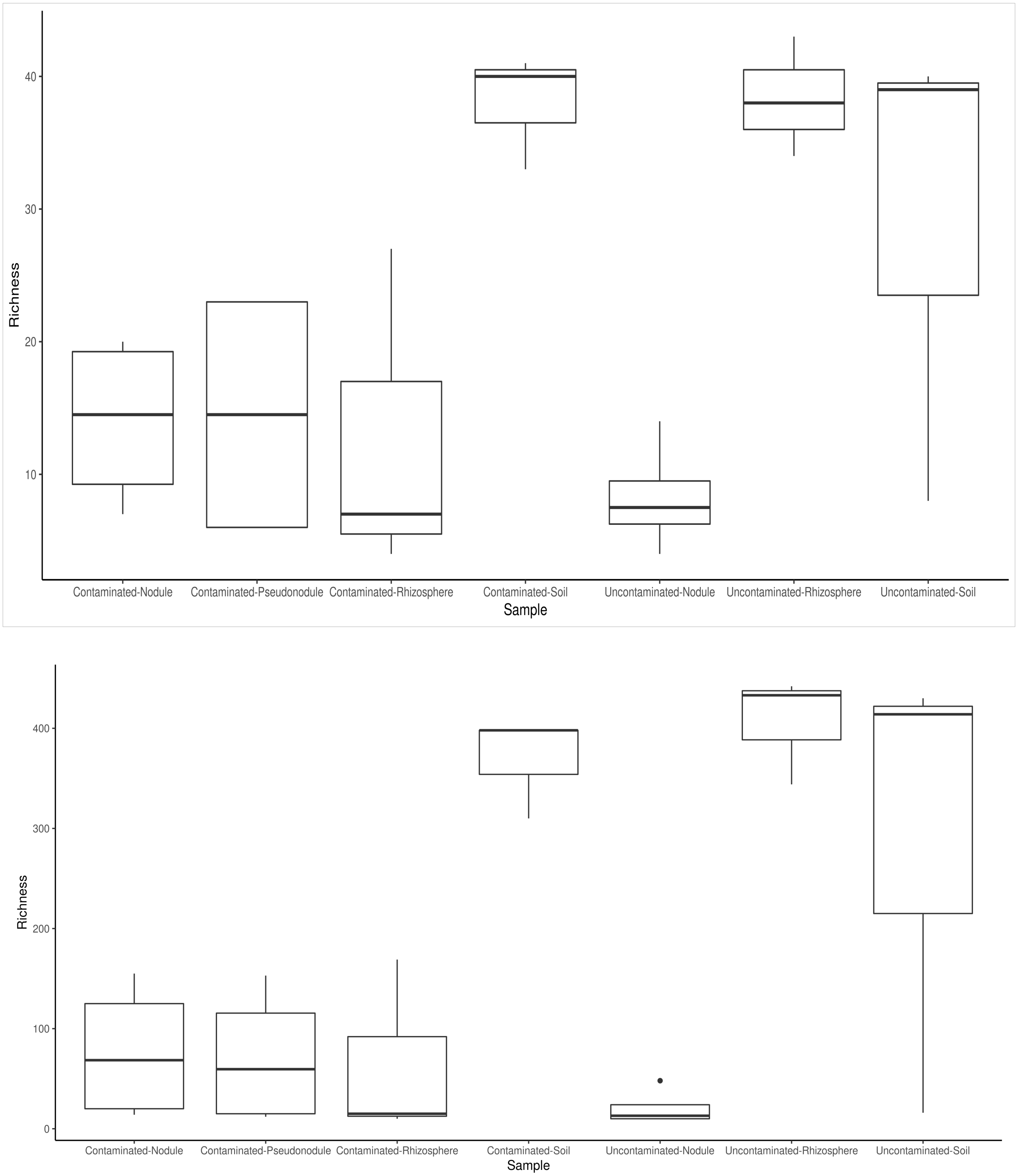


Figure 3.4: Phylum (upper) and genus (lower) level alpha diversity of C. Glauca nodules, rhizosphere, and nearby soil. Boxes represent 25th to 75th percentile variance around the mean. Whiskers represent 1.5 interval quartile ranges. Data points outside of the whiskers are considered outliers and are plotted separately.

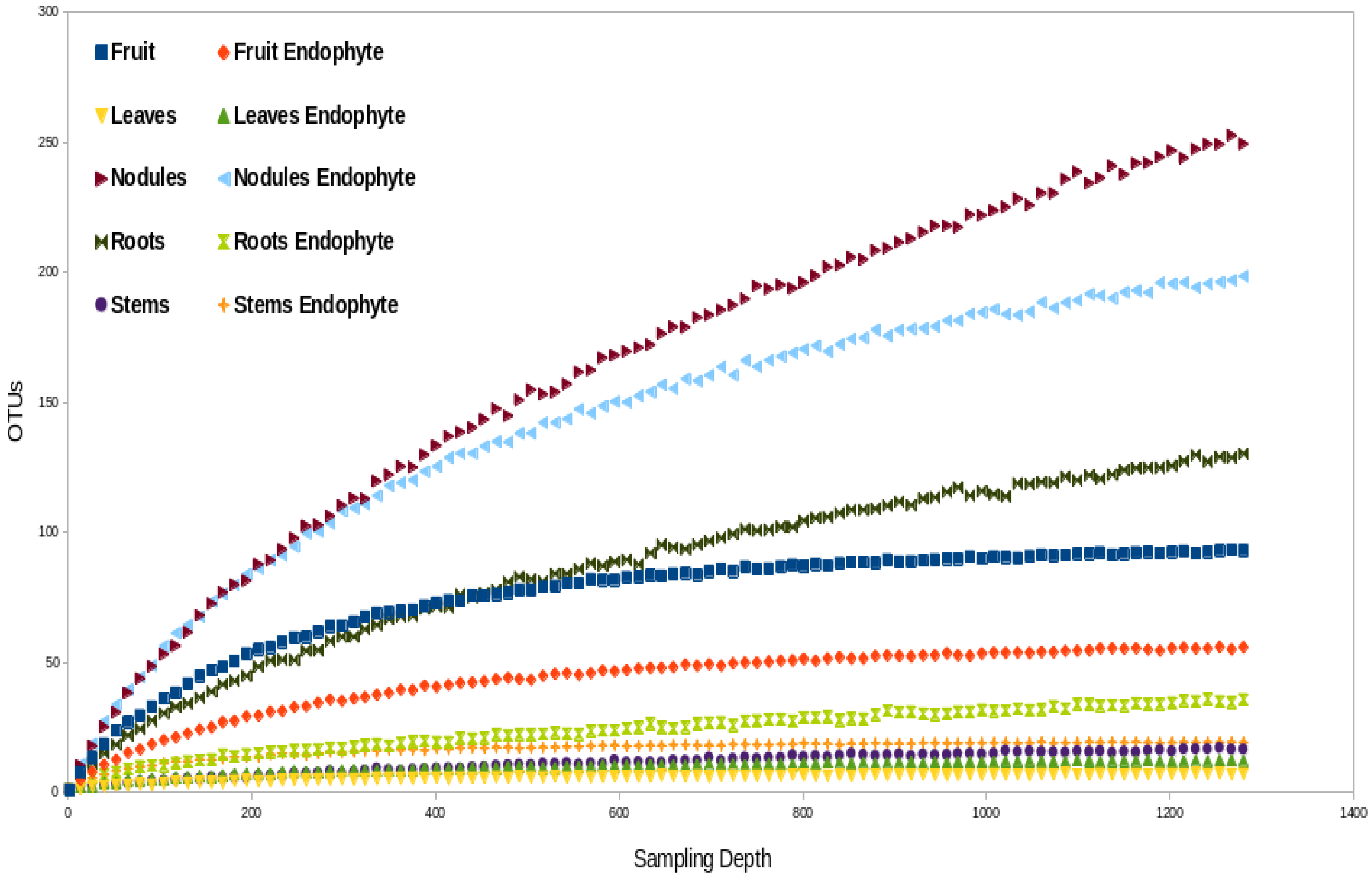


Figure 3.23: Alpha rarefaction curve of C. myrtifolia phytomicrobiome

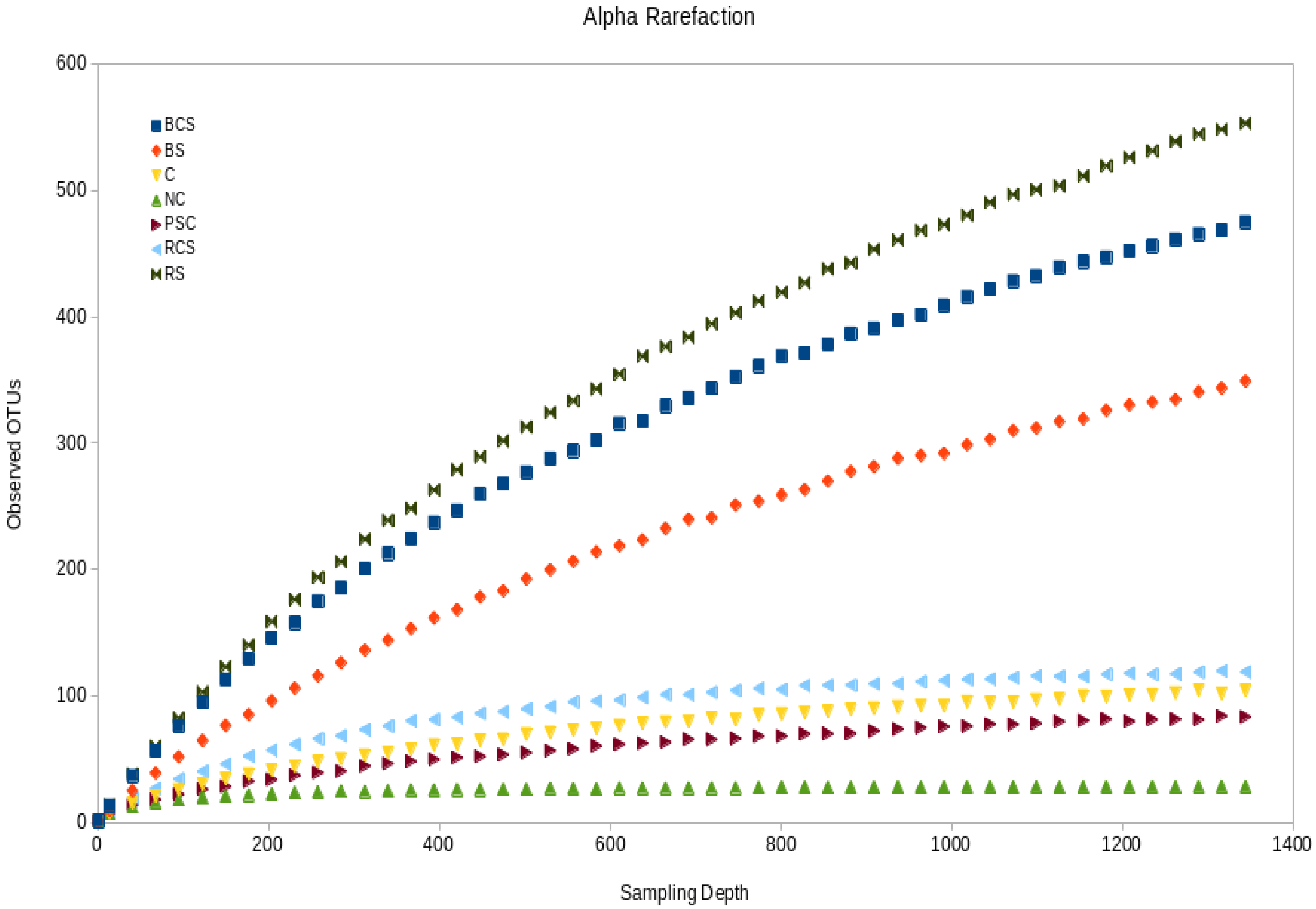


Figure 3.24: Alpha rarefaction of C. glauca rhizosphere, nodules, and nearby soil samples

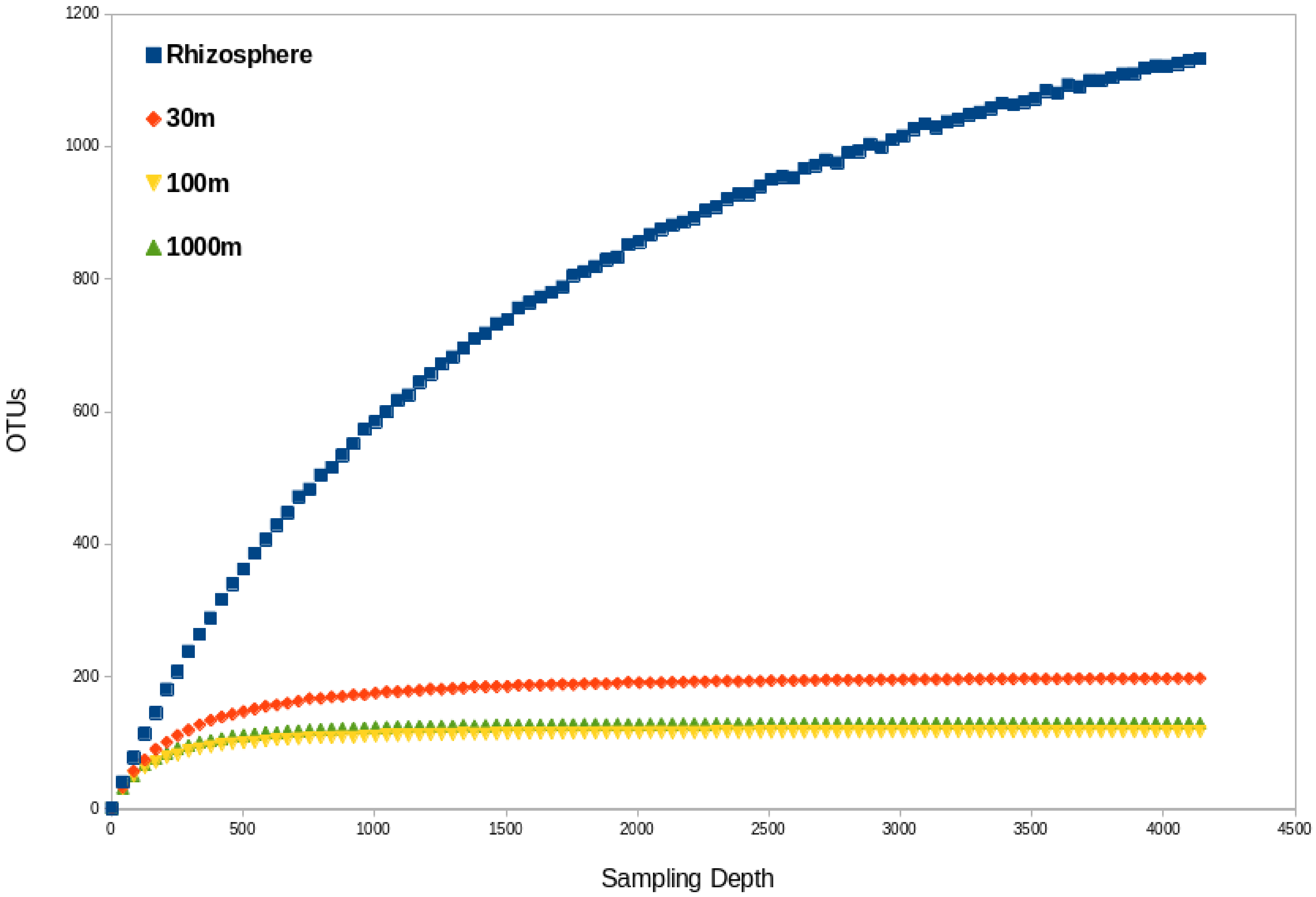


Figure 3.25: Alpha rarefaction of C. myrtifolia associated rhizosphere an soil samples

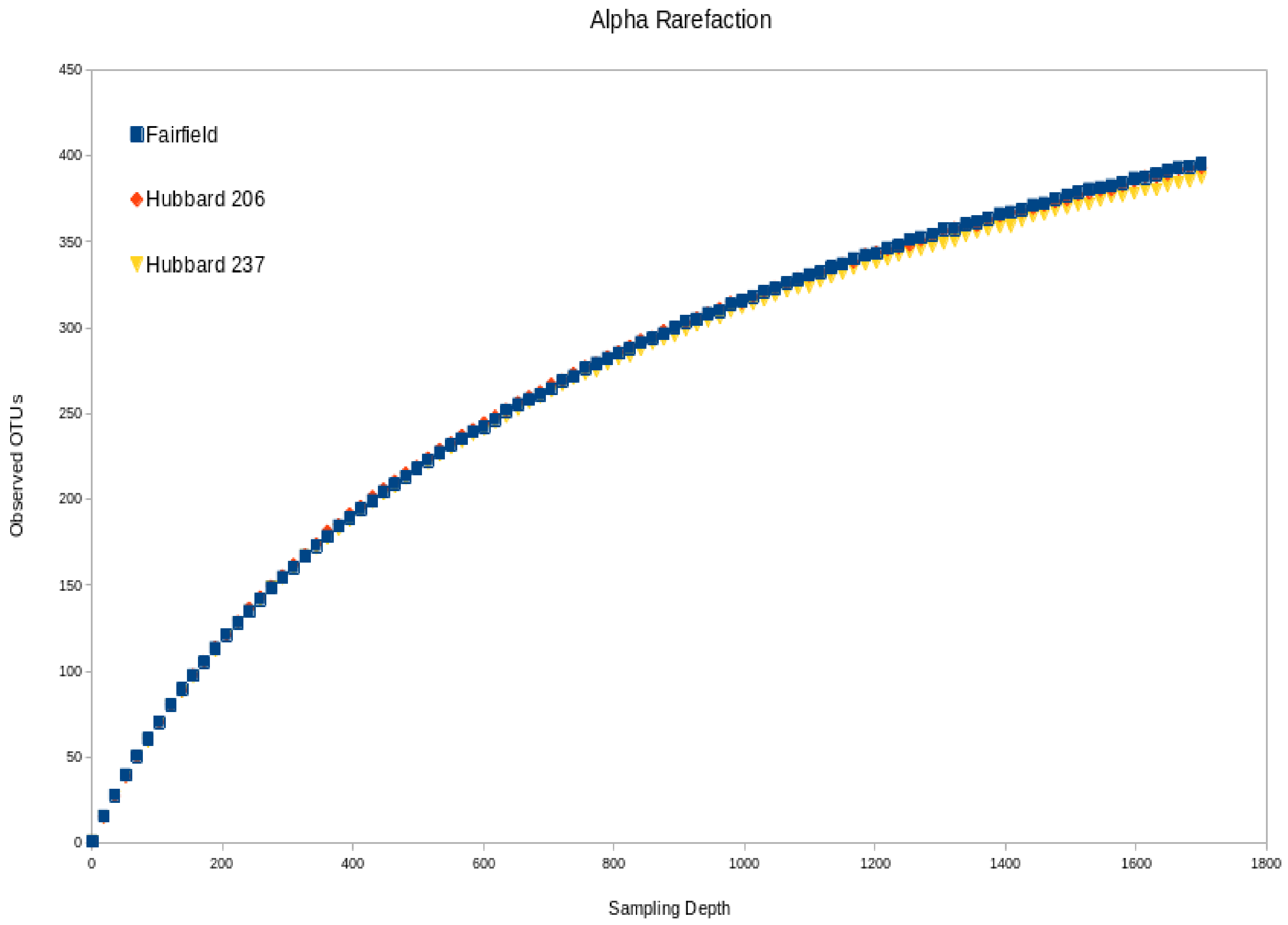


Figure 3.22: Alpha rarefaction curve of endolithic samples.

highest alpha diversity among *C. myrtifolia* samples from Algeria with an average diversity of 236.3 genus level OTUs per sample and 22.7 phyla level OTUs, while leaves were the lease diverse set of samples with 14.0 genus level OTUs per sample and 5.5 phyla level OTUs per sample. The most abundant phylum in the *C. myrtifolia* phytomicrobiome was α-proteobacteria. Other highly abundant taxa included Actinobacteria, Acidobacteria, and Firmicutes. Actinobacteria was particularly dominant in the root and nodules samples, while Acidobacteria was elevated in leaf samples. The most abundant genus level taxa group in the phytomicrobiome was identified only to the order level, Rickettsiales. Other highly abundant genera in the phytomicrobiome included *Frankia, Psychrobacter, Corynebacterium, Lactobacillales,* and *Pseudomonas*. *Kocuria* had increased abundance in nodule samples while *Bacillus* was more abundant in fruit tissue samples.

Soil and rhizosphere samples from Algeria were substantially more diverse than phytomicrobiome samples. Rhizosphere samples had the most alpha diversity with an average of 350.0 genus level OTUs per sample and 25.3 phyla level OTUs per sample. The alpha diversity of the soil samples decreased as distance the from the *C. myrtifolia* plant increased. Genus level OTU diversity was 168.0, 116.0, and 114.0 for soil samples that were 30, 100, and 1000m distant from the *C. myrtifolia* rhizosphere sample location respectively. Phyla level diversity was 20.0, 17.0, and 16.7 for 30, 100, and 1000m samples respectively. The dominant taxa in the soil and rhizosphere samples were similar to those in the phytomicrobiome. The most abundant phyla were actinobacteria, α-proteobacteria, Acidobacteria, γ-proteobacteria, and Bacteriodota. Chloroflexi, Myxococcota, and Verrucomicrobiota. The proportion of α-proteobacteria and Chloroflexi in each sample increased as distance from the *C. myrtifolia* rhizosphere source plant increased while the proportion of Verrucomicrobiota, Bacteroidota, and Myxococcota decreased with increased distance from the rhizospheres sampling location. The taxa with the highest frequency in the data set after genus level taxonomy assignment were *Solirubrobacterales*, including *Solirubrobacter, Lawsonella*, and *Blastococcus*. *Lawsonella* was substantially more abundant in the rhizosphere than in soil samples, while *Solirubrobacter* was more frequently present in soil samples at all three distances from the rhizosphere sample locations.

Soil and nodule samples from the Tunisian industrial site were more diverse overall than either the *C. myrtifolia* phytomicrobiome, rhizosphere, or soil samples. Uncontaminated control rhizosphere samples had the highest alpha diversity with an average of 406.3 genus level OTUs per sample and 38.3 phyla level OTUs per sample. Uncontaminated nodules had the lowest average alpha diversity with 8.3 phyla level OTUs per sample. The most abundant phyla in the Tunisian soil were similar to taxa identified in the Algerian soil samples. The most abundant microbial phyla in the Tunisian data set were Proteobacteria, Actinobacteria, Cyanobacteria, Bacteroidota, Acidobacteriota, Chloroflexi, and firmicutes. The most abundant genus level taxa identified in the data set were *Pseudomonas*, *Flavobacterium, Rickettsiales, Solirubrobacteriales, Nocardioides*, and *Frankia*.

The major microbial phyla in the Hubbard Brook and Vermont willow farm microbiomes were Proteobacteria, Firmicutes, and Halobacterota. The average genus

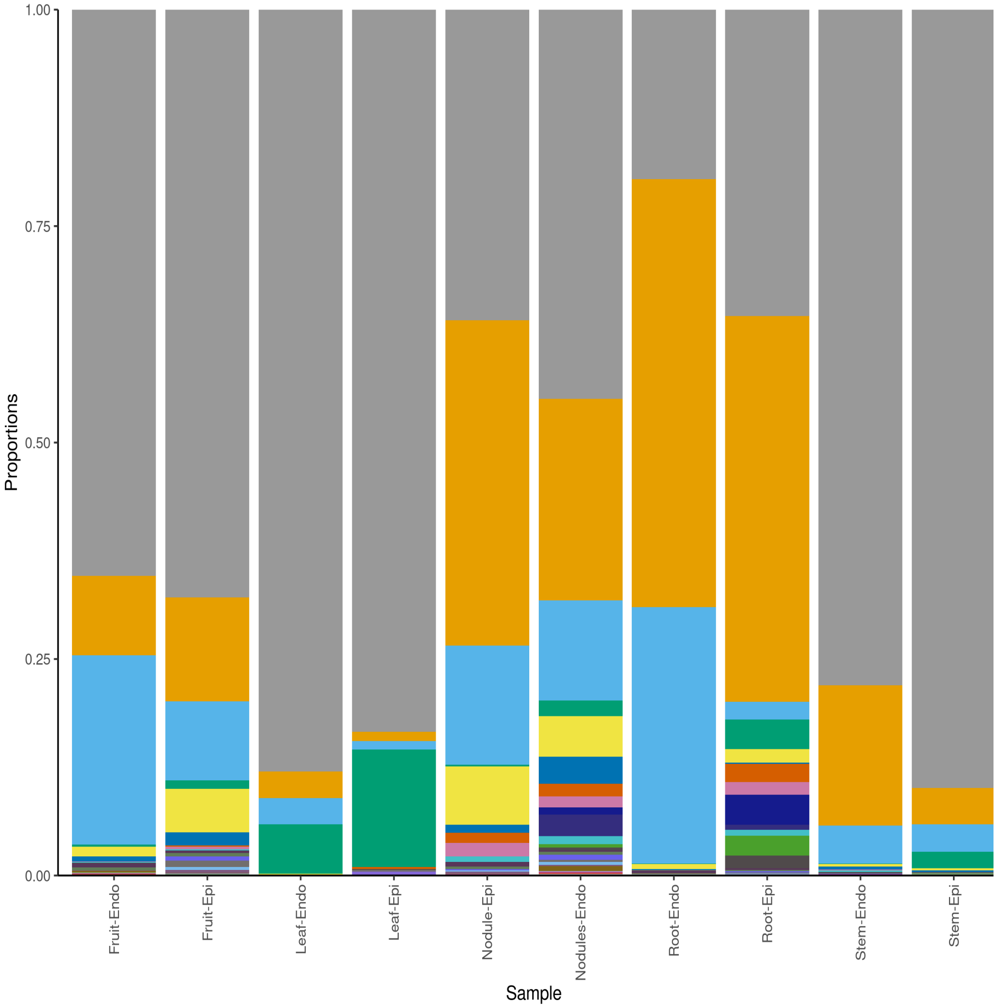


Figure 3.5: Relative abundance of C. myrtifolia phytomicrobiome phyla. Bars represent the average relative abundance of a given taxa across three samples.

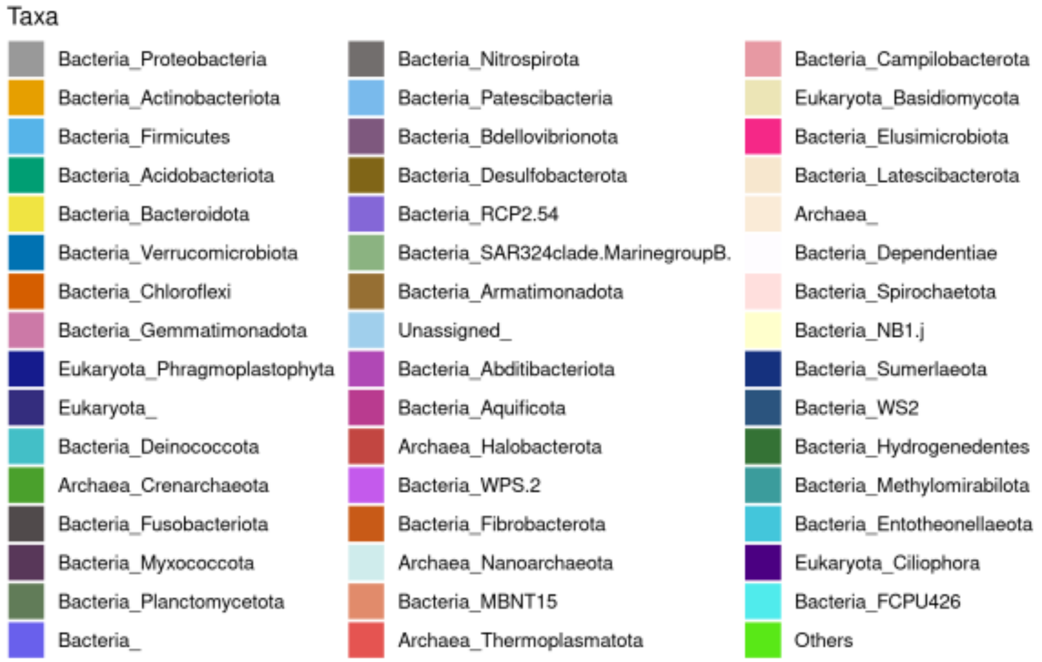


Figure 3.5 taxa key

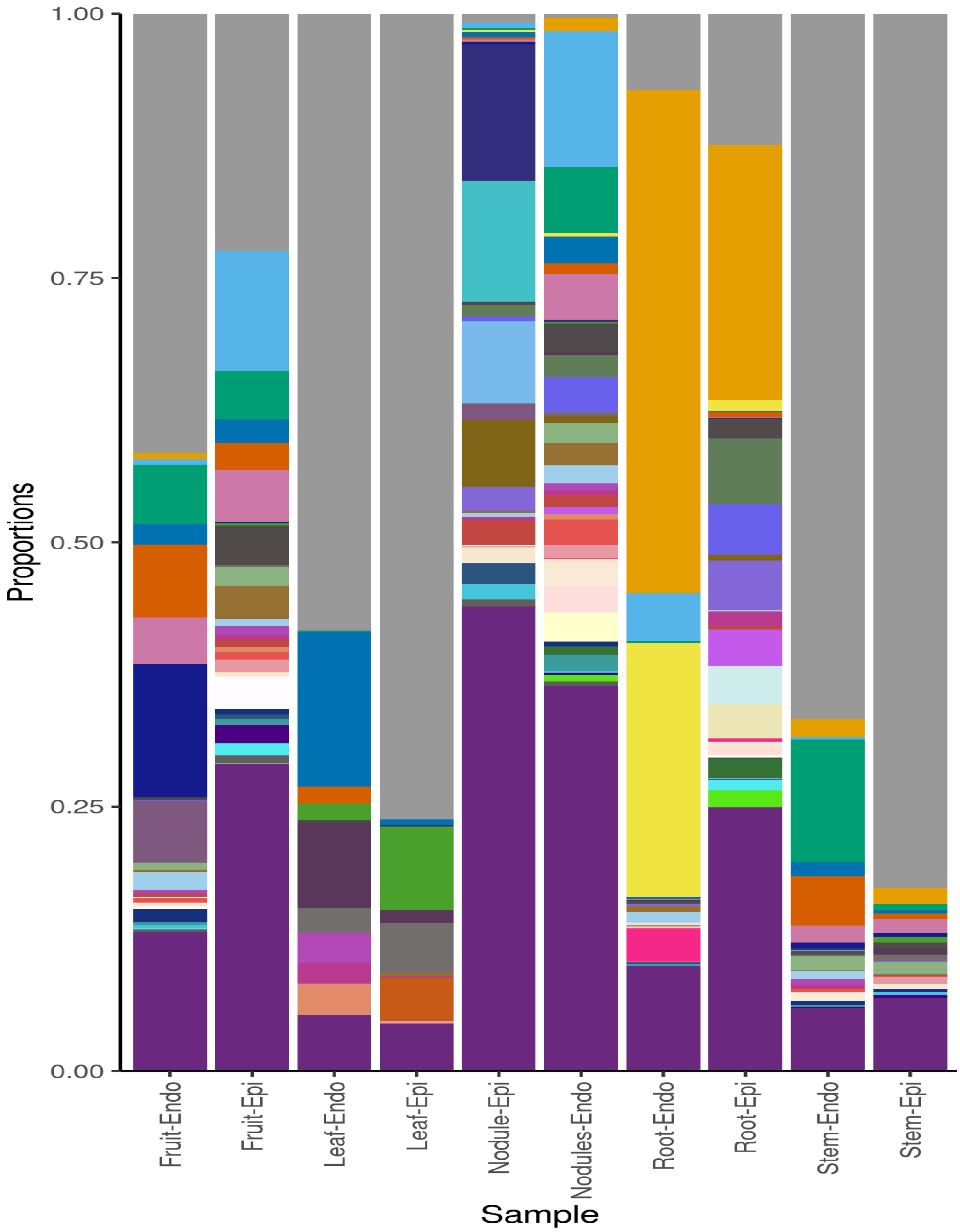


Figure 3.6:Relative abundance of C. myrtifolia phytomicrobiome genera. Bars represent the average relative abundance of a given taxa across three samples.

Figure 3.6 taxa key

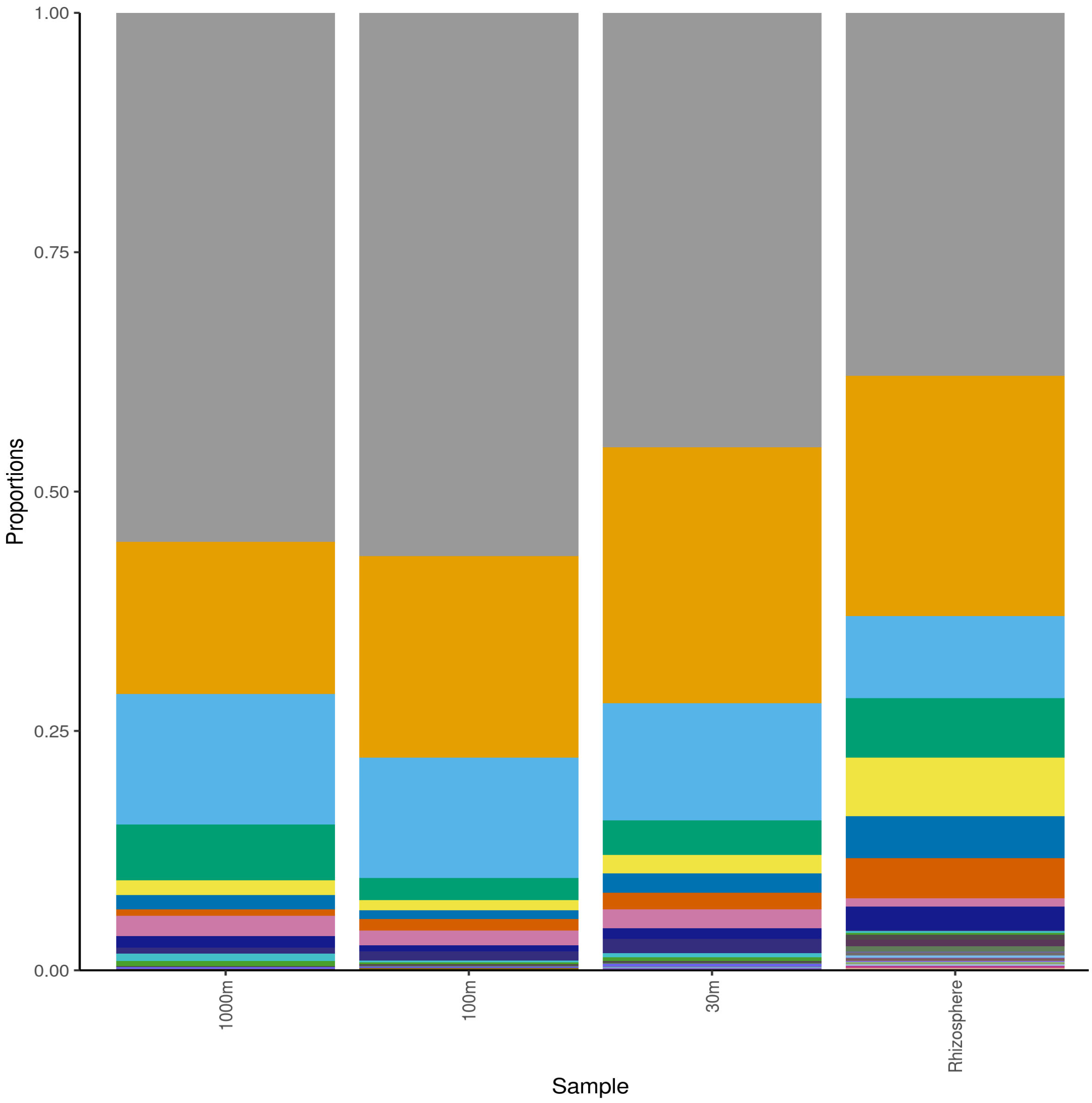


Figure 3.7: Relative abundance of phyla in the microbiome of C. myrtifolia rhizosphere and nearby soil samples. Bars represent the average relative abundance of a given taxa across three samples.

Figure 3.7 taxa key

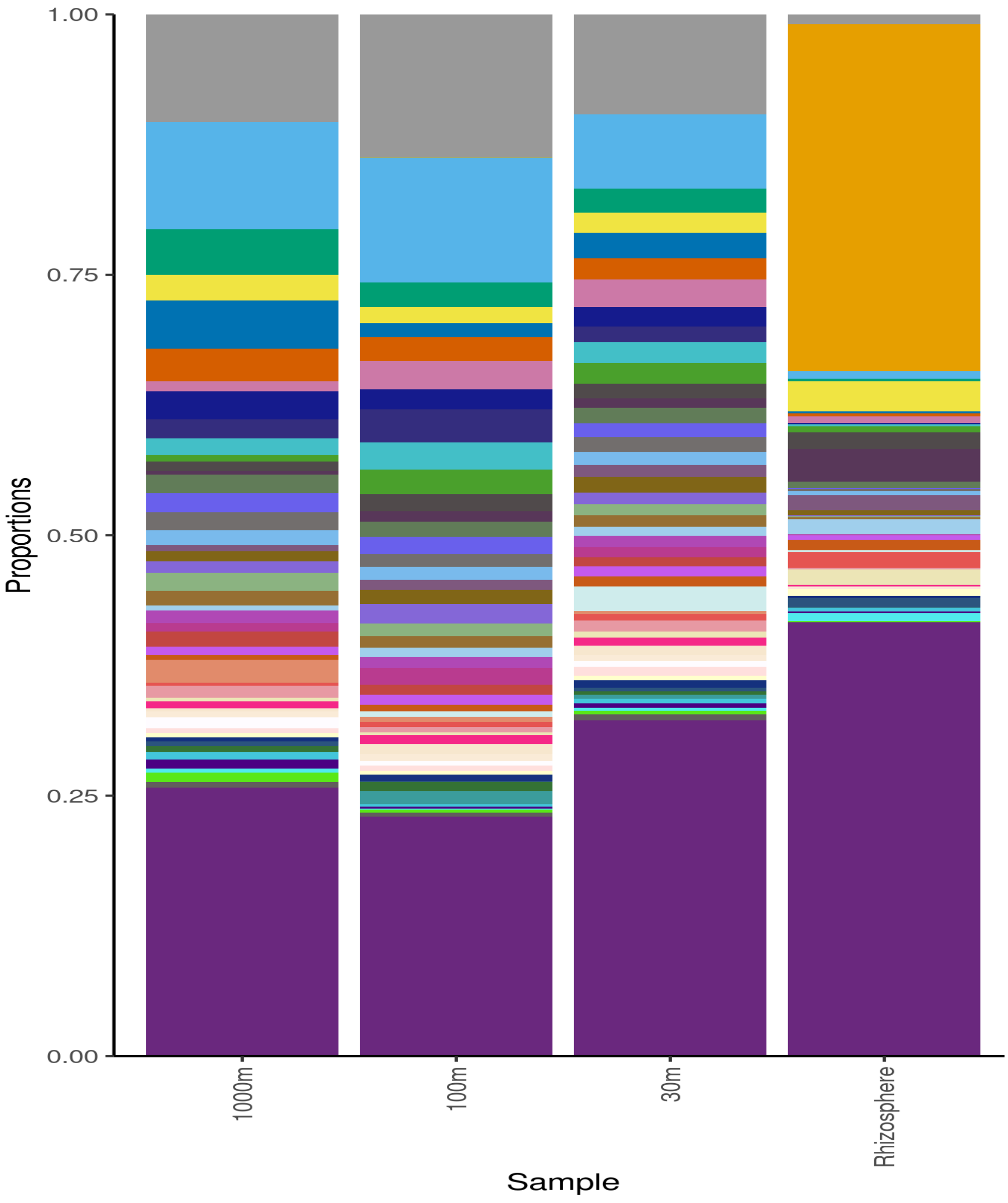


Figure 3.8:Relative abundance of genera in the microbiome of C. myrtifolia rhizosphere and nearby soil samples. Bars represent the average relative abundance of a given taxa across three samples.

Figure 3.8 taxa key

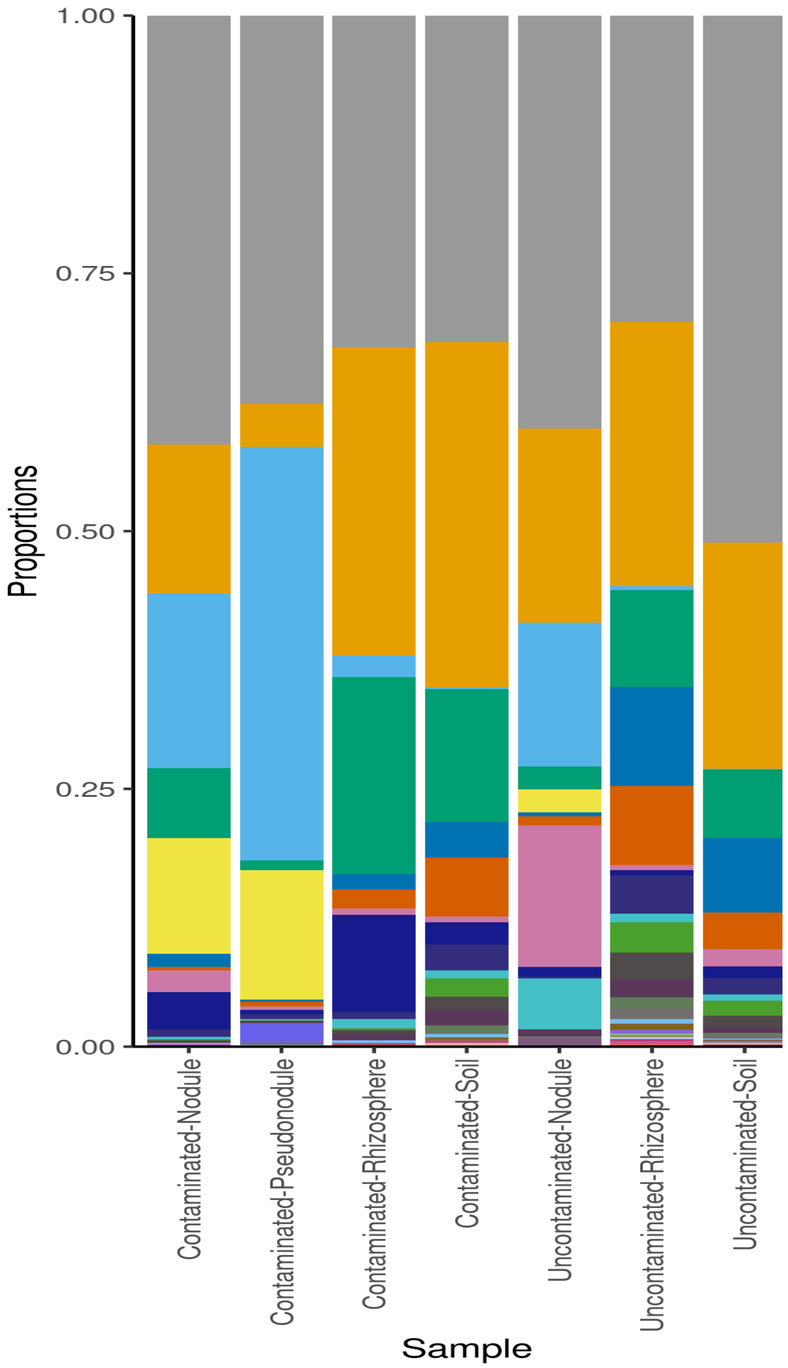


Figure 3.9: Relative abundance of phyla in the microbiome of C. glauca rhizosphere, nodule and nearby soil samples. Bars represent the average relative abundance of a given taxa across three samples.

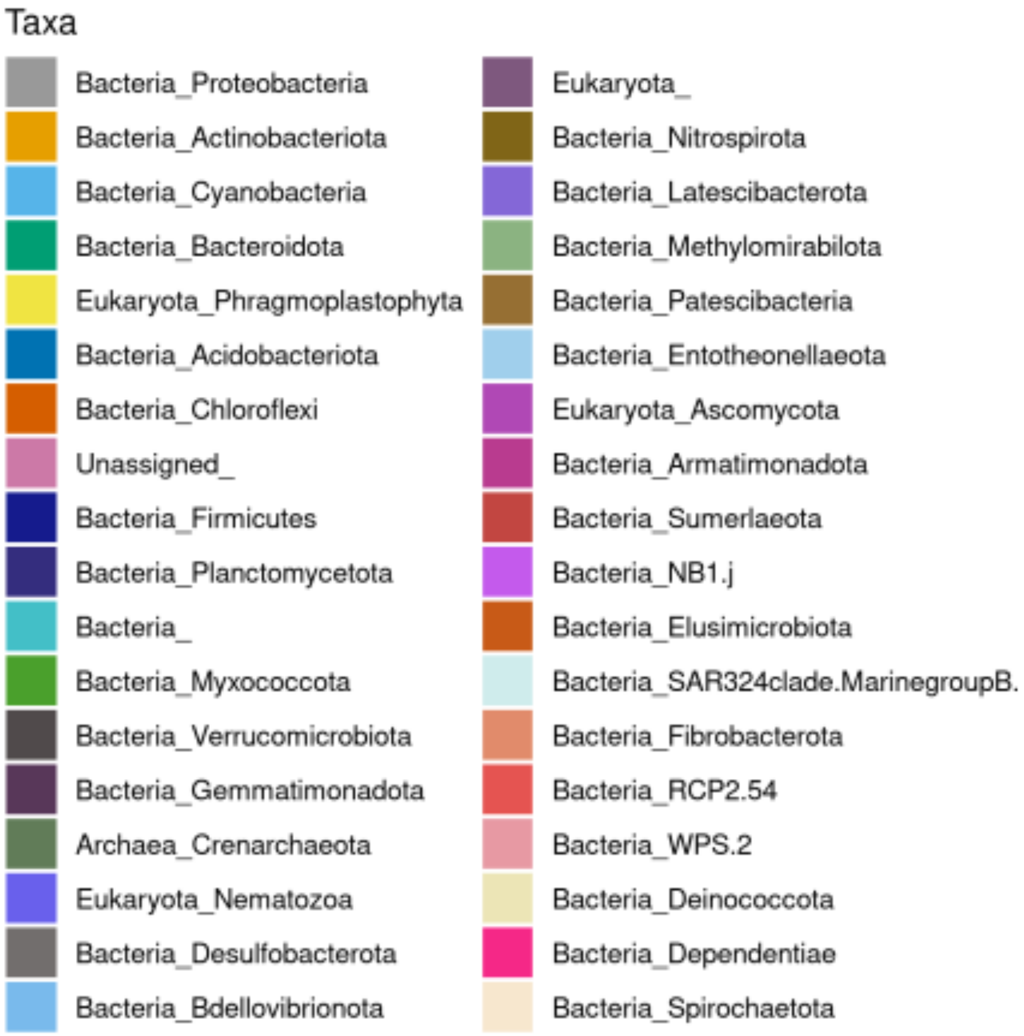


Figure 3.9 taxa key

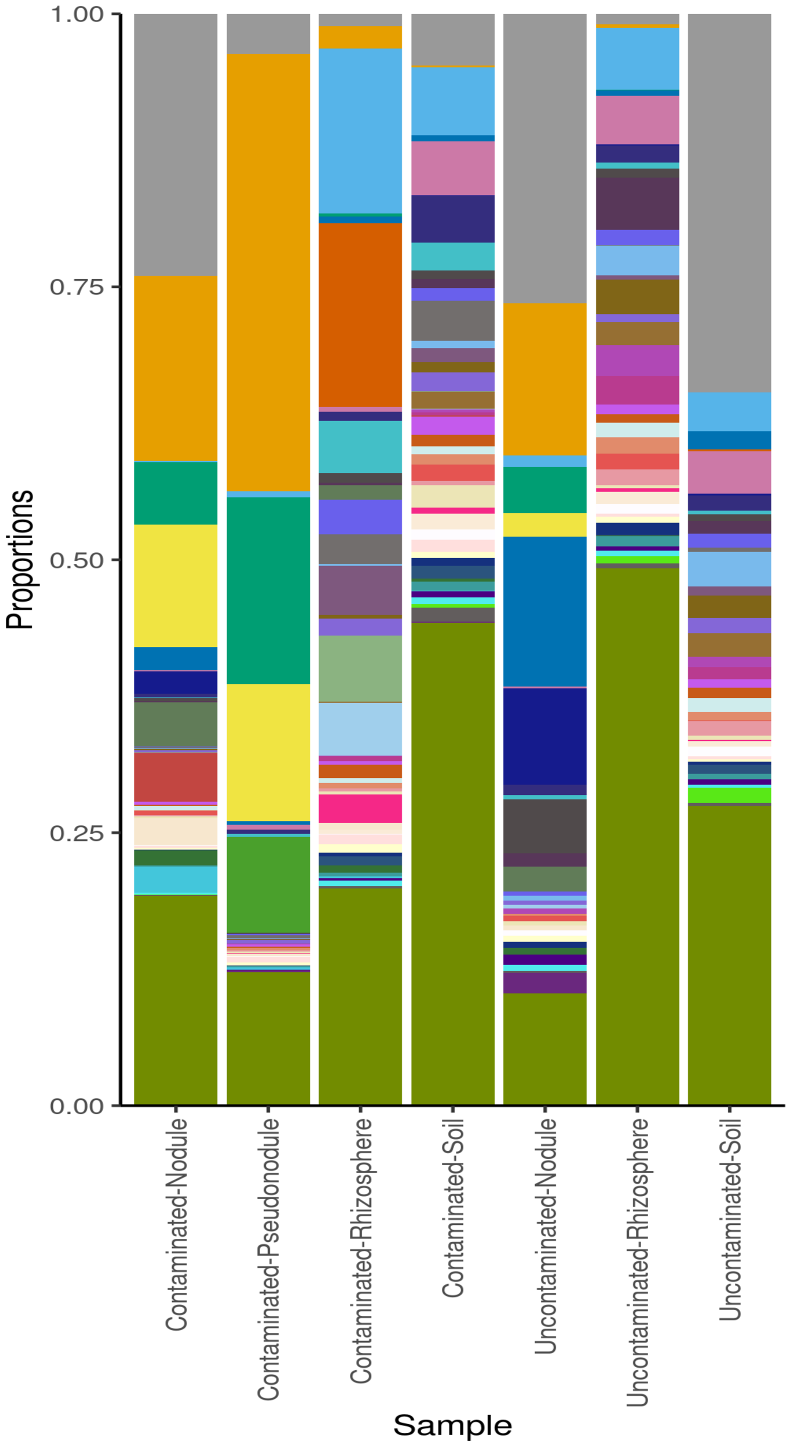


Figure 3.10: Relative abundance of genera in the microbiome of C. glauca rhizosphere, nodule and nearby soil samples. Bars represent the average relative abundance of a given taxa across three samples.

Figure 3.10 taxa key

level alpha diversity of the three endolithic communities was 143.2, 162.5, and 173.1 OTUs per sample at the BA dominated Hubbard site 206, the AS dominated Hubbard 237 site, and the SR dominated Fairfield, VT site respectively (table 3.2). The phyla level alpha diversity of the same three sites was 23.7, 28.8, and 26.8 OTUs per sample respectively. Across all three sites, soil samples has an average alpha diversity 25.1 phyla and 148.5 genera per sample while crushed rock samples had an average of 28.0 phyla and 179.4 genera per sample. Granite samples across all three site had an average of alpha diversity of 26.7 phyla and 158.7 genera per sample, and tonalite samples had an average alpha diversity of 28.0 phyla and 180.4 genera per sample. Soil samples collected concurrently with rock mesh-bag burial had an average alpha diversity of 24.5 phyla and 140.3 genera per sample. Soil samples collected when the rock mesh-bags were retrieved had an average alpha diversity of 26.3 phyla and 149.5 genera per sample. Interestingly, post-incubation soil samples from the SA dominated Fairfield, VT site had the highest alpha diversity based on both genera and phyla OTU counts, while post-incubation soil samples from the BA dominated Hubbard 206 site had the lowest overall alpha diversity based on both phyla and genera counts.

Beta Diversity: NMDS and PERMANOVA analysis

Beta diversity based on the amplicon data for each of the four data sets discussed above was assessed using NMDS ordinations. Bray-Curtis distance was used in all NMDS ordinations because it represents sparse data sets (data sets with many zeros) well. NMDS ordination and PERMANOVA analysis representing the phytomicrobiome showed significant differences between below-soil samples (roots and nodules), and above soil samples. However, ordination and PERMANOVA data showed no substantial or significant differences between endophyte and epiphyte samples. Roots were significantly distinct from all other tissue groups individually except nodules. Nodules were significantly distinct from stem and leaf samples, but not from fruit or root samples. Fruit and leaf tissue samples were also significantly distinct groups within the ordination. All sample types except stems were individually distinct from the sample types collectively. NMDS ordination and PERMANOVA analysis of rhizosphere and soil samples from Algeria indicate that the only significantly distinct sample type was rhizosphere.

NMDS ordination and PERMANOVA analysis of soil, nodule and pseudonodule samples in Tunisia indicate that the only sample type individually significantly distinct from other sample types was pseudonodules from the contaminated industrial site. Contaminated soil was also significantly distinct from both contaminated and uncontaminated nodule samples. Uncontaminated soil was significantly distinct from uncontaminated nodules and contaminated pseudonodules. Contaminated and uncontaminated nodules were significantly distinct from uncontaminated rhizosphere while pseudonodules were significantly distinct from both contaminated and uncontaminated rhizosphere samples.

PCoA ordination and PERMANOVA analysis of endolithic communities indicated that samples were significantly distinct based on location and dominate tree type.

Table 3.2: Genera level PERMANOVA analysis results for the C. myrtifolia phytomicrobiome. PERMANOVA scores were calculated using the adonis R function using Bray-Curtis distance and a genera level feature table generated using QIIME2. PERMANOVA comparisons were made for each pair-wise tissue type combination and between each tissue compared to all other tissue types collectively. AG =above ground tissue (Fruit, Leaf, Stem), BG = below ground tissue (root and nodule)

Comparison	***F Model***	***R^2***	***P Value***
Fruit vs. Stem	1.207	0.108	0.280
Fruit vs. Leaf	4.637	0.317	0.003
Fruit vs. Root	2.473	0.198	0.015
Fruit vs. Nodule	2.007	0.167	0.053
Stem vs. Leaf	3.564	0.263	0.016
Stem vs. Root	3.148	0.239	0.005
Stem vs. Nodule	3.676	0.269	0.002
Leaf vs. Root	7.646	0.433	0.005
Leaf vs. Nodule	8.344	0.455	0.003
Nodule vs. Root	1.862	0.157	0.050
Fruit vs. All	1.473	0.050	0.150
Leaf vs. All	3.410	0.109	0.005
Nodule vs. All	4.834	0.147	0.002
Root vs. All	2.171	0.072	0.046
Stem vs. All	1.193	0.040	0.257
AG vs. BG	5.543	0.165	0.002

Table 3.4: Phylum level PERMANOVA analysis results for the C. myrtifolia phytomicrobiome. PERMANOVA scores were calculated using the adonis R function using Bray-Curtis distance and a phylum level feature table generated using QIIME2. PERMANOVA comparisons were made for each pair-wise tissue type combination.

Comparison	***F Model***	***R^2***	***P Value***
Fruit vs. Stem	1.714	0.146	0.147
Fruit vs. Leaf	9.646	0.491	0.008
Fruit vs. Root	3.280	0.247	0.044
Fruit vs. Nodule	3.980	0.285	0.026
Stem vs. Leaf	1.734	0.148	0.133
Stem vs. Root	2.579	0.205	0.047
Stem vs. Nodule	5.444	0.353	0.002
Leaf vs. Root	6.576	0.397	0.004
Leaf vs. Nodule	13.694	0.578	0.004
Nodule vs. Root	1.342	0.118	0.191

Table 3.5: Genus level PERMANOVA analysis results microbiome of lithographic communities in Hubbard Brook and Fairfield, VT. PERMANOVA scores were calculated using the adonis R function using Bray-Curtis distance and a genus level feature table generated with QIIME2. PERMANOVA comparisons were made for each rock sample type combination, location combination, and tree type combination. "Pre" samples refer to soil collected at the beginning of the study, and "post" samples refer to soil samples collected at the conclusion of the experiment. BA = Betula alleghaniensis, AS = Acer saccharum, SR = Salix repens

Comparison	***F Model***	***R^2***	***P Value***
Pre vs. Post	0.722	0.035	0.783
Pre vs. Granite	1.024	0.027	0.353
Pre vs. Tonalite	1.257	0.034	0.164
Post vs. Granite	1.373	0.036	0.141
Post vs. Tonalite	1.635	0.043	0.069
Granite vs. Tonalite	0.834	0.015	0.659
Hubbard-206 vs. Hubbard-237	3.312	0.067	0.001
Hubbard-206 vs. Fairfield	8.655	0.145	0.001
Hubbard-237 vs. Fairfield	5.999	0.105	0.001
BA vs. AS	3.312	0.067	0.002
BA vs. SR	8.655	0.145	0.001
AS vs. SR	5.999	0.105	0.001
Soil vs. Crushed Rock	2.089	0.027	0.012

Table 3.6: Genera level PERMANOVA analysis results for the microbiome of the C. myrtifolia rhizosphere and nearby soil. PERMANOVA scores were calculated using the adonis R function using Bray-Curtis distance and a genera level feature table generated using QIIME2. PERMANOVA comparisons were made for each pair-wise sample type combination and each sample type vs. all other sample types.

Comparison	***F Model***	R^2	***P Value***
Rhizosphere vs. All	7.598	0.432	0.005
30m vs. All	0.657	0.062	0.706
100m vs. All	0.904	0.083	0.470
1000m vs. All	1.382	0.121	0.160
Rhizosphere vs. 100m	3.466	0.464	0.100
Rhizosphere vs. 1000m	4.258	0.516	0.100
Rhizosphere vs. 30m	2.901	0.420	0.100
100m vs. 1000m	2.011	0.335	0.100
100m vs. 30m	0.651	0.140	0.900
1000m vs. 30m	1.886	0.320	0.100

Table 3.7: Genera level PERMANOVA analysis results for the microbiome of C. glauca rhizosphere and nearby soil contaminated by industrial waste. PERMANOVA scores were calculated using the adonis R function using Bray-Curtis distance and a genera level feature table generated using QIIME2. PERMANOVA comparisons were made for each pair-wise sample type combination and each sample type vs. all other sample types.

Comparison	***F Model***	***R^2***	***P Value***
Contaminated Soil vs. Uncontaminated Soil	1.406	0.260	0.200
Contaminated Soil vs. Contaminated Nodule	2.632	0.345	0.031
Contaminated Soil vs. Uncontaminated Nodule	2.586	0.341	0.031
Contaminated Soil vs. Contaminated Pseudonodule	4.909	0.495	0.019
Contaminated Soil vs. Contaminated Rhizosphere	1.791	0.309	0.100
Contaminated Soil vs. Uncontaminated Rhizosphere	2.598	0.394	0.100
Uncontaminated Soil vs. Contaminated Nodule	1.621	0.245	0.215
Uncontaminated Soil vs. Uncontaminated Nodule	1.776	0.262	0.030
Uncontaminated Soil vs. Contaminated Pseudonodule	3.445	0.408	0.035
Uncontaminated Soil vs. Contaminated Rhizosphere	1.487	0.271	0.200
Uncontaminated Soil vs. Uncontaminated Rhizosphere	1.618	0.288	0.100
Contaminated Nodule vs. Uncontaminated Nodule	0.747	0.111	0.744
Contaminated Nodule vs. Contaminated Pseudonodule	0.903	0.131	0.548
Contaminated Nodule vs. Contaminated Rhizosphere	1.156	0.188	0.360
Contaminated Nodule vs. Uncontaminated Rhizosphere	3.283	0.396	0.035
Uncontaminated Nodule vs. Contaminated Pseudonodule	1.457	0.195	0.145
Uncontaminated Nodule vs. Contaminated Rhizosphere	0.951	0.160	0.666
Uncontaminated Nodule vs. Uncontaminated Rhizosphere	3.101	0.383	0.029
Contaminated Pseudonodule vs. Contaminated Rhizosphere	2.165	0.302	0.029
Contaminated Pseudonodule vs. Uncontaminated Rhizosphere	6.149	0.552	0.020
Contaminated Rhizosphere vs. Uncontaminated Rhizosphere	2.404	0.375	0.100

Contaminated Soil vs. All	1.727	0.073	0.077
Uncontaminated Soil vs. All	1.286	0.055	0.173
Uncontaminated Nodule vs. All	1.187	0.051	0.256
Contaminated Nodule vs. All	1.548	0.066	0.096
Contaminated Pseudonodule vs. All	2.352	0.097	0.012
Contaminated Rhizosphere vs. All	1.357	0.058	0.153
Uncontaminated Rhizosphere vs. All	1.357	0.058	0.158

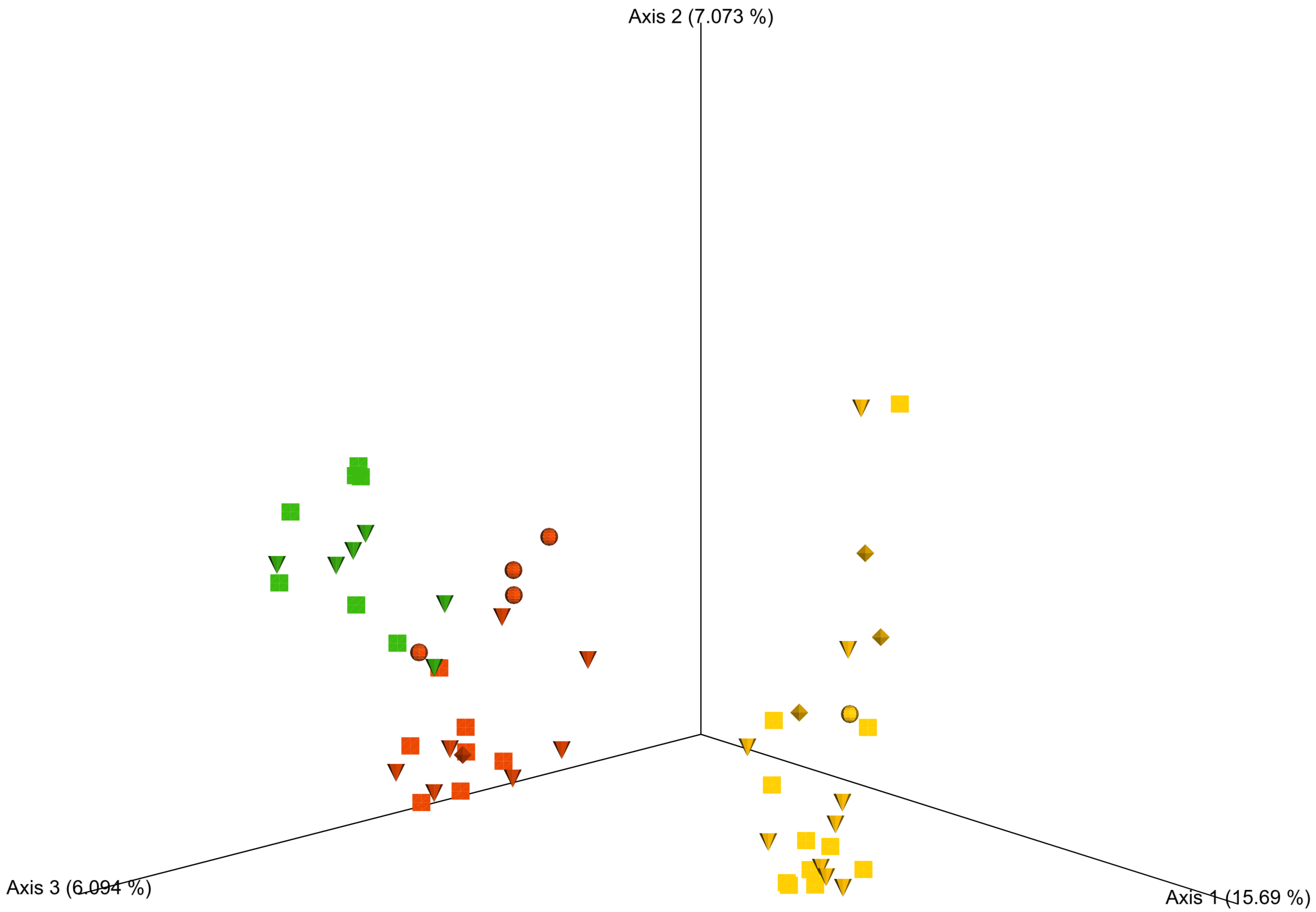


Figure 3.11: PCoA analysis results for lithographic community data from Hubbard Brook and Fairfield, VT. Green colored samples are from the A. saccharum dominated Hubbard-237 site, red colored samples are from the B. alleghaneinsis dominated Hubbard-206 site, and yellow colored samples are from the S. repens dominated Fairfield site. Sphere shaped points are "Pre" soil samples, diamond shaped points are "post" soil samples, square shaped points are Granite samples, and cone shaped points are tonalite samples. PCoA results were calculated using QIIME2 with Bray-Curtis distance.

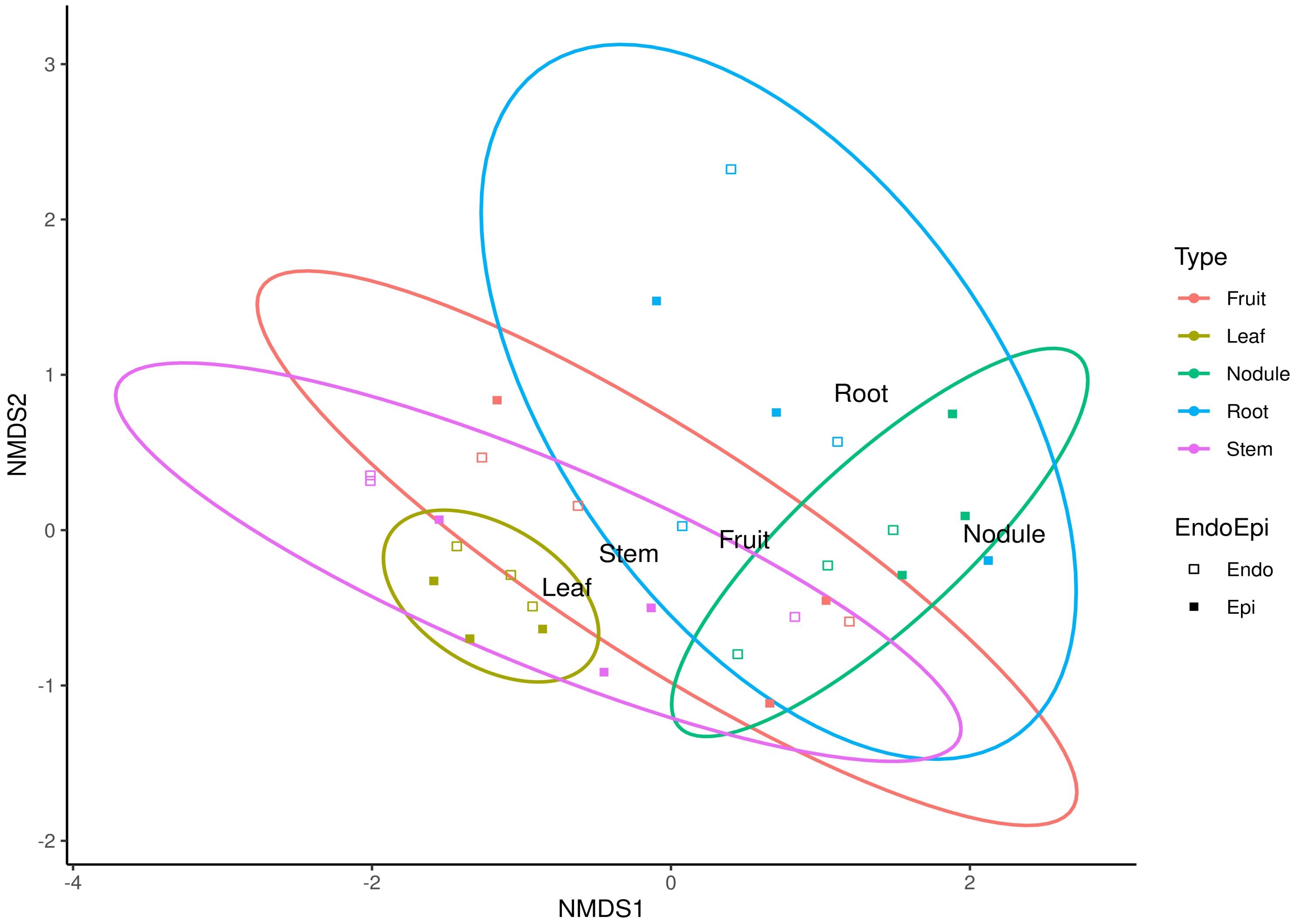


Figure 3.12: NMDS analysis results for the C. myrtifolia phytomicrobiome. Final ordination stress = 0.139, Procrustes rmse < 0.001, and max resid = 0.002. Point and ellipse color correspond to tissue times and point fill corresponds to endophyte (unfilled) and epiphyte (filled) samples.

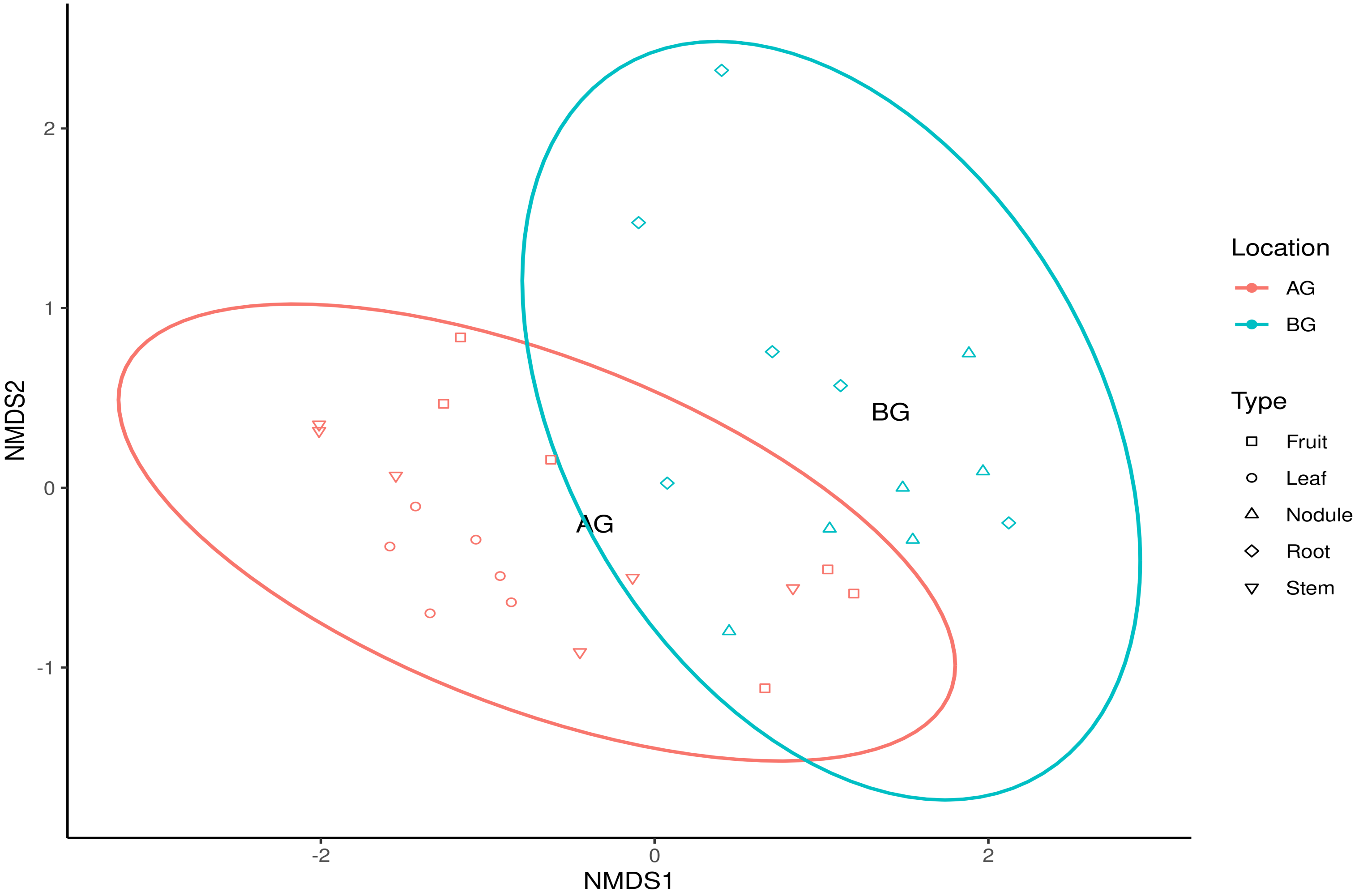


Figure 3.13: NMDS analysis results for the C. myrtifolia phytomicrobiome. Final ordination stress = 0.139, Procrustes rmse < 0.001, and max resid = 0.002. Point and ellipse color correspond to above ground samples (AG: fruit, leaf, and stem), and below ground samples (BG: root and nodule). Point shape corresponds to sample types with endophyte and epiphyte samples combined.

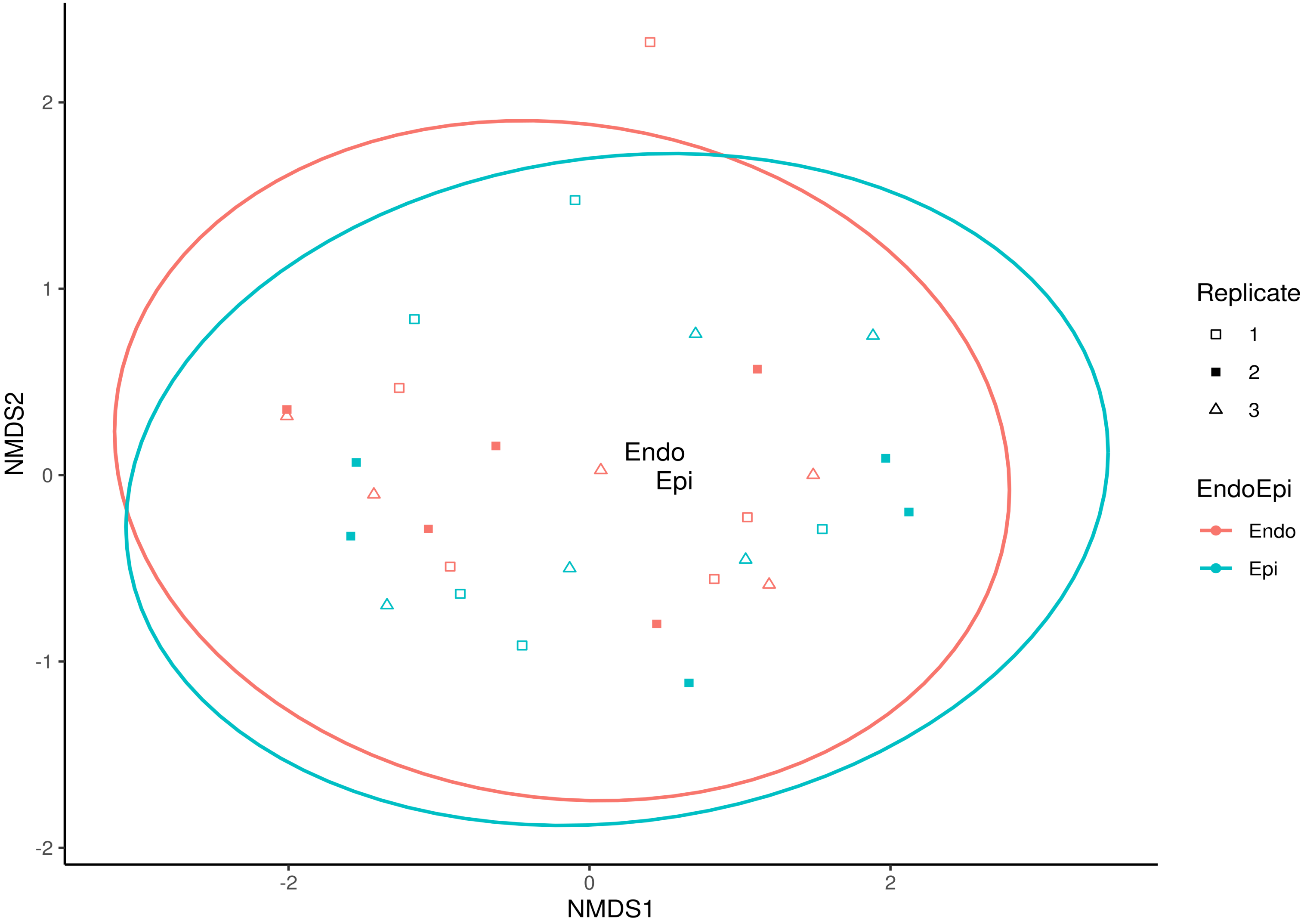


Figure 3.14: NMDS analysis results for the C. myrtifolia phytomicrobiome. Final ordination stress = 0.139, Procrustes rmse < 0.001, and max resid = 0.002. Point and ellipse color correspond to epiphyte (blue) and endophyte (red) samples. Point shape and fill correspond to sample replicate.

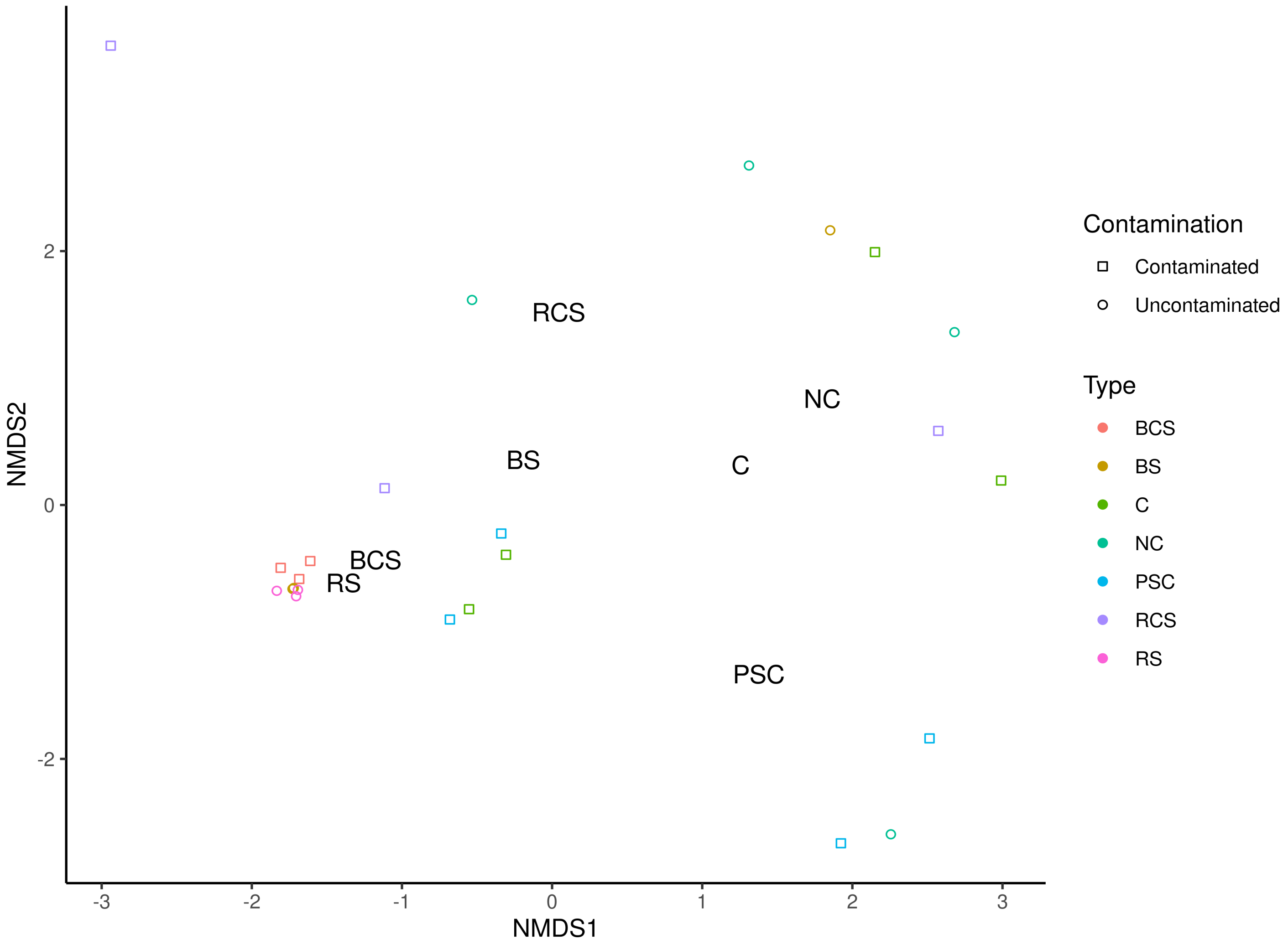


Figure 3.15: NMDS analysis results for the microbiome of C. glauca nodules, rhizosphere, and nearby soil at a Tunisian factory with industrial contamination. Final stress = 0.103, Procrustes rmse <0.001, max resid <0.001. Point colors correspond to samples types: BCS = Bulk Contaminated Soil, BS = Bulk Soil, C = Control nodules, NC = Nodules Contaminated, PSC = Pseudonodules Contaminated, RCS = Rhizosphere Contaminated, and RS = Rhizosphere. Point shapes corresponds to samples from the contaminated area (squares) and uncontaminated area (circles).

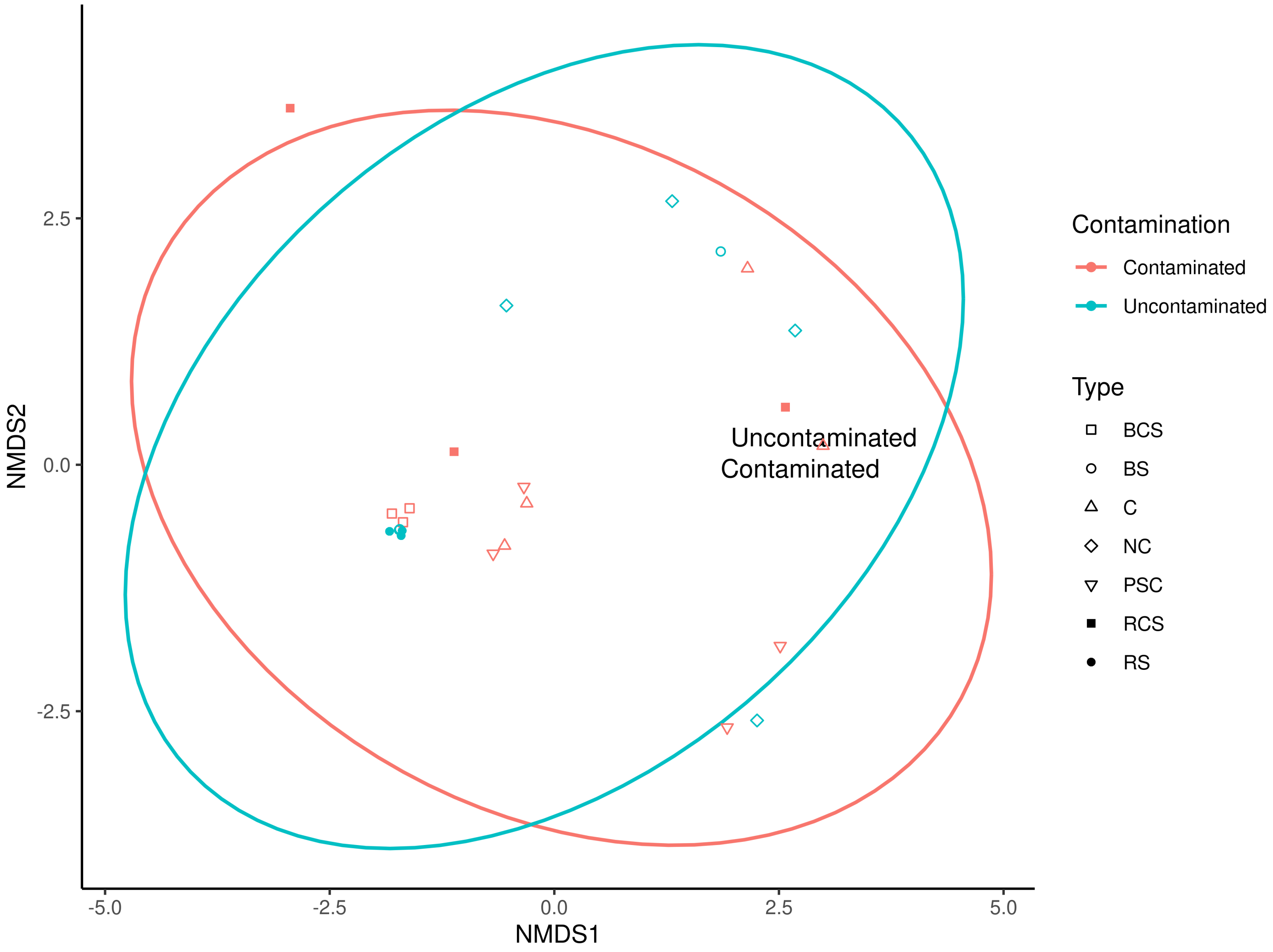


Figure 3.16: NMDS analysis results for the microbiome of C. glauca nodules, rhizosphere, and nearby soil at a Tunisian factory with industrial contamination. Final stress = 0.103, Procrustes rmse <0.001, max resid <0.001. Point shapes correspond to samples types: BCS = Bulk Contaminated Soil, BS = Bulk Soil, C = Control nodules, NC = Nodules Contaminated, PSC = Pseudonodules Contaminated, RCS = Rhizosphere Contaminated, and RS = Rhizosphere. Point and ellipse colors corresponds to samples from the contaminated area (red) and uncontaminated area (blue).

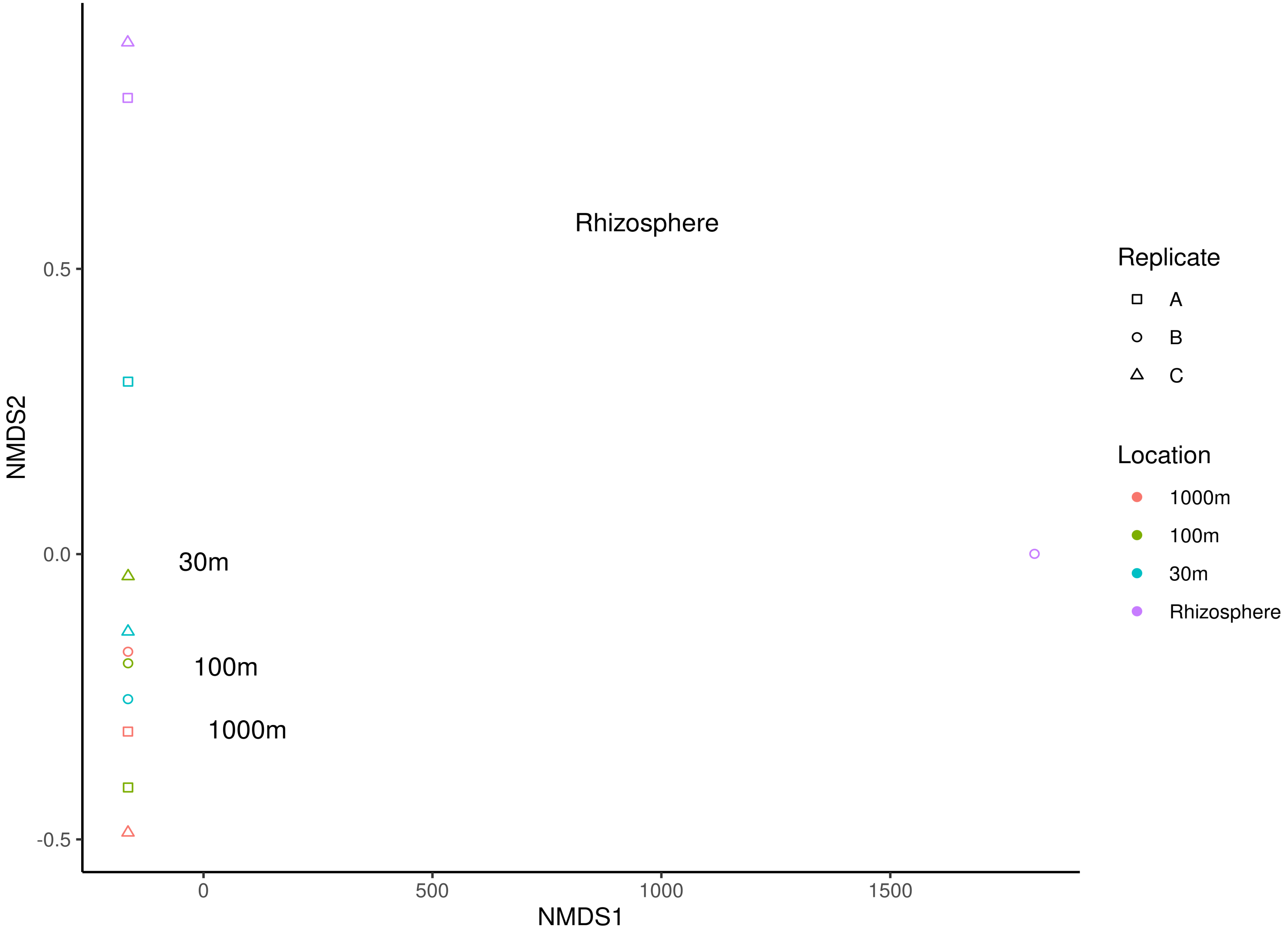


Figure 3.17: NMDS analysis results for the soil and rhizosphere microbiome of C. myrtifolia landscapes in Algeria. Final stress = 0.107, Procrustes rmse = 0.002, max resid = 0.004. Data point colors correspond to distance from the a C. myrtifolia plant. Data point shape corresponds to sample replicates.

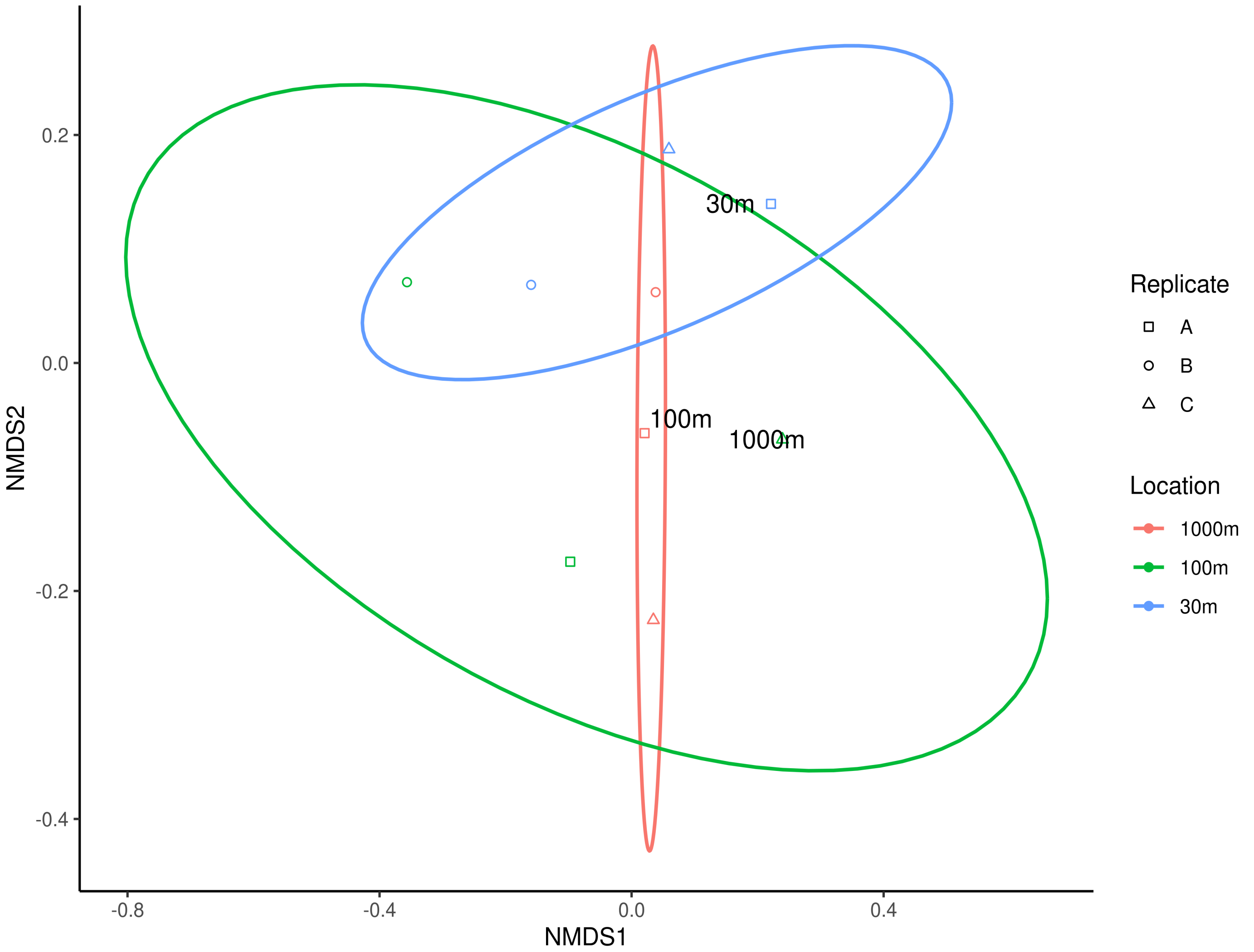


Figure 3.18: NMDS analysis results for the soil and rhizosphere microbiome of C. myrtifolia landscapes in Algeria. Final stress = 0.130, Procrustes rmse < 0.001, max resid < 0.001. Data point colors correspond to distance from the a C. myrtifolia plant. Data point shape corresponds to sample replicates.

However, Hubbard and Fairfield samples did not significantly group based on rock type or sample type.

Simper analysis showed that Proteobacteria, Firmicutes, Acidobacteriota, Actiobacteriota, and Bacteroidota were the most differentiating phyla level taxa between *C. myrtifolia* fruit and leaf tissue communities. Fruit and root communities, fruit and stem communities, leaf and nodule communities, leaf and stem communities, and nodule and root communities primarily differentiated by the same taxa: Proteobacteria, Firmicutes, Acidobacteriota, Actiobacteriota, and Bacteroidota. Protoebacteriota, Actinobacteriota, Firmicutes, Bacteroidota, and Verrucomicrobiota were the most differentiating taxa between fruit and nodule communities as well as nodule and stem communities. Leaf and root communities in addition to root and stem communities were differentiated most by Proteobacteria, Firmicutes, Acidobacteriota, Actiobacteriota, and Phragmoplastophyta. Simper analysis of *C. myrtifolia* communities at the genus level showed that *Frankia* plays a substantial role in differentiating the phytomicrobiomes of specific plant tissues despite being a relatively low abundance taxa. The genus *Frankia* was one of the top two most significant taxa characterizing the difference between fruit and nodule communities, leaf and root communities, nodule and root communities, and root and stem communities.

Actinobacteriota, Proteobacteria, Acidobacteriota, Gemmatimonadota, and Bacteroidota were the identified by Simper analysis as the most significant phyla contributing to the community differences between and among all rhizosphere and soil samples from Algeria. Genus level Simper analysis showed that *Solirubrobacter* and

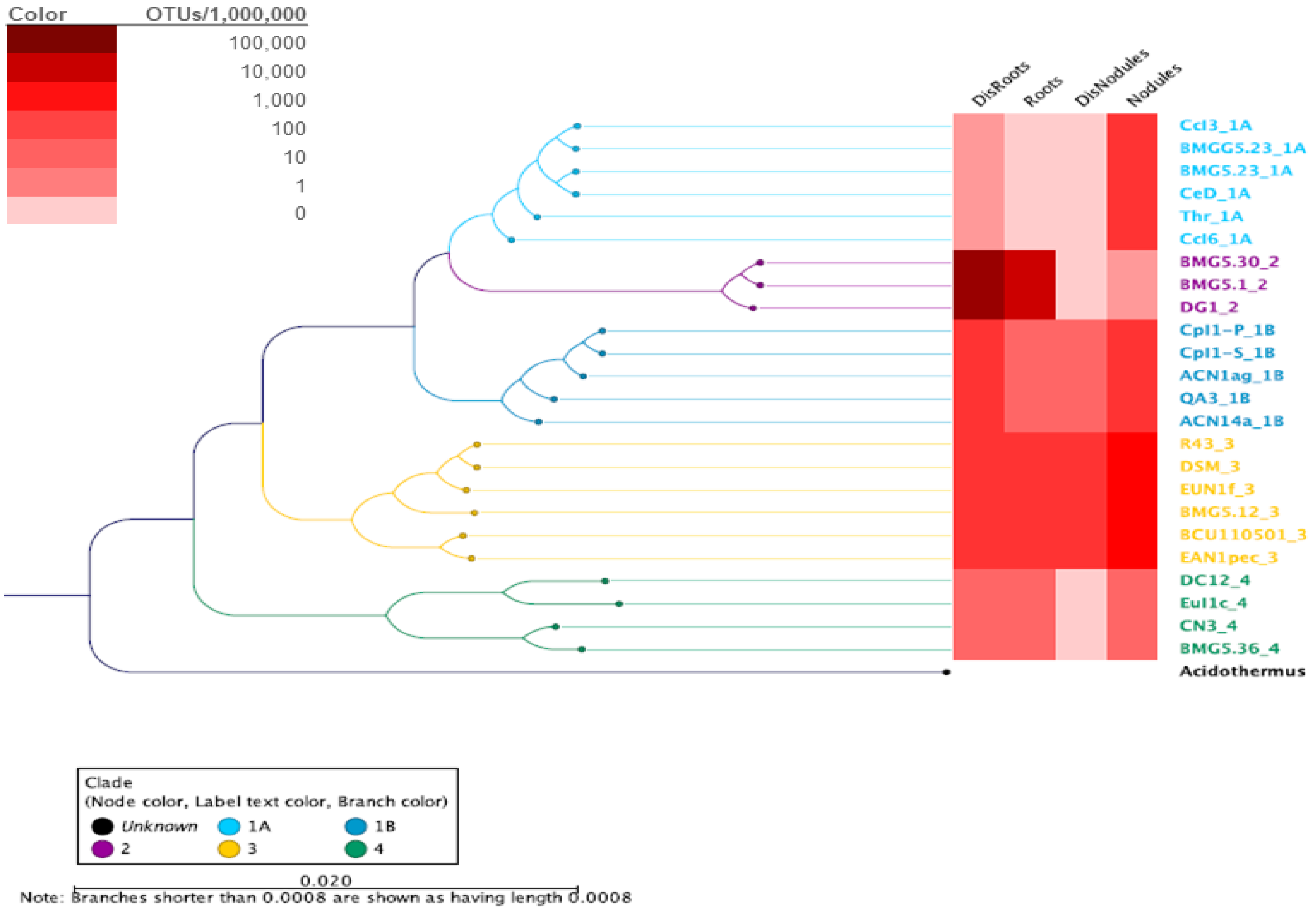


Figure 3.19: Remapped Frankia genus reads to clade level phylogeny. Heat-map colors correspond to reads per million in a given set of samples.

Lawsonella were the the most common taxa differentiating the rhizosphere and soil sample from Algerian *C. myrtifolia* collection sites.

Clade level binning of L6 *Frankia* reads from *C. myrtifolia* root and nodules samples indicated that all 5 major *Frankia* clades were present in the endophyte and epiphyte communities of both samples types.

Discussion

This work surveyed the microbial diversity represented in communities from highly varied niche space spanning two continents. Despite this geographic and environmental diversity, the microbial community profiles in Tunisia, Algeria, New Hampshire, and Vermont were dominated by many of the same taxa. Actinobacteriota, Proteobacteria, Acidobacteriota, Gemmatimonadota, Bacteroidota, Cyanobacteria, and Verrucomicrobiota were the most abundant bacteria in all of the communities surveyed in Tunisia and Algeria. Acidobacteriota, Actinobacteriota, and Bacteroidota were also highly abundant in endolithic communities at Hubbard Brook and Fairfield, but these communities were were also characterized by a high abundance of bacteria from the phyla Abditibacteriota and Armatimonadetes. Given that the metabolic characteristics of these phyla includes chemolithoautotrophy and chemoheterotrophy (Tahon et al. 2018, Tamaki et al. 2011), the presence Abditibacteriota and Armatimonadetes and their abundance in rock-associated soil communities is not surprising. Still, the high relative abundance of these taxa is a deviation from the other communities assessed in this work, and robust global trends established in other studies. A global meta-analysis found that Actinobacteriota, Proteobacteria, Acidobacteriota, Gemmatimonadota, Bacteroidota, Cyanobacteria, and Verrucomicrobiota, along with Chloroflexi, and Firmicutes were be the most common phyla in soil samples in numerous diverese environments including hot and cold deserts, tropical forests, temperate forests, boreal forests, prairies, and tundra (Fierer et al. 2012). Studies have also shown that microbial community diversity is an important driver of plant diversity and nitrogen cycling (van der Heijden et al. 2008, Hester et al. 2018, Schmidt et al. 2019, Ouyang and Norton 2020) and that climate change has a significant impact on microbial diversity (Classen et al. 2015). The interconnectedness of soil microbial diversity, plant diversity, and global change highlights the importance of understanding and preserving the composition of specific communities in order to preserve ecosystem functions. This work shows that even in communities dominated by common soil microbes, specific rare taxa can potentially play a significant role in a given environment.

Phytomicrobiome and endolithosphere microbiome alpha and beta diversity are also important indicators of overall ecosystem health (Wagg et al. 2019). This work showed that exposure heavy metal and hydrocarbon pollution slightly, but significantly, decreased alpha diversity at a Tunisian industrial site. Only contaminated rhizosphere samples were significantly less diverse than paired uncontaminated samples. Beta diversity analysis of the same site showed that this decrease in alpha diversity was not associated with a significant change to overall community structure. This observation is significant because of the importance microbial diversity plays ecosystem functioning. It is particularly important to identify the tolerance level and resilience of soil microbial communities to pollution to avoid snowballing losses to biodiversity. This is particularly true for nations undergoing rapid industrialization which are often also the home to important biodiversity reserves.

We also observed a correlation between increased alpha diversity in soil and phytomicrobiome samples and unique community structure as measured by beta diversity. At the Algerian study site containing *C. myrtifolia* soil, rhizosphere, nodule and root samples has the highest alpha diversity, ranging from approximately 90 phyla per sample for root endophyte samples to 350 phyla per sample for rhizosphere samples. Contrastingly, the alpha diversity of the *C. myrtifolia* above ground tissue microbiome (fruit, leaf, and stem samples) ranged from 76 phyla per sample for fruit epiphyte samples, down to 12.3 phyla per sample for leaf endophyte samples. NMDS and PERMANOVA results showed that rhizosphere samples were significantly distinct from soil samples, and that root and nodule samples were significantly distinct from the rest of the *C. myrtifolia* phytomicrobiome individually and jointly. We also observed differences in community structure between endolithic communities correlated with sample site and dominated tree variety. However, this structural variation was not mirrored by variation in the alpha diversity of the sites.

This work was particularly interested in the presence and function of *Frankia* in the phytomicrobiome of *C. myrtifolia*. *Frankia* was identified in root, nodule, rhizosphere, and soil samples at Les Gorges de Kharrata in Algeria. The presence of *Frankia* in the *C. myrtifolia* phytomicrobiome is not surprising since *C. myrtifolia* is an established member of the actinorhizal symbiosis and a common plant host for clade 2 *Frankia.* One of the few clade 2 *Frankia* isolates, strain BMG5.30, was isolated from the nodules of a *C. myrtifolia* plant and sequenced as a part of this study (Gueddou et al. 2019). Therefore, it is surprising that the most abundance *Frankia* clade represented in the *C. myrtifolia* nodule samples was clade 3, as indicated by the re-binnning of *Frankia* reads. Furthermore, since the actinorhizal symbiosis has historically been understood primarily as an interaction between specific *Frankia*-host pairings, the presence of all five *Frankia* clades in both the roots and nodules of *C. myrtifolia* is potentially significant. This could indicate that the nodulation process is less taxa-specific than previously thought, or that nodules are colonized by additional *Frankia* strains after initial nodulation.

The presence of non-*Frankia* taxa in the nodule community of *C. myrtifolia* and *C. glauca* is also noteworthy. These taxa could also be involved in the nodulation process, or nitrogen fixation after nodulation. They could also simply be occupying favorable niche space in relatively harsh environments (semi-arid conditions for *C. myrtifolia*, industrial contamination for *C. Glauca*). A similar phenomenon has been observed in *rhizobium* nodules (Review by Martinez-Hidalgo and Hirsch 2017). Many non-*rhizobium* plant-growth promoting bacteria have been isolated *rhizobium* nodules indicating that the nodule community and it’s impact on the host is more complex that previously thought. While there is currently less research on non-*Frankia* occupants of actinorhizal nodules, this work suggested that future studies will find a complex system rather than one dominated by *Frankia*.

Future analyses should also assess the *C. myrtifolia* and *C. glauca* phytomicrobiomes using shotgun metagenomics to better link community structure with community function. Additionally, analysis of the chemical composition of plant tissue in conjunction with higher resolution sequencing would greatly increase the explanatory power of future phytomicrobiome studies. The lack of data on the concentration of picrotoxane in our samples made it difficult to address one of the aims of this study.

CHAPTER FOUR

Dioxin-like compound degradation by members of the Frankia genus

Introduction

Rational

Anthropogenic sources of organic pollution continue to threaten human health, ecosystem services, and biodiversity. Dioxin-like compounds specifically are widespread in the environment and cause many health problems including cancer, contact dermatitis, teratogenesis, and endocrine disruption. Remediation efforts have either focused on highly disruptive industrial solvent extraction or bulk soil removal-based approaches. A limited number of bioremediation approaches have had mixed success. *Frankia* has been shown to be resistant to heavy metal pollution and some organic pollution, but the remediation potential of *Frankia* remains poorly understood. Previous studies have indicated that *Frankia* may have untapped remediation potential which should be determined. In particular, the unique symbiotic biology of the *Frankia*-actinorhizal association could help overcome one of the most challenging obstacles to effective bioremediation: persistent inoculation of contaminated areas with a remediating bacteria population. Actinorhizal host plants have been shown to be highly resistant to organic pollution and to function as reservoirs of *Frankia*. Past bacteria bioremediation efforts have often failed do to limited survival of introduced microbial cultures, and the *Frankia*-actinorhizal symbiosis could address that problem if *Frankia* has the traits necessary for remediation.

Purpose

The aim of the experiments discussed in this chapter was to identify and characterize novel degradation pathways in *Frankia*. Specifically, we sought to determine the efficacy of a putative *bph* operon in certain *Frankia* strains using a multifaceted approach to overcome the challenges associated with studying *Frankia,* an species with a slow growth rate and no well-developed genetic tools. This aim was addressed by assessing the ability of *Frankia* to grow under dioxin-like compound stress, degrade dioxin-like compounds, and utilize dioxin-like compounds as carbon and energy source. RNA sequencing and quantitative PCR were used to determine the genetic basis of any dioxin-like compound resistance traits possessed by *Frankia.*

Methods

Frankia Culture Methods

Frankia inefficax strain EuI1c (*Frankia inefficax* hereafter) and *Frankia* sp. strain EUN1f were selected for growth, metabolic, and degradation assays based on genomic data indicating that they both contain a putative *bph* operon. *Frankia asymbiotica* strain CN3 lacks the putative *bph* operon and was used as a negative control. All culture work involving *Frankia* was carried out in a laminar hood. *Frankia* stock cultures were maintained in basal growth medium supplemented with a nitrogen source, NH_4Cl, as previously described (Tisa et al. 1983, 1999). *Frankia* cultures were grown in 25 mL of MPN in125 mL Erlenmeyer flasks or 50 mL MPN medium in a 250 mL Erlenmeyer flasks. MPN medium was amended with 20 mM glucose as a carbon and energy source for *F. inefficax* cultures and 20 mM fructose as a carbon and energy source for EUN1f cultures. CN3 cultures were supplemented with 20 mM propionate.

To maintain exponential growth, *Frankia* stock cultures were subcultured and the hyphae were homogenized using a glass Dounce homogenizer every two to three weeks. For each subculture, a 125 or 250 mL *Frankia* culture was harvested and spun for 20 minutes at 10,000 g in a swinging bucket centrifuge. The supernatant containing the old media was decanted and the remaining cell pellet was washed in fresh MPN medium by briefly agitating the cells and media in a 50 mL conical tube with a bench-top vortex. After washing, the cells were re-pelleted for 20 minutes at 10,000 g. The supernatant was decanted and the *Frankia* cells were re-suspended in fresh MPN medium and transferred to a new 125 or 250 mL Erlenmeyer flask. Sterile 0.5 M stocks of either glucose of fructose were added to produce a final concentration of 20 mM. Sterile trace metals solution was added to bring the final concentrations to 1.7%. Cultures were incubated at 30 °C without agitation until for 7 to 14 days.

Identification of Frankia strains with bioremediation potential

The Joint Genome Institute's (JGI) online BLAST tool was used to identify potential *bphA* genes in *Frankia* with high similarity to the sequence of the *Rhodococcus* strain RHA1 *bphA* gene. *Frankia* strains with highly similar *bphA* alignments (Expect value below $1e^{-10}$) were assessed to determine the strain had a full putative *bph* operon. Subsequently, *Frankia* and non-*Frankia bphA* gene sequences identified using JGI BLAST were imported into CLC workbench and used to generate a *bphA* phylogeny using neighbor-joining and Jukes Cantor. Phylogeny strength was assessed using bootstrapping with 1000 replicates.

Protein Quantified Growth and Resistance Assays

The resistance of *Frankia* to dioxin-like compound toxicity was determined in growth assays with stains *inefficax*, EUN1f, and CN3. *Frankia* growth was measured during exposure to dioxin-like compound concentrations from 0.1 mM to 5.0 mM and MPN media amended with an additional carbon source. Additionally, the ability of the same three *Frankia* stains to utilize dioxin-like compounds as a sole carbon and energy source was assessed in growth assays lacking an alternate carbon source. At the start of both assays, three one-week old *Frankia* cultures were collected in three 50 mL conical tubes and centrifuged for 20 minutes at 10,000 g. The supernatant of each tube was decanted and the pellet was washed as previously described above. After washing, each pellet was re-suspended in 25 mL of MPN growth medium with the appropriate carbon source or lack of a carbon source.

Protein Determination: For each culture, a 1 mL aliquot was removed and added to a 1.5 microcentrifuge tube using a micropipette to determine the cell density in each suspension. Total cellular protein was determined using the Bradford protein quantification method (Bradford 1976). Bio-Rad coomassie stock reagent were diluted to the final working concentration (1:5) immediately before each assay. Bovine serum albumin (BSA) protein standards were diluted 1:2 in 0.25 M NaOH from 1.0 to 0.015 mg/mL. All samples from the three *Frankia* suspensions were centrifuged for 15 minutes at 13,000 x g in a room temperature bench-top microcentrifuge. The resulting supernatant was removed and discarded using a micropipette and 500 µL of 0.25 M NaOH was added for alkali cell lysis. The samples were then vortexed for approximately 30 seconds to disrupt the cell pellet and incubated at 100 °C for 30 minutes in a heat block. After incubation, the samples were centrifuged for 15 minutes at 13,000 x g to clarify the solution. Triplicate 10 µL samples were aliquoted from each lysis solution and BSA standard into a 96 well plate. Bradford working solution (200 µL) was added to each well and the samples were incubated at room temperature for 10 minutes. The samples were quantified using a Tecan 200 plated reader (Tecan, Durham, North Carolina) measuring absorbance at 595 nm. The protein concentration of each sample was determined using a standard curve generated from the BSA standards.

After determining the protein concentrations of the *Frankia* cell suspensions, growth and resistance assays was started. Dioxin-like compound resistance assays were carried out in 50 mL Erlenmeyer flasks containing 15 mL total volume. All flasks contained the volume of cell suspension necessary to reach 600 ng of protein, 1.7% trace metals, and 20 mM carbon source (glucose for *inefficax*, fructose EUN1f, and propionate for CN3). In dioxin-like compound stressed replicates, 100 mM stock solutions of biphenyl, 4-chlorobiphenyl, and dibenzofuran in 95% ethanol were added to bring final dioxin-like compound concentration to 0.1 mM, 0.2 mM, 1.0 mM, 2.0 mM, and 5.0 mM. MPN medium was added for the remainder of the volume to reach 15 mL. Negative controls contained cell suspension, trace metals and MPN to bring the volume to 15 mL. All flask in each assay were incubated at 30 °C for 30 days without agitation.

Each growth assay was carried out in 50 mL Erlenmeyer flasks containing 15 mL total volume. All flasks contained the volume of cell suspension necessary to reach 600 ng of protein and 1.7% trace metals. Positive control flasks contained only *Frankia* cells, trace metals, and 30 μL of 0.5 M carbon stock solution for a concentration of 1 mM (glucose for *inefficax*, fructose EUN1f, and propionate for CN3), and MPN for the remainder of the volume to reach 15 mL. Negative controls contained cell suspension, trace metals and MPN to bring the volume to 15 mL. Each assay included three experimental conditions: 0.25, 0.5, and 1 mM dioxin-like compounds concentrations. This experimental design was repeated for *inefficax*, EUN1f, and CN3 with biphenyl, 4-chlorobiphenyl, and dibenzofuran. All flask in each assay were incubated at 30 °C for 30 days without agitation.

After incubation, the the whole 15 mL volume in each Erlenmeyer flask was decanted into a 15 mL conical tube and centrifuged at 10,000 x g for 20 minutes. The supernatants were decanted and 1 mL aliquots of 0.25 M NaOH were added to each tube. The tubes were then vortexed for 30 seconds and subsequently incubated at 100 °C for 30 minutes in a heat block. Triplicate 10 μL aliquots of each protein extraction were transferred to a 96 well plate as well as 10 μL aliquots of BSA protein standards ranging from 0.015 to 1.0 mg/mL. 200 μL of Bradford working solution was then added to each well and incubated for 10 minute at room temperature. After incubation, the samples were quantified by measuring absorbance at 595 nm using a Tecan 200 plate reader. A standard curve was generated using the BSA standards and used to calculate the protein concentration of each sample. The relative growth of the positive controls and experimental conditions was then calculated by subtracting the protein concentration of the negative controls from each sample.

GC-FID Quantification of Biphenyl Degradation

Three one-week old *Frankia* cultures were collected in three 50 mL conical tubes and centrifuged for 20 minutes at 10,000 g The resulting supernatants were decanted and the pellets were washed, re-suspended, and quantified using the Bradford protein assay as previously described. The degradation assays were carried out in 25 x 200 mm glass test tubes with 20 mL total volume of media. The conditions tested were 1 mM biphenyl with either *Frankia inefficax* or EUN1f, 1 mM biphenyl with autoclaved *Frankia inefficax* or EUN1f , 1 mM biphenyl with no *Frankia* added, and *Frankia inefficax* or EUN1f without biphenyl. The volume of cell suspension need to add 200 µg of protein was added to each condition that contained *Frankia*. Conditions that included *Frankia* contained either glucose (*inefficax*) or fructose (EUN1f) at a final concentration of 20 mM and the biphenyl without *Frankia* control contained 20 mM glucose. All conditions also contained 1.7% trace metals, and the remainder of the volume needed to reach 20 mL was MPN media. 1 mL samples of each condition were transferred to 7 mL glass collection vials after agitating the tubes by hand immediately after the assay setup was completed. Additional samples were collected after 1, 7, and 14 days. All samples were stored at -20 °C until they were extracted. The assay was incubated at 30 °C without agitation between sampling days.

Immediately prior to extraction, the samples were thawed at room temperature for approximately 30 minutes. To determine whether *Frankia* metabolized or simply absorbed or sorbed biphenyl, parallel extractions were carried out for each sample measuring the biphenyl concentration in the media as well as the biphenyl in the *Frankia* cells pellet alone. To accomplish this, after the samples were thawed they were centrifuged for 30 minutes at 7000rpm and the supernatants were transferred to fresh 7 mL glass vials. 1 mL of ultrapure H_2O was then added to the each of the original sample vials that contained the *Frankia* pellets. Subsequently, 50 µL of 1 µg/µL naphthalene in dichloromethane was added to each vial using a Hamilton gas-tight syringe as an internal standard. The samples were then homogenized by mixing for 1 hour on a VWR VX-2500 platform vortex at medium speed to distribute the naphthalene. 1 mL of dichloromethane was then added to each sample vial and the samples were vortexed again for 1 hour. After vortexing, the samples were centrifuged for 2 minutes at 500 rpm to separate the organic and aqueous phases. The organic phase was them transferred to a 2 mL glass chromatography vial and an additional 1 mL of dichloromethane was added to the 7 mL sample vials. The sample vials were vortexed for an additional 30 minutes and then centrifuged for 2 minutes at 500 rpm. The second organic phase was then added to the initial organic phase in the chromatography vials. After extraction, the samples were concentrated to approximately 1 mL under a low pressure pure N_2 stream. The biphenyl extractions were either immediately quantified or were stored at -20 °C until quantification.

A method adapted from Mashayekhi et al. (2012) was used to determine the biphenyl concentration of each sample. A Perkin Elmer Clarus 580 gas chromatograph (GC) equipped with a split/splitless injector system, auto-sampler with a 5 µL syringe, and flame ionization detector (FID), was used to separate and quantify the biphenyl in each sample. Ultra pure N_2 gas (99.999%, Airgas) was used as the carried gas and was passed through an oxygen trap before entering the GC. The GC was equipped with a 30m HP5 column with an internal diameter of 0.53 nm and film thickness of 0.25 nm. Before and during injection, the injection port was operated in splitless mode with a pressure controlled flow of N_2 at 10 psi. A 2 µL sample was loaded with the auto-sampler, and after 1 minute the injector was switched to split mode decreasing to 2 psi at a rate of 20 psi/minute with a 5:1 split ratio. The injection port was held at 250 °C throughout. The initial oven temperature was set to 100 °C for 2 min and then increased to 250 °C at a rate of 10 °C/minute and held for 8 minutes. The FID temperature was held at 250 °C with an airflow (Ultra Pure 99.999%, Airgas) of 450 mL/minute and hydrogen (Ultra Pure 99.999% H2, Airgas) flow of 45 mL/minute. Perkin Elmer TotalChrome software was used to determine the biphenyl response ratios in each sample. The amount of biphenyl in *Frankia* pellet samples was minimal, so pellet and supernatant samples were recombined computationally for analysis and plotting.

RNA sequencing of Biphenyl Exposed Frankia

For this experiment, one-week old *F. inefficax* cultures used. Cells were harvested and treated as described above and used to inoculate growth medium under three condition: (1) 20 mM glucose as a sole carbon and energy source (2) , 20 mM glucose and 1 mM biphenyl as carbon and energy sources, and (3) 1 mM biphenyl as a sole carbon and energy source. The cultures were incubated at 30 °C for 3 days. The entire culture was harvested by centrifugation at 10,000 g for 20 mintues. After supernatant fluids were discarded and the pellets were stored at -80 °C until RNA extraction. Triplicate cultures of the three conditions were performed.

RNA was extracted using a modified version of the Qiagen RNeasy mini kit (Qiagen Sciences, Valencia, CA). All glassware was treated with 0.01 % DPEC to inactivate RNase activity. Briefly, frozen bacterial pellets were resuspended in 0.5 mL TE buffer, pH 8, supplemented with 5 mg/ml lysozyme and incubated at room temperature for 10 min. RLT buffer (2 ml) supplemented with 1 μl/ml β-Mercaptoethanol (β-ME) was added to each sample and the pellets were homogenized using Dounce homogenizers. Subsequently, the RNeasy mini kit procedure was followed as per the manufacturer's recommendation. RNA samples were treated with DNase I (New England Biolabs, Ipswich, Massachusetts) per the manufacturer's instructions. RNA was quantified using Qubit RNA assay (Invitrogen) and Nanodrop 2000c spectrophotometer (Thermo Scientific, Wilmington, Delaware) according to manufacturers' specifications. The quality of each RNA sample was determined using the Agilent 2100 Bioanalyzer (Agilent, Santa Clara, CA) according to the Prokaryote Total RNA Nano protocol. RNA quality was represented by RNA integrity number (RIN value), which ranged from 1 to 10, with 10 representing the most intact RNA. Samples with RIN value greater than or equal to 9 were used for downstream analysis. Ribosomal RNA was removed from total RNA using the MicrobeExpress kit (Ambion, Foster City, CA) according to the manufacturer's specifications. The MEGAclear kit (Life Technologies, Carlsbad, CA) was used to remove tRNA according to manufacturer's specifications. cDNA libraries were prepared using the TruSeq RNA Sample Prep Kit (Illumina, San Diego, CA) as described by the manufacturer. The cDNA library was verified for appropriate fragment size (approximately 250 bp) on an Agilent 2100 Bioanalyzer (Agilent, Santa Clara, CA) according to the DNA 1000 protocol described by the manufacturer. The Qubit dsDNA BR Assay (Invitrogen, Carlsbad, CA) was used to determine the cDNA concentration of each library according to manufacturer's recommendations. Libraries were normalized to 10 nM with 10 mM Tris-HCl, pH 8.5, supplemented with 0.1% Tween 20. Illumina sequencing was carried out at Hubbard Genome Center at the University of New Hampshire on an Illumina HiSeq2500 platform. Reads (150 bp paired-end) were separated on adapter assignment and pre-processed through CASAVA 1.8.3. The resulting FASTQ files of sequence reads were processed using CLC Genomics Workbench 9.0 (CLC bio, Cambridge, MD). Adapters were trimmed from reads by searching on the forward and reverse strands. The ends of reads were quality trimmed based on quality scores from a base-caller algorithm using a limit value of 0.05. The high-quality trimmed reads were mapped to *Frankia* strain *inefficax* gene regions. Reads mapping to rRNA operons were excluded from downstream analysis. Mapping parameters were as follows: The maximum number of mismatches allowed was 2. The minimum length fraction was set so that at least 50% of the read length aligns to the reference sequence. The minimum fraction of identity between the read and the reference sequence was set at 80%. A read that matched to more than 10 distinct places in the reference was not mapped. If the read matched to multiple distinct places, but below 10 different locations, it was randomly assigned to one of the distinct places. After mapping, the expression level for each gene was tabulated in terms of the unique number of reads mapping to that gene. All RNA-seq experiments were normalized by the total number of reads. A gene was expressed if it had at least one unique sequence read aligned with it. Principal coordinates analysis (PCA) was performed to determine the clustering of samples from each sample type. Differential expression analysis using a negative binomial generalized liner model was performed using CLCs integrated method.

After differentially regulated genes were determined, separate FASTA files were generated for up and down-regulated gene sets for both biphenyl only, and biphenyl with glucose conditions. Blast2GO was then used to annotate each data set with gene ontology information and summarize biological processes and molecular functions represented in each set of genes.

Comparison of RNA sequencing and pan-genome

Frankia RNA sequencing results were combined with the core genome data produced in this study to determine what functions are both highly conserved *Frankia* clade 4 strains and up regulated in response to dioxin-like compounds. Genes that were present in both the *Frankia* core genome and differentially regulated under dioxin-like compound stress were determined using BLAST. Specifically, a BLAST database with all differentially regulated genes from the dioxin-stressed RNA sequencing library was generated, and *Frankia* core or *Frankia* clade core genes were queried against it. *Frankia* core gene hits with and expect values below $1e^{-5}$ where saved. The functional characteristics of these gene sets was then determine using Blast2Go as described above for the entire core genome. The core genomes of *Frankia*, *Rhizobium*, and *Bradyrhizobium* were also compared to identify any genes common to each core genome.

Quantitative RT-PCR of Dioxin-like Compound Exposed Frankia

The expression of a putative *bph* operon in *F. inefficax* in response to biphenyl, 4-chlorobiphenyl, and dibenzofuran exposure was measured by quantitative RT-PCR . One-week-old *Frankia* cultures were used to inoculate growth medium under three conditions: (1) 20 mM glucose as a sole carbon and energy source (2) , 20 mM glucose and 1 mM test dioxin-like compound as carbon and energy sources, and (3) 1 mM test dioxin-like compound as a sole carbon and energy source. Cultures were incubated at 30 °C without agitation. At 1, 3, and 7 days, samples were removed from the culture and harvested by centrifugation in a microfuge tube. After the supernatant fluid was decanted, the pelleted cells were stored at -80 °C until extraction. The experiment was performed in triplicate.

RNA extractions were performed by the Triton X100 method as previously described (Niemann & Tisa 2008). RNA samples were treated with DNase I (New England Biolabs) according to the manufacturer's recommendations. RNA samples were quantified with a Nanodrop 2000c spectrophotometer (Thermo Scientific) and stored at −80∘C until use.

RNA was transcribed into cDNA using GoScript reverse transcriptase (Promega) following the manufacturer's instructions. The cDNA was quantified by a Nanodrop 2000c spectrophotometer, diluted to 10 ng/μL working stocks in DNAse-free, RNAse-free H_2O, and stored at −20∘C until use. Amplification and detection of gene expression were performed using a Mx3000P QPCR system (Agilent Technologies, Santa Clara, California). The primers used for these experiments are listed in Table 4.1.

Briefly, each 25 µL reaction contained 50 ng template cDNA, 300 nM of the forward and reverse primer mix, and SYBRGreen PCR Master Mix. Parameters for the Agilent MP3000 were as follows: (1) 95∘C for 15 min, (2) 40 cycles of 95∘C for 15 s and 60∘C for 30 s, and (3) thermal disassociation cycle of 95∘C for 60s, 55∘C for 30 s, and incremental increases in temperature to 95∘C for 30 s. Reactions were performed in triplicates and the comparative threshold-cycle method was used to quantify gene expression. The results were standardized with *rps*A expression levels. The ΔΔCt method (Scheittgen and Livak 2008) was used to calculate relative expression (fold changes) with the control as the calibrator. Three biological replicates of the triplicate samples were averaged. The ΔΔCT values of each sample were determined and plotted in R.

Plant infectivity

Alnus glutinosa seeds were soaked overnight at room temperature in sterile tap water in 50 mL screw-cap glass centrifuge tubes. After overnight incubation, the water was removed, and the seeds were rinsed once with 10 mL sterile tap water. The seeds were surface sterilized with 15 mL of 30% hydrogen peroxide solution with 20 µL Tween-20. The mixture was incubated at room temperature with agitation for 1 hour. Following the agitation period, the seeds were incubated overnight at room temperature without agitation in the same peroxide solution. The sterilized alder seeds were rinsed 5 times with 15 mL sterile tap water to remove residual peroxide solution. The surface-sterilized seeds were germinated in Magenta GA-7 boxes containing100 mL of sterilized perlite of in 50 mL sterile Brougton and Dilworth medium with nitrogen (BDN)

(Broughton and Dilworth 1971). The germination boxes were kept in an environmentally-controlled growth chamber at 28 °C with a 16-h light period and 8-h dark period.

After the seeds germinated, two-week old alder seedlings were aseptically transplanted to a Brite-Kote aluminum screen in a Magenta GA-7 box suspended over 50 mL of BDN medium as described previously (Beauchemin et al. 2012). The plants were incubated at 28 °C with a 16 h light period for a minimum of 4 weeks, replacing the spent BDN medium every 2 weeks. Two weeks prior to inoculation, the 6-week-old plants were starved of nitrogen by replacing the BDN medium with nitrogen-deficient BD medium. For the inoculum, 2-week-old *Frankia* cultures were collected as previously described and subcultured in nitrogen deficient media (BD) for an additional two weeks. The nitrogen-starved *Frankia* cultures were harvested and resuspended in BD medium. The cell density of the culture was determined by protein quantification using the Bradford Assay as described above. The plant boxes were inoculated with the equivalent of 450 µg protein for the culture. To five Magenta boxes 50 µL of 100 mM biphenyl in 95% ethanol was added to achieve a 0.1 mM biphenyl stress level. Four control Magenta boxes had 50 µL of 95% ethanol was added to them. The plants were incubated at 28 ◦C with a 16 h light period. The root systems in each magenta box were observed approximately every two weeks for five months. Five months after inoculation, the plants were removed from the Magenta boxes for closer observation and nodule quantification.

Results

Bph operon identification

Two *Frankia* strains with a putative *bph* operon were identified by searching publicly available genomes on the National Center for Biotechnology Information

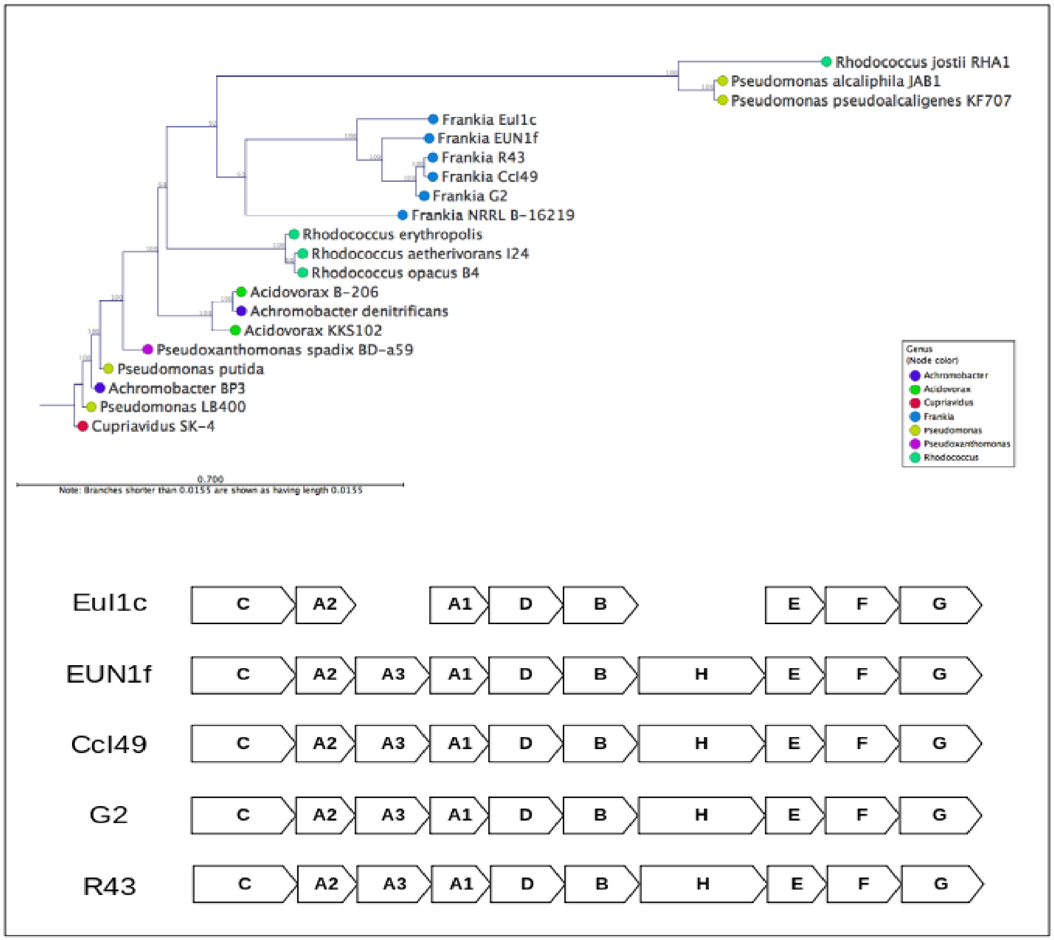


Figure 4.1: bph operon organization in Frankia strains and phylogenetic relatedness of the Frankia bph operon to other bacterial bph operons.

(NCBI) and Joint Genome Institute (JGI). *Frankia inefficax* and *Frankia* EUN1f both contain genes similar to known biphenyl degrading genes in *Rhodococcus* sp.

Resistance and Growth assays

Frankia EUN1f and *inefficax* were both able to grow under biphenyl, 4-chlorobiphenyl, and dibenzofuran stress up to 5.0 mM. *Frankia* CN3 showed significantly reduced growth starting at 1.0 mM concentrations of dioxin-like compounds. *Frankia inefficax* and *Frankia* EUN1f were both able to growth with biphenyl or dibenzofuran as a sole carbon source. Additionally, *Frankia* EUN1f was able to grow with 4-chlorobiphenyl as a sole carbon source.

Degradation assay

Both *Frankia inefficax* and *Frankia* EUN1f were able to degrade Biphenyl. *Frankia inefficax* degraded biphenyl at an average rate of 9.4 µg/day and *Frankia* EUN1f degraded biphenyl at a rate of 8.2 µg/day. Degradation rate was highest after 7 days of exposure and the concentration of biphenyl in samples inoculated with either *Frankia inefficax* or *Frankia* EUN1f was reduced to near zero after 14 days of incubation.

RNA Sequencing

Shotgun sequencing of RNA from biphenyl exposed *Frankia* cells produced over 6 million reads. After processing using tools from CLC genomics software 3.8 million reads were mapped to the *Frankia inefficax* reference genome. Principal Coordinates Analysis of

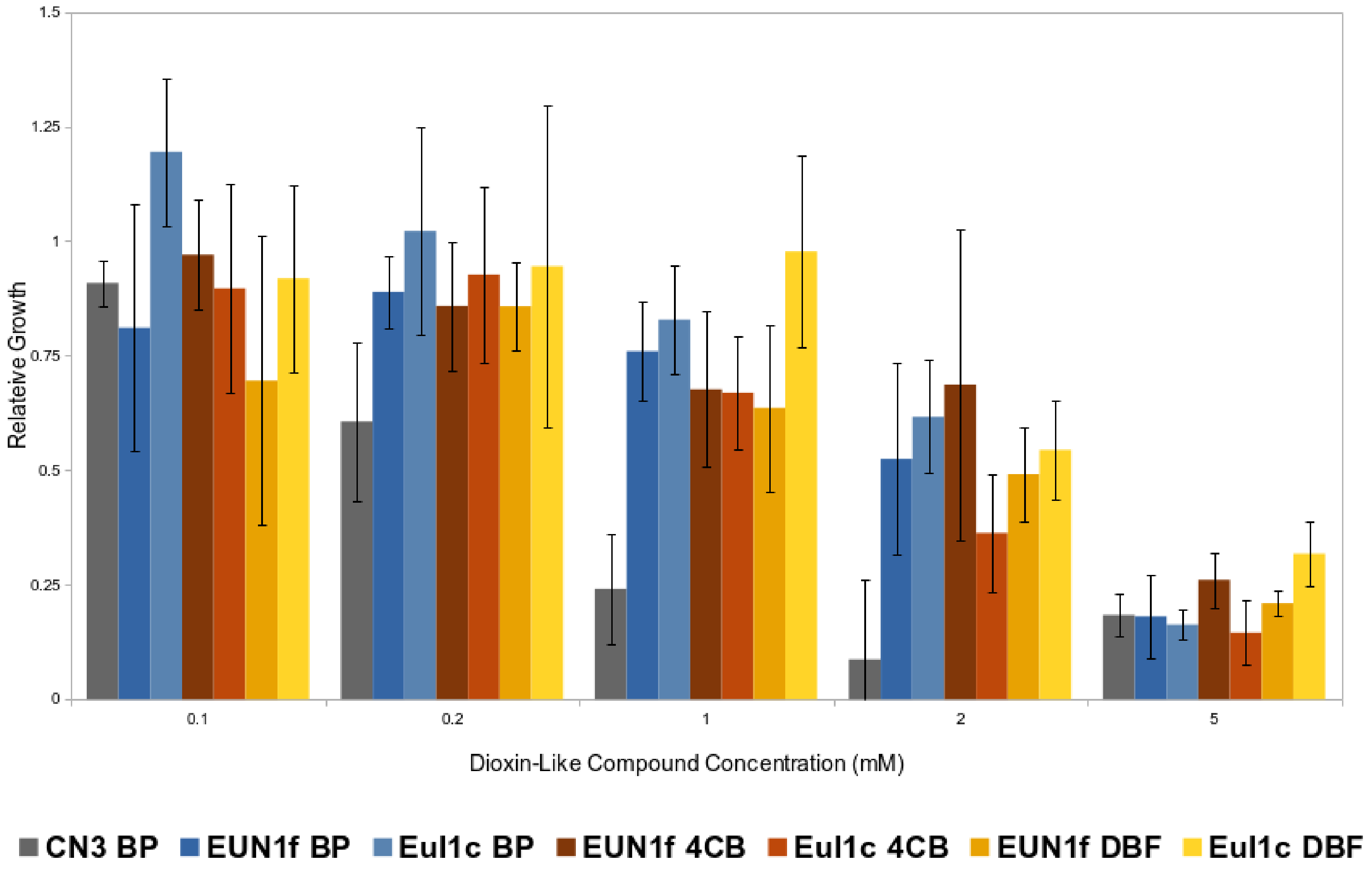


Figure 4.2: Relative growth of Frankia strains inefficax, EUN1f, and CN3 under dioxin-like compound stress with alternative carbarn sources. BP = biphenyl treatment, 4CB = 4-Chlorobiphenyl treatment, DBF = Dibenzofuran treatment. Error bars represent standard deviation.

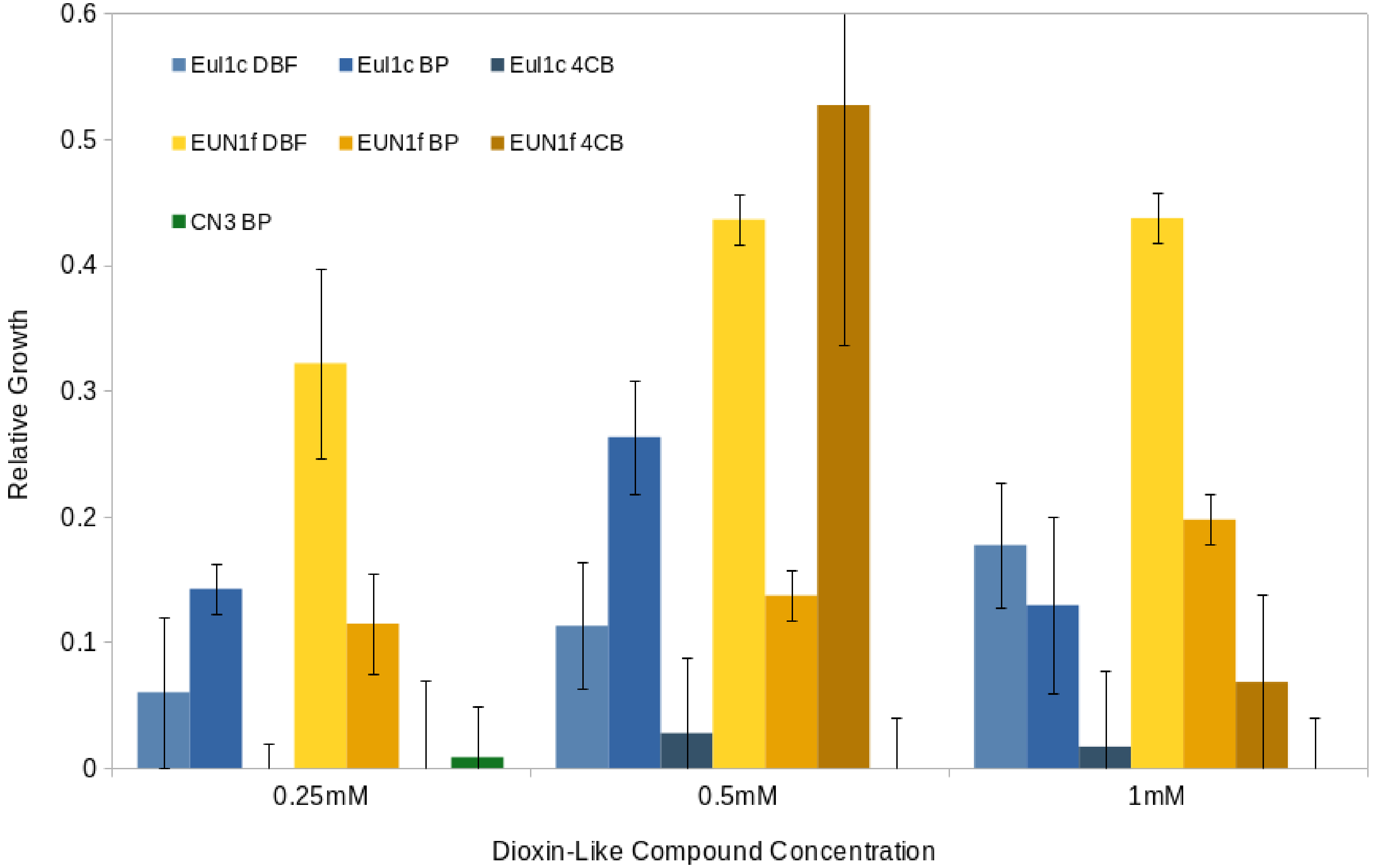


Figure 4.3: Growth of Frankia strains inefficax, EUN1c, and CN3 with biphenyl (BP), 4-chlorobiphenyl (4CB), and dibenzofuran (DBF) as a sole carbon and energy source. Error bars represent standard deviation.

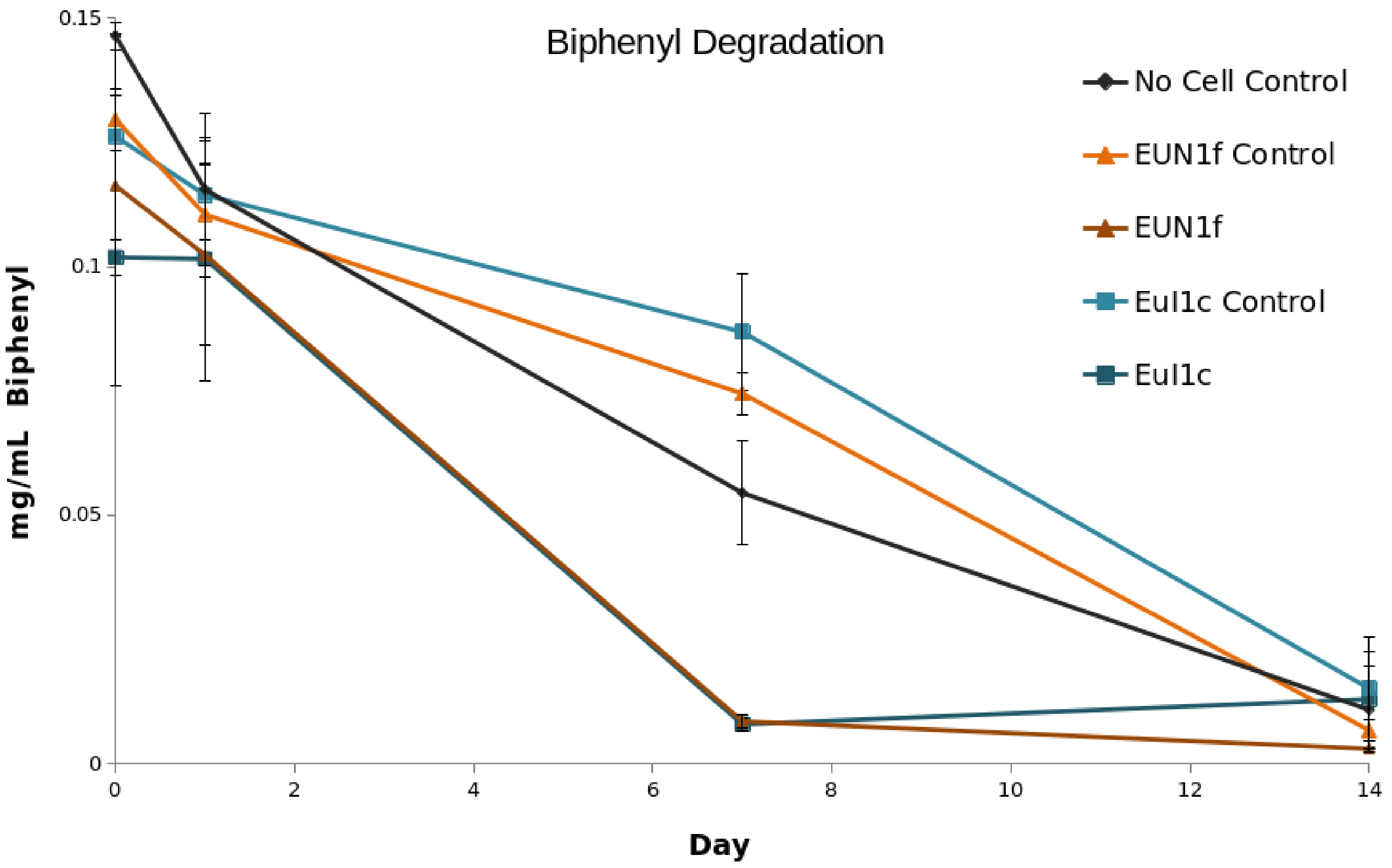


Figure 4.4: Determination of biphenyl concentrations after degradation by Frankia. No cell control samples contained only MPN media spiked with biphenyl. EUN1f and inefficax controls contained autoclaved Frankia cells equal to the live Frankia samples. Error bars represent standard deviation.

the mapped reads showed clustering based on sample type with control samples, biphenyl exposed samples, and biphenyl exposed samples supplemented with glucose all forming groups. Control samples clustered much more tightly, while there was some overlap between biphenyl only samples and biphenyl with glucose.

Biphenyl exposed samples had 808 differentially regulated genes that were at least 2 fold up or down regulated with a P value below 0.05. Biphenyl exposed samples supplemented with glucose had 284 differentially regulated genes that were at least 2 fold up or down regulated with a P value below 0.05. There were 407 and 161 up regulated genes in the biphenyl only and biphenyl with glucose samples respectively, and there where 401 and 123 down regulated genes in the biphenyl only and biphenyl with glucose samples respectively. 61 genes were up-regulated at least 2 fold with a P value below 0.05 in both the biphenyl only condition and the biphenyl plus glucose condition while 49 genes were down-regulated in both conditions.

Gene ontology annotation results showed that transmembrane transport was the most common biological process among up-regulated genes in the biphenyl only condition. Phosphorylation activity, carbohydrate metabolic processes, transcription regulation, and organonitrogen compound metabolism processes were also highly up-regulated. In *Frankia* exposed to biphenyl with an alternative carbon source, the most frequently up-regulated biological process was transcription regulation followed by phosphorylation, amino acid biosynthesis, and methylation phosphorelay signal transduction systems. Many of the same biological processes were represented in the set of genes down-regulated in response to biphenyl, with or without an alternative carbon and energy source.

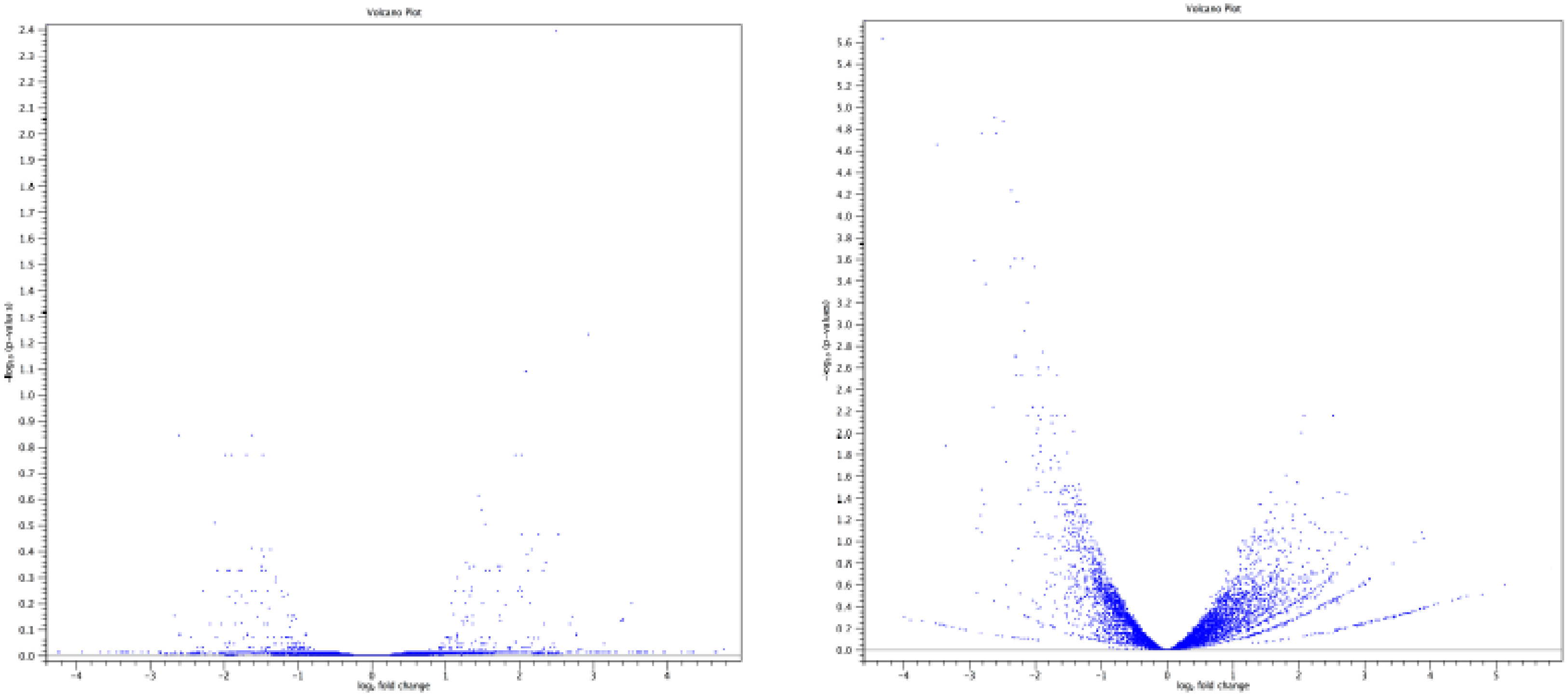


Figure 4.5 Volcano plots of all differentially regulated genes between control and biphenyl with supplemental glucose conditions (left) and control and biphenyl only conditions (right).

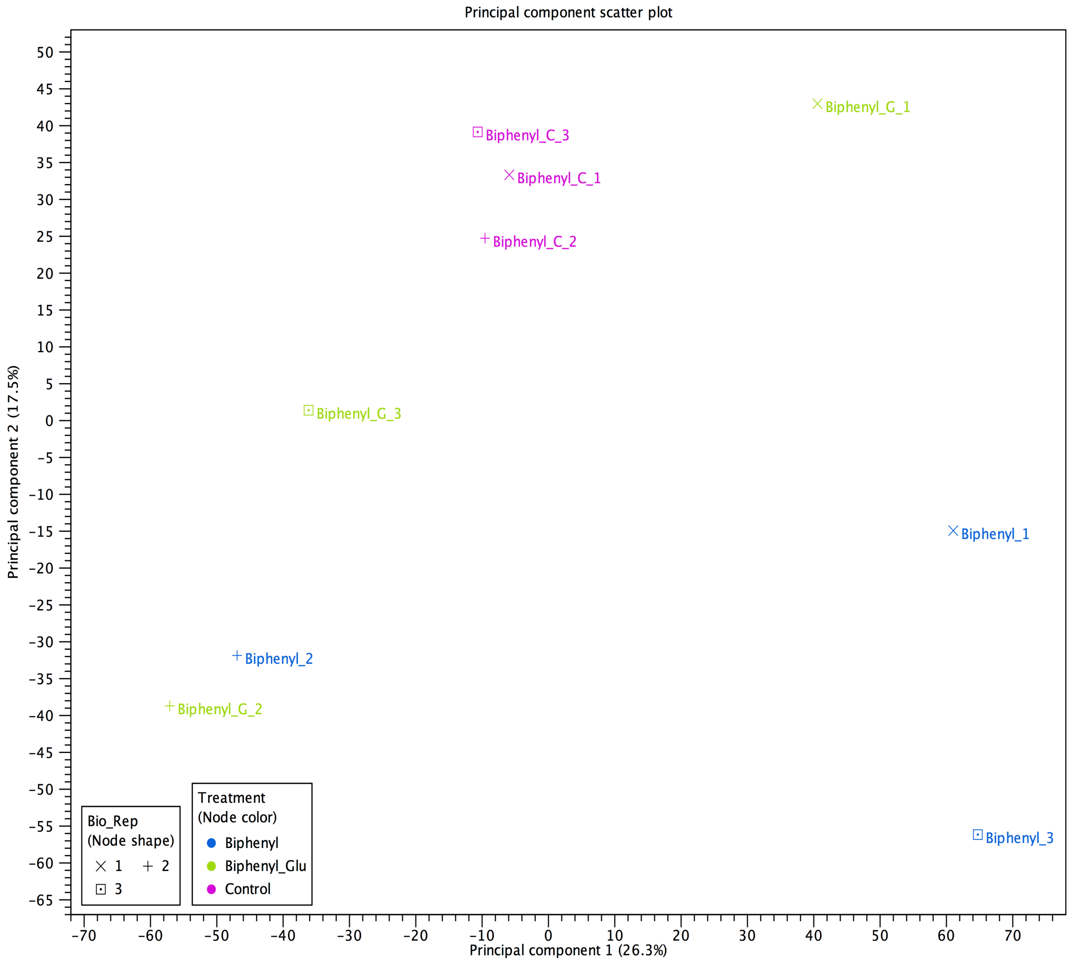


Figure 4.6: PCA representing RNA sequening results. "Biphenyl_C_#" samples are controls, "Biphenyl_#" samples are biphneyl as a sole carbon source samples, and "Biphenyl_G_#" samples are biphenyl plus supplemental glucose samples.

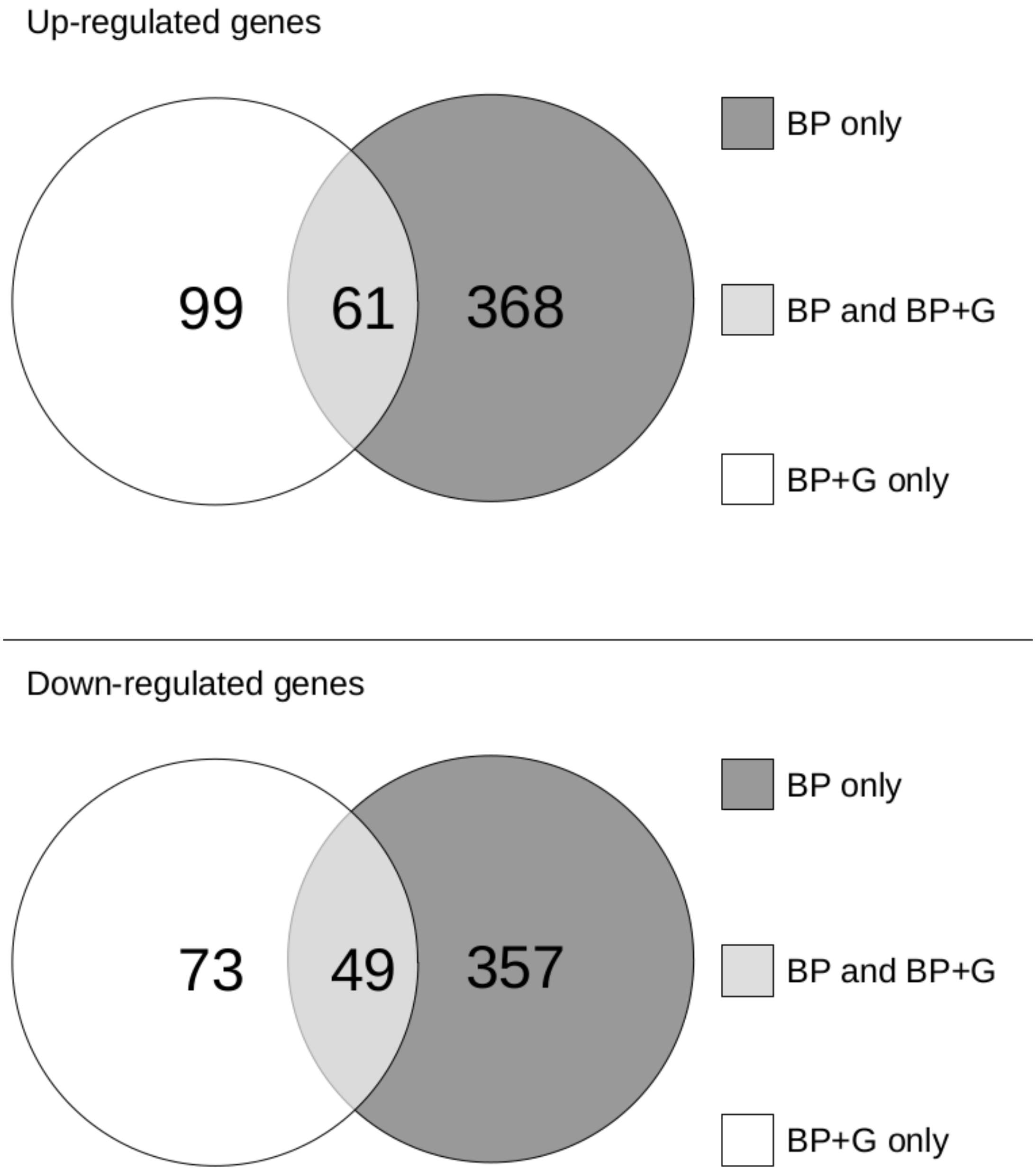


Figure 4.7: Venn diagram of up and down-regulated genes in the biphenyl only condition and the biphenyl with sublimental glucose condition. BP = Bipenyl only, BP+G = Biphenyl plus suplimental glucose

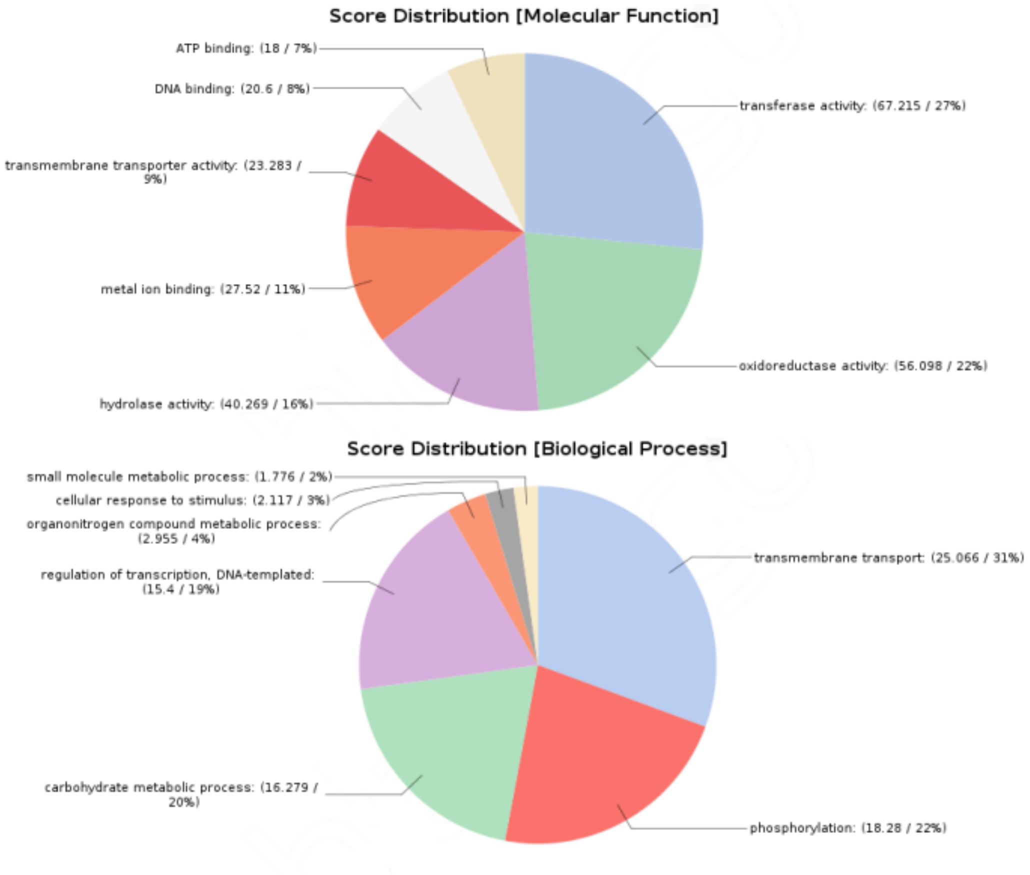


Figure 4.8:Blast2GO gene ontology assignments of up-regulated genes in Frankia inefficax exposed to biphenyl without glucose as an alternative carbon source.

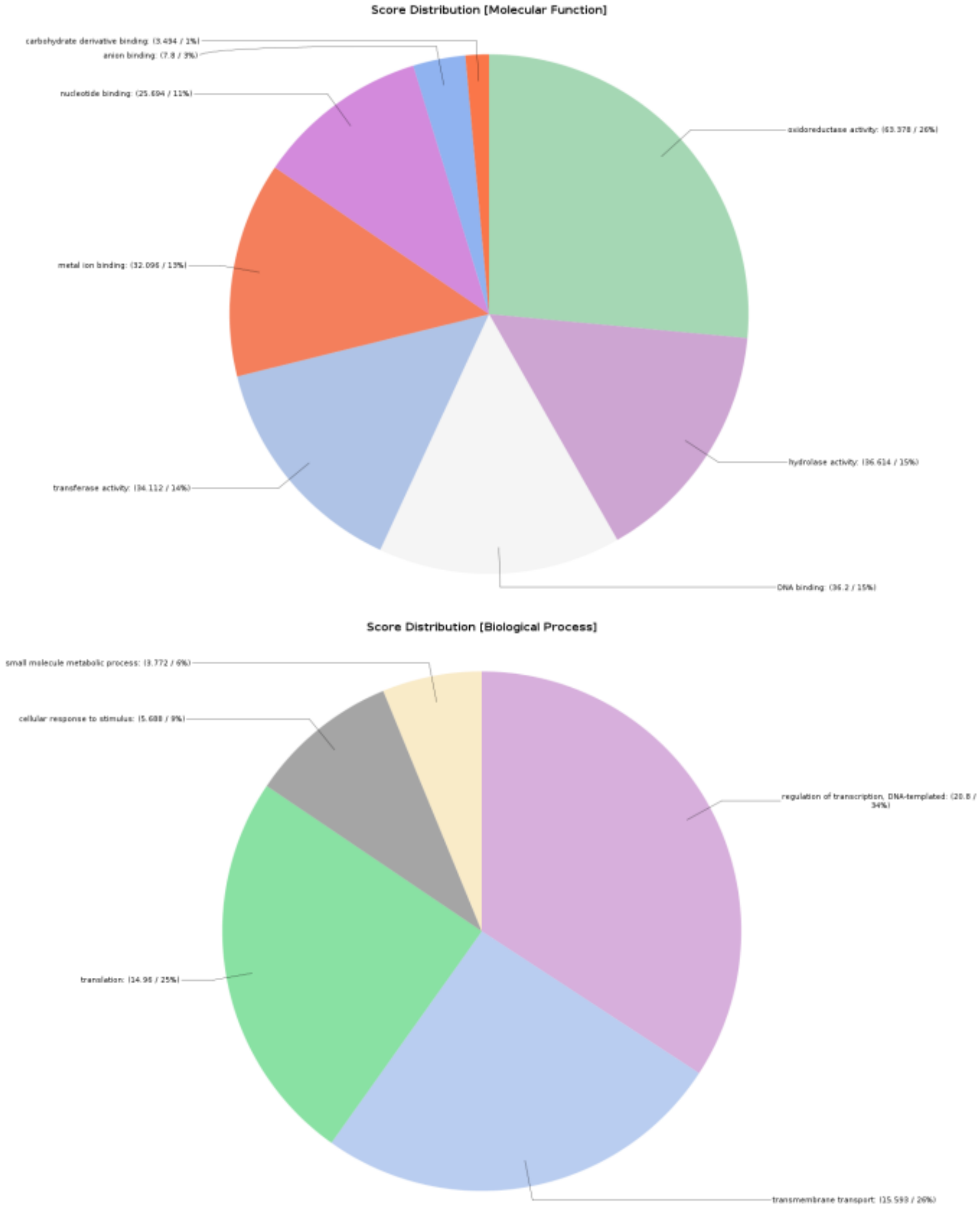


Figure 4.9: Blast2GO gene ontology assignments of down-regulated genes in Frankia inefficax exposed to biphenyl without glucose as an alternative carbon source.

Specifically, the two most frequently down-regulated biological processes in both conditions were transcription regulation and transmembrane transport. The down-regulated molecular functions in the biphenyl-only condition included oxidoreductase activity, hydrolase activity, DNA binding, transferase activity, metal ion binding, nucleotide binding, anion binding, and carbohydrate derivative binding. In *Frankia* exposed to biphenyl with an alternative carbon source, oxidoreductase and transferase activity, transmembrane transport, DNA binding, hydrolase, transition metal ion binding, and anion binding molecular functions were down-regulated.

Quantitative PCR

Quantitative PCR was used to validate the RNA sequencing results assessing the *bph* operon with rpoA as a housekeeping reference gene. Quantitative PCR results were consistent with RNA sequencing results with individual genes in the *bph* operon up-regulated by 2-4 fold.

Quantitative PCR was also carried out on a separate set of RNA samples from *Frankia inefficax* exposed to three different dioxin-like compounds sampled at three time points, 1,3, and 7 days after exposure. Results showed that the *Frankia bph* operon is up-regulated in response to all three compounds with the highest responses induced by dibenzofuran and biphenyl after three days of exposure.

Clade 4 Stress Response

Twentyone percent of *Frankia* genes in the clade 4 core genome that are also up-regulated under dioxin stress are oxidoreductase genes indicating that more than the *bph* operon is activated during dioxin-like compound stress, and that these are important genes in clade 4.

Actinorhizal nodulation under biphenyl stress

After inoculation with *Frankia,* the BD media in each of the 9 alder hydroponic magenta boxes became cloudy and made it difficult to identify the progression of nodulation. Therefore, the nodule quantification after five months of incubation is the only time point. After five months of incubation with *Frankia,* 53.3% of biphenyl stressed alders were nodulated and none of the unstressed alders were nodulated.

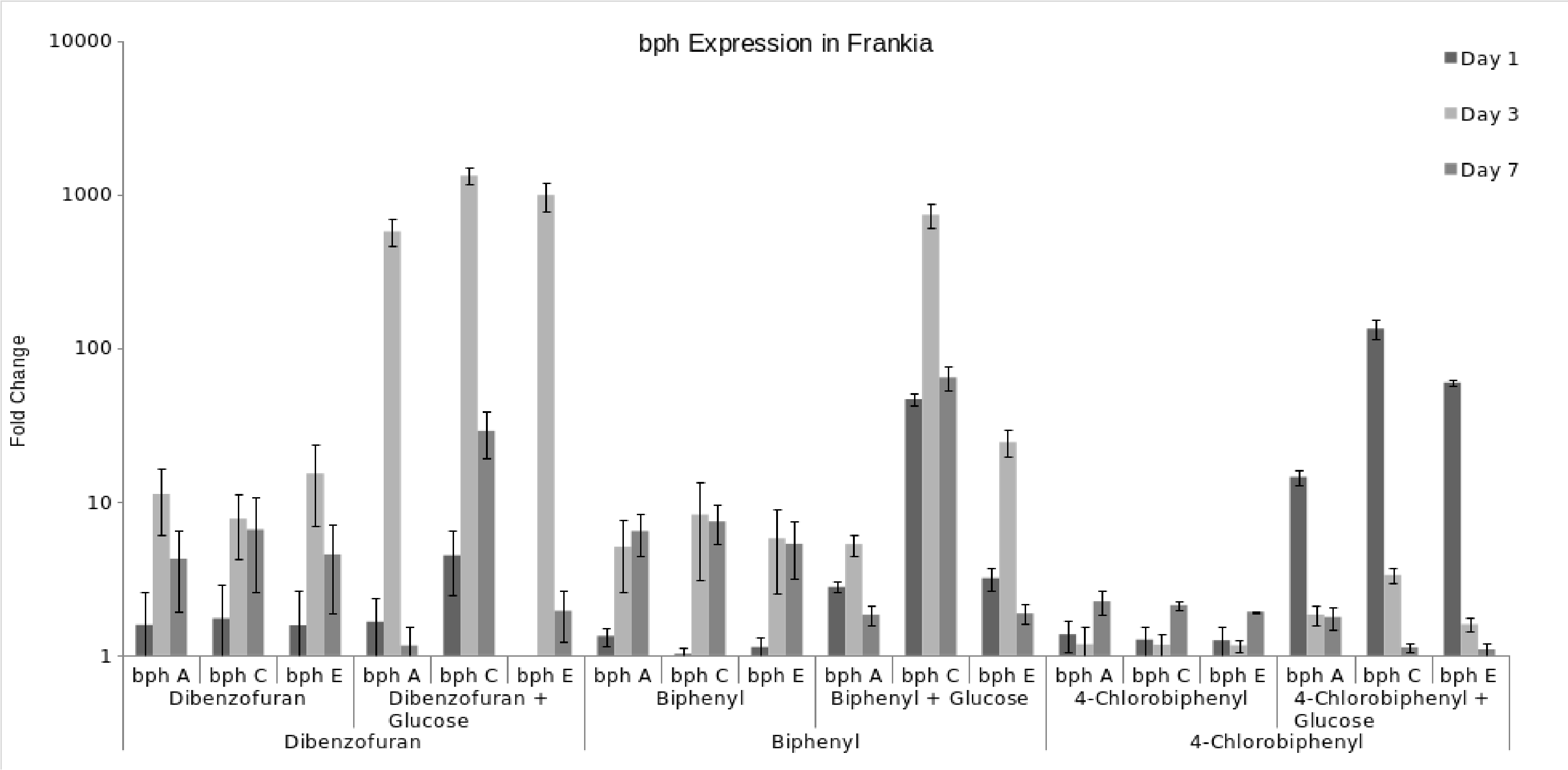


Figure 4.10: Relative expression of bph operon genes after exposure to dioxin-like compounds.

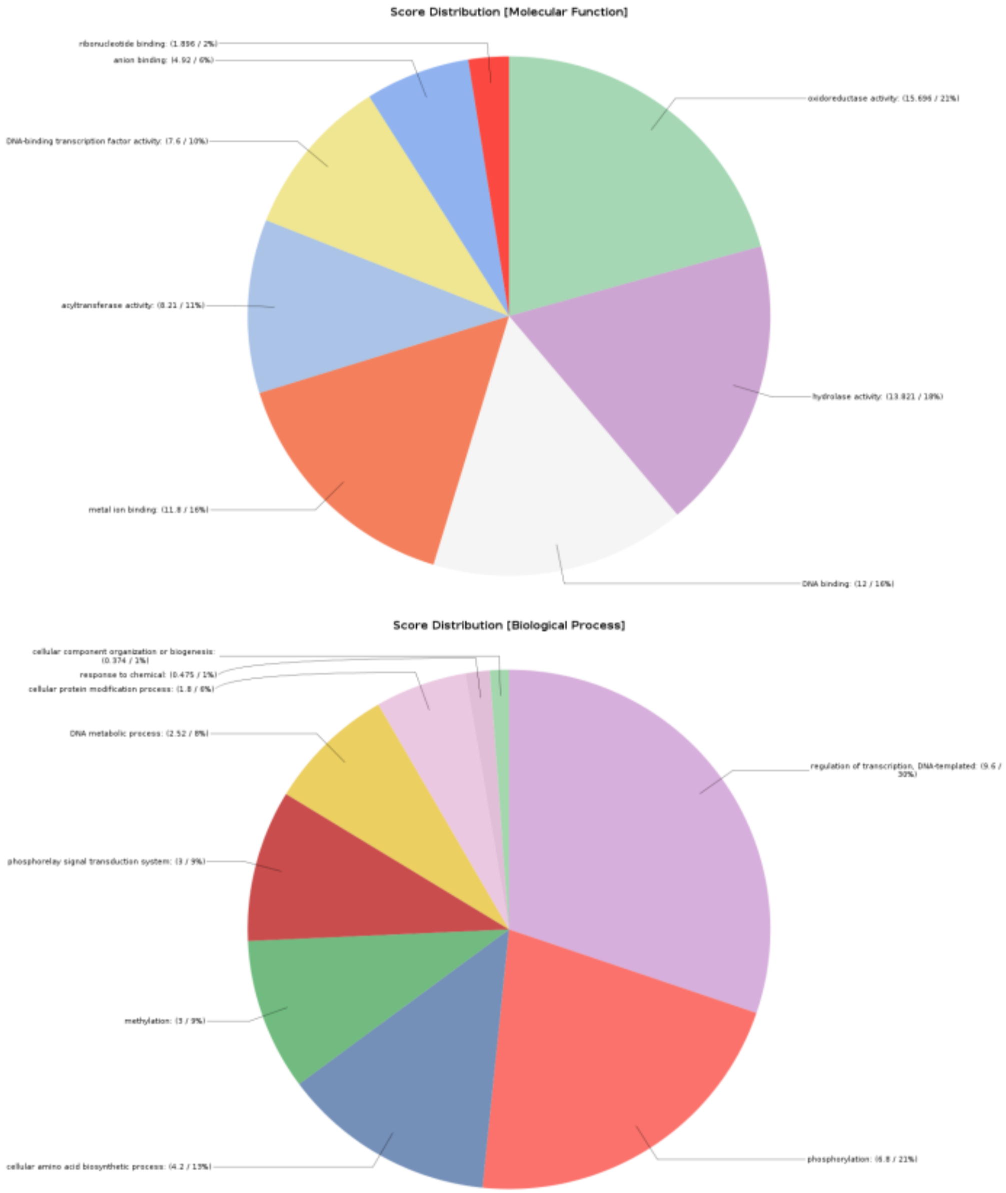
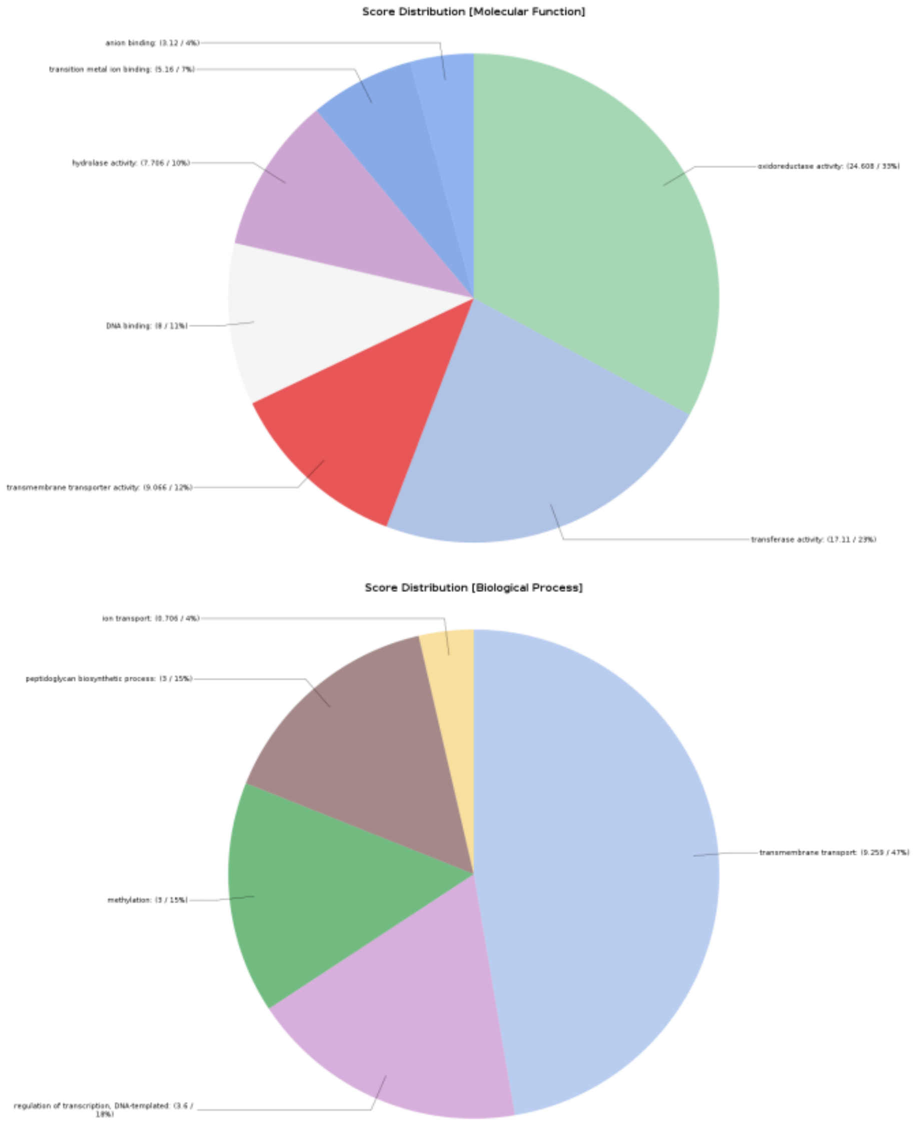


Figure 4.11:Blast2GO gene ontology assignments of up-regulated genes in Frankia inefficax exposed to biphenyl with glucose as an alternative carbon source.


Score Distribution [Molecular Function]

Score Distribution [Biological Process]

Figure 4.12: Blast2GO gene ontology assignments of down-regulated genes in Frankia inefficax exposed to biphenyl with glucose as an alternative carbon source.

Figure 4.13: Nodulation rates among biphenyl stressed and unstressed alder plants by atypical Frankia.

Table 4.1: Nodulation rates among biphenyl stressed and unstressed alder plants by atypical Frankia.

	0.1mM Biphenyl Stress		
Box #	***Nodules/Box***	***% Nodulated Plants***	***Nodules/Plant***
1	32	1.00	16.0
2	0	0.00	0.0
3	11	0.67	3.7
4	51	1.00	12.8
5	0	0.00	0.0
Average	**18.8**	**53.33**	**6.5**
	Unstressed		
1	0	0	0
2	0	0	0
3	0	0	0
4	0	0	0
Average	**0**	**0**	**0**

Discussion

This work shows that *Frankia* is resistant to biphenyl, 4-chlorobiphenyl, and dibenzofuran toxicity up to levels substantially higher than those typically found in contaminate soils. The concentration of dioxin-like compounds in environmental samples from disastrous point source events such as the Seveso factory explosion are still at or below 600 μg/m^2 annual deposition (Bertazzi et al. 1998). Long term soil concentrations of dioxins are typically in the pg/m^3 range. Higher environmental concentrations of less toxic non-chlorinated or mono-chlorinated congeners of biphenyl have been reported, sometimes as hight as 10,000 μg/cm^3. However, these are still well below the resistance limits determined in this work. This is especially true when considering the sorption of dioxin-like compounds to soil particles and the associated decrease in bioavailability.

These results also show that while *Frankia* strains without the *bph* operon (CN3) have some resistance to dioxin-like compounds, strains with the operon (*F. inefficax* and EUN1f) have substantially higher levels of resistance. Furthermore, both *Frankia* strains with the *bph* operon were able to grow with dioxin-like compounds as their only carbon and energy source and expressed key genes in the operon in response to biphenyl exposure. *Frankia* strain CN3 (which lacks the *bph* operon) was not able to grow on any of the three dioxin-like compounds tested without propionate as a supplemental carbon and energy source. Additionally, GC-FID results showed that both *Frankia inefficax* and *Frankia* strain EUN1f measurably degraded biphenyl.

Interestingly, while strain EUN1f was able to utilize biphenyl, 4-chlorobiphenyl, or dibenzofuran as a sole carbon and energy source, *F. inefficax* was only able grow with

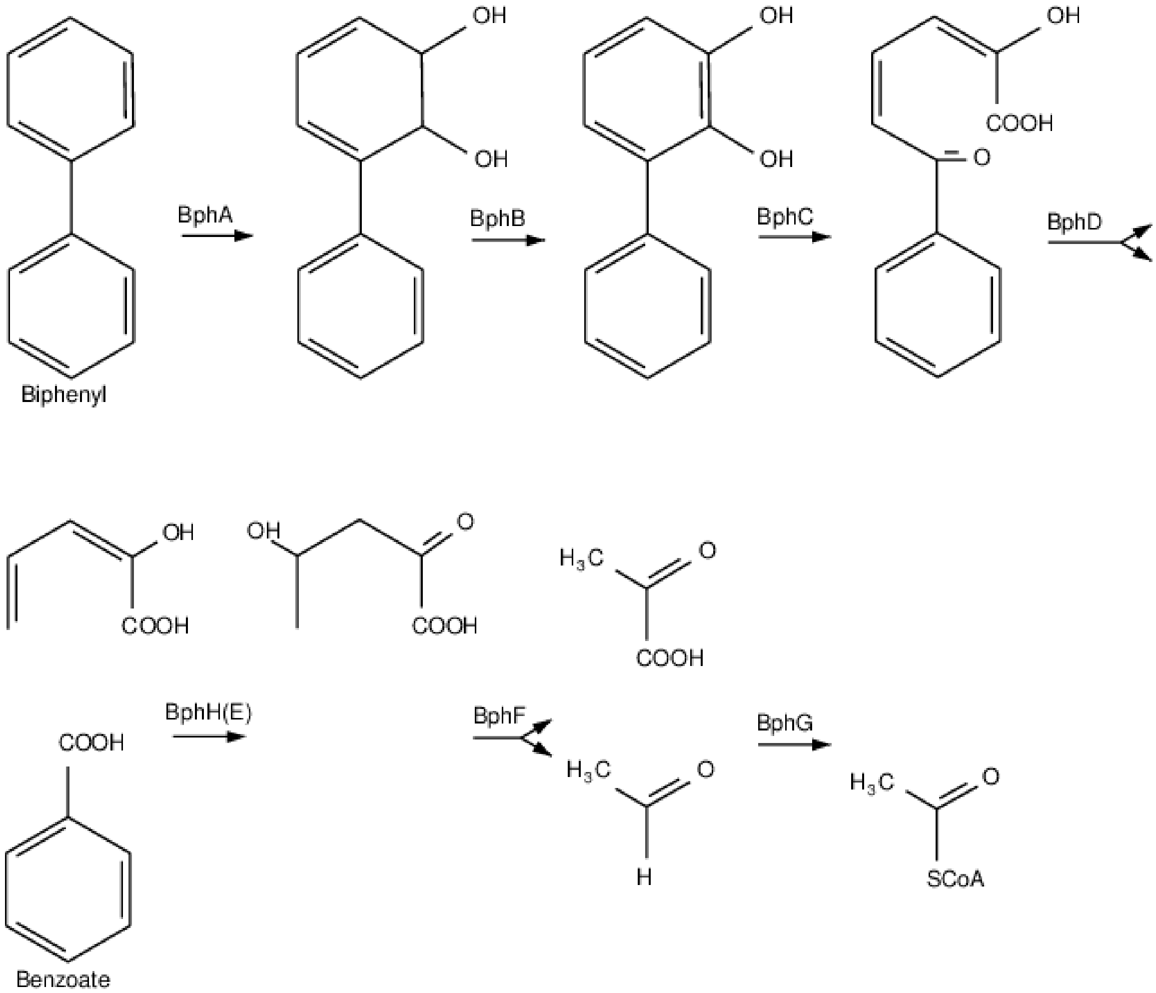


Figure 4.14: Proposed Dioxin-like compound (Biphenyl) degradation pathway based on

biphenyl and dibenzofuran as sole carbon and energy sources. This could be do to the differences in *bphA* or *bphH* between *Frankia inefficax* and *Frankia* strain EUN1f. The substrate specificity of the *bph* operon is largely determined by *bphA*, which performs the initial ring cleavage during the first stage of degradation. The first four genes (bphABCD) in the the *bph* operon convert biphenyl or another dioxin-like compound to benzoate in a process called the upper pathway. Studies have shown that the exact range of substrates a specific *bphA* enzyme is capable of cleaving is quite broad, and representative of the highly diverse assemblages of microbes that carry out degradation of naturally occurring dioxin-like compounds and polyaromatic compounds in nature. The *bph* operon is often flanked by transposase, and the *bphA* gene in *Frankia inefficax* separates phylogenetically from the *bphA* gene in *Frankia* strain EUN1f. Therefore, the difference we observed in substrate usage could be do to separate acquisition events between the two strains leading to different ring cleavage ranges. Alternatively, the absence of *bphH* in *Frankia inefficax* could results in a failure to convert the initial cleavage product into a usable energy source by truncating the lower pathway of the *bph* operon, conventionally defined as *bphEFG*. Additional accessory genes such as *bphK* have been shown to increase the efficacy of the *bph* operon by catalyzing the degradation of 4-chlorobenzoate, and *bphH,* which catalyzes an important step in the meta-cleavage branch of the pathway, could allow *Frankia* strain EUN1f to utilize chlorinated biphenyls in addition to non-chlorinated biphenyl and dibenzofuran.

Additionally, RNA sequencing results show that numerous other uncharacterized hypothetical genes with oxygenase and cytochrome motifs are upregulated under biphenyl-only growth conditions, suggesting that the incorporation of carbon and production of energy from dioxin-like compounds involves additional pathways and enzymes. *Frankia* exposed to biphenyl without a supplemental carbon source also increased transcription of *CorA*, a Mg^{2+} transmembrane transport gene. Magnesium is an important cofactor for a number of oxygenases involved in aromatic compound degradation, including *bphH.* A magnesium chelatase was also significantly up-regulated in both the RNA sequencing conditions.

Two additional genes up-regulated in biphenyl stressed *Frankia* without alternative carbon sources could facilitate the balancing of toxicity with energetic demands. *EmrB* and a putative inner membrane bound translocator were both significantly up-regulated in biphenyl stressed *Frankia.* A number of genes related to transposon or plasmid integration were also up-regulated in both conditions along with NusA and RecX. NusA has been associated with stress induced mutagenesis and RecX is involved stress induced DNA repair. Conversely, 4 different putative tetR-like repressors were down-regulated in both RNA sequencing conditions. The differential activity of these genes in response to dioxin-like compound stress could indicate a global cellular response to biphenyl stress, including facilitating the acquisition of novel resistance traits through horizontal gene transfer. Interestingly, the *bph* operon in *Frankia* is flanked by insertion sequences.

Blast2GO results also showed that many of the same categories of biological processes and molecular functions were differentially regulated in the biphenyl only samples and the biphenyl plus glucose samples. Similarly, many of the gene ontology groups that were represented in the set of up-regulated genes were also represented in the down-regulated genes. The high proportion of differentially regulated oxidoreductases, transmembrane transporters, and metal ion binding is consistent with a transition from growth utilizing a simple carbon and energy sources (glucose) to a more complex and toxic one such as biphenyl. Metal cofactors, transporters to uptake polar compounds, and additional reductive pathways are critical elements of alternative metabolic function.

Together, the work discussed here shows that multiple *Frankia* strains are resistant to dioxin-like compounds, and are able to degrade and utilize biphenyl, dibenzofuran, and 4-chlorobiphenyl as sole carbon and energy sources. The *bph* operon is necessary for dioxin-like compound utilization in *Frankia*, but many other genes appear to be involved. This is significant because it indicates that the *Frankia*-actinorhizal symbiosis could be used as a bioaugmentation system to remediate PCB contaminated sites, which exist around the world. Future work should address this potential in the field, and further investigate the role genes identified in this work could play in degradation.

Summary and Conclusions

Hydrocarbon pollution and the associated ecological damage and reduction of ecosystem services has an enormous negative impact on the ability of nearly all organisms ability to survive and flourish. The human toll associated with atmospheric hydrocarbon pollution is on the order of millions of deaths per year, and many more millions of people are negatively impacted by increased rates of many chronic illnesses and lost opportunity for work. In addition to reducing the sources of air, soil, and water pollution, remediation methods are needed to effectively address the scope of the pollution already present in environments around the world.

Microbial bioremediation has been considered a promising strategy for remediation for decades, and the extent of microbial metabolic diversity that could be applied to remediation efforts is now becoming even more apparent with second and third generation sequencing technologies. The catalog of genetic pathways that code for the degradation of compounds at one time considered dead-end xenobiotics is constantly expanding, supporting the proposed concept of microbial metabolic infallibility. Framing research with the idea that there is a microbe somewhere in the world that is able to metabolize every potential carbon source or molecular with redox potential is a motivating perspective. This work sought to take advantage of “microbial infallibility” and elucidate the potential role that *Frankia* and the actinorhizal symbiosis could play in toxic hydrocarbon remediation from the metagenomic, genomic, and molecular perspectives. In particular, this work focused on the potential ability of specific *Frankia* strains to degrade dioxin-like compounds and use them as both a carbon and an energy source.

Three primary aims were addressed within the overarching goal of expanding our understanding of resistance traits in microbial communities: 1.) to determine the pan-genome characteristics of *Frankia,* 2.) to survey the microbial diversity of ecological niches that contain the actinorhizal symbiosis, and 3.) to elucidate the potential ability of *Frankia* to degrade toxic dioxin-like compounds.

This work showed that both the *Frankia* and *Rhizobium* genera have an open pan-genome structure with Heap's alpha values below 1 (0.86 and 0.66 respectively). *Bradyrhizobium* on the other hand has a closed pan-genome with a Heap's alpha value of 1.05. The substantial difference between the genomic characteristics of *Bradyrhizobium* and *Rhizobium* is interesting given their close phylogenetic relationship and comparable nodulation functions. The variation in pan-genome characteristics within the *Frankia* genus is also interesting and suggests active divergence at the clade level. Particularly interesting the the fact that the *Frankia* clade with the most reduced genome size, clade 1C, is also the clade with the highest Heap's alpha value (2.00). Clade 1C *Frankia* are also one of the most restrictive clades in the *Frankia* genus in terms of host specificity. While each individual *Frankia* clade has a Heap's alpha values above 1, indicating a closed pan-genome structure, pan-genome analysis is heavily influenced by the number of strains considered, particularly when few genomes are analyzed. This could explain why the *Frankia* genus as a whole has a open pan-genome structure despite the closed pan-genomes of each clade.

The *Frankia* clade with the lowest Heap's alpha was clade 3 with a value of 1.53. *Frankia* strains in clade 3 also tend to have the largest genome size and the broadest host range. The contrast between *Frankia* clade 1C and 3 could illustrate their genomic divergence with clade 1C undergoing a period of genome reduction while clade 3 is rapidly acquiring new genetic information through horizontal gene transfer and expanding it's niche range. The ability to degrade dioxin-like compounds may be one example of this expansion since the *bph* operon in *Frankia* is flanked by transposon insertion sequences suggesting that it is a relatively recent gene acquisition. The *bph* operon in *Frankia* also appears to have been acquired at least twice since phylogenic analysis of the operon shows two distinct lineages.

This work also found that actinorhizal nodules on *Coriaria myrtifolia* plants contain a diverse microbial assemblage rather than being dominated by *Frankia* as previously thought. This is corroborates other recent metagenomics studies that have identified a broad range of species in actinorhizal nodules (D'Angelo et al. 2016). The diversity of bacteria found in *Frankia* nodules suggests the potential for considerable trans-species processes in the nodule. Some evidence of these functions has previously been found associated with *Nocardia* sp. strains (Tisa, unpublished data). *Nocardia-Frankia* co-infections of actinorhizal plants increased nodulation efficacy indicating a trans-species interaction that benefits the actinorhizal symbiosis. The cosmopolitan nature of the actinorhizal symbiosis may also help explain why some *Frankia* isolates are unable to reinfect the plant host species that they were isolated from and how some *Frankia* strains have remained stable without nitrogen fixing *Nif* genes. The role of cooperative metabolic processes and nodulation among *Frankia* sp. strains and between *Frankia* and other members of the *Frankia* nodule community should be an area of continued research.

In addition to the diversity of actinorhizal communities themselves, this work surveyed the diversity of microbial communities associated with the actinorhizal symbiosis. Sequencing results showed that *C. myrtifolia* structures (leaves, stems, fruit, roots, and nodules) have distinct and diverse communities and that the *C. myrtifolia* roots and rhizosphere appeared to influence the microbial diversity of nearby bulk soil. However, the analysis of *C. myrtifolia* was limited by the lack of associated environmental data about the physical and chemical characteristics of the soil and plant tissues surveyed. Future analysis should include soil and plant tissue analysis to measure nitrogen and plant secondary compounds to begin differentiating between microbial population structuring by other microbes and microbial population structuring by host plants. The presence and concentration of phenolic root exudates would be especially interesting to link to microbial population structuring giving their similarity to some toxic pollutants. Members of the *Frankia* genus contain multiple pathways for the degradation of aromatic compounds including naphthalene, biphenyl, and dibenzofuran (Baker et al. 2015, this study). Metabolizing aromatic compounds either to neutralize any associated toxicity or as supplementary carbon source would be a selective pressure that could explain the presence of degradation pathways in *Frankia* and guide future investigation into bacterial bioremediation.

The ability of *F. inefficax* and *Frankia* sp. strain EUN1f to degrade dioxin-like compounds and utilize them as a sole carbon and energy source is a major finding of this work. Our results showed that *F. inefficax* is able to grow with biphenyl and dibenzofuran as sole carbon and energy sources, and that *Frankia* sp. strain EUN1f is able to grow with biphenyl, 4-chlorobiphenyl, or dibenzofuran as a sole carbon and energy. Additionally, this work showed that the *bph* operon in *F. inefficax* and *Frankia* strain EUN1f is highly up-regulated in response to biphenyl exposure, with peak expression 3 days after initial exposure. Gas-Chromatography results showed that biphenyl concentrations in *Frankia* cultures where also reduced from 1mM down to the detection limit of the assay in three days. These results strongly indicate that *F. inefficax* a *Frankia* strain EUN1f are both able to break down dioxin-like compounds and both rely on the *bph* operon to carry out the transformation. This indicates that the additional *Frankia* strains with the *bph* operon and other desirable traits could be used in a variety of dioxin-like compound remediation contexts. Recently developed techniques to transform *Frankia* (Pesce et al. 2019) could also be used to insert the *bph* operon into *Frankia* strains with specific actinorhizal host plants or additional remediation abilities.

The unique attributes of the *Frankia*-actinorhizal symbiosis amplify potential bioremediation applications with *Frankia* strains. Actinorhizal plants are already used in soil stabilization and reclamation projects around the world, including remediation efforts in Canadian tar sands areas contaminated with a aromatic compounds. The remediation ability of *Frankia* spp. strains combined with the persistence of *Frankia* bacteria in soil surrounding actinorhizal plants overcomes one of the major challenges associated with bacterial bioremediation: maintaining a population of remediating bacteria in a contaminated area.

Future Directions

Future work should advance this research to include field or mesocosm studies of dioxin-like compound remediation by the *Frankia*-actinorhizal symbiosis. Additionally, future studies should merge the approaches implemented in this work to gain a more comprehensive understanding of the ecology and remediation efficacy of microbial communities in contaminated soils. Directly linking shotgun metagenomic analysis with more detailed environmental data would help explain how abiotic factors structure the microbial community in polluted soil.

Appendix A

Frankia GCA Number	Frankia Strain Name	Clade	Accession Number
GCA_001414035.1	ACN1ag	1A	SAMN03353435
GCA_001421075.1	CpI1_p	1A	SAMN02798501
GCA_001756285.1	CgIM4	1A	SAMN04196701
GCA_000262465.1	QA3	1A	SAMN02256510
GCA_000948395.1	CpI1_S	1A	SAMN02798190
GCA_001420875.1	AvcI1	1A	SAMN03360499
GCA_001636575.1	BR	1C	SAMN03579665
GCA_001854725.1	CgIS1	1C	SAMN04211879
GCA_001983015.1	CcI156	1C	SAMN04211878
GCA_002099325.1	KB5	1C	SAMN04962126
GCA_002099355.1	Cg70_9	1C	SAMN03360501
GCA_004405155.1	B2	1C	SAMN11038663
GCA_000611815.2	Thr	1C	SAMN02639461
GCA_000733325.1	Allo2	1C	SAMN02344566
GCA_000685765.2	BMG5_23	1C	SAMN02338736
GCA_000503735.2	CcI6	1C	SAMN02216979
GCA_000732115.1	CeD	1C	SAMN02344567
GCA_000013345.1	CcI3	1C	SAMN02199398
GCA_001017755.1	BMG5_1	2	SAMN03121018
GCA_000177615.2	Dg1	2	SAMN00713636
GCA_001983005.1	BMG5_30	2	SAMN04851312
GCA_900635395.1	Cj1_Dg_vc	2	SAMEA5187594
GCA_900634755.1	Cm1_Cm_nod	2	SAMEA5176174
GCA_900634785.1	Cm1_Dg_nod	2	SAMEA5176885
GCA_900634735.1	Cppng1_Ca_nod	2	SAMEA5176171
GCA_900634745.1	Cv1_Ct_nod1	2	SAMEA5176172
GCA_900634715.1	Dd1_Dg_vc	2	SAMEA5176170
GCA_900634705.1	Dg1_Dg_nod2	2	SAMEA5176169
GCA_001306465.1	R43	3	SAMN03463641
GCA_001636565.1	EI5c	3	SAMN03353334
GCA_000177675.1	EUN1f	3	SAMN02441797
GCA_000018005.1	EAN1pec	3	SAMN02598325
GCA_001854655.1	Cc1_17	3	SAMN02343076
GCA_001854695.1	NRRL_B_16219	3	SAMN04851309
GCA_001983215.1	CcI49	3	SAMN04211910
GCA_000373365.1	BCU110501	3	SAMN02441714
GCA_000374165.1	BMG5_12	3	SAMN02440438

GCA_004337455.1	BMG5_11	3	SAMN04856672
GCA_001536285.1	G2	3	SAMN04233181
GCA_000166135.1	EuI1c	4	SAMN02232023
GCA_001854805.1	BMG5_36	4	SAMN04851314
GCA_001854645.1	EUN1h	4	SAMN04851311
GCA_001983105.1	NRRL_B_16386	4	SAMN04851310
GCA_000235425.3	CN3	4	SAMN02256511
GCA_000966285.1	DC12	4	SAMN00114978

Rhizobium Strain	**Accession Number**	**Bradyrhizobium Strain**	**Accession Number**
N1341	SAMN03998639	amphicarpaeae 39S1MB	SAMN07448754
Phaseoli N261	SAMN03998625	guangdongense CCBAU 51649	SAMN02415993
phaseoli N831	SAMN03998628	KBS0725	SAMN11620955
N731	SAMN03998643	symbiodeficiens 85S1MB	SAMN07448748
phaseoli N161	SAMN03998624	SG09	SAMD00179679
phaseoli R744	SAMN03998636	japonicum E109	SAMN03262953
phaseoli R630	SAMN03998633	diazoefficiens USDA110	SAMD00061083
phaseoli R723	SAMN03998635	betea PL7HG1	SAMN12900461
phaseoli R620	SAMN03998632	ORS278	SAMEA3138227
esperanzae N561	SAMN03998640	cosmicum 58S1	SAMN12262001
phaseoli N931	SAMN03998630	diazoefficiens NK6	SAMD00022775
N1314	SAMN03998638	BF49	SAMEA3647810
N621	SAMN03998641	japonicum USDA 6	SAMD00060992
N113	SAMN03998637	LCT2	SAMN10475296
phaseoli N671	SAMN03998626	symbiodeficiens 65S1MB	SAMN12079237
phaseoli R650	SAMN03998634	cosmicum S23321	SAMD00060998
phaseoli N771	SAMN03998627	ORS 285	SAMEA103957792
phaseoli N841	SAMN03998629	diazoefficiens XF7	SAMN09205184
phaseoli R611	SAMN03998631	CCGE-LA001	SAMN02469422
N6212	SAMN03998642	diazoefficiens 110spc4	SAMN10141985
N324	SAMN03998646	diazoefficiens USDA 110	SAMN03573437
N871	SAMN03998645	oligotrophicum S58	SAMD00061052
N741	SAMN03998644	SK17	SAMN08116651
leguminosarum Vaf10	SAMN05285389	diazoefficiens USDA 122	SAMN04191488

S41	SAMN05323143	elkanii USDA 61	SAMD00067082
Kim5	SAMN02469451	japonicum J5	SAMN05890661
phaseoli Brazil 5	SAMN02469449	guangdongense CCBAU 51670	SAMN03459144
CIAT894	SAMN02469455	vignae ORS3257	SAMEA104196492
leguminosarum Vaf-108	SAMN05990783	symbiodeficiens 141S2	SAMN14365434
etli 8C-3	SAMN04017682	BTAi1	SAMN02598359
gallicum IE4872	SAMN04010568	KBS0727	SAMN11620956
etli CIAT 652	SAMN02603107	63S1MB	SAMN14355123
NXC14	SAMN06767451	icense LMTR 13	SAMN05230120
TAL182	SAMN05928285	TM102	SAMD00179693
etli NXC12	SAMN06767430	1S3	SAMN14174716
leguminosarum WSM2304	SAMN00000679	diazoefficiens 172S4	SAMN14364959
leguminosarum BIHB 1148	SAMN04849238	ottawaense OO99	SAMN07448707
leguminosarum BIHB 1217	SAMN07414824	CCBAU 051011	SAMN03459128
11515TR	SAMN07522840	symbiodeficiens 101S1MB	SAMN14365685
leguminosarum WSM1325	SAMN00000703		
acidisoli FH23	SAMN07627169		
ACO-34A	SAMN06830640		
Y9	SAMN05958282		
NXC24	SAMN07823526		
leguminosarum UPM791	SAMN07965043		
leguminosarum Norway	SAMN07985393		
leguminosarum ATCC 14479	SAMN09255527		
tropici CIAT 899	SAMN02604105		
jaguaris CCGE525	SAMN10118526		
CCGE532	SAMN10118470		
CCGE531	SAMN10118218		
etli Mim1	SAMN02603105		
leguminosarum WSM1689	SAMN02769650		
leguminosarum CB782	SAMN02769652		
pusense CFBP5875	SAMN11489452		
NIBRBAC000502774	SAMN12098111		

IE4771	SAMN02423216
WL3	SAMN12513120
gallicum R602	SAMN02393724
etli CFN 42	SAMN02603106
Leguminosarum 3841	SAMEA1705944
grahamii BG7	SAMN12661675
bafiediae NT-26	SAMEA3283108
TCK	SAMEA104296050
YW14	SAMEA104296051
Khangiran2	SAMEA104296052
pusense IRBG74	SAMEA3138824

Appendix B

Table 3.1: Genus level Simper analysis results for the microbiome of C. myrtifolia rhizosphere and nearby soil. Taxa are listed as assigned by QIMME2 at level 6 (L6). Average and cumsum scores for each pair of sample types are listed below the labeled headers. Average refers to average contribution to dissimilarity for a given taxa and cumsum refers to the cumulative sum of dissimilarity for all taxa listed above a give row.

Rhizosphere vs. 100m

	average	cumsum
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Lawsonella	0.167	0.243
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Solirubrobacter	0.035	0.295
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_67-14_67-14	0.034	0.345
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_uncultured	0.012	0.363
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Nitrosomonadaceae_MND1	0.011	0.378
Bacteria_Actinobacteriota_Rubrobacteria_Rubrobacterales_Rubrobacteriaceae_Rubrobacter	0.010	0.393
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_uncultured	0.010	0.408
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_	0.009	0.422
Bacteria_Acidobacteriota_Acidobacteriae_Subgroup2_Subgroup2_Subgroup2	0.009	0.435
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_uncultured_uncultured	0.009	0.448
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Blastococcus	0.008	0.459
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_	0.006	0.468
Bacteria_Actinobacteriota_Thermoleophilia_Gaiellales_Gaiellaceae_Gaiella	0.006	0.477
Bacteria_Acidobacteriota_Vicinamibacteria_Vicinamibacterales_Vicinamibacteraceae_Vicinamibacteraceae	0.006	0.485
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_Pedosphaeraceae	0.006	0.493
Bacteria_Acidobacteriota_Vicinamibacteria_Vicinamibacterales_uncultured_uncultured	0.005	0.501
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_TRA3-20_TRA3-20	0.005	0.509
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Pseudonocardia	0.005	0.516
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Conexibacter	0.005	0.524
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingomonas	0.005	0.531
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_	0.005	0.539
Bacteria_Acidobacteriota_Blastocatellia_Pyrinomonadales_Pyrinomonadaceae_RB41	0.005	0.546
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_uncultured	0.005	0.553
Bacteria_Actinobacteriota_Acidimicrobiia___	0.005	0.560
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Crossiella	0.005	0.567
Bacteria_Actinobacteriota_Thermoleophilia_Gaiellales_uncultured_uncultured	0.005	0.574
Bacteria_Acidobacteriota_Acidobacteriae_Bryobacterales_Bryobacteraceae_Bryobacter	0.004	0.580
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Nitrosomonadaceae_Ellin6067	0.004	0.586
Bacteria_Actinobacteriota_Actinobacteria_Micromonosporales_Micromonosporaceae_	0.004	0.592
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Microvirga	0.004	0.597
Bacteria_Proteobacteria_Gammaproteobacteria_Steroidobacterales_Steroidobacteraceae_Steroidobacter	0.004	0.603
Bacteria_Gemmatimonadota_S0134terrestrialgroup_S0134terrestrialgroup_S0134terrestrialgroup_S0134terrestrialgroup	0.004	0.608
Bacteria_Myxococcota_Polyangia_Haliangiales_Haliangiaceae_Haliangium	0.003	0.613
Bacteria_Myxococcota_Polyangia_Polyangiales_Sandaracinaceae_uncultured	0.003	0.618
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_uncultured_uncultured	0.003	0.623
Bacteria_Proteobacteria_Gammaproteobacteria_GammaproteobacteriaIncertaeSedis_UnknownFamily_Acidibacter	0.003	0.628
Bacteria_Actinobacteriota_Actinobacteria_0319-7L14_0319-7L14_0319-7L14	0.003	0.632

Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_Gemmatimonas	0.003	0.637
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Geodermatophilus	0.003	0.642
Bacteria_Acidobacteriota_Holophagae_Subgroup7_Subgroup7_Subgroup7	0.003	0.647
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Microscillaceae_uncultured	0.003	0.651
Bacteria_Proteobacteria_Gammaproteobacteria_CCD24_CCD24_CCD24	0.003	0.656
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Parviterribacter	0.003	0.660
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales__	0.003	0.664
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonadaceae_Rheinheimera	0.003	0.668
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_	0.003	0.672
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_YC-ZSS-LKJ147	0.003	0.676
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Acidothermaceae_Acidothermus	0.003	0.679
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Rubellimicrobium	0.002	0.683
Bacteria_Acidobacteriota_Thermoanaerobaculia_Thermoanaerobaculales_Thermoanaerobaculaceae_Subgroup10	0.002	0.686
Bacteria_Myxococcota_Polyangia_Polyangiales_BIrii41_BIrii41	0.002	0.689
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Saprospiraceae_uncultured	0.002	0.693
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Occallatibacter	0.002	0.696
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Phormidiaceae_TychonemaCCAP1459-11B	0.002	0.699
Bacteria_Nitrospirota_Nitrospiria_Nitrospirales_Nitrospiraceae_Nitrospira	0.002	0.702
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_uncultured	0.002	0.705
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_	0.002	0.708
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Granulicella	0.002	0.711
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_uncultured	0.002	0.714
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Nakamurellaceae_Nakamurella	0.002	0.717
Bacteria_Myxococcota_Myxococcia_Myxococcales_Myxococcaceae_	0.002	0.720
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_Ellin517	0.002	0.723
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Nocardioides	0.002	0.725
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Beutenbergiaceae_Beutenbergia	0.002	0.728
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Hyphomonadaceae_SWB02	0.002	0.730
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Aeromicrobium	0.002	0.733
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Cellulomonadaceae_Cellulomonas	0.002	0.736
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Chthoniobacterales_Chthoniobacteraceae_CandidatusUdaeobacter	0.002	0.738
Bacteria_Chloroflexi_TK10_TK10_TK10_TK10	0.002	0.741
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Arthrobacter	0.002	0.743
Bacteria_Proteobacteria_Gammaproteobacteria___	0.002	0.745
Bacteria_Proteobacteria_Alphaproteobacteria_Dongiales_Dongiaceae_Dongia	0.002	0.748
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Terrimonas	0.002	0.750
Bacteria_Actinobacteriota_Actinobacteria_Micromonosporales_Micromonosporaceae_Krasilnikovia	0.002	0.753
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Bradyrhizobium	0.002	0.755
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Flavisolibacter	0.002	0.757
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Bacillus	0.002	0.760
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Hyphomonadaceae_Hirschia	0.002	0.762
Bacteria_Myxococcota_bacteriap25_bacteriap25_bacteriap25_bacteriap25	0.002	0.764
Archaea_Crenarchaeota_Nitrososphaeria_Nitrososphaerales_Nitrososphaeraceae_CandidatusNitrocosmicus	0.002	0.767
Bacteria_Proteobacteria_Gammaproteobacteria_PLTA13_PLTA13_PLTA13	0.002	0.769
Bacteria_____	0.002	0.771
Bacteria_Chloroflexi_KD4-96_KD4-96_KD4-96_KD4-96	0.001	0.773
Bacteria_Planctomycetota_Phycisphaerae_Tepidisphaerales_WD2101soilgroup_WD2101soilgroup	0.001	0.775
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Alcaligenaceae_	0.001	0.777

Bacteria_Planctomycetota_OM190_OM190_OM190_OM190	0.001	0.779
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_uncultured	0.001	0.782
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobium	0.001	0.784
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_Mitochondria_Mitochondria	0.001	0.786
Bacteria_Firmicutes_Bacilli_Alicyclobacillales_Alicyclobacillaceae_Tumebacillus	0.001	0.788
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_KF-JG30-B3_KF-JG30-B3	0.001	0.790
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_	0.001	0.792
Bacteria_Gemmatimonadota_BD2-11terrestrialgroup_BD2-11terrestrialgroup_BD2-11terrestrialgroup_BD2-11terrestrialgroup	0.001	0.794
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Actinophytocola	0.001	0.796
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_env.OPS17_env.OPS17	0.001	0.798
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Massilia	0.001	0.800
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Hyphomicrobiaceae_	0.001	0.802
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_uncultured_uncultured	0.001	0.803
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_	0.001	0.805
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Psychroglaciecola	0.001	0.807
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Ramlibacter	0.001	0.809
Bacteria_Acidobacteriota_Acidobacteriae_Solibacterales_Solibacteraceae_CandidatusSolibacter	0.001	0.811
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_Aridibacter	0.001	0.813
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Chthoniobacterales_Chthoniobacteraceae_Chthoniobacter	0.001	0.814
Bacteria_Actinobacteriota_MB-A2-108_MB-A2-108_MB-A2-108_MB-A2-108	0.001	0.816
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_	0.001	0.818
Bacteria_Firmicutes_Bacilli_Bacillales__	0.001	0.819
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Novosphingobium	0.001	0.821
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_uncultured	0.001	0.823
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_uncultured	0.001	0.825
Bacteria_Acidobacteriota_Blastocatellia_11-24_11-24_11-24	0.001	0.826
Bacteria_Desulfobacterota_uncultured_uncultured_uncultured_uncultured	0.001	0.828
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Devosiaceae_Devosia	0.001	0.829
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Puia	0.001	0.831
Bacteria_Bdellovibrionota_Oligoflexia_0319-6G20_0319-6G20_0319-6G20	0.001	0.833
Bacteria_Planctomycetota_vadinHA49_vadinHA49_vadinHA49_vadinHA49	0.001	0.834
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Ellin6055	0.001	0.836
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_Craurococcus-Caldovatus	0.001	0.837
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Opitutales_Opitutaceae_Lacunisphaera	0.001	0.839
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Microscillaceae_Ohtaekwangia	0.001	0.840
Bacteria_Actinobacteriota_Acidimicrobiia_uncultured_uncultured_uncultured	0.001	0.842
Bacteria_Myxococcota_Polyangia_Polyangiales_Phaselicystidaceae_Phaselicystis	0.001	0.843
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Opitutales_Opitutaceae_Opitutus	0.001	0.845
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobiaceae	0.001	0.846
Bacteria_RCP2-54_RCP2-54_RCP2-54_RCP2-54_RCP2-54	0.001	0.848
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Edaphobaculum	0.001	0.849
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_Sphingobacteriaceae_Mucilaginibacter	0.001	0.851
Bacteria_Actinobacteriota_Acidimicrobiia_IMCC26256_IMCC26256_IMCC26256	0.001	0.852
Bacteria_Proteobacteria_Gammaproteobacteria_Steroidobacterales_Steroidobacteraceae_uncultured	0.001	0.853
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Ferruginibacter	0.001	0.855
Bacteria_Proteobacteria_Gammaproteobacteria_WD260_WD260_WD260	0.001	0.856
Bacteria_NB1-j_NB1-j_NB1-j_NB1-j_NB1-j	0.001	0.857
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Phenylobacterium	0.001	0.858

Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_Blastocatella	0.001	0.860
Bacteria_Firmicutes_Bacilli_Bacillales_Planococcaceae_	0.001	0.861
Bacteria_Cyanobacteria_Cyanobacteriia_Chloroplast_Chloroplast_Chloroplast	0.001	0.862
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Rhodanobacteraceae_uncultured	0.001	0.864
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Acidipila	0.001	0.865
Bacteria_Acidobacteriota_Subgroup5_Subgroup5_Subgroup5_Subgroup5	0.001	0.866
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_ADurb.Bin063-1	0.001	0.867
Bacteria_Proteobacteria_Alphaproteobacteria_uncultured_uncultured_uncultured	0.001	0.868
Bacteria_Myxococcota_Polyangia_Polyangiales_Polyangiaceae_Pajaroellobacter	0.001	0.870
Bacteria_Proteobacteria_Gammaproteobacteria_JG36-TzT-191_JG36-TzT-191_JG36-TzT-191	0.001	0.871
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Altererythrobacter	0.001	0.872
Bacteria_Actinobacteriota_Acidimicrobiia_Microtrichales_uncultured_uncultured	0.001	0.873
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Roseiarcus	0.001	0.874
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.001	0.875
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Sporichthyaceae_uncultured	0.001	0.877
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_PMMR1	0.001	0.878
Bacteria_Planctomycetota_Planctomycetes_Gemmatales_Gemmataceae_uncultured	0.001	0.879
Bacteria_Chloroflexi_Chloroflexia_Kallotenuales_AKIW781_AKIW781	0.001	0.880
Bacteria_Chloroflexi_Gitt-GS-136_Gitt-GS-136_Gitt-GS-136_Gitt-GS-136	0.001	0.881
Unassigned_____	0.001	0.882
Bacteria_Actinobacteriota_Acidimicrobiia_Microtrichales_Iamiaceae_Iamia	0.001	0.883
Bacteria_Myxococcota_Polyangia_Polyangiales_Polyangiaceae_uncultured	0.001	0.884
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_uncultured	0.001	0.886
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Mycobacteriaceae_Mycobacterium	0.001	0.887
Bacteria_Actinobacteriota_Acidimicrobiia_Microtrichales_Ilumatobacteraceae_uncultured	0.001	0.888
Bacteria_Proteobacteria_Alphaproteobacteria_Azospirillales_Azospirillaceae_Skermanella	0.001	0.889
Bacteria_Actinobacteriota_Actinobacteria_Kineosporiales_Kineosporiaceae_	0.001	0.890
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_Stenotrophobacter	0.001	0.891
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Rhodanobacteraceae_Ahniella	0.001	0.892
Bacteria_Proteobacteria_Gammaproteobacteria_R7C24_R7C24_R7C24	0.001	0.893
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Ensifer	0.001	0.894
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Actinomycetospora	0.001	0.895
Bacteria_Proteobacteria_Alphaproteobacteria_Tistrellales_Geminicoccaceae_CandidatusAlysiosphaera	0.001	0.896

Rhizosphere vs. 1000m

	average	cumsum
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_67-14_67-14	0.028	0.060
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Solirubrobacter	0.024	0.109
Bacteria_Actinobacteriota_Rubrobacteria_Rubrobacterales_Rubrobacteriaceae_Rubrobacter	0.011	0.133
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Blastococcus	0.010	0.153
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_	0.009	0.173
Bacteria_Acidobacteriota_Acidobacteriae_Subgroup2_Subgroup2_Subgroup2	0.009	0.191
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_uncultured_uncultured	0.008	0.207
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_uncultured	0.008	0.223
Bacteria_Actinobacteriota_Thermoleophilia_Gaiellales_uncultured_uncultured	0.007	0.238
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_uncultured	0.007	0.253
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Nitrosomonadaceae_MND1	0.007	0.267
Bacteria_Actinobacteriota_Actinobacteria_Streptomycetales_Streptomycetaceae_Streptomyces	0.006	0.280
Bacteria_Actinobacteriota_Thermoleophilia_Gaiellales_Gaiellaceae_Gaiella	0.006	0.292

Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_uncultured	0.005	0.303
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Crossiella	0.005	0.314
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Conexibacter	0.005	0.324
Bacteria_Acidobacteriota_Vicinamibacteria_Vicinamibacterales_Vicinamibacteraceae_Vicinamibacteraceae	0.005	0.333
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_Pedosphaeraceae	0.004	0.343
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_TRA3-20_TRA3-20	0.004	0.351
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Pseudonocardia	0.004	0.359
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_	0.004	0.368
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales__	0.004	0.375
Bacteria_Actinobacteriota_Actinobacteria_0319-7L14_0319-7L14_0319-7L14	0.004	0.383
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Nitrosomonadaceae_Ellin6067	0.003	0.390
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Geodermatophilus	0.003	0.397
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_Gemmatimonas	0.003	0.404
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Parviterribacter	0.003	0.410
Bacteria_Actinobacteriota_Acidimicrobiia___	0.003	0.417
Bacteria_Acidobacteriota_Vicinamibacteria_Vicinamibacterales_uncultured_uncultured	0.003	0.423
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Ellin6055	0.003	0.430
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Microvirga	0.003	0.436
Bacteria_Myxococcota_Polyangia_Haliangiales_Haliangiaceae_Haliangium	0.003	0.442
Bacteria_Gemmatimonadota_S0134terrestrialgroup_S0134terrestrialgroup_S0134terrestrialgroup_S0134terrestrialgroup	0.003	0.448
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingomonas	0.003	0.454
Bacteria_Myxococcota_Polyangia_Polyangiales_Sandaracinaceae_uncultured	0.003	0.460
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Actinomycetospora	0.003	0.465
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_uncultured	0.003	0.471
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Phormidiaceae_TychonemaCCAP1459-11B	0.003	0.477
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_YC-ZSS-LKJ147	0.003	0.482
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_	0.003	0.488
Bacteria_Proteobacteria_Gammaproteobacteria_CCD24_CCD24_CCD24	0.003	0.493
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Chthoniobacterales_Chthoniobacteraceae_CandidatusUdaeobacter	0.003	0.499
Bacteria_Acidobacteriota_Blastocatellia_Pyrinomonadales_Pyrinomonadaceae_RB41	0.003	0.504
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Arthrobacter	0.003	0.510
Bacteria_Actinobacteriota_Actinobacteria_Micromonosporales_Micromonosporaceae_	0.003	0.515
Bacteria_Proteobacteria_Gammaproteobacteria_Steroidobacterales_Steroidobacteraceae_Steroidobacter	0.002	0.520
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Microscillaceae_uncultured	0.002	0.526
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Rubellimicrobium	0.002	0.531
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Pseudomonadaceae_Pseudomonas	0.002	0.536
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Acidipila	0.002	0.541
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Acidothermaceae_Acidothermus	0.002	0.546
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_	0.002	0.551
Bacteria_Actinobacteriota_MB-A2-108_MB-A2-108_MB-A2-108_MB-A2-108	0.002	0.556
Bacteria_Proteobacteria_Gammaproteobacteria_GammaproteobacteriaIncertaeSedis_UnknownFamily_Acidibacter	0.002	0.561
Bacteria_Acidobacteriota_Acidobacteriae_Bryobacterales_Bryobacteraceae_Bryobacter	0.002	0.566
Bacteria_Firmicutes_Bacilli_Bacillales__	0.002	0.571
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Granulicella	0.002	0.576
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Bacillus	0.002	0.581
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Massilia	0.002	0.585
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_	0.002	0.590
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_uncultured_uncultured	0.002	0.594

Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobium	0.002	0.599
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_	0.002	0.603
Bacteria_Actinobacteriota_Thermoleophilia_uncultured_uncultured_uncultured	0.002	0.607
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Sporichthyaceae_uncultured	0.002	0.611
Bacteria_Chloroflexi_KD4-96_KD4-96_KD4-96_KD4-96	0.002	0.615
Bacteria_Myxococcota_Polyangia_Polyangiales_BIrii41_BIrii41	0.002	0.620
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Nocardioides	0.002	0.624
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Cellulomonadaceae_Cellulomonas	0.002	0.628
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Aeromicrobium	0.002	0.632
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_uncultured	0.002	0.635
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Saprospiraceae_uncultured	0.002	0.639
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Actinophytocola	0.002	0.643
Bacteria_Actinobacteriota_Acidimicrobiia_uncultured_uncultured_uncultured	0.002	0.647
Bacteria_Chloroflexi_TK10_TK10_TK10_TK10	0.002	0.650
Archaea_Crenarchaeota_Nitrososphaeria_Nitrososphaerales_Nitrososphaeraceae_CandidatusNitrocosmicus	0.002	0.654
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Psychroglaciecola	0.002	0.657
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Hyphomonadaceae_SWB02	0.002	0.660
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Hyphomicrobiaceae_Hyphomicrobium	0.002	0.664
Bacteria_Firmicutes_Bacilli_Alicyclobacillales_Alicyclobacillaceae_Tumebacillus	0.002	0.667
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Occallatibacter	0.002	0.670
Bacteria_Proteobacteria_Alphaproteobacteria_Dongiales_Dongiaceae_Dongia	0.002	0.674
Bacteria_Acidobacteriota_Holophagae_Subgroup7_Subgroup7_Subgroup7	0.002	0.677
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_Ellin517	0.002	0.680
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_	0.002	0.683
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_uncultured	0.002	0.687
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Devosiaceae_Devosia	0.001	0.690
Bacteria_Acidobacteriota_Thermoanaerobaculia_Thermoanaerobaculales_Thermoanaerobaculaceae_Subgroup10	0.001	0.693
Bacteria_Proteobacteria_Alphaproteobacteria_Elsterales_uncultured_uncultured	0.001	0.696
Bacteria_Proteobacteria_Gammaproteobacteria_PLTA13_PLTA13_PLTA13	0.001	0.699
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Flavisolibacter	0.001	0.702
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_KF-JG30-B3_KF-JG30-B3	0.001	0.705
Bacteria_Planctomycetota_Phycisphaerae_Tepidisphaerales_WD2101soilgroup_WD2101soilgroup	0.001	0.707
Bacteria_Acidobacteriota_Acidobacteriae_Solibacterales_Solibacteraceae_CandidatusSolibacter	0.001	0.710
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_Mitochondria_Mitochondria	0.001	0.713
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Ferruginibacter	0.001	0.716
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_	0.001	0.719
Bacteria_Myxococcota_Myxococcia_Myxococcales_Myxococcaceae_	0.001	0.721
Bacteria_RCP2-54_RCP2-54_RCP2-54_RCP2-54_RCP2-54	0.001	0.724
Bacteria_Nitrospirota_Nitrospiria_Nitrospirales_Nitrospiraceae_Nitrospira	0.001	0.727
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Hyphomicrobiaceae_	0.001	0.729
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_uncultured_uncultured	0.001	0.732
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Altererythrobacter	0.001	0.735
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Hyphomonadaceae_Hirschia	0.001	0.738
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_Roseisolibacter	0.001	0.740
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Neo-b11	0.001	0.743
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_Aridibacter	0.001	0.745
Bacteria_Actinobacteriota_Acidimicrobiia_Microtrichales_Iamiaceae_Iamia	0.001	0.748
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Puia	0.001	0.750

Bacteria_Gemmatimonadota_BD2-11terrestrialgroup_BD2-11terrestrialgroup_BD2-11terrestrialgroup_BD2-11terrestrialgroup	0.001	0.753
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_Craurococcus-Caldovatus	0.001	0.755
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales__	0.001	0.758
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Chthoniobacterales_Chthoniobacteraceae_Chthoniobacter	0.001	0.760
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_	0.001	0.763
Bacteria_Acidobacteriota_Blastocatellia_11-24_11-24_11-24	0.001	0.765
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_uncultured	0.001	0.768
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Terrimonas	0.001	0.770
Bacteria_Proteobacteria_Gammaproteobacteria___	0.001	0.772
Bacteria_Planctomycetota_OM190_OM190_OM190_OM190	0.001	0.775
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Novosphingobium	0.001	0.777
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_env.OPS17_env.OPS17	0.001	0.779
Bacteria_Proteobacteria_Alphaproteobacteria_Azospirillales_Azospirillaceae_Skermanella	0.001	0.782
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Bradyrhizobium	0.001	0.784
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_uncultured	0.001	0.786
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_Blastocatella	0.001	0.788
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Hyphomicrobiaceae_Pedomicrobium	0.001	0.790
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobiaceae	0.001	0.792
Bacteria_Proteobacteria_Gammaproteobacteria_WD260_WD260_WD260	0.001	0.794
Bacteria_Myxococcota_Polyangia_Polyangiales_Phaselicystidaceae_Phaselicystis	0.001	0.796
Bacteria_Bdellovibrionota_Oligoflexia_0319-6G20_0319-6G20_0319-6G20	0.001	0.798
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Phenylobacterium	0.001	0.800
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Microscillaceae_Ohtaekwangia	0.001	0.802
Bacteria_Cyanobacteria_Cyanobacteriia_Chloroplast_Chloroplast_Chloroplast	0.001	0.804
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Marmoricola	0.001	0.806
Bacteria_Myxococcota_bacteriap25_bacteriap25_bacteriap25_bacteriap25	0.001	0.808
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_Sphingobacteriaceae_Mucilaginibacter	0.001	0.810
Bacteria_Myxococcota_Polyangia_Polyangiales_Polyangiaceae_Pajaroellobacter	0.001	0.812
Bacteria_Latescibacterota_Latescibacterota_Latescibacterota_Latescibacterota_Latescibacterota	0.001	0.814
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Roseiarcus	0.001	0.816
Bacteria_Desulfobacterota_uncultured_uncultured_uncultured_uncultured	0.001	0.818
Bacteria_Planctomycetota_vadinHA49_vadinHA49_vadinHA49_vadinHA49	0.001	0.820
Bacteria_Myxococcota_Polyangia_Polyangiales_Polyangiaceae_uncultured	0.001	0.822
Bacteria_Actinobacteriota_Acidimicrobiia_IMCC26256_IMCC26256_IMCC26256	0.001	0.824
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Opitutales_Opitutaceae_Lacunisphaera	0.001	0.826
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Opitutales_Opitutaceae_Opitutus	0.001	0.827
Bacteria_Actinobacteriota_Acidimicrobiia_Microtrichales_Ilumatobacteraceae_uncultured	0.001	0.829
Bacteria_Chloroflexi_Chloroflexia_Kallotenuales_AKIW781_AKIW781	0.001	0.831
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_JGI0001001-H03	0.001	0.833
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Edaphobaculum	0.001	0.834
Bacteria_Proteobacteria_Gammaproteobacteria_JG36-TzT-191_JG36-TzT-191_JG36-TzT-191	0.001	0.836
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_PMMR1	0.001	0.838
Bacteria_Actinobacteriota_Acidimicrobiia_Microtrichales_uncultured_uncultured	0.001	0.839
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Rhodanobacteraceae_uncultured	0.001	0.841
Bacteria_Chloroflexi_Gitt-GS-136_Gitt-GS-136_Gitt-GS-136_Gitt-GS-136	0.001	0.843
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Alcaligenaceae_	0.001	0.844
Bacteria_Acidobacteriota_Vicinamibacteria_Subgroup17_Subgroup17_Subgroup17	0.001	0.846
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonadaceae_Rheinheimera	0.001	0.847

Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Kibdelosporangium	0.001	0.849
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhodomicrobiaceae_Rhodomicrobium	0.001	0.850
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Intrasporangiaceae_	0.001	0.852
Bacteria_Actinobacteriota_Acidimicrobiia_Actinomarinales_uncultured_uncultured	0.001	0.854
Bacteria_Proteobacteria_Alphaproteobacteria_uncultured_uncultured_uncultured	0.001	0.855
Bacteria_Proteobacteria_Gammaproteobacteria_Steroidobacterales_Steroidobacteraceae_uncultured	0.001	0.857
Bacteria_Chloroflexi_Chloroflexia_Thermomicrobiales_JG30-KF-CM45_JG30-KF-CM45	0.001	0.858
Bacteria_Actinobacteriota_Actinobacteria_Kineosporiales_Kineosporiaceae_	0.001	0.859
Bacteria_Actinobacteriota_Actinobacteria_Kineosporiales_Kineosporiaceae_Kineosporia	0.001	0.861

Rhizosphere vs. 30m

	average	cumsum
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Solirubrobacter	0.023	0.047
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_67-14_67-14	0.019	0.085
Bacteria_Actinobacteriota_Rubrobacteria_Rubrobacterales_Rubrobacteriaceae_Rubrobacter	0.013	0.110
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Pseudomonadaceae_Pseudomonas	0.012	0.134
Bacteria_Acidobacteriota_Acidobacteriae_Subgroup2_Subgroup2_Subgroup2	0.010	0.153
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Phormidiaceae_TychonemaCCAP1459-11B	0.009	0.171
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Blastococcus	0.009	0.189
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_uncultured_uncultured	0.009	0.206
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_	0.008	0.222
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Nitrosomonadaceae_MND1	0.008	0.237
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_uncultured	0.007	0.252
Bacteria_Actinobacteriota_Thermoleophilia_Gaiellales_uncultured_uncultured	0.006	0.263
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_uncultured	0.005	0.273
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_uncultured	0.005	0.283
Bacteria_Acidobacteriota_Vicinamibacteria_Vicinamibacterales_Vicinamibacteraceae_Vicinamibacteraceae	0.005	0.293
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_	0.005	0.302
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Conexibacter	0.004	0.311
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_TRA3-20_TRA3-20	0.004	0.319
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_Pedosphaeraceae	0.004	0.328
Bacteria_Actinobacteriota_Thermoleophilia_Gaiellales_Gaiellaceae_Gaiella	0.004	0.336
Bacteria_Acidobacteriota_Vicinamibacteria_Vicinamibacterales_uncultured_uncultured	0.004	0.344
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Geodermatophilus	0.004	0.352
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_	0.004	0.359
Bacteria_Actinobacteriota_Acidimicrobiia___	0.004	0.367
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Crossiella	0.004	0.374
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingomonas	0.004	0.381
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Occallatibacter	0.004	0.388
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Nitrosomonadaceae_Ellin6067	0.003	0.395
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_	0.003	0.402
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Ellin6055	0.003	0.409
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Microvirga	0.003	0.415
Bacteria_Acidobacteriota_Blastocatellia_Pyrinomonadales_Pyrinomonadaceae_RB41	0.003	0.422
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Bacillus	0.003	0.428
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Psychroglaciecola	0.003	0.434
Bacteria_Actinobacteriota_Actinobacteria_0319-7L14_0319-7L14_0319-7L14	0.003	0.440
Bacteria_Chloroflexi_TK10_TK10_TK10_TK10	0.003	0.446
Bacteria_Actinobacteriota_Acidimicrobiia_IMCC26256_IMCC26256_IMCC26256	0.003	0.453

Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Nocardioides	0.003	0.459
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Enterobacteriaceae_	0.003	0.465
Bacteria_Proteobacteria_Gammaproteobacteria_GammaproteobacteriaIncertaeSedis_UnknownFamily_Acidibacter	0.003	0.471
Bacteria_Gemmatimonadota_S0134terrestrialgroup_S0134terrestrialgroup_S0134terrestrialgroup_S0134terrestrialgroup	0.003	0.477
Bacteria_Myxococcota_Polyangia_Polyangiales_Sandaracinaceae_uncultured	0.003	0.482
Bacteria_Myxococcota_Polyangia_Haliangiales_Haliangiaceae_Haliangium	0.003	0.488
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_	0.003	0.494
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales__	0.003	0.499
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobium	0.003	0.505
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Pseudonocardia	0.003	0.511
Bacteria_Proteobacteria_Gammaproteobacteria_CCD24_CCD24_CCD24	0.003	0.516
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Coleofasciculaceae_uncultured	0.003	0.521
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Microscillaceae_uncultured	0.003	0.527
Bacteria_Proteobacteria_Gammaproteobacteria_Steroidobacterales_Steroidobacteraceae_Steroidobacter	0.003	0.532
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Sporichthyaceae_uncultured	0.003	0.537
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_Gemmatimonas	0.002	0.542
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_	0.002	0.547
Bacteria_Actinobacteriota_Actinobacteria_Micromonosporales_Micromonosporaceae_	0.002	0.551
Bacteria_Acidobacteriota_Acidobacteriae_Bryobacterales_Bryobacteraceae_Bryobacter	0.002	0.556
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Acidothermaceae_Acidothermus	0.002	0.561
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Granulicella	0.002	0.565
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Chthoniobacterales_Chthoniobacteraceae_CandidatusUdaeobacter	0.002	0.570
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Parviterribacter	0.002	0.574
Bacteria_Acidobacteriota_Acidobacteriae_Solibacterales_Solibacteraceae_CandidatusSolibacter	0.002	0.579
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_uncultured_uncultured	0.002	0.583
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_uncultured	0.002	0.588
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_YC-ZSS-LKJ147	0.002	0.592
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Flavisolibacter	0.002	0.597
Bacteria_Actinobacteriota_Actinobacteria_Kineosporiales_Kineosporiaceae_	0.002	0.601
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_	0.002	0.605
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Rubellimicrobium	0.002	0.609
Bacteria_Myxococcota_Polyangia_Polyangiales_BIrii41_BIrii41	0.002	0.614
Bacteria_Planctomycetota_Planctomycetes_Isosphaerales_Isosphaeraceae_uncultured	0.002	0.618
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Aeromicrobium	0.002	0.622
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Puia	0.002	0.626
Bacteria_Actinobacteriota_Acidimicrobiia_Microtrichales_Ilumatobacteraceae_uncultured	0.002	0.629
Bacteria_Acidobacteriota_Holophagae_Subgroup7_Subgroup7_Subgroup7	0.002	0.633
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Saprospiraceae_uncultured	0.002	0.637
Bacteria_Proteobacteria_Gammaproteobacteria_WD260_WD260_WD260	0.002	0.640
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Coleofasciculaceae_MicrocoleusSAG1449-1a	0.002	0.644
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Mycobacteriaceae_Mycobacterium	0.002	0.647
Bacteria_Firmicutes_Bacilli_Bacillales__	0.002	0.651
Bacteria_Actinobacteriota_Actinobacteria_Streptomycetales_Streptomycetaceae_Streptomyces	0.002	0.654
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_uncultured	0.002	0.658
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Arthrobacter	0.002	0.661
Bacteria_Proteobacteria_Alphaproteobacteria_Dongiales_Dongiaceae_Dongia	0.002	0.664
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Hyphomonadaceae_SWB02	0.002	0.668
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_Ellin517	0.002	0.671

Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_	0.002	0.674
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Acidipila	0.002	0.677
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Ramlibacter	0.002	0.680
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_uncultured	0.001	0.683
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Actinophytocola	0.001	0.686
Archaea_Crenarchaeota_Nitrososphaeria_Nitrososphaerales_Nitrososphaeraceae_CandidatusNitrocosmicus	0.001	0.689
Bacteria_Actinobacteriota_Thermoleophilia_uncultured_uncultured_uncultured	0.001	0.691
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_Mitochondria_Mitochondria	0.001	0.694
Bacteria_Firmicutes_Bacilli_Alicyclobacillales_Alicyclobacillaceae_Tumebacillus	0.001	0.697
Bacteria_Planctomycetota_Phycisphaerae_Tepidisphaerales_WD2101soilgroup_WD2101soilgroup	0.001	0.700
Bacteria_Acidobacteriota_Thermoanaerobaculia_Thermoanaerobaculales_Thermoanaerobaculaceae_Subgroup10	0.001	0.703
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Novosphingobium	0.001	0.705
Bacteria_Proteobacteria_Gammaproteobacteria_PLTA13_PLTA13_PLTA13	0.001	0.708
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_KF-JG30-B3_KF-JG30-B3	0.001	0.711
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_	0.001	0.713
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_	0.001	0.716
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Cellulomonadaceae_Cellulomonas	0.001	0.719
Bacteria_Actinobacteriota_Acidimicrobiia_Microtrichales_Iamiaceae_Iamia	0.001	0.721
Bacteria_Cyanobacteria_Cyanobacteriia_Chloroplast_Chloroplast_Chloroplast	0.001	0.724
Bacteria_Myxococcota_Myxococcia_Myxococcales_Myxococcaceae_	0.001	0.726
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Terrimonas	0.001	0.729
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Hyphomicrobiaceae_	0.001	0.731
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_uncultured_uncultured	0.001	0.734
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Hyphomonadaceae_Hirschia	0.001	0.736
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_uncultured	0.001	0.739
Bacteria_Actinobacteriota_Thermoleophilia_Gaiellales__	0.001	0.741
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_	0.001	0.744
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Devosiaceae_Devosia	0.001	0.746
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Bradyrhizobium	0.001	0.749
Bacteria_Nitrospirota_Nitrospiria_Nitrospirales_Nitrospiraceae_Nitrospira	0.001	0.751
Bacteria_Actinobacteriota_Acidimicrobiia_uncultured_uncultured_uncultured	0.001	0.754
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Coleofasciculaceae_MicrocoleusPCC-7113	0.001	0.756
Bacteria_Gemmatimonadota_BD2-11terrestrialgroup_BD2-11terrestrialgroup_BD2-11terrestrialgroup_BD2-11terrestrialgroup	0.001	0.758
Bacteria_Planctomycetota_OM190_OM190_OM190_OM190	0.001	0.761
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_Roseisolibacter	0.001	0.763
Bacteria_Proteobacteria_Alphaproteobacteria_Azospirillales_Azospirillaceae_Skermanella	0.001	0.765
Bacteria_Proteobacteria_Gammaproteobacteria___	0.001	0.768
Bacteria_Actinobacteriota_MB-A2-108_MB-A2-108_MB-A2-108_MB-A2-108	0.001	0.770
Bacteria_Chloroflexi_KD4-96_KD4-96_KD4-96_KD4-96	0.001	0.772
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_Craurococcus-Caldovatus	0.001	0.774
Bacteria_Actinobacteriota_Acidimicrobiia_Microtrichales__	0.001	0.776
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Massilia	0.001	0.779
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_env.OPS17_env.OPS17	0.001	0.781
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Chthoniobacterales_Chthoniobacteraceae_Chthoniobacter	0.001	0.783
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Burkholderia-Caballeronia-Paraburkholderia	0.001	0.785
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Phenylobacterium	0.001	0.787
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobiaceae	0.001	0.789
Bacteria_Myxococcota_bacteriap25_bacteriap25_bacteriap25_bacteriap25	0.001	0.791

Bacteria_Verrucomicrobiota_Verrucomicrobiae_Opitutales_Opitutaceae_Opitutus	0.001	0.793
Bacteria_Chloroflexi_Chloroflexia_Kallotenuales_AKIW781_AKIW781	0.001	0.795
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Promicromonosporaceae_Isoptericola	0.001	0.797
Bacteria_Bdellovibrionota_Oligoflexia_0319-6G20_0319-6G20_0319-6G20	0.001	0.799
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_uncultured	0.001	0.801
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Microscillaceae_Ohtaekwangia	0.001	0.803
Bacteria_Myxococcota_Polyangia_Polyangiales_Phaselicystidaceae_Phaselicystis	0.001	0.805
Bacteria_Proteobacteria_Alphaproteobacteria_Tistrellales_Geminicoccaceae_CandidatusAlysiosphaera	0.001	0.806
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_Sphingobacteriaceae_Mucilaginibacter	0.001	0.808
Bacteria_Desulfobacterota_uncultured_uncultured_uncultured_uncultured	0.001	0.810
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Opitutales_Opitutaceae_Lacunisphaera	0.001	0.812
Bacteria_Proteobacteria_Alphaproteobacteria_Micropepsales_Micropepsaceae_uncultured	0.001	0.814
Bacteria_Acidobacteriota_Blastocatellia_11-24_11-24_11-24	0.001	0.816
Bacteria_Proteobacteria_Gammaproteobacteria_JG36-TzT-191_JG36-TzT-191_JG36-TzT-191	0.001	0.818
Bacteria_Chloroflexi_Gitt-GS-136_Gitt-GS-136_Gitt-GS-136_Gitt-GS-136	0.001	0.819
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Edaphobaculum	0.001	0.821
Bacteria_Planctomycetota_vadinHA49_vadinHA49_vadinHA49_vadinHA49	0.001	0.823
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Intrasporangiaceae_Phycicoccus	0.001	0.825
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_Blastocatella	0.001	0.826
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_uncultured	0.001	0.828
Bacteria_Myxococcota_Polyangia_Polyangiales_Polyangiaceae_Pajaroellobacter	0.001	0.830
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Rhodoplanes	0.001	0.831
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Hyphomicrobiaceae_Pedomicrobium	0.001	0.833
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Alcaligenaceae_	0.001	0.834
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Altererythrobacter	0.001	0.836
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Hymenobacteraceae_Adhaeribacter	0.001	0.838
Bacteria_Myxococcota_Polyangia_Polyangiales_Polyangiaceae_uncultured	0.001	0.839
Bacteria_Entotheonellaeota_Entotheonellia_Entotheonellales_Entotheonellaceae_Entotheonellaceae	0.001	0.841
Bacteria_Proteobacteria_Gammaproteobacteria_Steroidobacterales_Steroidobacteraceae_uncultured	0.001	0.842
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_PMMR1	0.001	0.844
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Neo-b11	0.001	0.845
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Rhizobacter	0.001	0.847
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Ferruginibacter	0.001	0.848

100m vs. 1000m

	average	cumsum
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Lawsonella	0.167	0.237
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_67-14_67-14	0.043	0.298
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Solirubrobacter	0.042	0.359
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_uncultured	0.013	0.378
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_uncultured_uncultured	0.013	0.395
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Blastococcus	0.012	0.412
Bacteria_Acidobacteriota_Acidobacteriae_Subgroup2_Subgroup2_Subgroup2	0.011	0.428
Bacteria_Actinobacteriota_Rubrobacteria_Rubrobacterales_Rubrobacteriaceae_Rubrobacter	0.010	0.442
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_	0.009	0.455
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Nitrosomonadaceae_MND1	0.009	0.468
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_uncultured	0.009	0.481
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_uncultured	0.008	0.492
Bacteria_Actinobacteriota_Thermoleophilia_Gaiellales_Gaiellaceae_Gaiella	0.008	0.504

Bacteria_Actinobacteriota_Thermoleophilia_Gaiellales_uncultured_uncultured	0.008	0.516
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_	0.006	0.525
Bacteria_Actinobacteriota_Actinobacteria_Streptomycetales_Streptomycetaceae_Streptomyces	0.006	0.534
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Crossiella	0.006	0.542
Bacteria_Actinobacteriota_Acidimicrobiia___	0.006	0.550
Bacteria_Acidobacteriota_Acidobacteriae_Bryobacterales_Bryobacteraceae_Bryobacter	0.006	0.558
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingomonas	0.005	0.566
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Pseudonocardia	0.005	0.574
Bacteria_Acidobacteriota_Blastocatellia_Pyrinomonadales_Pyrinomonadaceae_RB41	0.005	0.581
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Conexibacter	0.005	0.588
Bacteria_Acidobacteriota_Vicinamibacteria_Vicinamibacterales_Vicinamibacteraceae_Vicinamibacteraceae	0.005	0.594
Bacteria_Actinobacteriota_Actinobacteria_Micromonosporales_Micromonosporaceae_	0.005	0.601
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_TRA3-20_TRA3-20	0.005	0.607
Bacteria_Acidobacteriota_Vicinamibacteria_Vicinamibacterales_uncultured_uncultured	0.004	0.614
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Geodermatophilus	0.004	0.620
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_	0.004	0.626
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_uncultured_uncultured	0.004	0.632
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_Pedosphaeraceae	0.004	0.638
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Parviterribacter	0.004	0.644
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales__	0.004	0.650
Bacteria_Acidobacteriota_Holophagae_Subgroup7_Subgroup7_Subgroup7	0.004	0.655
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Microvirga	0.004	0.660
Bacteria_Actinobacteriota_Actinobacteria_0319-7L14_0319-7L14_0319-7L14	0.004	0.665
Bacteria_Actinobacteriota_MB-A2-108_MB-A2-108_MB-A2-108_MB-A2-108	0.004	0.671
Bacteria_Proteobacteria_Gammaproteobacteria_Steroidobacterales_Steroidobacteraceae_Steroidobacter	0.003	0.675
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Ellin6055	0.003	0.680
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_	0.003	0.684
Bacteria_Chloroflexi_KD4-96_KD4-96_KD4-96_KD4-96	0.003	0.688
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Phormidiaceae_TychonemaCCAP1459-11B	0.003	0.692
Bacteria_Proteobacteria_Gammaproteobacteria_GammaproteobacteriaIncertaeSedis_UnknownFamily_Acidibacter	0.003	0.696
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Actinomycetospora	0.003	0.700
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Acidipila	0.003	0.704
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Nocardioides	0.003	0.708
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_	0.003	0.711
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Pseudomonadaceae_Pseudomonas	0.003	0.715
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Occallatibacter	0.003	0.719
Bacteria_Myxococcota_Polyangia_Polyangiales_Sandaracinaceae_uncultured	0.002	0.722
Bacteria_Gemmatimonadota_S0134terrestrialgroup_S0134terrestrialgroup_S0134terrestrialgroup_S0134terrestrialgroup	0.002	0.725
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonadaceae_Rheinheimera	0.002	0.729
Bacteria_Acidobacteriota_Thermoanaerobaculia_Thermoanaerobaculales_Thermoanaerobaculaceae_Subgroup10	0.002	0.732
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Acidothermaceae_Acidothermus	0.002	0.736
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Nitrosomonadaceae_Ellin6067	0.002	0.739
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_uncultured	0.002	0.742
Bacteria_Firmicutes_Bacilli_Bacillales__	0.002	0.745
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Sporichthyaceae_uncultured	0.002	0.749
Bacteria_Proteobacteria_Gammaproteobacteria_CCD24_CCD24_CCD24	0.002	0.752
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_uncultured	0.002	0.755
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobium	0.002	0.758

Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Microscillaceae_uncultured	0.002	0.761
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Chthoniobacterales_Chthoniobacteraceae_CandidatusUdaeobacter	0.002	0.764
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Bradyrhizobium	0.002	0.767
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Rubellimicrobium	0.002	0.770
Bacteria_Myxococcota_Polyangia_Haliangiales_Haliangiaceae_Haliangium	0.002	0.773
Bacteria_Actinobacteriota_Thermoleophilia_uncultured_uncultured_uncultured	0.002	0.775
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Arthrobacter	0.002	0.778
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Nakamurellaceae_Nakamurella	0.002	0.781
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Massilia	0.002	0.784
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Psychroglaciecola	0.002	0.787
Bacteria_Nitrospirota_Nitrospiria_Nitrospirales_Nitrospiraceae_Nitrospira	0.002	0.789
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Bacillus	0.002	0.792
Archaea_Crenarchaeota_Nitrososphaeria_Nitrososphaerales_Nitrososphaeraceae_CandidatusNitrocosmicus	0.002	0.794
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Hyphomicrobiaceae_Hyphomicrobium	0.002	0.796
Bacteria_Myxococcota_Myxococcia_Myxococcales_Myxococcaceae_	0.002	0.799
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Flavisolibacter	0.002	0.801
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_Gemmatimonas	0.002	0.804
Bacteria_Actinobacteriota_Actinobacteria_Micromonosporales_Micromonosporaceae_Krasilnikovia	0.002	0.806
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_	0.002	0.808
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_Ellin517	0.002	0.811
Bacteria_Proteobacteria_Alphaproteobacteria_Elsterales_uncultured_uncultured	0.002	0.813
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Beutenbergiaceae_Beutenbergia	0.002	0.815
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_Aridibacter	0.002	0.817
Bacteria_RCP2-54_RCP2-54_RCP2-54_RCP2-54_RCP2-54	0.002	0.820
Bacteria_Myxococcota_Polyangia_Polyangiales_BIrii41_BIrii41	0.002	0.822
Bacteria_Actinobacteriota_Acidimicrobiia_uncultured_uncultured_uncultured	0.002	0.824
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Ramlibacter	0.001	0.826
Bacteria_____	0.001	0.828
Bacteria_Proteobacteria_Gammaproteobacteria_WD260_WD260_WD260	0.001	0.830
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Saprospiraceae_uncultured	0.001	0.832
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Cellulomonadaceae_Cellulomonas	0.001	0.833
Bacteria_Proteobacteria_Gammaproteobacteria___	0.001	0.835
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Actinophytocola	0.001	0.837
Bacteria_Proteobacteria_Alphaproteobacteria_Dongiales_Dongiaceae_Dongia	0.001	0.839
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Altererythrobacter	0.001	0.841
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Terrimonas	0.001	0.843
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Ferruginibacter	0.001	0.844
Bacteria_Myxococcota_bacteriap25_bacteriap25_bacteriap25_bacteriap25	0.001	0.846
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Alcaligenaceae_	0.001	0.848
Bacteria_Proteobacteria_Alphaproteobacteria_Azospirillales_Azospirillaceae_Skermanella	0.001	0.850
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Devosiaceae_Devosia	0.001	0.851
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_Roseisolibacter	0.001	0.853
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales__	0.001	0.855
Bacteria_Planctomycetota_Phycisphaerae_Tepidisphaerales_WD2101soilgroup_WD2101soilgroup	0.001	0.856
Bacteria_Planctomycetota_OM190_OM190_OM190_OM190	0.001	0.858
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Chthoniobacterales_Chthoniobacteraceae_Chthoniobacter	0.001	0.859
Bacteria_Actinobacteriota_Acidimicrobiia_Microtrichales_uncultured_uncultured	0.001	0.861
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_uncultured	0.001	0.862

Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Aeromicrobium	0.001	0.864
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Roseiarcus	0.001	0.865
Bacteria_Proteobacteria_Gammaproteobacteria_PLTA13_PLTA13_PLTA13	0.001	0.867
Bacteria_Acidobacteriota_Acidobacteriae_Solibacterales_Solibacteraceae_CandidatusSolibacter	0.001	0.868
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Neo-b11	0.001	0.870
Bacteria_Actinobacteriota_Acidimicrobiia_Microtrichales_Iamiaceae_Iamia	0.001	0.871
Bacteria_Desulfobacterota_uncultured_uncultured_uncultured_uncultured	0.001	0.872
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Hyphomicrobiaceae_Pedomicrobium	0.001	0.874
Bacteria_Proteobacteria_Alphaproteobacteria_Tistrellales_Geminicoccaceae_CandidatusAlysiosphaera	0.001	0.875
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_uncultured	0.001	0.877
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_env.OPS17_env.OPS17	0.001	0.878
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Novosphingobium	0.001	0.879
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Phenylobacterium	0.001	0.881
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Hyphomonadaceae_SWB02	0.001	0.882
Bacteria_Chloroflexi_Gitt-GS-136_Gitt-GS-136_Gitt-GS-136_Gitt-GS-136	0.001	0.883
Bacteria_Latescibacterota_Latescibacterota_Latescibacterota_Latescibacterota_Latescibacterota	0.001	0.884
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Hyphomonadaceae_Hirschia	0.001	0.886
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_KF-JG30-B3_KF-JG30-B3	0.001	0.887
Bacteria_Gemmatimonadota_BD2-11terrestrialgroup_BD2-11terrestrialgroup_BD2-11terrestrialgroup_BD2-11terrestrialgroup	0.001	0.888
Bacteria_Chloroflexi_TK10_TK10_TK10_TK10	0.001	0.889
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Rhodanobacteraceae_uncultured	0.001	0.891
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Marmoricola	0.001	0.892
Bacteria_Myxococcota_Polyangia_Polyangiales_Polyangiaceae_uncultured	0.001	0.893
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Mycobacteriaceae_Mycobacterium	0.001	0.894
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobiaceae	0.001	0.895
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.001	0.896
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_Nordella	0.001	0.897
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_JGI0001001-H03	0.001	0.898
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Promicromonosporaceae_Promicromonospora	0.001	0.899
Bacteria_Firmicutes_Bacilli_Bacillales_Planococcaceae_	0.001	0.901
Bacteria_NB1-j_NB1-j_NB1-j_NB1-j_NB1-j	0.001	0.902
Bacteria_Acidobacteriota_Vicinamibacteria_Subgroup17_Subgroup17_Subgroup17	0.001	0.903
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Opitutales_Opitutaceae_Opitutus	0.001	0.904
Bacteria_Actinobacteriota_Acidimicrobiia_Actinomarinales_uncultured_uncultured	0.001	0.905
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_uncultured	0.001	0.906
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Intrasporangiaceae_	0.001	0.907
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_YC-ZSS-LKJ147	0.001	0.908
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_	0.001	0.909
Bacteria_Acidobacteriota_Blastocatellia_11-24_11-24_11-24	0.001	0.910
Bacteria_Planctomycetota_Planctomycetes_Gemmatales_Gemmataceae_uncultured	0.001	0.911
Bacteria_Myxococcota_Polyangia_Polyangiales_Phaselicystidaceae_Phaselicystis	0.001	0.912
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_ADurb.Bin063-1	0.001	0.913
Bacteria_Actinobacteriota_Actinobacteria_Micromonosporales_Micromonosporaceae_Virgisporangium	0.001	0.914
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Granulicella	0.001	0.915
Bacteria_Planctomycetota_Planctomycetes_Isosphaerales_Isosphaeraceae_uncultured	0.001	0.916
Bacteria_Actinobacteriota_Acidimicrobiia_IMCC26256_IMCC26256_IMCC26256	0.001	0.917
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_	0.001	0.918
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Microscillaceae_Ohtaekwangia	0.001	0.919

Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_Mitochondria_Mitochondria	0.001	0.919
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhodomicrobiaceae_Rhodomicrobium	0.001	0.920
Bacteria_Proteobacteria_Gammaproteobacteria_Steroidobacterales_Steroidobacteraceae_uncultured	0.001	0.921
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_Craurococcus-Caldovatus	0.001	0.922
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Burkholderia-Caballeronia-Paraburkholderia	0.001	0.923
Bacteria_Chloroflexi_Anaerolineae_SBR1031_A4b_A4b	0.001	0.924
Bacteria_Planctomycetota_vadinHA49_vadinHA49_vadinHA49_vadinHA49	0.001	0.924
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Koribacteraceae_CandidatusKoribacter	0.001	0.925
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Ensifer	0.001	0.926

100m vs. 30m

	average	cumsum
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Lawsonella	0.167	0.235
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Solirubrobacter	0.042	0.294
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_67-14_67-14	0.040	0.350
Bacteria_Actinobacteriota_Rubrobacteria_Rubrobacterales_Rubrobacteriaceae_Rubrobacter	0.013	0.368
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_uncultured	0.013	0.386
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Pseudomonadaceae_Pseudomonas	0.012	0.403
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Blastococcus	0.011	0.419
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_uncultured_uncultured	0.010	0.433
Bacteria_Acidobacteriota_Acidobacteriae_Subgroup2_Subgroup2_Subgroup2	0.010	0.447
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Nitrosomonadaceae_MND1	0.009	0.460
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Phormidiaceae_TychonemaCCAP1459-11B	0.009	0.473
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_uncultured	0.008	0.484
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Pseudonocardia	0.006	0.493
Bacteria_Actinobacteriota_Thermoleophilia_Gaiellales_Gaiellaceae_Gaiella	0.006	0.501
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Crossiella	0.006	0.508
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_	0.005	0.516
Bacteria_Acidobacteriota_Blastocatellia_Pyrinomonadales_Pyrinomonadaceae_RB41	0.005	0.524
Bacteria_Acidobacteriota_Acidobacteriae_Bryobacterales_Bryobacteraceae_Bryobacter	0.005	0.531
Bacteria_Actinobacteriota_Thermoleophilia_Gaiellales_uncultured_uncultured	0.005	0.538
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_uncultured	0.005	0.545
Bacteria_Acidobacteriota_Vicinamibacteria_Vicinamibacterales_Vicinamibacteraceae_Vicinamibacteraceae	0.005	0.552
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_TRA3-20_TRA3-20	0.005	0.559
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Geodermatophilus	0.005	0.565
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Conexibacter	0.004	0.571
Bacteria_Actinobacteriota_Actinobacteria_Micromonosporales_Micromonosporaceae_	0.004	0.577
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingomonas	0.004	0.583
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_Pedosphaeraceae	0.004	0.589
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Microvirga	0.004	0.595
Bacteria_Acidobacteriota_Vicinamibacteria_Vicinamibacterales_uncultured_uncultured	0.004	0.601
Bacteria_Actinobacteriota_Acidimicrobiia___	0.004	0.607
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Psychroglaciecola	0.004	0.612
Bacteria_Actinobacteriota_Acidimicrobiia_IMCC26256_IMCC26256_IMCC26256	0.004	0.618
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_	0.004	0.623
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_uncultured_uncultured	0.004	0.628
Bacteria_Chloroflexi_TK10_TK10_TK10_TK10	0.004	0.633
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_	0.004	0.638
Bacteria_Proteobacteria_Gammaproteobacteria_Steroidobacterales_Steroidobacteraceae_Steroidobacter	0.003	0.643

Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Ellin6055	0.003	0.648
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Sporichthyaceae_uncultured	0.003	0.652
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Nocardioides	0.003	0.657
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_	0.003	0.661
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Occallatibacter	0.003	0.666
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Bacillus	0.003	0.670
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Enterobacteriaceae_	0.003	0.674
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales__	0.003	0.679
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_	0.003	0.683
Bacteria_Myxococcota_Polyangia_Polyangiales_Sandaracinaceae_uncultured	0.003	0.687
Bacteria_Proteobacteria_Gammaproteobacteria_GammaproteobacteriaIncertaeSedis_UnknownFamily_Acidibacter	0.003	0.691
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Coleofasciculaceae_uncultured	0.003	0.694
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobium	0.003	0.698
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_	0.003	0.702
Bacteria_Gemmatimonadota_S0134terrestrialgroup_S0134terrestrialgroup_S0134terrestrialgroup_S0134terrestrialgroup	0.003	0.706
Bacteria_Actinobacteriota_Actinobacteria_Kineosporiales_Kineosporiaceae_	0.003	0.709
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Microscillaceae_uncultured	0.002	0.712
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonadaceae_Rheinheimera	0.002	0.716
Bacteria_Actinobacteriota_Acidimicrobiia_Microtrichales_Ilumatobacteraceae_uncultured	0.002	0.719
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_uncultured	0.002	0.722
Bacteria_Planctomycetota_Planctomycetes_Isosphaerales_Isosphaeraceae_uncultured	0.002	0.726
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Acidothermaceae_Acidothermus	0.002	0.729
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Cellulomonadaceae_Cellulomonas	0.002	0.732
Bacteria_Proteobacteria_Gammaproteobacteria_CCD24_CCD24_CCD24	0.002	0.735
Bacteria_Myxococcota_Polyangia_Haliangiales_Haliangiaceae_Haliangium	0.002	0.738
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_Gemmatimonas	0.002	0.741
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Nitrosomonadaceae_Ellin6067	0.002	0.744
Archaea_Crenarchaeota_Nitrososphaeria_Nitrososphaerales_Nitrososphaeraceae_CandidatusNitrocosmicus	0.002	0.747
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Aeromicrobium	0.002	0.750
Bacteria_Actinobacteriota_MB-A2-108_MB-A2-108_MB-A2-108_MB-A2-108	0.002	0.753
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Nakamurellaceae_Nakamurella	0.002	0.755
Bacteria_Proteobacteria_Gammaproteobacteria_WD260_WD260_WD260	0.002	0.758
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Parviterribacter	0.002	0.761
Bacteria_Acidobacteriota_Acidobacteriae_Solibacterales_Solibacteraceae_CandidatusSolibacter	0.002	0.763
Bacteria_Acidobacteriota_Holophagae_Subgroup7_Subgroup7_Subgroup7	0.002	0.766
Bacteria_Chloroflexi_KD4-96_KD4-96_KD4-96_KD4-96	0.002	0.769
Bacteria_Nitrospirota_Nitrospiria_Nitrospirales_Nitrospiraceae_Nitrospira	0.002	0.771
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Coleofasciculaceae_MicrocoleusSAG1449-1a	0.002	0.774
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Puia	0.002	0.776
Bacteria_Myxococcota_Polyangia_Polyangiales_BIrii41_BIrii41	0.002	0.778
Bacteria_Actinobacteriota_Actinobacteria_Micromonosporales_Micromonosporaceae_Krasilnikovia	0.002	0.781
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_Ellin517	0.002	0.783
Bacteria_Actinobacteriota_Actinobacteria_Streptomycetales_Streptomycetaceae_Streptomyces	0.002	0.785
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Rubellimicrobium	0.002	0.788
Bacteria_Acidobacteriota_Thermoanaerobaculia_Thermoanaerobaculales_Thermoanaerobaculaceae_Subgroup10	0.002	0.790
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Flavisolibacter	0.002	0.792
Bacteria_Proteobacteria_Alphaproteobacteria_Tistrellales_Geminicoccaceae_CandidatusAlysiosphaera	0.002	0.795
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Beutenbergiaceae_Beutenbergia	0.002	0.797

Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Mycobacteriaceae_Mycobacterium	0.002	0.799
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Massilia	0.002	0.801
Bacteria_RCP2-54_RCP2-54_RCP2-54_RCP2-54_RCP2-54	0.001	0.803
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Granulicella	0.001	0.805
Bacteria_____	0.001	0.807
Bacteria_Actinobacteriota_Thermoleophilia_uncultured_uncultured_uncultured	0.001	0.809
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Terrimonas	0.001	0.811
Bacteria_Actinobacteriota_Actinobacteria_0319-7L14_0319-7L14_0319-7L14	0.001	0.813
Bacteria_Myxococcota_Myxococcia_Myxococcales_Myxococcaceae_	0.001	0.815
Bacteria_Actinobacteriota_Thermoleophilia_Gaiellales__	0.001	0.817
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Saprospiraceae_uncultured	0.001	0.819
Bacteria_Firmicutes_Bacilli_Bacillales__	0.001	0.821
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Bradyrhizobium	0.001	0.823
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Ramlibacter	0.001	0.825
Bacteria_Proteobacteria_Alphaproteobacteria_Dongiales_Dongiaceae_Dongia	0.001	0.827
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_	0.001	0.829
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Acidipila	0.001	0.831
Bacteria_Proteobacteria_Gammaproteobacteria___	0.001	0.832
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Chthoniobacterales_Chthoniobacteraceae_CandidatusUdaeobacter	0.001	0.834
Bacteria_Actinobacteriota_Acidimicrobiia_Microtrichales_uncultured_uncultured	0.001	0.836
Bacteria_Proteobacteria_Alphaproteobacteria_Azospirillales_Azospirillaceae_Skermanella	0.001	0.838
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Alcaligenaceae_	0.001	0.839
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_	0.001	0.841
Bacteria_Planctomycetota_OM190_OM190_OM190_OM190	0.001	0.843
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Coleofasciculaceae_MicrocoleusPCC-7113	0.001	0.844
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_Aridibacter	0.001	0.846
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_Roseisolibacter	0.001	0.847
Bacteria_Cyanobacteria_Cyanobacteriia_Chloroplast_Chloroplast_Chloroplast	0.001	0.849
Bacteria_Actinobacteriota_Acidimicrobiia_Microtrichales__	0.001	0.851
Bacteria_Actinobacteriota_Acidimicrobiia_Microtrichales_Iamiaceae_Iamia	0.001	0.852
Bacteria_Planctomycetota_Phycisphaerae_Tepidisphaerales_WD2101soilgroup_WD2101soilgroup	0.001	0.854
Bacteria_Myxococcota_bacteriap25_bacteriap25_bacteriap25_bacteriap25	0.001	0.855
Bacteria_Chloroflexi_Gitt-GS-136_Gitt-GS-136_Gitt-GS-136_Gitt-GS-136	0.001	0.856
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_uncultured	0.001	0.858
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_uncultured	0.001	0.859
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Phenylobacterium	0.001	0.861
Bacteria_Desulfobacterota_uncultured_uncultured_uncultured_uncultured	0.001	0.862
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Novosphingobium	0.001	0.864
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_env.OPS17_env.OPS17	0.001	0.865
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Burkholderia-Caballeronia-Paraburkholderia	0.001	0.867
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Chthoniobacterales_Chthoniobacteraceae_Chthoniobacter	0.001	0.868
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Promicromonosporaceae_Isoptericola	0.001	0.869
Bacteria_Proteobacteria_Gammaproteobacteria_PLTA13_PLTA13_PLTA13	0.001	0.871
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Hyphomonadaceae_SWB02	0.001	0.872
Bacteria_Proteobacteria_Alphaproteobacteria_Elsterales_uncultured_uncultured	0.001	0.873
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Hyphomonadaceae_Hirschia	0.001	0.875
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.001	0.876
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_YC-ZSS-LKJ147	0.001	0.877

Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobiaceae	0.001	0.878
Bacteria_Actinobacteriota_Acidimicrobiia_uncultured_uncultured_uncultured	0.001	0.880
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Intrasporangiaceae_Phycicoccus	0.001	0.881
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_Mitochondria_Mitochondria	0.001	0.882
Bacteria_NB1-j_NB1-j_NB1-j_NB1-j_NB1-j	0.001	0.883
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Roseiarcus	0.001	0.884
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_uncultured	0.001	0.886
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_Craurococcus-Caldovatus	0.001	0.887
Bacteria_Gemmatimonadota_BD2-11terrestrialgroup_BD2-11terrestrialgroup_BD2-11terrestrialgroup_BD2-11terrestrialgroup	0.001	0.888
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_ADurb.Bin063-1	0.001	0.889
Bacteria_Planctomycetota_Planctomycetes_Gemmatales_Gemmataceae_uncultured	0.001	0.890
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Rhodoplanes	0.001	0.891
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_KF-JG30-B3_KF-JG30-B3	0.001	0.893
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Actinomycetospora	0.001	0.894
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_	0.001	0.895
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Altererythrobacter	0.001	0.896
Bacteria_Acidobacteriota_Blastocatellia_11-24_11-24_11-24	0.001	0.897
Bacteria_Proteobacteria_Alphaproteobacteria_Micropepsales_Micropepsaceae_uncultured	0.001	0.898
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Hyphomicrobiaceae_Pedomicrobium	0.001	0.899
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Rhodanobacteraceae_uncultured	0.001	0.900
Bacteria_Firmicutes_Bacilli_Bacillales_Planococcaceae_	0.001	0.901
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Mesorhizobium	0.001	0.902
Bacteria_Myxococcota_Polyangia_Polyangiales_Polyangiaceae_uncultured	0.001	0.903
Bacteria_Acidobacteriota_Vicinamibacteria_Subgroup17_Subgroup17_Subgroup17	0.001	0.904
Bacteria_Myxococcota_Polyangia_Polyangiales_Phaselicystidaceae_Phaselicystis	0.001	0.905
Bacteria_Entotheonellaeota_Entotheonellia_Entotheonellales_Entotheonellaceae_Entotheonellaceae	0.001	0.906
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Limnohabitans	0.001	0.907
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Paracoccus	0.001	0.908
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Devosiaceae_Devosia	0.001	0.909
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Rhizobacter	0.001	0.910
Bacteria_Actinobacteriota_Actinobacteria_Micromonosporales_Micromonosporaceae_Virgisporangium	0.001	0.911
Bacteria_Chloroflexi_Chloroflexia_Kallotenuales_AKIW781_AKIW781	0.001	0.912
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_Agromyces	0.001	0.913

1000m vs. 30m

	average	cumsum
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Pseudomonadaceae_Pseudomonas	0.012	0.032
Bacteria_Actinobacteriota_Rubrobacteria_Rubrobacterales_Rubrobacteriaceae_Rubrobacter	0.012	0.062
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_67-14_67-14	0.010	0.087
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Blastococcus	0.009	0.110
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Phormidiaceae_TychonemaCCAP1459-11B	0.009	0.134
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_uncultured_uncultured	0.008	0.154
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Solirubrobacter	0.008	0.174
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_uncultured	0.008	0.193
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_	0.007	0.213
Bacteria_Acidobacteriota_Acidobacteriae_Subgroup2_Subgroup2_Subgroup2	0.006	0.229
Bacteria_Actinobacteriota_Actinobacteria_Streptomycetales_Streptomycetaceae_Streptomyces	0.006	0.245
Bacteria_Actinobacteriota_Acidimicrobiia___	0.005	0.258
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_uncultured	0.005	0.271

Bacteria_Actinobacteriota_Thermoleophilia_Gaiellales_uncultured_uncultured	0.005	0.283
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Crossiella	0.004	0.294
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Ellin6055	0.004	0.305
Bacteria_Actinobacteriota_Thermoleophilia_Gaiellales_Gaiellaceae_Gaiella	0.004	0.315
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales__	0.004	0.325
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingomonas	0.004	0.335
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Geodermatophilus	0.004	0.345
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Conexibacter	0.004	0.354
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Parviterribacter	0.004	0.363
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_	0.004	0.372
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Pseudonocardia	0.004	0.382
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_	0.003	0.391
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_	0.003	0.399
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Bacillus	0.003	0.407
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_TRA3-20_TRA3-20	0.003	0.415
Bacteria_Actinobacteriota_Acidimicrobiia_IMCC26256_IMCC26256_IMCC26256	0.003	0.423
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Occallatibacter	0.003	0.431
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Psychroglaciecola	0.003	0.439
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Enterobacteriaceae_	0.003	0.447
Bacteria_Chloroflexi_TK10_TK10_TK10_TK10	0.003	0.454
Bacteria_Actinobacteriota_Actinobacteria_0319-7L14_0319-7L14_0319-7L14	0.003	0.462
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobium	0.003	0.469
Bacteria_Acidobacteriota_Vicinamibacteria_Vicinamibacterales_Vicinamibacteraceae_Vicinamibacteraceae	0.003	0.476
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Coleofasciculaceae_uncultured	0.003	0.483
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Nitrosomonadaceae_MND1	0.003	0.490
Bacteria_Acidobacteriota_Blastocatellia_Pyrinomonadales_Pyrinomonadaceae_RB41	0.003	0.497
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Actinomycetospora	0.003	0.503
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_	0.003	0.510
Bacteria_Actinobacteriota_Actinobacteria_Kineosporiales_Kineosporiaceae_	0.003	0.517
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_uncultured	0.003	0.524
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_	0.003	0.530
Bacteria_Acidobacteriota_Vicinamibacteria_Vicinamibacterales_uncultured_uncultured	0.003	0.537
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Nocardioides	0.002	0.543
Bacteria_Firmicutes_Bacilli_Bacillales__	0.002	0.549
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Acidipila	0.002	0.555
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Microvirga	0.002	0.561
Bacteria_Acidobacteriota_Holophagae_Subgroup7_Subgroup7_Subgroup7	0.002	0.567
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_uncultured_uncultured	0.002	0.573
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Massilia	0.002	0.578
Bacteria_Acidobacteriota_Acidobacteriae_Solibacterales_Solibacteraceae_CandidatusSolibacter	0.002	0.584
Bacteria_Acidobacteriota_Acidobacteriae_Bryobacterales_Bryobacteraceae_Bryobacter	0.002	0.589
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Cellulomonadaceae_Cellulomonas	0.002	0.595
Bacteria_Actinobacteriota_Thermoleophilia_uncultured_uncultured_uncultured	0.002	0.600
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Aeromicrobium	0.002	0.605
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_uncultured	0.002	0.610
Bacteria_Actinobacteriota_Acidimicrobiia_Microtrichales_Ilumatobacteraceae_uncultured	0.002	0.616
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Chthoniobacterales_Chthoniobacteraceae_CandidatusUdaeobacter	0.002	0.621
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Arthrobacter	0.002	0.626

Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Mycobacteriaceae_Mycobacterium	0.002	0.631
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_Gemmatimonas	0.002	0.636
Bacteria_Planctomycetota_Planctomycetes_Isosphaerales_Isosphaeraceae_uncultured	0.002	0.640
Archaea_Crenarchaeota_Nitrososphaeria_Nitrososphaerales_Nitrososphaeraceae_CandidatusNitrocosmicus	0.002	0.645
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Coleofasciculaceae_MicrocoleusSAG1449-1a	0.002	0.649
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Acidothermaceae_Acidothermus	0.002	0.654
Bacteria_Proteobacteria_Gammaproteobacteria_GammaproteobacteriaIncertaeSedis_UnknownFamily_Acidibacter	0.002	0.658
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Rubellimicrobium	0.002	0.663
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Hyphomicrobiaceae_Hyphomicrobium	0.002	0.667
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Flavisolibacter	0.002	0.671
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Ramlibacter	0.002	0.676
Bacteria_Actinobacteriota_MB-A2-108_MB-A2-108_MB-A2-108_MB-A2-108	0.002	0.680
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Puia	0.002	0.684
Bacteria_Actinobacteriota_Acidimicrobiia_uncultured_uncultured_uncultured	0.002	0.688
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Sporichthyaceae_uncultured	0.002	0.692
Bacteria_Gemmatimonadota_S0134terrestrialgroup_S0134terrestrialgroup_S0134terrestrialgroup_S0134terrestrialgroup	0.002	0.696
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_	0.002	0.700
Bacteria_Proteobacteria_Gammaproteobacteria_WD260_WD260_WD260	0.001	0.704
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Bradyrhizobium	0.001	0.707
Bacteria_Acidobacteriota_Thermoanaerobaculia_Thermoanaerobaculales_Thermoanaerobaculaceae_Subgroup10	0.001	0.711
Bacteria_RCP2-54_RCP2-54_RCP2-54_RCP2-54_RCP2-54	0.001	0.715
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_Roseisolibacter	0.001	0.718
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Actinophytocola	0.001	0.722
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_Aridibacter	0.001	0.725
Bacteria_Actinobacteriota_Acidimicrobiia_Microtrichales_Iamiaceae_Iamia	0.001	0.729
Bacteria_Chloroflexi_KD4-96_KD4-96_KD4-96_KD4-96	0.001	0.732
Bacteria_Proteobacteria_Alphaproteobacteria_Elsterales_uncultured_uncultured	0.001	0.735
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Devosiaceae_Devosia	0.001	0.739
Bacteria_Myxococcota_Polyangia_Polyangiales_Sandaracinaceae_uncultured	0.001	0.742
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_	0.001	0.745
Bacteria_Proteobacteria_Alphaproteobacteria_Dongiales_Dongiaceae_Dongia	0.001	0.748
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Altererythrobacter	0.001	0.752
Bacteria_Actinobacteriota_Thermoleophilia_Gaiellales__	0.001	0.755
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Granulicella	0.001	0.758
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Coleofasciculaceae_MicrocoleusPCC-7113	0.001	0.761
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales__	0.001	0.764
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Burkholderia-Caballeronia-Paraburkholderia	0.001	0.767
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Neo-b11	0.001	0.770
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_uncultured	0.001	0.773
Bacteria_Planctomycetota_Phycisphaerae_Tepidisphaerales_WD2101soilgroup_WD2101soilgroup	0.001	0.776
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Novosphingobium	0.001	0.779
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_	0.001	0.782
Bacteria_Myxococcota_Polyangia_Polyangiales_BIrii41_BIrii41	0.001	0.785
Bacteria_Actinobacteriota_Actinobacteria_Micromonosporales_Micromonosporaceae_	0.001	0.788
Bacteria_Proteobacteria_Gammaproteobacteria_Steroidobacterales_Steroidobacteraceae_Steroidobacter	0.001	0.790
Bacteria_Actinobacteriota_Acidimicrobiia_Microtrichales__	0.001	0.793
Bacteria_Cyanobacteria_Cyanobacteriia_Chloroplast_Chloroplast_Chloroplast	0.001	0.796
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Ferruginibacter	0.001	0.799

Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Hyphomicrobiaceae_Pedomicrobium	0.001	0.802
Bacteria_Proteobacteria_Gammaproteobacteria_CCD24_CCD24_CCD24	0.001	0.804
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_uncultured	0.001	0.807
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Roseiarcus	0.001	0.809
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Promicromonosporaceae_Isoptericola	0.001	0.812
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_uncultured	0.001	0.814
Bacteria_Proteobacteria_Alphaproteobacteria_Azospirillales_Azospirillaceae_Skermanella	0.001	0.817
Bacteria_Actinobacteriota_Acidimicrobiia_Microtrichales_uncultured_uncultured	0.001	0.819
Bacteria_Myxococcota_Myxococcia_Myxococcales_Myxococcaceae_	0.001	0.822
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Microscillaceae_uncultured	0.001	0.824
Bacteria_Latescibacterota_Latescibacterota_Latescibacterota_Latescibacterota_Latescibacterota	0.001	0.827
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_Craurococcus-Caldovatus	0.001	0.829
Bacteria_Myxococcota_bacteriap25_bacteriap25_bacteriap25_bacteriap25	0.001	0.831
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Intrasporangiaceae_Phycicoccus	0.001	0.834
Bacteria_Myxococcota_Polyangia_Polyangiales_Polyangiaceae_uncultured	0.001	0.836
Bacteria_Actinobacteriota_Actinobacteria_Micromonosporales_Micromonosporaceae_Virgisporangium	0.001	0.838
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Phenylobacterium	0.001	0.840
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Marmoricola	0.001	0.842
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_YC-ZSS-LKJ147	0.001	0.844
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_Mitochondria_Mitochondria	0.001	0.846
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Nitrosomonadaceae_Ellin6067	0.001	0.848
Bacteria_Proteobacteria_Alphaproteobacteria_Micropepsales_Micropepsaceae_uncultured	0.001	0.850
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_Nordella	0.001	0.852
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Intrasporangiaceae_	0.001	0.854
Bacteria_Myxococcota_Polyangia_Haliangiales_Haliangiaceae_Haliangium	0.001	0.856
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_JGI0001001-H03	0.001	0.858
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_KF-JG30-B3_KF-JG30-B3	0.001	0.860
Bacteria_Acidobacteriota_Blastocatellia_11-24_11-24_11-24	0.001	0.862
Bacteria_Acidobacteriota_Vicinamibacteria_Subgroup17_Subgroup17_Subgroup17	0.001	0.863
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Limnohabitans	0.001	0.865
Bacteria_Entotheonellaeota_Entotheonellia_Entotheonellales_Entotheonellaceae_Entotheonellaceae	0.001	0.867
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Paracoccus	0.001	0.869
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_Pedosphaeraceae	0.001	0.871
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Rhizobacter	0.001	0.872
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_uncultured	0.001	0.874
Bacteria_Planctomycetota_Planctomycetes_Gemmatales_Gemmataceae_uncultured	0.001	0.876
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_uncultured	0.001	0.878
Bacteria_Actinobacteriota_Acidimicrobiia_Actinomarinales_uncultured_uncultured	0.001	0.879
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.001	0.881
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Rhodoplanes	0.001	0.883
Bacteria_Chloroflexi_Chloroflexia_Kallotenuales_AKIW781_AKIW781	0.001	0.884
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_	0.001	0.886
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_Agromyces	0.001	0.888
Bacteria_Proteobacteria_Gammaproteobacteria_JG36-TzT-191_JG36-TzT-191_JG36-TzT-191	0.001	0.890
Bacteria_Proteobacteria_Alphaproteobacteria_Tistrellales_Geminicoccaceae_CandidatusAlysiosphaera	0.001	0.891
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Mesorhizobium	0.001	0.893
Bacteria_Chloroflexi_Gitt-GS-136_Gitt-GS-136_Gitt-GS-136_Gitt-GS-136	0.001	0.894
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales__	0.001	0.896

Bacteria_Entotheonellaeota_Entotheonellia_Entotheonellales_Entotheonellaceae_CandidatusEntotheonella	0.001	0.898
Bacteria_Desulfobacterota_uncultured_uncultured_uncultured_uncultured	0.001	0.899
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobiaceae	0.001	0.901
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_	0.001	0.902
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Koribacteraceae_CandidatusKoribacter	0.001	0.904
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Promicromonosporaceae_Promicromonospora	0.001	0.905
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Hymenobacteraceae_Adhaeribacter	0.001	0.906
Bacteria_Nitrospirota_Nitrospiria_Nitrospirales_Nitrospiraceae_Nitrospira	0.001	0.908
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhodomicrobiaceae_Rhodomicrobium	0.001	0.909

Table 3.2: Phyla level Simper analysis results microbiome of C. myrtifolia rhizosphere and nearby soil. Taxa are listed as assigned by QIMME2 at level 2(L2). Average and cumsum scores for each pair of sample types are listed below the labeled headers. Average refers to average contribution to dissimilarity for a given taxa and cumsum refers to the cumulative sum of dissimilarity for all taxa listed above a give row.

	Rhizosphere vs. 100m	
	average	cumsum
Bacteria_Actinobacteriota	0.220	0.479
Bacteria_Proteobacteria	0.088	0.671
Bacteria_Acidobacteriota	0.038	0.754
Bacteria_Gemmatimonadota	0.023	0.804
Bacteria_Bacteroidota	0.022	0.852
Bacteria_Myxococcota	0.017	0.888
Bacteria_Verrucomicrobiota	0.015	0.920
Bacteria_Planctomycetota	0.009	0.939
Bacteria_Chloroflexi	0.006	0.951
Bacteria_Firmicutes	0.004	0.961
Bacteria_Bdellovibrionota	0.003	0.967
Bacteria_Desulfobacterota	0.002	0.972
Bacteria_Nitrospirota	0.002	0.977
Bacteria_	0.002	0.980
Archaea_Crenarchaeota	0.001	0.983
Bacteria_RCP2-54	0.001	0.985
Bacteria_NB1-j	0.001	0.987
Unassigned_	0.001	0.989
Bacteria_Armatimonadota	0.001	0.990
Bacteria_Entotheonellaeota	0.001	0.992
Bacteria_Elusimicrobiota	0.001	0.993
Bacteria_Methylomirabilota	0.000	0.994
Eukaryota_	0.000	0.995
Bacteria_Latescibacterota	0.000	0.996
Bacteria_Dependentiae	0.000	0.996
Bacteria_Patescibacteria	0.000	0.997
Bacteria_WPS-2	0.000	0.997
Bacteria_Abditibacteriota	0.000	0.998
Bacteria_Fibrobacterota	0.000	0.998

Bacteria_SAR324clade(MarinegroupB)	0.000	0.999
Bacteria_FCPU426	0.000	0.999
Archaea_Nanoarchaeota	0.000	0.999
Bacteria_Spirochaetota	0.000	1.000
Bacteria_MBNT15	0.000	1.000
Archaea_Thermoplasmatota	0.000	1.000
Bacteria_Sumerlaeota	0.000	1.000
Bacteria_WS2	0.000	1.000
Bacteria_Hydrogenedentes	0.000	1.000
Bacteria_Deinococcota	0.000	1.000

Rhizosphere vs. 1000m

	average	cumsum
Bacteria_Actinobacteriota	0.103	0.407
Bacteria_Proteobacteria	0.045	0.584
Bacteria_Bacteroidota	0.019	0.658
Bacteria_Gemmatimonadota	0.019	0.732
Bacteria_Acidobacteriota	0.014	0.789
Bacteria_Myxococcota	0.013	0.839
Bacteria_Verrucomicrobiota	0.011	0.881
Bacteria_Planctomycetota	0.006	0.903
Bacteria_Firmicutes	0.005	0.922
Bacteria_Chloroflexi	0.005	0.941
Bacteria_Bdellovibrionota	0.002	0.950
Bacteria_Desulfobacterota	0.002	0.958
Archaea_Crenarchaeota	0.002	0.964
Bacteria_RCP2-54	0.001	0.969
Bacteria_Nitrospirota	0.001	0.974
Bacteria_Latescibacterota	0.001	0.978
Bacteria_Entotheonellaeota	0.001	0.981
Unassigned_	0.001	0.983
Bacteria_Armatimonadota	0.001	0.985
Bacteria_	0.000	0.987
Bacteria_NB1-j	0.000	0.989
Bacteria_Elusimicrobiota	0.000	0.991
Bacteria_Methylomirabilota	0.000	0.993
Bacteria_Patescibacteria	0.000	0.994
Bacteria_Abditibacteriota	0.000	0.995
Bacteria_Dependentiae	0.000	0.996
Bacteria_Fibrobacterota	0.000	0.996
Bacteria_WPS-2	0.000	0.997
Archaea_Nanoarchaeota	0.000	0.998
Bacteria_FCPU426	0.000	0.998
Archaea_Thermoplasmatota	0.000	0.999
Bacteria_SAR324clade(MarinegroupB)	0.000	0.999
Bacteria_Spirochaetota	0.000	1.000
Bacteria_MBNT15	0.000	1.000
Bacteria_Sumerlaeota	0.000	1.000
Bacteria_Deinococcota	0.000	1.000

Bacteria_Hydrogenedentes	0.000	1.000
Bacteria_WS2	0.000	1.000
Eukaryota_	0.000	1.000

Rhizosphere vs. 30m

	average	cumsum
Bacteria_Actinobacteriota	0.099	0.386
Bacteria_Proteobacteria	0.052	0.587
Bacteria_Acidobacteriota	0.021	0.666
Bacteria_Bacteroidota	0.017	0.731
Bacteria_Gemmatimonadota	0.016	0.795
Bacteria_Myxococcota	0.011	0.839
Bacteria_Verrucomicrobiota	0.011	0.882
Bacteria_Planctomycetota	0.006	0.906
Bacteria_Chloroflexi	0.006	0.928
Bacteria_Firmicutes	0.005	0.946
Bacteria_Bdellovibrionota	0.002	0.955
Bacteria_Desulfobacterota	0.002	0.963
Archaea_Crenarchaeota	0.001	0.968
Bacteria_Nitrospirota	0.001	0.973
Bacteria_RCP2-54	0.001	0.976
Bacteria_Entotheonellaeota	0.001	0.978
Unassigned_	0.001	0.981
Bacteria_NB1-j	0.001	0.983
Bacteria_Armatimonadota	0.001	0.985
Bacteria_	0.000	0.987
Bacteria_WPS-2	0.000	0.989
Bacteria_Elusimicrobiota	0.000	0.991
Bacteria_Methylomirabilota	0.000	0.992
Bacteria_Latescibacterota	0.000	0.994
Bacteria_Patescibacteria	0.000	0.995
Bacteria_Dependentiae	0.000	0.996
Bacteria_Fibrobacterota	0.000	0.996
Bacteria_Abditibacteriota	0.000	0.997
Archaea_Nanoarchaeota	0.000	0.998
Bacteria_FCPU426	0.000	0.998
Bacteria_SAR324clade(MarinegroupB)	0.000	0.999
Bacteria_Deinococcota	0.000	0.999
Bacteria_Spirochaetota	0.000	1.000
Bacteria_MBNT15	0.000	1.000
Bacteria_Sumerlaeota	0.000	1.000
Archaea_Thermoplasmatota	0.000	1.000
Bacteria_Hydrogenedentes	0.000	1.000
Bacteria_WS2	0.000	1.000
Eukaryota_	0.000	1.000

100m vs. 1000m

	average	cumsum
Bacteria_Actinobacteriota	0.184	0.483
Bacteria_Proteobacteria	0.078	0.688

Bacteria_Acidobacteriota	0.038	0.788
Bacteria_Gemmatimonadota	0.017	0.831
Bacteria_Bacteroidota	0.013	0.866
Bacteria_Verrucomicrobiota	0.012	0.897
Bacteria_Myxococcota	0.010	0.923
Bacteria_Planctomycetota	0.007	0.941
Bacteria_Chloroflexi	0.004	0.952
Bacteria_Firmicutes	0.004	0.962
Bacteria_Nitrospirota	0.002	0.967
Archaea_Crenarchaeota	0.002	0.971
Bacteria_RCP2-54	0.002	0.975
Bacteria_Bdellovibrionota	0.001	0.979
Bacteria_	0.001	0.982
Bacteria_Desulfobacterota	0.001	0.985
Bacteria_Latescibacterota	0.001	0.987
Bacteria_NB1-j	0.001	0.989
Bacteria_Entotheonellaeota	0.001	0.991
Bacteria_Armatimonadota	0.001	0.993
Unassigned_	0.000	0.994
Eukaryota_	0.000	0.995
Bacteria_Methylomirabilota	0.000	0.996
Bacteria_Elusimicrobiota	0.000	0.997
Bacteria_Patescibacteria	0.000	0.998
Bacteria_Dependentiae	0.000	0.998
Bacteria_SAR324clade(MarinegroupB)	0.000	0.998
Archaea_Thermoplasmatota	0.000	0.999
Bacteria_WPS-2	0.000	0.999
Bacteria_Spirochaetota	0.000	0.999
Bacteria_FCPU426	0.000	0.999
Bacteria_Fibrobacterota	0.000	1.000
Archaea_Nanoarchaeota	0.000	1.000
Bacteria_MBNT15	0.000	1.000
Bacteria_Abditibacteriota	0.000	1.000
Bacteria_Sumerlaeota	0.000	1.000
Bacteria_WS2	0.000	1.000
Bacteria_Hydrogenedentes	0.000	1.000
Bacteria_Deinococcota	0.000	1.000

100m vs. 30m

	average	cumsum
Bacteria_Actinobacteriota	0.188	0.485
Bacteria_Proteobacteria	0.079	0.689
Bacteria_Acidobacteriota	0.033	0.776
Bacteria_Gemmatimonadota	0.018	0.822
Bacteria_Bacteroidota	0.014	0.857
Bacteria_Verrucomicrobiota	0.011	0.887
Bacteria_Myxococcota	0.011	0.915
Bacteria_Planctomycetota	0.008	0.934
Bacteria_Chloroflexi	0.007	0.952

Bacteria_Firmicutes	0.004	0.962
Archaea_Crenarchaeota	0.002	0.967
Bacteria_Nitrospirota	0.002	0.971
Bacteria_RCP2-54	0.002	0.975
Bacteria_	0.001	0.979
Bacteria_Bdellovibrionota	0.001	0.983
Bacteria_Desulfobacterota	0.001	0.985
Bacteria_NB1-j	0.001	0.988
Bacteria_Entotheonellaeota	0.001	0.990
Bacteria_Armatimonadota	0.001	0.991
Unassigned_	0.000	0.992
Bacteria_WPS-2	0.000	0.994
Eukaryota_	0.000	0.995
Bacteria_Methylomirabilota	0.000	0.996
Bacteria_Elusimicrobiota	0.000	0.997
Bacteria_Latescibacterota	0.000	0.997
Bacteria_Patescibacteria	0.000	0.998
Bacteria_Dependentiae	0.000	0.998
Bacteria_SAR324clade(MarinegroupB)	0.000	0.998
Bacteria_Spirochaetota	0.000	0.999
Bacteria_Deinococcota	0.000	0.999
Bacteria_FCPU426	0.000	0.999
Bacteria_Fibrobacterota	0.000	0.999
Archaea_Thermoplasmatota	0.000	1.000
Bacteria_Abditibacteriota	0.000	1.000
Archaea_Nanoarchaeota	0.000	1.000
Bacteria_MBNT15	0.000	1.000
Bacteria_Sumerlaeota	0.000	1.000
Bacteria_WS2	0.000	1.000
Bacteria_Hydrogenedentes	0.000	1.000

1000m vs. 30m

	average	cumsum
Bacteria_Proteobacteria	0.042	0.326
Bacteria_Actinobacteriota	0.032	0.572
Bacteria_Acidobacteriota	0.019	0.716
Bacteria_Gemmatimonadota	0.011	0.803
Bacteria_Bacteroidota	0.004	0.835
Bacteria_Myxococcota	0.003	0.859
Bacteria_Verrucomicrobiota	0.003	0.881
Bacteria_Chloroflexi	0.003	0.901
Bacteria_Planctomycetota	0.003	0.920
Bacteria_Firmicutes	0.002	0.937
Archaea_Crenarchaeota	0.002	0.950
Bacteria_RCP2-54	0.001	0.961
Bacteria_Latescibacterota	0.001	0.968
Bacteria_Entotheonellaeota	0.001	0.974
Bacteria_Desulfobacterota	0.001	0.979
Bacteria_Nitrospirota	0.001	0.983

Bacteria_WPS-2	0.000	0.986
Bacteria_Bdellovibrionota	0.000	0.989
Bacteria_NB1-j	0.000	0.992
Bacteria_Methylomirabilota	0.000	0.994
Bacteria_	0.000	0.996
Bacteria_Armatimonadota	0.000	0.998
Archaea_Thermoplasmatota	0.000	0.998
Bacteria_Deinococcota	0.000	0.999
Bacteria_Patescibacteria	0.000	1.000
Bacteria_Abditibacteriota	0.000	1.000
Unassigned_	0.000	1.000
Archaea_Nanoarchaeota	0.000	1.000
Bacteria_Dependentiae	0.000	1.000
Bacteria_Elusimicrobiota	0.000	1.000
Bacteria_FCPU426	0.000	1.000
Bacteria_Fibrobacterota	0.000	1.000
Bacteria_Hydrogenedentes	0.000	1.000
Bacteria_MBNT15	0.000	1.000
Bacteria_SAR324clade(MarinegroupB)	0.000	1.000
Bacteria_Spirochaetota	0.000	1.000
Bacteria_Sumerlaeota	0.000	1.000
Bacteria_WS2	0.000	1.000
Eukaryota_	0.000	1.000

Table 3.3: Genus level Simper analysis results for the phytomicrobiome of C. myrtifolia. Taxa are listed as assigned by QIMME2 at level 6 (L6). Average and cumsum scores for each pair of sample types are listed below the labeled headers. Average refers to average contribution to dissimilarity for a given taxa and cumsum refers to the cumulative sum of dissimilarity for all taxa listed above a give row.

	Fruit vs. Leaf	
	average	cumsum
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_Mitochondria_Mitochondria	0.1904	0.2857
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Pseudomonadaceae_Pseudomonas	0.0363	0.3403
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Bacillus	0.0319	0.3881
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Psychrobacter	0.0298	0.4328
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Corynebacterium	0.0251	0.4705
Bacteria_Acidobacteriota_Acidobacteriae_Subgroup2_Subgroup2_Subgroup2	0.0235	0.5058
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Acinetobacter	0.0233	0.5407
Bacteria_Firmicutes_Bacilli_Staphylococcales_Staphylococcaceae_Staphylococcus	0.0232	0.5756
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Erwiniaceae_Pantoea	0.0231	0.6102
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_uncultured_uncultured	0.0173	0.6362
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Paracoccus	0.0145	0.6580
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Lautropia	0.0102	0.6733
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_	0.0098	0.6881
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Brevundimonas	0.0086	0.7009
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Enterobacteriaceae_Escherichia-Shigella	0.0082	0.7132

Bacteria_Firmicutes_Bacilli_Exiguobacterales_Exiguobacteraceae_Exiguobacterium	0.0074	0.7243
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Massilia	0.0072	0.7350
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Lawsonella	0.0060	0.7441
Bacteria_Firmicutes_Bacilli_Lactobacillales_Streptococcaceae_Streptococcus	0.0060	0.7530
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingomonas	0.0050	0.7605
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Anaerococcus	0.0043	0.7669
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_uncultured	0.0043	0.7733
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_Pseudarcicella	0.0041	0.7795
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Phenylobacterium	0.0032	0.7843
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xanthomonadaceae_Stenotrophomonas	0.0031	0.7889
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_	0.0031	0.7936
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Sporichthyaceae_hgcIclade	0.0030	0.7981
Bacteria_Actinobacteriota_Actinobacteria_Kineosporiales_Kineosporiaceae_Kineococcus	0.0029	0.8024
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Verrucomicrobiales_Verrucomicrobiaceae_uncultured	0.0028	0.8067
Bacteria_Bacteroidota_Bacteroidia_Flavobacteriales_Flavobacteriaceae_Flavobacterium	0.0025	0.8104
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Delftia	0.0024	0.8141
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_	0.0024	0.8177
Bacteria_Firmicutes_Bacilli_Lactobacillales_Enterococcaceae_Enterococcus	0.0023	0.8211
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Polynucleobacter	0.0021	0.8242
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Fictibacillus	0.0020	0.8273
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Bradyrhizobium	0.0020	0.8303
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Acidipila	0.0020	0.8332
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Occallatibacter	0.0020	0.8362
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Granulicella	0.0020	0.8391
Bacteria_Nitrospirota_Nitrospiria_Nitrospirales_Nitrospiraceae_Nitrospira	0.0020	0.8420
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Acidothermaceae_Acidothermus	0.0019	0.8448
Bacteria_Actinobacteriota_Actinobacteria_PeM15_PeM15_PeM15	0.0018	0.8476
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales__	0.0017	0.8501
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Frankiaceae_Frankia	0.0017	0.8526
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Micrococcus	0.0016	0.8550
Bacteria_Firmicutes_Clostridia___	0.0016	0.8574
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_	0.0015	0.8597
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Ferruginibacter	0.0015	0.8620
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_	0.0015	0.8643
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_CandidatusPlanktoluna	0.0015	0.8665
Bacteria_Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae_Dolosigranulum	0.0015	0.8688
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Hydrogenophaga	0.0015	0.8710
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Stappiaceae_Pannonibacter	0.0015	0.8732
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Acidovorax	0.0014	0.8753
Bacteria_Proteobacteria_Alphaproteobacteria___	0.0014	0.8774
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Moraxella	0.0013	0.8794
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Finegoldia	0.0013	0.8814
Bacteria_____	0.0013	0.8833
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Novosphingobium	0.0013	0.8852
Bacteria_Proteobacteria_Gammaproteobacteria_Cellvibrionales_Halieaceae_	0.0013	0.8871
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Sporichthyaceae_Sporichthyaceae	0.0012	0.8890
Bacteria_RCP2-54_RCP2-54_RCP2-54_RCP2-54_RCP2-54	0.0012	0.8908
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_AB1_AB1	0.0012	0.8926

Bacteria_Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae_Lactobacillus	0.0011	0.8943
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Afipia	0.0011	0.8959
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.0011	0.8976
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonadaceae_Rheinheimera	0.0011	0.8992
Bacteria_Proteobacteria_Gammaproteobacteria_Diplorickettsiales_Diplorickettsiaceae_uncultured	0.0011	0.9008
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_Aurantimicrobium	0.0010	0.9023
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Shewanellaceae_Shewanella	0.0010	0.9038
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_	0.0010	0.9053
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Arthrobacter	0.0010	0.9068
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_uncultured	0.0009	0.9082
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Chthoniobacterales_Chthoniobacteraceae_LD29	0.0009	0.9096
Bacteria_Actinobacteriota_Actinobacteria_Actinomycetales_Actinomycetaceae_Actinomyces	0.0009	0.9110
Bacteria_Myxococcota_Polyangia_Polyangiales_Sandaracinaceae_uncultured	0.0009	0.9123
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_Pseudoclavibacter	0.0009	0.9137
Bacteria_Acidobacteriota_Acidobacteriae_Bryobacterales_Bryobacteraceae_Bryobacter	0.0009	0.9150
Bacteria_Proteobacteria_Gammaproteobacteria_Cellvibrionales_Halieaceae_Halioglobus	0.0008	0.9163
Bacteria_Proteobacteria_Gammaproteobacteria_Legionellales_Legionellaceae_Legionella	0.0008	0.9175
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Janthinobacterium	0.0008	0.9186
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Rhodobacter	0.0008	0.9198
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingoaurantiacus	0.0007	0.9209
Bacteria_Proteobacteria_Gammaproteobacteria_WD260_WD260_WD260	0.0007	0.9219
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Verrucomicrobiales_Rubritaleaceae_Luteolibacter	0.0007	0.9230
Bacteria_Proteobacteria_Gammaproteobacteria___	0.0007	0.9240
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_SM2D12_SM2D12	0.0007	0.9250
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_Lentimicrobiaceae_	0.0007	0.9261
Bacteria_Chloroflexi_Ktedonobacteria_Ktedonobacterales_Ktedonobacteraceae_HSBOF53-F07	0.0006	0.9270
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Actinophytocola	0.0006	0.9279
Bacteria_Firmicutes_Bacilli_Staphylococcales_Gemellaceae_Gemella	0.0006	0.9289
Bacteria_Proteobacteria_Gammaproteobacteria_Pasteurellales_Pasteurellaceae_Haemophilus	0.0006	0.9298
Bacteria_Gemmatimonadota_PAUC43fmarinebenthicgroup_PAUC43	0.0006	0.9307
Bacteria_Proteobacteria_Gammaproteobacteria_Methylococcales_Methylomonadaceae_	0.0006	0.9317
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Brevibacteriaceae_Brevibacterium	0.0006	0.9325
Bacteria_Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae_Granulicatella	0.0006	0.9334
Bacteria_Bacteroidota_Bacteroidia_Flavobacteriales_Flavobacteriaceae_Gillisia	0.0006	0.9342
Bacteria_Proteobacteria_Gammaproteobacteria_Methylococcales_Methylomonadaceae_Methylobacter	0.0006	0.9350
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Nocardiaceae_Rhodococcus	0.0005	0.9359
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Polaromonas	0.0005	0.9367
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Solirubrobacter	0.0005	0.9375
Bacteria_Proteobacteria_Gammaproteobacteria_Steroidobacterales_Woeseiaceae_Woeseia	0.0005	0.9383
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_67-14_67-14	0.0005	0.9391
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Noviherbaspirillum	0.0005	0.9399
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Nitrosomonadaceae_Ellin6067	0.0005	0.9407
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_Sphingobacteriaceae_Pedobacter	0.0005	0.9414
Bacteria_Proteobacteria_Alphaproteobacteria_AlphaproteobacteriaIncertaeSedis_UnknownFamily_	0.0005	0.9422
Bacteria_Myxococcota_Myxococcia_Myxococcales_Anaeromyxobacteraceae_Anaeromyxobacter	0.0005	0.9429
Bacteria_Proteobacteria_Gammaproteobacteria_B2M28_B2M28_B2M28	0.0005	0.9437
Bacteria_Firmicutes_Negativicutes_Veillonellales-Selenomonadales_Veillonellaceae_Veillonella	0.0005	0.9444

Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Rothia	0.0005	0.9451
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_	0.0005	0.9459
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Hymenobacteraceae_Hymenobacter	0.0005	0.9466
Bacteria_Actinobacteriota_Thermoleophilia_Gaiellales_uncultured_uncultured	0.0005	0.9473
Bacteria_Bdellovibrionota_Oligoflexia_0319-6G20_0319-6G20_0319-6G20	0.0005	0.9479
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Malikia	0.0004	0.9486
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Anaerovoracaceae_S5-A14a	0.0004	0.9493
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Hyphomicrobiaceae_Pedomicrobium	0.0004	0.9499
Bacteria_Bdellovibrionota_Bdellovibrionia_Bdellovibrionales_Bdellovibrionaceae_Bdellovibrio	0.0004	0.9506
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Methylobacterium-Methylorubrum	0.0004	0.9512
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Kocuria	0.0004	0.9519
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_	0.0004	0.9525
Bacteria_Planctomycetota_Planctomycetes_Gemmatales_Gemmataceae_uncultured	0.0004	0.9531
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Dermabacteraceae_Brachybacterium	0.0004	0.9538
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Azorhizobium	0.0004	0.9544
Bacteria_SAR324clade(MarinegroupB)	0.0004	0.9550
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_uncultured	0.0004	0.9556
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Koribacteraceae_CandidatusKoribacter	0.0004	0.9562
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_Rhodoluna	0.0004	0.9569
Bacteria_Bacteroidota_Bacteroidia_Flavobacteriales_Weeksellaceae_Chryseobacterium	0.0004	0.9575
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_Emticicia	0.0004	0.9580
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Blastomonas	0.0004	0.9586
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Rhodoferax	0.0004	0.9592
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Halocynthiibacter	0.0004	0.9598
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_env.OPS17_env.OPS17	0.0004	0.9603
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Enterobacteriaceae_	0.0004	0.9609
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Methylophilaceae_Methylotenera	0.0004	0.9614
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Sediminibacterium	0.0003	0.9619
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_Sphingobacteriaceae_Mucilaginibacter	0.0003	0.9624
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Rhizorhapis	0.0003	0.9629
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Aquabacterium	0.0003	0.9634
Bacteria_Myxococcota_Polyangia_Polyangiales_Polyangiaceae_uncultured	0.0003	0.9639
Bacteria_Planctomycetota_Planctomycetes_Pirellulales_Pirellulaceae_Rhodopirellula	0.0003	0.9644
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_Roseomonas	0.0003	0.9649
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_Dyadobacter	0.0003	0.9653
Bacteria_Verrucomicrobiota_Chlamydiae_Chlamydiales_cvE6_cvE6	0.0003	0.9658
Bacteria_Chloroflexi_KD4-96_KD4-96_KD4-96_KD4-96	0.0003	0.9663
Bacteria_Deinococcota_Deinococci_Deinococcales_Deinococcaceae_uncultured	0.0003	0.9667
Bacteria_Patescibacteria_Saccharimonadia_Saccharimonadales__	0.0003	0.9672
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_	0.0003	0.9677
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_Anderseniella	0.0003	0.9681
Bacteria_Proteobacteria_Gammaproteobacteria_Diplorickettsiales_Diplorickettsiaceae_Aquicella	0.0003	0.9686
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Rurimicrobium	0.0003	0.9691
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_	0.0003	0.9695
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Dietziaceae_Dietzia	0.0003	0.9700
Bacteria_Aquificota_Aquificae_Aquificales_Aquificaceae_Hydrogenobacter	0.0003	0.9704
Bacteria_Proteobacteria_Alphaproteobacteria_Elsterales_Elsteraceae_uncultured	0.0003	0.9708
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhodomicrobiaceae_Rhodomicrobium	0.0003	0.9713

Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Hyphomicrobiaceae_	0.0003	0.9717
Bacteria_Acidobacteriota_Acidobacteriae_Solibacterales_Solibacteraceae_CandidatusSolibacter	0.0003	0.9722
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Fenollaria	0.0003	0.9726
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingopyxis	0.0003	0.9730
Bacteria_Proteobacteria_Gammaproteobacteria_Methylococcales_Methylomonadaceae_Methyloglobulus	0.0003	0.9735
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Morganellaceae_Proteus	0.0003	0.9739
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_AKYH767_AKYH767	0.0003	0.9743
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_A0839_A0839	0.0003	0.9747

Fruit vs. Nodule

	average	cumsum
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_Mitochondria_Mitochondria	0.1587	0.1809
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Psychrobacter	0.0454	0.2327
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Kocuria	0.0328	0.2700
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Bacillus	0.0316	0.3061
Bacteria_Firmicutes_Bacilli_Paenibacillales_Paenibacillaceae_Paenibacillus	0.0286	0.3387
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Corynebacterium	0.0256	0.3678
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Acinetobacter	0.0230	0.3940
Bacteria_Firmicutes_Bacilli_Staphylococcales_Staphylococcaceae_Staphylococcus	0.0223	0.4194
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Rhodocyclaceae_uncultured	0.0193	0.4414
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Blastococcus	0.0173	0.4612
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Paracoccus	0.0170	0.4805
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_	0.0114	0.4935
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Brevundimonas	0.0102	0.5052
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Pseudomonadaceae_Pseudomonas	0.0098	0.5164
Bacteria_Actinobacteriota_Rubrobacteria_Rubrobacterales_Rubrobacteriaceae_Rubrobacter	0.0095	0.5272
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Enterobacteriaceae_Escherichia-Shigella	0.0082	0.5365
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_uncultured	0.0080	0.5457
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_	0.0076	0.5544
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Verrucomicrobiales_Verrucomicrobiaceae_uncultured	0.0073	0.5627
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Lawsonella	0.0070	0.5707
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Morganellaceae_Photorhabdus	0.0068	0.5784
Bacteria_Firmicutes_Bacilli_Lactobacillales_Streptococcaceae_Streptococcus	0.0064	0.5857
Eukaryota_____	0.0062	0.5928
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Enterobacteriaceae_	0.0057	0.5993
Bacteria_Actinobacteriota_Actinobacteria_Streptomycetales_Streptomycetaceae_Streptomyces	0.0057	0.6058
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.0056	0.6122
Bacteria_Firmicutes_Bacilli_Entomoplasmatales_Entomoplasmataceae_Mesoplasma	0.0049	0.6178
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xanthomonadaceae_Stenotrophomonas	0.0048	0.6232
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_uncultured	0.0045	0.6283
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Frankiaceae_Frankia	0.0045	0.6334
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_Pseudarcicella	0.0043	0.6384
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Polynucleobacter	0.0042	0.6432
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Hydrogenophaga	0.0042	0.6480
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Anaerococcus	0.0041	0.6527
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_	0.0041	0.6574
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Bogoriellaceae_Georgenia	0.0041	0.6620
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_	0.0040	0.6666

Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Intrasporangiaceae_Ornithinimicrobium	0.0039	0.6710
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Rubellimicrobium	0.0037	0.6752
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Sporichthyaceae_hgcIclade	0.0034	0.6791
Bacteria_Bacteroidota_Bacteroidia_Flavobacteriales_Flavobacteriaceae_Flavobacterium	0.0034	0.6830
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobiaceae	0.0033	0.6868
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Modestobacter	0.0033	0.6906
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Phenylobacterium	0.0032	0.6943
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Massilia	0.0029	0.6975
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Microscillaceae_uncultured	0.0028	0.7008
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Nocardiaceae_Rhodococcus	0.0028	0.7039
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_D05-2_D05-2	0.0028	0.7071
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Geodermatophilus	0.0026	0.7101
Bacteria_Chloroflexi_Chloroflexia_Thermomicrobiales_JG30-KF-CM45_JG30-KF-CM45	0.0026	0.7130
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Shewanellaceae_Shewanella	0.0025	0.7159
Bacteria_Proteobacteria_Gammaproteobacteria_Cellvibrionales_Cellvibrionaceae_Cellvibrio	0.0025	0.7188
Bacteria_____	0.0025	0.7216
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Delftia	0.0025	0.7244
Bacteria_Firmicutes_Bacilli_Lactobacillales_Enterococcaceae_Enterococcus	0.0024	0.7272
Bacteria_Bacteroidota_Bacteroidia_Bacteroidales_Dysgonomonadaceae_Dysgonomonas	0.0024	0.7300
Bacteria_Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae_Dolosigranulum	0.0024	0.7327
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_Aliterella	0.0024	0.7355
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Rhodocyclaceae_Azoarcus	0.0024	0.7382
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_uncultured_uncultured	0.0022	0.7407
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Hymenobacteraceae_Pontibacter	0.0022	0.7432
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Cellulomonadaceae_Cellulomonas	0.0022	0.7457
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_GloeocapsaPCC-7428	0.0021	0.7482
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingomonas	0.0021	0.7506
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Devosiaceae_Devosia	0.0021	0.7530
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Micrococcus	0.0021	0.7553
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Verrucomicrobiales_Rubritaleaceae_Luteolibacter	0.0021	0.7577
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_67-14_67-14	0.0021	0.7600
Bacteria_Deinococcota_Deinococci_Deinococcales_Deinococcaceae_Deinococcus	0.0020	0.7623
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Solirubrobacter	0.0019	0.7645
Bacteria_Firmicutes_Bacilli_Exiguobacterales_Exiguobacteraceae_Exiguobacterium	0.0019	0.7667
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales__	0.0019	0.7689
Bacteria_Nitrospirota_Nitrospiria_Nitrospirales_Nitrospiraceae_Nitrospira	0.0018	0.7710
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_Arcicella	0.0018	0.7731
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_uncultured_uncultured	0.0018	0.7751
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Ferruginibacter	0.0018	0.7772
Bacteria_Actinobacteriota_Actinobacteria_PeM15_PeM15_PeM15	0.0018	0.7793
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Alcaligenaceae_	0.0018	0.7813
Eukaryota_Phragmoplastophyta_Embryophyta_Magnoliophyta_Magnoliophyta_Magnoliophyta	0.0017	0.7833
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_	0.0016	0.7852
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonadaceae_Rheinheimera	0.0016	0.7871
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_CandidatusPlanktoluna	0.0016	0.7889
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Dermabacteraceae_Brachybacterium	0.0016	0.7907
Bacteria_Firmicutes_Clostridia___	0.0016	0.7925
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Cyclobacteriaceae_Algoriphagus	0.0016	0.7943

Bacteria_Actinobacteriota_Actinobacteria_Micromonosporales_Micromonosporaceae_Actinoplanes	0.0016	0.7961
Bacteria_Deinococcota_Deinococci_Deinococcales_Trueperaceae_Truepera	0.0015	0.7978
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_DapisostemonumCCIBt3536	0.0015	0.7995
Bacteria_Proteobacteria_Gammaproteobacteria_Methylococcales_Methylomonadaceae_Methylomonas	0.0015	0.8011
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Novosphingobium	0.0015	0.8028
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Stappiaceae_Pannonibacter	0.0015	0.8045
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Acidovorax	0.0014	0.8061
Bacteria_Proteobacteria_Alphaproteobacteria___	0.0014	0.8077
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Nocardioides	0.0014	0.8093
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_uncultured	0.0014	0.8109
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_uncultured	0.0014	0.8124
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Moraxella	0.0014	0.8140
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_	0.0014	0.8156
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Finegoldia	0.0013	0.8171
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_Sphingobacteriaceae_Pedobacter	0.0013	0.8186
Bacteria_Proteobacteria_Gammaproteobacteria_Diplorickettsiales_Diplorickettsiaceae_uncultured	0.0013	0.8200
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Ellin6055	0.0013	0.8215
Bacteria_Proteobacteria_Gammaproteobacteria_Cellvibrionales_Halieaceae_	0.0013	0.8229
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales__	0.0013	0.8243
Bacteria_Firmicutes_Bacilli_Lactobacillales__	0.0012	0.8258
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_YC-ZSS-LKJ147	0.0012	0.8272
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Arthrobacter	0.0012	0.8286
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Sporichthyaceae_Sporichthyaceae	0.0012	0.8300
Bacteria_Firmicutes_Bacilli_Staphylococcales_Gemellaceae_Gemella	0.0012	0.8314
Bacteria_Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae_Lactobacillus	0.0012	0.8327
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_AB1_AB1	0.0012	0.8341
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Aquabacterium	0.0012	0.8354
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Janthinobacterium	0.0012	0.8368
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Afipia	0.0011	0.8380
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_PMMR1	0.0011	0.8393
Bacteria_Firmicutes_Bacilli_Bacillales_Planococcaceae_Planococcus	0.0010	0.8404
Bacteria_Chloroflexi_KD4-96_KD4-96_KD4-96_KD4-96	0.0010	0.8416
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_ChroococcidiopsisSAG2023	0.0010	0.8428
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_Aurantimicrobium	0.0010	0.8440
Bacteria_Actinobacteriota_Actinobacteria_Frankiales__	0.0010	0.8451
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Intrasporangiaceae_Ornithinicoccus	0.0010	0.8463
Bacteria_Myxococcota_Polyangia_Polyangiales_Sandaracinaceae_uncultured	0.0010	0.8474
Bacteria_Actinobacteriota_Actinobacteria_Kineosporiales_Kineosporiaceae_	0.0010	0.8486
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_uncultured	0.0010	0.8497
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_uncultured_uncultured	0.0010	0.8508
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_Pseudoclavibacter	0.0010	0.8519
Bacteria_Actinobacteriota_Actinobacteria_Euzebyales_Euzebyaceae_uncultured	0.0009	0.8530
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobium	0.0009	0.8541
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Chthoniobacterales_Chthoniobacteraceae_LD29	0.0009	0.8551
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Rothia	0.0009	0.8562
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Rhodobacter	0.0009	0.8572
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Sediminibacterium	0.0009	0.8583
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_uncultured_uncultured	0.0009	0.8593

Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_uncultured	0.0009	0.8603
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingopyxis	0.0009	0.8613
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Intrasporangiaceae_	0.0009	0.8623
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Noviherbaspirillum	0.0009	0.8633
Bacteria_Proteobacteria_Gammaproteobacteria_Cellvibrionales_Halieaceae_Halioglobus	0.0008	0.8642
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Rhodanobacteraceae_uncultured	0.0008	0.8652
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_SM2D12_SM2D12	0.0008	0.8661
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Niastella	0.0008	0.8670
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Saprospiraceae_uncultured	0.0008	0.8680
Bacteria_Proteobacteria_Gammaproteobacteria_Legionellales_Legionellaceae_Legionella	0.0008	0.8689
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Undibacterium	0.0008	0.8698
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Dermabacteraceae_	0.0008	0.8706
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingoaurantiacus	0.0008	0.8715
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Methylobacterium-Methylorubrum	0.0008	0.8724
Bacteria_Proteobacteria_Gammaproteobacteria___	0.0008	0.8733
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_	0.0008	0.8741
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_uncultured	0.0008	0.8750
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_Craurococcus-Caldovatus	0.0007	0.8758
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Rhizorhapis	0.0007	0.8767
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Dietziaceae_Dietzia	0.0007	0.8775
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Propionibacteriaceae_Cutibacterium	0.0007	0.8784
Bacteria_Desulfobacterota_Desulfuromonadia_Geobacterales_Geobacteraceae_Citrifermentans	0.0007	0.8792
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Brevibacteriaceae_Brevibacterium	0.0007	0.8801
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_Dyadobacter	0.0007	0.8809
Bacteria_Firmicutes_Bacilli_Bacillales_Planococcaceae_	0.0007	0.8817
Bacteria_Proteobacteria_Alphaproteobacteria_Azospirillales_Azospirillaceae_Skermanella	0.0007	0.8825
Bacteria_Proteobacteria_Gammaproteobacteria_Pasteurellales_Pasteurellaceae_Haemophilus	0.0007	0.8832
Bacteria_Proteobacteria_Gammaproteobacteria_Methylococcales_Methylomonadaceae_Methylobacter	0.0007	0.8840
Archaea_Crenarchaeota_Nitrososphaeria_Nitrososphaerales_Nitrososphaeraceae_	0.0007	0.8848
Bacteria_Bdellovibrionota_Bdellovibrionia_Bdellovibrionales_Bdellovibrionaceae_Bdellovibrio	0.0007	0.8856
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Erwiniaceae_Pantoea	0.0007	0.8864
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Polaromonas	0.0007	0.8871
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Aureimonas	0.0007	0.8879

Fruit vs. Root

	average	cumsum
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Frankiaceae_Frankia	0.1793	0.1952
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_Mitochondria_Mitochondria	0.1581	0.3673
Bacteria_Firmicutes_Bacilli_Lactobacillales__	0.0627	0.4356
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Psychrobacter	0.0331	0.4717
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Bacillus	0.0318	0.5063
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Corynebacterium	0.0248	0.5333
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Acinetobacter	0.0234	0.5588
Bacteria_Firmicutes_Bacilli_Staphylococcales_Staphylococcaceae_Staphylococcus	0.0230	0.5838
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_uncultured	0.0156	0.6008
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Paracoccus	0.0145	0.6166
Bacteria_Actinobacteriota_Actinobacteria_Streptomycetales_Streptomycetaceae_Streptomyces	0.0120	0.6297
Bacteria_Actinobacteriota_Rubrobacteria_Rubrobacterales_Rubrobacteriaceae_Rubrobacter	0.0120	0.6427
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_	0.0113	0.6550

Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Pseudomonadaceae_Pseudomonas	0.0103	0.6663
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhodomicrobiaceae_Rhodomicrobium	0.0094	0.6765
Eukaryota_Phragmoplastophyta_Embryophyta_Magnoliophyta_Magnoliophyta_Magnoliophyta	0.0087	0.6860
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Brevundimonas	0.0086	0.6954
Bacteria_Proteobacteria_Gammaproteobacteria_Steroidobacterales_Steroidobacteraceae_Steroidobacter	0.0085	0.7047
Bacteria_Proteobacteria_Gammaproteobacteria_Cardiobacteriales_Wohlfahrtiimonadaceae_Ignatzschineria	0.0084	0.7138
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Enterobacteriaceae_Escherichia-Shigella	0.0082	0.7227
Bacteria_Firmicutes_Bacilli_Lactobacillales_Streptococcaceae_Streptococcus	0.0060	0.7293
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Lawsonella	0.0060	0.7358
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Phenylobacterium	0.0047	0.7410
Bacteria_Proteobacteria_Gammaproteobacteria_GammaproteobacteriaIncertaeSedis_UnknownFamily_Acidibacter	0.0047	0.7461
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_GloeocapsaPCC-7428	0.0044	0.7509
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_uncultured	0.0043	0.7555
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Anaerococcus	0.0043	0.7602
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_Pseudarcicella	0.0041	0.7647
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_DapisostemonumCCIBt3536	0.0040	0.7691
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Tissierella	0.0040	0.7734
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingomonas	0.0038	0.7776
Bacteria_Fusobacteriota_Fusobacteriia_Fusobacteriales_Fusobacteriaceae_Fusobacterium	0.0038	0.7817
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Hyphomonadaceae_SWB02	0.0032	0.7852
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xanthomonadaceae_Stenotrophomonas	0.0031	0.7885
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Sporichthyaceae_hgcIclade	0.0030	0.7917
Archaea_Crenarchaeota_Nitrososphaeria_Nitrososphaerales_Nitrososphaeraceae_	0.0029	0.7949
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Verrucomicrobiales_Verrucomicrobiaceae_uncultured	0.0029	0.7980
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Massilia	0.0028	0.8011
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_	0.0027	0.8040
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_	0.0027	0.8069
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_uncultured_uncultured	0.0026	0.8097
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Neisseriaceae_	0.0026	0.8125
Bacteria_Bacteroidota_Bacteroidia_Flavobacteriales_Flavobacteriaceae_Flavobacterium	0.0025	0.8152
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Delftia	0.0024	0.8179
Bacteria_Firmicutes_Bacilli_Lactobacillales_Enterococcaceae_Enterococcus	0.0023	0.8204
Bacteria_Firmicutes_Bacilli_Bacillales__	0.0021	0.8227
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Polynucleobacter	0.0021	0.8249
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Burkholderia-Caballeronia-Paraburkholderia	0.0020	0.8271
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_67-14_67-14	0.0020	0.8293
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_Blastocatella	0.0020	0.8314
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_ChroococcidiopsisSAG2023	0.0020	0.8335
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Geodermatophilus	0.0019	0.8356
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales__	0.0019	0.8376
Bacteria_Nitrospirota_Nitrospiria_Nitrospirales_Nitrospiraceae_Nitrospira	0.0019	0.8396
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Promicromonosporaceae_Cellulosimicrobium	0.0018	0.8416
Bacteria_Actinobacteriota_Actinobacteria_PeM15_PeM15_PeM15	0.0018	0.8436
Bacteria_Proteobacteria_Gammaproteobacteria_Pasteurellales_Pasteurellaceae_	0.0017	0.8455
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales__	0.0017	0.8474
Bacteria_Firmicutes_Bacilli_Erysipelotrichales_Erysipelotrichaceae_ZOR0006	0.0017	0.8493
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Ferruginibacter	0.0017	0.8511
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Micrococcus	0.0016	0.8529

Eukaryota_____	0.0016	0.8547
Bacteria_Firmicutes_Clostridia___	0.0016	0.8564
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_Aliterella	0.0016	0.8582
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_	0.0015	0.8598
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Tepidimicrobium	0.0015	0.8615
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_	0.0015	0.8632
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_CandidatusPlanktoluna	0.0015	0.8648
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobiaceae	0.0015	0.8665
Bacteria_Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae_Dolosigranulum	0.0015	0.8681
Bacteria_Firmicutes_Clostridia_Oscillospirales_Ruminococcaceae_CandidatusSoleaferrea	0.0015	0.8697
Bacteria_____	0.0015	0.8713
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Hydrogenophaga	0.0015	0.8729
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Stappiaceae_Pannonibacter	0.0015	0.8745
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Acidovorax	0.0014	0.8760
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Novosphingobium	0.0014	0.8776
Bacteria_Proteobacteria_Alphaproteobacteria___	0.0014	0.8791
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.0013	0.8805
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_	0.0013	0.8820
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Moraxella	0.0013	0.8834
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Finegoldia	0.0013	0.8849
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Blastococcus	0.0013	0.8863
Bacteria_Proteobacteria_Gammaproteobacteria_Cellvibrionales_Halieaceae_	0.0013	0.8877
Bacteria_Chloroflexi_Chloroflexia_Kallotenuales_AKIW781_AKIW781	0.0012	0.8890
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Sporichthyaceae_Sporichthyaceae	0.0012	0.8903
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_AB1_AB1	0.0012	0.8916
Bacteria_Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae_Lactobacillus	0.0012	0.8929
Bacteria_Firmicutes_Bacilli_Exiguobacterales_Exiguobacteraceae_Exiguobacterium	0.0012	0.8942
Bacteria_Myxococcota_Polyangia_Polyangiales_Sandaracinaceae_uncultured	0.0012	0.8955
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Niastella	0.0011	0.8967
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Afipia	0.0011	0.8979
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonadaceae_Rheinheimera	0.0011	0.8991
Bacteria_Proteobacteria_Gammaproteobacteria_Diplorickettsiales_Diplorickettsiaceae_uncultured	0.0011	0.9003
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_Aurantimicrobium	0.0010	0.9014
Bacteria_Firmicutes_Bacilli_Erysipelotrichales_Erysipelotrichaceae_	0.0010	0.9025
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Shewanellaceae_Shewanella	0.0010	0.9036
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Arthrobacter	0.0010	0.9046
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_uncultured	0.0009	0.9057
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Chthoniobacterales_Chthoniobacteraceae_LD29	0.0009	0.9067
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_Pseudoclavibacter	0.0009	0.9077
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_	0.0009	0.9087
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Nocardiaceae_Rhodococcus	0.0009	0.9096
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_	0.0009	0.9106
Bacteria_Proteobacteria_Gammaproteobacteria_Cellvibrionales_Halieaceae_Halioglobus	0.0008	0.9115
Bacteria_Acidobacteriota_Blastocatellia_Pyrinomonadales_Pyrinomonadaceae_RB41	0.0008	0.9124
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Morganellaceae_Photorhabdus	0.0008	0.9133
Bacteria_Proteobacteria_Gammaproteobacteria_Legionellales_Legionellaceae_Legionella	0.0008	0.9141
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Janthinobacterium	0.0008	0.9150

Bacteria_Verrucomicrobiota_Verrucomicrobiae_Verrucomicrobiales_Rubritaleaceae_Luteolibacter	0.0008	0.9158
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingoaurantiacus	0.0008	0.9166
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Rhodobacter	0.0008	0.9175
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_	0.0007	0.9183
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Nocardioides	0.0007	0.9191
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_uncultured_uncultured	0.0007	0.9199
Bacteria_Deinococcota_Deinococci_Deinococcales_Deinococcaceae_Deinococcus	0.0007	0.9206
Bacteria_Proteobacteria_Gammaproteobacteria___	0.0007	0.9214
Bacteria_Chloroflexi_Anaerolineae_Ardenticatenales_Ardenticatenaceae_uncultured	0.0007	0.9222
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_SM2D12_SM2D12	0.0007	0.9229
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_Lentimicrobiaceae_	0.0007	0.9236
Bacteria_Chloroflexi_Chloroflexia_Thermomicrobiales_AKYG1722_AKYG1722	0.0007	0.9243
Bacteria_Proteobacteria_Gammaproteobacteria_Pasteurellales_Pasteurellaceae_Haemophilus	0.0007	0.9251
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_uncultured_uncultured	0.0006	0.9258
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Actinophytocola	0.0006	0.9264
Bacteria_Firmicutes_Bacilli_Staphylococcales_Gemellaceae_Gemella	0.0006	0.9271
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_ChroococcidiopsisPCC7203	0.0006	0.9278
Bacteria_Gemmatimonadota_PAUC43fmarinebenthicgroup	0.0006	0.9285
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_	0.0006	0.9291
Bacteria_Proteobacteria_Gammaproteobacteria_Methylococcales_Methylomonadaceae_	0.0006	0.9298
Bacteria_Bacteroidota_Bacteroidia_Flavobacteriales_Flavobacteriaceae_Gillisia	0.0006	0.9304
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Brevibacteriaceae_Brevibacterium	0.0006	0.9310
Bacteria_Proteobacteria_Gammaproteobacteria_Methylococcales_Methylomonadaceae_Methylobacter	0.0006	0.9316
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Solirubrobacter	0.0005	0.9322
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Polaromonas	0.0005	0.9328
Bacteria_Proteobacteria_Gammaproteobacteria_Steroidobacterales_Woeseiaceae_Woeseia	0.0005	0.9334
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Granulicella	0.0005	0.9340
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_Acidocella	0.0005	0.9346
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Nitrosomonadaceae_Ellin6067	0.0005	0.9352
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Noviherbaspirillum	0.0005	0.9357
Bacteria_Firmicutes_Clostridia_Oscillospirales_Ruminococcaceae_uncultured	0.0005	0.9363
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_Sphingobacteriaceae_Pedobacter	0.0005	0.9369
Bacteria_Acidobacteriota_Acidobacteriae_Subgroup2_Subgroup2_Subgroup2	0.0005	0.9374
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_	0.0005	0.9380
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Ellin6055	0.0005	0.9385
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Microvirga	0.0005	0.9391
Bacteria_Proteobacteria_Alphaproteobacteria_AlphaproteobacteriaIncertaeSedis_UnknownFamily_	0.0005	0.9396
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Hymenobacteraceae_Hymenobacter	0.0005	0.9402
Bacteria_Cyanobacteria_Cyanobacteriia_Thermosynechococcales_Acaryochloridaceae_AcaryochlorisMBIC11017	0.0005	0.9407
Bacteria_Myxococcota_Myxococcia_Myxococcales_Anaeromyxobacteraceae_Anaeromyxobacter	0.0005	0.9413
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingopyxis	0.0005	0.9418
Bacteria_Proteobacteria_Gammaproteobacteria_B2M28_B2M28_B2M28	0.0005	0.9424
Bacteria_Firmicutes_Negativicutes_Veillonellales-Selenomonadales_Veillonellaceae_Veillonella	0.0005	0.9429
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Rothia	0.0005	0.9434
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_uncultured	0.0005	0.9439
Bacteria_Deinococcota_Deinococci_Deinococcales_Trueperaceae_Truepera	0.0005	0.9445
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Hyphomicrobiaceae_Pedomicrobium	0.0005	0.9450
Bacteria_Acidobacteriota_Acidobacteriae_Bryobacterales_Bryobacteraceae_Bryobacter	0.0005	0.9455

Bacteria_Actinobacteriota_Actinobacteria_Frankiales_uncultured_uncultured	0.0005	0.9460
Bacteria_Bdellovibrionota_Oligoflexia_0319-6G20_0319-6G20_0319-6G20	0.0005	0.9465
Archaea_Crenarchaeota_Nitrososphaeria_Nitrososphaerales_Nitrososphaeraceae_CandidatusNitrocosmicus	0.0005	0.9470
Bacteria_Bdellovibrionota_Bdellovibrionia_Bdellovibrionales_Bdellovibrionaceae_Bdellovibrio	0.0005	0.9475
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Malikia	0.0004	0.9480
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Anaerovoracaceae_S5-A14a	0.0004	0.9485
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Methylobacterium-Methylorubrum	0.0004	0.9489
Bacteria_Bacteroidota_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	0.0004	0.9494
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_	0.0004	0.9499
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_uncultured	0.0004	0.9503

Fruit vs. Stem

	average	cumsum
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_Mitochondria_Mitochondria	0.2637	0.3943
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Corynebacterium	0.0445	0.4609
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Bacillus	0.0315	0.5080
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Psychrobacter	0.0298	0.5525
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Acinetobacter	0.0289	0.5957
Bacteria_Firmicutes_Bacilli_Staphylococcales_Staphylococcaceae_Staphylococcus	0.0190	0.6242
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Paracoccus	0.0145	0.6459
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Pseudomonadaceae_Pseudomonas	0.0104	0.6615
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_	0.0102	0.6767
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Frankiaceae_Frankia	0.0088	0.6899
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Brevundimonas	0.0085	0.7026
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Lawsonella	0.0083	0.7150
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Enterobacteriaceae_Escherichia-Shigella	0.0082	0.7272
Bacteria_Firmicutes_Bacilli_Lactobacillales_Streptococcaceae_Streptococcus	0.0061	0.7364
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_uncultured	0.0046	0.7433
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_Pseudarcicella	0.0041	0.7494
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Anaerococcus	0.0039	0.7553
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xanthomonadaceae_Stenotrophomonas	0.0037	0.7609
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Massilia	0.0033	0.7658
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Phenylobacterium	0.0032	0.7706
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Verrucomicrobiales_Verrucomicrobiaceae_uncultured	0.0031	0.7752
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Sporichthyaceae_hgcIclade	0.0030	0.7797
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_	0.0026	0.7835
Bacteria_Bacteroidota_Bacteroidia_Flavobacteriales_Flavobacteriaceae_Flavobacterium	0.0025	0.7873
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Delftia	0.0024	0.7909
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Enterobacteriaceae_	0.0024	0.7945
Bacteria_Firmicutes_Bacilli_Lactobacillales_Enterococcaceae_Enterococcus	0.0023	0.7979
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Polynucleobacter	0.0021	0.8011
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_uncultured_uncultured	0.0020	0.8040
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Shewanellaceae_Shewanella	0.0019	0.8069
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Novosphingobium	0.0019	0.8097
Bacteria_Actinobacteriota_Actinobacteria_PeM15_PeM15_PeM15	0.0019	0.8125
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Micrococcus	0.0019	0.8153
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_	0.0018	0.8180
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonadaceae_Rheinheimera	0.0018	0.8207
Bacteria_Nitrospirota_Nitrospiria_Nitrospirales_Nitrospiraceae_Nitrospira	0.0018	0.8234

Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales__	0.0017	0.8259
Bacteria_Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae_Dolosigranulum	0.0017	0.8284
Bacteria_Acidobacteriota_Acidobacteriae_Subgroup2_Subgroup2_Subgroup2	0.0016	0.8308
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingomonas	0.0016	0.8332
Bacteria_Firmicutes_Clostridia___	0.0016	0.8356
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Ferruginibacter	0.0015	0.8379
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_	0.0015	0.8402
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_CandidatusPlanktoluna	0.0015	0.8424
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Hydrogenophaga	0.0015	0.8447
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Geobacillus	0.0015	0.8469
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Stappiaceae_Pannonibacter	0.0015	0.8491
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Finegoldia	0.0014	0.8512
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Acidovorax	0.0014	0.8534
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Erwiniaceae_Pantoea	0.0014	0.8554
Bacteria_Proteobacteria_Alphaproteobacteria___	0.0014	0.8575
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_	0.0014	0.8596
Bacteria_____	0.0014	0.8616
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Moraxella	0.0013	0.8636
Bacteria_Proteobacteria_Gammaproteobacteria_Cellvibrionales_Halieaceae_	0.0013	0.8655
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Rhodoferax	0.0013	0.8674
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Sporichthyaceae_Sporichthyaceae	0.0012	0.8692
Bacteria_Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae_Lactobacillus	0.0012	0.8710
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_AB1_AB1	0.0012	0.8728
Bacteria_Firmicutes_Bacilli_Exiguobacterales_Exiguobacteraceae_Exiguobacterium	0.0012	0.8746
Bacteria_Proteobacteria_Gammaproteobacteria_Diplorickettsiales_Diplorickettsiaceae_uncultured	0.0011	0.8762
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_uncultured	0.0011	0.8779
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Afipia	0.0011	0.8795
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.0011	0.8811
Bacteria_Proteobacteria_Gammaproteobacteria_B2M28_B2M28_B2M28	0.0010	0.8827
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_Aurantimicrobium	0.0010	0.8842
Bacteria_Acidobacteriota_Acidobacteriae_Bryobacterales_Bryobacteraceae_Bryobacter	0.0010	0.8857
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Arthrobacter	0.0010	0.8871
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Halobacillus	0.0010	0.8886
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Chthoniobacterales_Chthoniobacteraceae_LD29	0.0009	0.8900
Bacteria_Myxococcota_Polyangia_Polyangiales_Sandaracinaceae_uncultured	0.0009	0.8913
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_Pseudoclavibacter	0.0009	0.8927
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Janthinobacterium	0.0009	0.8940
Bacteria_Proteobacteria_Gammaproteobacteria_Cellvibrionales_Halieaceae_Halioglobus	0.0008	0.8953
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Acidipila	0.0008	0.8965
Bacteria_Proteobacteria_Gammaproteobacteria_Legionellales_Legionellaceae_Legionella	0.0008	0.8977
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Granulicella	0.0008	0.8988
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Rhodobacter	0.0008	0.8999
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingoaurantiacus	0.0007	0.9010
Bacteria_Firmicutes_Bacilli_Staphylococcales_Gemellaceae_Gemella	0.0007	0.9021
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_Sphingobacteriaceae_Pedobacter	0.0007	0.9032
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_67-14_67-14	0.0007	0.9043
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Verrucomicrobiales_Rubritaleaceae_Luteolibacter	0.0007	0.9053

Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Kocuria	0.0007	0.9064
Bacteria_Proteobacteria_Gammaproteobacteria___	0.0007	0.9074
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_SM2D12_SM2D12	0.0007	0.9084
Bacteria_Proteobacteria_Gammaproteobacteria_Pasteurellales_Pasteurellaceae_Haemophilus	0.0007	0.9094
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_Lentimicrobiaceae_	0.0007	0.9104
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Nitrosomonadaceae_Ellin6067	0.0007	0.9114
Bacteria_Firmicutes_Bacilli_Bacillales_Planococcaceae_	0.0006	0.9124
Bacteria_Deinococcota_Deinococci_Deinococcales_Deinococcaceae_Deinococcus	0.0006	0.9133
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Actinophytocola	0.0006	0.9143
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Acidothermaceae_Acidothermus	0.0006	0.9152
Bacteria_Gemmatimonadota_PAUC43fmarinebenthic	0.0006	0.9161
Bacteria_SAR324clade(MarinegroupB)	0.0006	0.9170
Bacteria_Proteobacteria_Gammaproteobacteria_Methylococcales_Methylomonadaceae_	0.0006	0.9179
Bacteria_Proteobacteria_Gammaproteobacteria_WD260_WD260_WD260	0.0006	0.9188
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Dermabacteraceae_Brachybacterium	0.0006	0.9197
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_Phreatobacter	0.0006	0.9206
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Brevibacteriaceae_Brevibacterium	0.0006	0.9215
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Hymenobacteraceae_Hymenobacter	0.0006	0.9223
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Rothia	0.0006	0.9232
Bacteria_Bacteroidota_Bacteroidia_Flavobacteriales_Flavobacteriaceae_Gillisia	0.0006	0.9240
Bacteria_Proteobacteria_Gammaproteobacteria_Methylococcales_Methylomonadaceae_Methylobacter	0.0006	0.9248
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Nocardiaceae_Rhodococcus	0.0005	0.9257
Bacteria_Proteobacteria_Gammaproteobacteria_GammaproteobacteriaIncertaeSedis_UnknownFamily_Acidibacter	0.0005	0.9265
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Polaromonas	0.0005	0.9273
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_	0.0005	0.9281
Bacteria_Proteobacteria_Gammaproteobacteria_Steroidobacterales_Woeseiaceae_Woeseia	0.0005	0.9289
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_	0.0005	0.9297
Bacteria_Proteobacteria_Gammaproteobacteria_Thiohalorhabdales_Thiohalorhabdaceae_uncultured	0.0005	0.9305
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Noviherbaspirillum	0.0005	0.9312
Bacteria_Proteobacteria_Alphaproteobacteria_AlphaproteobacteriaIncertaeSedis_UnknownFamily_	0.0005	0.9320
Bacteria_Myxococcota_Myxococcia_Myxococcales_Anaeromyxobacteraceae_Anaeromyxobacter	0.0005	0.9327
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_alphaIcluster	0.0005	0.9335
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Pseudorhodoplanes	0.0005	0.9342
Bacteria_Planctomycetota_Planctomycetes_Gemmatales_Gemmataceae_uncultured	0.0005	0.9349
Bacteria_Firmicutes_Negativicutes_Veillonellales-Selenomonadales_Veillonellaceae_Veillonella	0.0005	0.9357
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_	0.0005	0.9364
Bacteria_Proteobacteria_Gammaproteobacteria_Chromatiales_Chromatiaceae_CandidatusThiobios	0.0005	0.9371
Bacteria_Bdellovibrionota_Oligoflexia_0319-6G20_0319-6G20_0319-6G20	0.0005	0.9378
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Yersiniaceae_	0.0005	0.9384
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Malikia	0.0004	0.9391
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Anaerovoracaceae_S5-A14a	0.0004	0.9398
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Hyphomicrobiaceae_Pedomicrobium	0.0004	0.9404
Bacteria_Actinobacteriota_Actinobacteria_Actinomycetales_Actinomycetaceae_Actinomyces	0.0004	0.9411
Bacteria_Bdellovibrionota_Bdellovibrionia_Bdellovibrionales_Bdellovibrionaceae_Bdellovibrio	0.0004	0.9418
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Dinghuibacter	0.0004	0.9424
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Sutterellaceae_uncultured	0.0004	0.9431
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Methylobacterium-Methylorubrum	0.0004	0.9437
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Azorhizobium	0.0004	0.9443

Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_uncultured	0.0004	0.9449
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_Rhodoluna	0.0004	0.9455
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcaceae_Paraclostridium	0.0004	0.9461
Bacteria_Bacteroidota_Bacteroidia_Flavobacteriales_Weeksellaceae_Chryseobacterium	0.0004	0.9467
Bacteria_Planctomycetota_Phycisphaerae_Tepidisphaerales_WD2101soilgroup_WD2101soilgroup	0.0004	0.9473
Bacteria_Aquificota_Aquificae_Aquificales_Aquificaceae_Hydrogenobacter	0.0004	0.9479
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_Emticicia	0.0004	0.9485
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Blastomonas	0.0004	0.9491
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Halocynthiibacter	0.0004	0.9497
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Turicella	0.0004	0.9502
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_env.OPS17_env.OPS17	0.0004	0.9508
Bacteria_Proteobacteria_Gammaproteobacteria_KI89Aclade_KI89Aclade_KI89Aclade	0.0004	0.9513
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Roseiarcus	0.0004	0.9519
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Rhodocyclaceae_	0.0004	0.9524
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_	0.0004	0.9530
Bacteria_Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae_Granulicatella	0.0004	0.9535
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Methylophilaceae_Methylotenera	0.0004	0.9540
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Neisseriaceae_Neisseria	0.0003	0.9546
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_MWH-Ta3	0.0003	0.9551
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Sediminibacterium	0.0003	0.9556
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_Sphingobacteriaceae_Mucilaginibacter	0.0003	0.9561
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Rhizorhapis	0.0003	0.9566
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Aquabacterium	0.0003	0.9571
Bacteria_Bacteroidota_Bacteroidia_Flavobacteriales_Weeksellaceae_Cloacibacterium	0.0003	0.9576
Bacteria_Myxococcota_Polyangia_Polyangiales_Polyangiaceae_uncultured	0.0003	0.9581
Bacteria_Planctomycetota_Planctomycetes_Pirellulales_Pirellulaceae_Rhodopirellula	0.0003	0.9585
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_Roseomonas	0.0003	0.9590
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_Dyadobacter	0.0003	0.9595
Bacteria_Verrucomicrobiota_Chlamydiae_Chlamydiales_cvE6_cvE6	0.0003	0.9600
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Enhydrobacter	0.0003	0.9604
Bacteria_Chloroflexi_KD4-96_KD4-96_KD4-96_KD4-96	0.0003	0.9609
Bacteria_Deinococcota_Deinococci_Deinococcales_Deinococcaceae_uncultured	0.0003	0.9613
Bacteria_Patescibacteria_Saccharimonadia_Saccharimonadales__	0.0003	0.9618
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_	0.0003	0.9623
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_Anderseniella	0.0003	0.9627

Leaf vs. Nodule

	average	cumsum
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_Mitochondria_Mitochondria	0.3336	0.3445
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Pseudomonadaceae_Pseudomonas	0.0363	0.3820
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Psychrobacter	0.0334	0.4165
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Kocuria	0.0328	0.4503
Bacteria_Firmicutes_Bacilli_Paenibacillales_Paenibacillaceae_Paenibacillus	0.0286	0.4799
Bacteria_Acidobacteriota_Acidobacteriae_Subgroup2_Subgroup2_Subgroup2	0.0236	0.5043
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Erwiniaceae_Pantoea	0.0224	0.5274
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Rhodocyclaceae_uncultured	0.0193	0.5473
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_uncultured_uncultured	0.0174	0.5653
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Blastococcus	0.0173	0.5832
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Corynebacterium	0.0159	0.5996

Bacteria_Firmicutes_Bacilli_Staphylococcales_Staphylococcaceae_Staphylococcus	0.0114	0.6114
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Lautropia	0.0102	0.6219
Bacteria_Actinobacteriota_Rubrobacteria_Rubrobacterales_Rubrobacteriaceae_Rubrobacter	0.0095	0.6317
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_	0.0086	0.6405
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_uncultured	0.0080	0.6489
Bacteria_Firmicutes_Bacilli_Exiguobacterales_Exiguobacteraceae_Exiguobacterium	0.0074	0.6565
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_	0.0072	0.6639
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Massilia	0.0072	0.6713
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Morganellaceae_Photorhabdus	0.0068	0.6783
Eukaryota_____	0.0062	0.6847
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Verrucomicrobiales_Verrucomicrobiaceae_uncultured	0.0061	0.6910
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Brevundimonas	0.0058	0.6969
Bacteria_Actinobacteriota_Actinobacteria_Streptomycetales_Streptomycetaceae_Streptomyces	0.0057	0.7028
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Enterobacteriaceae_	0.0056	0.7086
Bacteria_Firmicutes_Bacilli_Lactobacillales_Streptococcaceae_Streptococcus	0.0051	0.7139
Bacteria_Firmicutes_Bacilli_Entomoplasmatales_Entomoplasmataceae_Mesoplasma	0.0049	0.7190
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.0049	0.7240
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Lawsonella	0.0048	0.7289
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingomonas	0.0047	0.7337
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Paracoccus	0.0043	0.7382
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_	0.0043	0.7426
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Acinetobacter	0.0043	0.7470
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Bogoriellaceae_Georgenia	0.0041	0.7512
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_	0.0039	0.7553
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Intrasporangiaceae_Ornithinimicrobium	0.0039	0.7593
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Polynucleobacter	0.0037	0.7632
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Rubellimicrobium	0.0037	0.7670
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xanthomonadaceae_Stenotrophomonas	0.0035	0.7706
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Frankiaceae_Frankia	0.0034	0.7741
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobiaceae	0.0033	0.7776
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Modestobacter	0.0033	0.7810
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Hydrogenophaga	0.0033	0.7844
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Nocardiaceae_Rhodococcus	0.0032	0.7876
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_	0.0031	0.7908
Bacteria_Actinobacteriota_Actinobacteria_Kineosporiales_Kineosporiaceae_Kineococcus	0.0029	0.7938
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Microscillaceae_uncultured	0.0028	0.7967
Bacteria_Bacteroidota_Bacteroidia_Flavobacteriales_Flavobacteriaceae_Flavobacterium	0.0028	0.7996
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_D05-2_D05-2	0.0028	0.8025
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Geodermatophilus	0.0026	0.8052
Bacteria_Chloroflexi_Chloroflexia_Thermomicrobiales_JG30-KF-CM45_JG30-KF-CM45	0.0026	0.8078
Bacteria_Proteobacteria_Gammaproteobacteria_Cellvibrionales_Cellvibrionaceae_Cellvibrio	0.0025	0.8104
Bacteria_Bacteroidota_Bacteroidia_Bacteroidales_Dysgonomonadaceae_Dysgonomonas	0.0024	0.8129
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_Aliterella	0.0024	0.8154
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Rhodocyclaceae_Azoarcus	0.0024	0.8178
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_uncultured_uncultured	0.0022	0.8201
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Hymenobacteraceae_Pontibacter	0.0022	0.8224
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Cellulomonadaceae_Cellulomonas	0.0022	0.8247

Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_GloeocapsaPCC-7428	0.0021	0.8269
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Devosiaceae_Devosia	0.0021	0.8291
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Bradyrhizobium	0.0021	0.8312
Bacteria_Deinococcota_Deinococci_Deinococcales_Deinococcaceae_Deinococcus	0.0021	0.8333
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Fictibacillus	0.0021	0.8355
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Solirubrobacter	0.0021	0.8376
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Shewanellaceae_Shewanella	0.0019	0.8396
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Occallatibacter	0.0019	0.8415
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Acidothermaceae_Acidothermus	0.0019	0.8435
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_Arcicella	0.0018	0.8454
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_uncultured_uncultured	0.0018	0.8473
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Alcaligenaceae_	0.0018	0.8491
Bacteria_____	0.0018	0.8509
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Acidipila	0.0018	0.8528
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_67-14_67-14	0.0017	0.8546
Eukaryota_Phragmoplastophyta_Embryophyta_Magnoliophyta_Magnoliophyta_Magnoliophyta	0.0017	0.8564
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Granulicella	0.0017	0.8581
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Verrucomicrobiales_Rubritaleaceae_Luteolibacter	0.0017	0.8598
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Cyclobacteriaceae_Algoriphagus	0.0016	0.8615
Bacteria_Actinobacteriota_Actinobacteria_Micromonosporales_Micromonosporaceae_Actinoplanes	0.0016	0.8631
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Sporichthyaceae_hgcIclade	0.0016	0.8647
Bacteria_Deinococcota_Deinococci_Deinococcales_Trueperaceae_Truepera	0.0015	0.8662
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_DapisostemonumCCIBt3536	0.0015	0.8677
Bacteria_Proteobacteria_Gammaproteobacteria_Methylococcales_Methylomonadaceae_Methylomonas	0.0015	0.8693
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Dermabacteraceae_Brachybacterium	0.0015	0.8708
Bacteria_Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae_Dolosigranulum	0.0014	0.8722
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_uncultured	0.0014	0.8737
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_uncultured	0.0013	0.8751
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Nocardioides	0.0013	0.8764
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Ellin6055	0.0013	0.8777
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales__	0.0013	0.8790
Bacteria_Firmicutes_Bacilli_Lactobacillales__	0.0012	0.8803
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_YC-ZSS-LKJ147	0.0012	0.8816
Bacteria_RCP2-54_RCP2-54_RCP2-54_RCP2-54_RCP2-54	0.0012	0.8828
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Micrococcus	0.0011	0.8840
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_Sphingobacteriaceae_Pedobacter	0.0011	0.8851
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Anaerococcus	0.0011	0.8863
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_PMMR1	0.0011	0.8874
Bacteria_Firmicutes_Bacilli_Bacillales_Planococcaceae_Planococcus	0.0010	0.8885
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_ChroococcidiopsisSAG2023	0.0010	0.8896
Bacteria_Actinobacteriota_Actinobacteria_Frankiales__	0.0010	0.8906
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Intrasporangiaceae_Ornithinicoccus	0.0010	0.8917
Bacteria_Actinobacteriota_Actinobacteria_Kineosporiales_Kineosporiaceae_	0.0010	0.8927
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Aquabacterium	0.0010	0.8937
Bacteria_Actinobacteriota_Actinobacteria_Euzebyales_Euzebyaceae_uncultured	0.0009	0.8947
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobium	0.0009	0.8956
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_uncultured_uncultured	0.0009	0.8966
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_uncultured	0.0009	0.8975

Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Intrasporangiaceae_	0.0009	0.8984
Bacteria_Chloroflexi_KD4-96_KD4-96_KD4-96_KD4-96	0.0009	0.8993
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonadaceae_Rheinheimera	0.0008	0.9002
Bacteria_Firmicutes_Bacilli_Staphylococcales_Gemellaceae_Gemella	0.0008	0.9010
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Rhodanobacteraceae_uncultured	0.0008	0.9019
Bacteria_Actinobacteriota_Actinobacteria_Actinomycetales_Actinomycetaceae_Actinomyces	0.0008	0.9027
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_Pseudarcicella	0.0008	0.9035
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Niastella	0.0008	0.9044
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Sediminibacterium	0.0008	0.9052
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Undibacterium	0.0008	0.9060
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Dermabacteraceae_	0.0008	0.9068
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_	0.0008	0.9076
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_uncultured	0.0008	0.9084
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_Craurococcus-Caldovatus	0.0007	0.9091
Bacteria_Desulfobacterota_Desulfuromonadia_Geobacterales_Geobacteraceae_Citrifermentans	0.0007	0.9099
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Saprospiraceae_uncultured	0.0007	0.9106
Bacteria_Proteobacteria_Gammaproteobacteria_WD260_WD260_WD260	0.0007	0.9114
Bacteria_Firmicutes_Bacilli_Bacillales_Planococcaceae_	0.0007	0.9121
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingopyxis	0.0007	0.9128
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_CandidatusPlanktoluna	0.0007	0.9135
Archaea_Crenarchaeota_Nitrososphaeria_Nitrososphaerales_Nitrososphaeraceae_	0.0007	0.9142
Bacteria_Acidobacteriota_Acidobacteriae_Bryobacterales_Bryobacteraceae_Bryobacter	0.0007	0.9149
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Aureimonas	0.0007	0.9156
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Bacillus	0.0007	0.9163
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Altererythrobacter	0.0007	0.9170
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Propionibacteriaceae_Cutibacterium	0.0007	0.9177
Bacteria_Proteobacteria_Alphaproteobacteria_Azospirillales_Azospirillaceae_Skermanella	0.0007	0.9184
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales__	0.0007	0.9190
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_uncultured	0.0006	0.9197
Bacteria_Chloroflexi_Ktedonobacteria_Ktedonobacterales_Ktedonobacteraceae_HSBOF53-F07	0.0006	0.9204
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Rothia	0.0006	0.9210
Bacteria_Chloroflexi_Anaerolineae_Ardenticatenales_Ardenticatenaceae_uncultured	0.0006	0.9217
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Dietziaceae_Dietzia	0.0006	0.9223
Bacteria_Proteobacteria_Gammaproteobacteria_GammaproteobacteriaIncertaeSedis_UnknownFamily_CandidatusBerkiella	0.0006	0.9229
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_	0.0006	0.9236
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_uncultured	0.0006	0.9242
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Ferruginibacter	0.0006	0.9248
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_Dyadobacter	0.0006	0.9254
Bacteria_Proteobacteria_Gammaproteobacteria_EV818SWSAP88_EV818SWSAP88_EV818SWSAP88	0.0006	0.9261
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Chitinophaga	0.0006	0.9267
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Citricoccus	0.0006	0.9273
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Rhizorhapis	0.0006	0.9279
Bacteria_Nitrospirota_Nitrospiria_Nitrospirales_Nitrospiraceae_Nitrospira	0.0006	0.9285
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Janthinobacterium	0.0006	0.9291
Bacteria_Proteobacteria_Gammaproteobacteria_Diplorickettsiales_Diplorickettsiaceae_uncultured	0.0006	0.9297
Bacteria_Actinobacteriota_Actinobacteria___	0.0006	0.9303
Bacteria_Acidobacteriota_Thermoanaerobaculia_Thermoanaerobaculales_Thermoanaerobaculaceae_Subgroup10	0.0005	0.9308
Bacteria_Acidobacteriota_Blastocatellia_Pyrinomonadales_Pyrinomonadaceae_RB41	0.0005	0.9314

Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Conexibacter	0.0005	0.9319
Bacteria_Proteobacteria_Gammaproteobacteria_Oceanospirillales_Halomonadaceae_Halomonas	0.0005	0.9325
Bacteria_Firmicutes_Bacilli_Lactobacillales_Vagococcaceae_Vagococcus	0.0005	0.9330
Bacteria_Fusobacteriota_Fusobacteriia_Fusobacteriales_Fusobacteriaceae_Fusobacterium	0.0005	0.9336
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Hyphomicrobiaceae_Hyphomicrobium	0.0005	0.9341
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Noviherbaspirillum	0.0005	0.9346
Bacteria_Actinobacteriota_Thermoleophilia_Gaiellales_uncultured_uncultured	0.0005	0.9352
Bacteria_Actinobacteriota_Actinobacteria_Kineosporiales_Kineosporiaceae_Quadrisphaera	0.0005	0.9357
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Curvibacter	0.0005	0.9362
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Novosphingobium	0.0005	0.9368
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xanthomonadaceae_Pseudoxanthomonas	0.0005	0.9373
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Ralstonia	0.0005	0.9378

Leaf vs. Root

	average	cumsum
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_Mitochondria_Mitochondria	0.2874	0.3215
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Frankiaceae_Frankia	0.1793	0.5220
Bacteria_Firmicutes_Bacilli_Lactobacillales__	0.0627	0.5921
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Pseudomonadaceae_Pseudomonas	0.0377	0.6343
Bacteria_Acidobacteriota_Acidobacteriae_Subgroup2_Subgroup2_Subgroup2	0.0238	0.6609
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Erwiniaceae_Pantoea	0.0231	0.6867
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_uncultured_uncultured	0.0177	0.7065
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_uncultured	0.0156	0.7239
Bacteria_Actinobacteriota_Actinobacteria_Streptomycetales_Streptomycetaceae_Streptomyces	0.0121	0.7374
Bacteria_Actinobacteriota_Rubrobacteria_Rubrobacterales_Rubrobacteriaceae_Rubrobacter	0.0119	0.7507
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Psychrobacter	0.0113	0.7633
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Lautropia	0.0103	0.7748
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhodomicrobiaceae_Rhodomicrobium	0.0094	0.7853
Eukaryota_Phragmoplastophyta_Embryophyta_Magnoliophyta_Magnoliophyta_Magnoliophyta	0.0087	0.7950
Bacteria_Proteobacteria_Gammaproteobacteria_Steroidobacterales_Steroidobacteraceae_Steroidobacter	0.0086	0.8046
Bacteria_Proteobacteria_Gammaproteobacteria_Cardiobacteriales_Wohlfahrtiimonadaceae_Ignatzschineria	0.0084	0.8140
Bacteria_Firmicutes_Bacilli_Exiguobacterales_Exiguobacteraceae_Exiguobacterium	0.0074	0.8223
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Massilia	0.0072	0.8303
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingomonas	0.0057	0.8367
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_	0.0054	0.8427
Bacteria_Proteobacteria_Gammaproteobacteria_GammaproteobacteriaIncertaeSedis_UnknownFamily_Acidibacter	0.0047	0.8480
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_GloeocapsaPCC-7428	0.0044	0.8529
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Acinetobacter	0.0042	0.8575
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_DapisostemonumCCIBt3536	0.0040	0.8620
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Tissierella	0.0040	0.8665
Bacteria_Fusobacteriota_Fusobacteriia_Fusobacteriales_Fusobacteriaceae_Fusobacterium	0.0037	0.8706
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Hyphomonadaceae_SWB02	0.0032	0.8742
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_	0.0031	0.8777
Bacteria_Actinobacteriota_Actinobacteria_Kineosporiales_Kineosporiaceae_Kineococcus	0.0029	0.8809
Archaea_Crenarchaeota_Nitrososphaeria_Nitrososphaerales_Nitrososphaeraceae_	0.0029	0.8841
Bacteria_Firmicutes_Bacilli_Lactobacillales_Streptococcaceae_Streptococcus	0.0027	0.8871
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_uncultured_uncultured	0.0026	0.8900
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Neisseriaceae_	0.0026	0.8929
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Phenylobacterium	0.0025	0.8956

Bacteria_Firmicutes_Bacilli_Bacillales__	0.0021	0.8980
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Burkholderia-Caballeronia-Paraburkholderia	0.0021	0.9003
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Fictibacillus	0.0020	0.9026
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Bradyrhizobium	0.0020	0.9049
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_Blastocatella	0.0020	0.9070
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_ChroococcidiopsisSAG2023	0.0020	0.9092
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Geodermatophilus	0.0019	0.9114
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Occallatibacter	0.0019	0.9135
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Acidothermaceae_Acidothermus	0.0019	0.9156
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales__	0.0019	0.9176
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Promicromonosporaceae_Cellulosimicrobium	0.0018	0.9197
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Brevundimonas	0.0018	0.9218
Bacteria_Proteobacteria_Gammaproteobacteria_Pasteurellales_Pasteurellaceae_	0.0017	0.9237
Bacteria_Firmicutes_Bacilli_Erysipelotrichales_Erysipelotrichaceae_ZOR0006	0.0017	0.9256
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Acidipila	0.0017	0.9276
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_	0.0017	0.9294
Eukaryota_____	0.0016	0.9312
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_67-14_67-14	0.0016	0.9330
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Granulicella	0.0016	0.9348
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_Aliterella	0.0016	0.9366
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Tepidimicrobium	0.0015	0.9383
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobiaceae	0.0015	0.9400
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_	0.0015	0.9417
Bacteria_Firmicutes_Clostridia_Oscillospirales_Ruminococcaceae_CandidatusSoleaferrea	0.0015	0.9433
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Blastococcus	0.0013	0.9448
Bacteria_Chloroflexi_Chloroflexia_Kallotenuales_AKIW781_AKIW781	0.0012	0.9462
Bacteria_RCP2-54_RCP2-54_RCP2-54_RCP2-54_RCP2-54	0.0012	0.9475
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Niastella	0.0011	0.9487
Bacteria_Firmicutes_Bacilli_Erysipelotrichales_Erysipelotrichaceae_	0.0010	0.9499
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_	0.0009	0.9509
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_	0.0009	0.9519
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xanthomonadaceae_Stenotrophomonas	0.0009	0.9528
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.0008	0.9538
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Nocardioides	0.0008	0.9547
Bacteria_Actinobacteriota_Actinobacteria_Actinomycetales_Actinomycetaceae_Actinomyces	0.0008	0.9556
Bacteria_Acidobacteriota_Blastocatellia_Pyrinomonadales_Pyrinomonadaceae_RB41	0.0008	0.9565
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Morganellaceae_Photorhabdus	0.0008	0.9573
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_	0.0008	0.9582
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Solirubrobacter	0.0007	0.9590
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_	0.0007	0.9598
Bacteria_Chloroflexi_Anaerolineae_Ardenticatenales_Ardenticatenaceae_uncultured	0.0007	0.9606
Bacteria_Chloroflexi_Chloroflexia_Thermomicrobiales_AKYG1722_AKYG1722	0.0007	0.9613
Bacteria_Acidobacteriota_Acidobacteriae_Bryobacterales_Bryobacteraceae_Bryobacter	0.0006	0.9620
Bacteria_Chloroflexi_Ktedonobacteria_Ktedonobacterales_Ktedonobacteraceae_HSBOF53-F07	0.0006	0.9628
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_uncultured_uncultured	0.0006	0.9635
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Nocardiaceae_Rhodococcus	0.0006	0.9642
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_ChroococcidiopsisPCC7203	0.0006	0.9649

Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Corynebacterium	0.0006	0.9655
Bacteria_Nitrospirota_Nitrospiria_Nitrospirales_Nitrospiraceae_Nitrospira	0.0006	0.9662
Bacteria_Proteobacteria_Gammaproteobacteria_WD260_WD260_WD260	0.0006	0.9668
Bacteria_Myxococcota_Polyangia_Polyangiales_Sandaracinaceae_uncultured	0.0006	0.9675
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_	0.0005	0.9681
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_Acidocella	0.0005	0.9687
Bacteria_Firmicutes_Clostridia_Oscillospirales_Ruminococcaceae_uncultured	0.0005	0.9693
Bacteria_Deinococcota_Deinococci_Deinococcales_Deinococcaceae_Deinococcus	0.0005	0.9698
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Ellin6055	0.0005	0.9704
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Microvirga	0.0005	0.9710
Bacteria_Cyanobacteria_Cyanobacteriia_Thermosynechococcales_Acaryochloridaceae_AcaryochlorisMBIC11017	0.0005	0.9715
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_uncultured	0.0005	0.9721
Bacteria_Deinococcota_Deinococci_Deinococcales_Trueperaceae_Truepera	0.0005	0.9726
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_uncultured_uncultured	0.0005	0.9731
Archaea_Crenarchaeota_Nitrososphaeria_Nitrososphaerales_Nitrososphaeraceae_CandidatusNitrocosmicus	0.0005	0.9736
Bacteria_Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae_Granulicatella	0.0005	0.9742
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Kocuria	0.0004	0.9746
Bacteria_Bacteroidota_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	0.0004	0.9751
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Koribacteraceae_CandidatusKoribacter	0.0004	0.9755
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Ferruginibacter	0.0004	0.9760
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_YC-ZSS-LKJ147	0.0004	0.9765
Bacteria_Actinobacteriota_Actinobacteria_Frankiales__	0.0004	0.9769
Unassigned_____	0.0004	0.9773
Bacteria_Actinobacteriota_Thermoleophilia_Gaiellales_uncultured_uncultured	0.0004	0.9777
Bacteria_Actinobacteriota_Actinobacteria___	0.0003	0.9781
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Novosphingobium	0.0003	0.9785
Bacteria_Firmicutes_Bacilli_Entomoplasmatales_Entomoplasmataceae_Mesoplasma	0.0003	0.9788
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingopyxis	0.0003	0.9792
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Neisseriaceae_Vitreoscilla	0.0003	0.9795
Bacteria_Proteobacteria_Gammaproteobacteria_Cardiobacteriales_Wohlfahrtiimonadaceae_	0.0003	0.9798
Bacteria_Actinobacteriota_Actinobacteria_Kineosporiales_Kineosporiaceae_	0.0003	0.9802
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Conexibacter	0.0003	0.9805
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Parviterribacter	0.0003	0.9808
Bacteria_Acidobacteriota_Acidobacteriae_Solibacterales_Solibacteraceae_CandidatusSolibacter	0.0003	0.9811
Bacteria_Actinobacteriota_Actinobacteria_Euzebyales_Euzebyaceae_uncultured	0.0003	0.9814
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xanthomonadaceae_Vulcaniibacterium	0.0003	0.9817
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Puia	0.0003	0.9819
Bacteria_Firmicutes_Bacilli_Paenibacillales_Paenibacillaceae_Saccharibacillus	0.0003	0.9822
Bacteria_WPS-2_WPS-2_WPS-2_WPS-2_WPS-2	0.0003	0.9825
Bacteria_Planctomycetota_Planctomycetes_Gemmatales_Gemmataceae_Fimbriiglobus	0.0003	0.9828
Bacteria_Firmicutes_Bacilli_Staphylococcales_Staphylococcaceae_Staphylococcus	0.0003	0.9831
Bacteria_____	0.0002	0.9834
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Microscillaceae_uncultured	0.0002	0.9836
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Mesorhizobium	0.0002	0.9839
Bacteria_Bacteroidota_Rhodothermia_Rhodothermales_Rhodothermaceae_uncultured	0.0002	0.9842
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_uncultured	0.0002	0.9844
Bacteria_Chloroflexi_Chloroflexia_Thermomicrobiales_JG30-KF-CM45_JG30-KF-CM45	0.0002	0.9847
Bacteria_Fusobacteriota_Fusobacteriia_Fusobacteriales_Fusobacteriaceae_Cetobacterium	0.0002	0.9849

Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Rubellimicrobium	0.0002	0.9852
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Psychroglaciecola	0.0002	0.9854
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_PMMR1	0.0002	0.9857
Bacteria_Bacteroidota_Bacteroidia_Bacteroidales_Dysgonomonadaceae_Dysgonomonas	0.0002	0.9859
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Flavisolibacter	0.0002	0.9862
Bacteria_Proteobacteria_Alphaproteobacteria_Dongiales_Dongiaceae_Dongia	0.0002	0.9864
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Mycobacteriaceae_Mycobacterium	0.0002	0.9866
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Microscillaceae_Chryseolinea	0.0002	0.9868
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Cupriavidus	0.0002	0.9870
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_	0.0002	0.9872
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Cnuella	0.0002	0.9874
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_	0.0002	0.9875
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Actinokineospora	0.0001	0.9877
Bacteria_Actinobacteriota_Actinobacteria_Glycomycetales_Glycomycetaceae_Glycomyces	0.0001	0.9878
Bacteria_Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae_Lactobacillus	0.0001	0.9880
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Nostocaceae_MastigocladopsisPCC-10914	0.0001	0.9882
Bacteria_Actinobacteriota_Acidimicrobiia_Microtrichales_Microtrichaceae_uncultured	0.0001	0.9883
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_uncultured	0.0001	0.9884
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Robbsia	0.0001	0.9886
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Caulobacter	0.0001	0.9887
Bacteria_Proteobacteria_Alphaproteobacteria___	0.0001	0.9889
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Pleomorphomonadaceae_Chthonobacter	0.0001	0.9890
Bacteria_Actinobacteriota_Actinobacteria_Pseudonocardiales_Pseudonocardiaceae_Pseudonocardia	0.0001	0.9892
Bacteria_Actinobacteriota_Acidimicrobiia___	0.0001	0.9893
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Chthoniobacterales_Chthoniobacteraceae_Chthoniobacter	0.0001	0.9894
Bacteria_Campilobacterota_Campylobacteria_Campylobacterales_Campylobacteraceae_Campylobacter	0.0001	0.9896
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales__	0.0001	0.9897
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Nostocaceae_StigonemaSAG48.90	0.0001	0.9898
Bacteria_Actinobacteriota_Actinobacteria_Kineosporiales_Kineosporiaceae_Quadrisphaera	0.0001	0.9899
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Marmoricola	0.0001	0.9901
Bacteria_Chloroflexi____	0.0001	0.9902
Bacteria_Cyanobacteria_Cyanobacteriia_Thermosynechococcales_Thermosynechococcaceae_uncultured	0.0001	0.9903
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Bacillus	0.0001	0.9904
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Nostocaceae_uncultured	0.0001	0.9905
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Hylemonella	0.0001	0.9906
Bacteria_Actinobacteriota_Acidimicrobiia_uncultured_uncultured_uncultured	0.0001	0.9907
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Devosiaceae_Devosia	0.0001	0.9909

Leaf vs. Stem

	average	cumsum
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_Mitochondria_Mitochondria	0.1476	0.3532
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Pseudomonadaceae_Pseudomonas	0.0372	0.4423
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Corynebacterium	0.0304	0.5150
Bacteria_Acidobacteriota_Acidobacteriae_Subgroup2_Subgroup2_Subgroup2	0.0231	0.5702
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Erwiniaceae_Pantoea	0.0217	0.6220
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_uncultured_uncultured	0.0168	0.6621
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Acinetobacter	0.0146	0.6969
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Lautropia	0.0102	0.7214
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Frankiaceae_Frankia	0.0083	0.7412

Bacteria_Firmicutes_Bacilli_Exiguobacterales_Exiguobacteraceae_Exiguobacterium	0.0074	0.7588
Bacteria_Firmicutes_Bacilli_Staphylococcales_Staphylococcaceae_Staphylococcus	0.0073	0.7763
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Massilia	0.0072	0.7934
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Lawsonella	0.0063	0.8085
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingomonas	0.0049	0.8203
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_	0.0031	0.8278
Bacteria_Actinobacteriota_Actinobacteria_Kineosporiales_Kineosporiaceae_Kineococcus	0.0029	0.8347
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_	0.0026	0.8410
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Enterobacteriaceae_	0.0023	0.8464
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xanthomonadaceae_Stenotrophomonas	0.0022	0.8517
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Acidipila	0.0021	0.8567
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Fictibacillus	0.0020	0.8616
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Bacillus	0.0020	0.8664
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Bradyrhizobium	0.0020	0.8711
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Occallatibacter	0.0019	0.8756
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Acidothermaceae_Acidothermus	0.0019	0.8801
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Granulicella	0.0019	0.8846
Bacteria_Firmicutes_Bacilli_Lactobacillales_Streptococcaceae_Streptococcus	0.0019	0.8891
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Anaerococcus	0.0017	0.8931
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Geobacillus	0.0015	0.8966
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Novosphingobium	0.0013	0.8996
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Shewanellaceae_Shewanella	0.0012	0.9026
Bacteria_RCP2-54_RCP2-54_RCP2-54_RCP2-54_RCP2-54	0.0012	0.9054
Bacteria_Acidobacteriota_Acidobacteriae_Bryobacterales_Bryobacteraceae_Bryobacter	0.0012	0.9082
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Brevundimonas	0.0011	0.9108
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonadaceae_Rheinheimera	0.0011	0.9133
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Rhodoferax	0.0010	0.9157
Bacteria_Actinobacteriota_Actinobacteria_Actinomycetales_Actinomycetaceae_Actinomyces	0.0010	0.9181
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Halobacillus	0.0010	0.9204
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_uncultured	0.0009	0.9226
Bacteria_Proteobacteria_Gammaproteobacteria_WD260_WD260_WD260	0.0009	0.9247
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Kocuria	0.0008	0.9267
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Verrucomicrobiales_Verrucomicrobiaceae_uncultured	0.0008	0.9286
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_	0.0008	0.9305
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Micrococcus	0.0007	0.9322
Bacteria_Proteobacteria_Gammaproteobacteria_B2M28_B2M28_B2M28	0.0007	0.9339
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_	0.0007	0.9355
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Polynucleobacter	0.0007	0.9371
Bacteria_Firmicutes_Bacilli_Bacillales_Planococcaceae_	0.0006	0.9386
Bacteria_Chloroflexi_Ktedonobacteria_Ktedonobacterales_Ktedonobacteraceae_HSBOF53-F07	0.0006	0.9401
Bacteria_Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae_Granulicatella	0.0006	0.9416
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Psychrobacter	0.0006	0.9429
Bacteria_Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae_Dolosigranulum	0.0005	0.9442
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_Phreatobacter	0.0005	0.9455
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_	0.0005	0.9467
Bacteria_Proteobacteria_Gammaproteobacteria_Thiohalorhabdales_Thiohalorhabdaceae_uncultured	0.0005	0.9480
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_alphaIcluster	0.0005	0.9492
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Pseudorhodoplanes	0.0005	0.9504

Bacteria_Nitrospirota_Nitrospiria_Nitrospirales_Nitrospiraceae_Nitrospira	0.0005	0.9515
Bacteria_Proteobacteria_Gammaproteobacteria_GammaproteobacteriaIncertaeSedis_UnknownFamily_Acidibacter	0.0005	0.9526
Bacteria_Proteobacteria_Gammaproteobacteria_Chromatiales_Chromatiaceae_CandidatusThiobios	0.0005	0.9537
Bacteria_Deinococcota_Deinococci_Deinococcales_Deinococcaceae_Deinococcus	0.0005	0.9548
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_	0.0004	0.9559
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Burkholderia-Caballeronia-Paraburkholderia	0.0004	0.9569
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Dinghuibacter	0.0004	0.9579
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Sutterellaceae_uncultured	0.0004	0.9590
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Solirubrobacter	0.0004	0.9600
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Koribacteraceae_CandidatusKoribacter	0.0004	0.9610
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcaceae_Paraclostridium	0.0004	0.9619
Bacteria_Acidobacteriota_Acidobacteriae_Solibacterales_Solibacteraceae_CandidatusSolibacter	0.0004	0.9629
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Turicella	0.0004	0.9638
Bacteria_Actinobacteriota_Actinobacteria_PeM15_PeM15_PeM15	0.0004	0.9647
Bacteria_Proteobacteria_Gammaproteobacteria_KI89Aclade_KI89Aclade_KI89Aclade	0.0004	0.9656
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_MWH-Ta3	0.0003	0.9664
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Hydrogenophaga	0.0003	0.9673
Bacteria_SAR324clade(MarinegroupB)	0.0003	0.9681
Bacteria_WPS-2_WPS-2_WPS-2_WPS-2_WPS-2	0.0003	0.9688
Bacteria_Actinobacteriota_Thermoleophilia_Gaiellales_uncultured_uncultured	0.0003	0.9696
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_uncultured	0.0003	0.9703
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_Sphingobacteriaceae_Pedobacter	0.0003	0.9711
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Enhydrobacter	0.0003	0.9718
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Yersiniaceae_	0.0003	0.9726
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Nocardioides	0.0003	0.9733
Bacteria_Actinobacteriota_Actinobacteria_Actinomycetales_Actinomycetaceae_Actinotignum	0.0003	0.9740
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Dermabacteraceae_Brachybacterium	0.0003	0.9747
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_67-14_67-14	0.0003	0.9753
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xanthomonadaceae_Xanthomonas	0.0003	0.9760
Bacteria_Firmicutes_Bacilli_Bacillales_Planococcaceae_Domibacillus	0.0003	0.9767
Bacteria_Planctomycetota_Phycisphaerae_Tepidisphaerales_WD2101soilgroup_WD2101soilgroup	0.0003	0.9773
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_Pedosphaeraceae	0.0003	0.9780
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Puia	0.0003	0.9786
Bacteria_Firmicutes_Bacilli_Paenibacillales_Paenibacillaceae_Saccharibacillus	0.0003	0.9792
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Roseiarcus	0.0003	0.9798
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_	0.0002	0.9804
Bacteria_Firmicutes_Bacilli_Staphylococcales_Gemellaceae_Gemella	0.0002	0.9810
Bacteria_Fusobacteriota_Fusobacteriia_Fusobacteriales_Leptotrichiaceae_Leptotrichia	0.0002	0.9815
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Rhodocyclaceae_	0.0002	0.9821
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_uncultured	0.0002	0.9827
Bacteria_Actinobacteriota_Actinobacteria_Streptomycetales_Streptomycetaceae_Streptomyces	0.0002	0.9833
Bacteria_Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae_Lactobacillus	0.0002	0.9838
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Conexibacter	0.0002	0.9844
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Yersiniaceae_Serratia	0.0002	0.9850
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Neisseriaceae_Neisseria	0.0002	0.9855
Bacteria_Fusobacteriota_Fusobacteriia_Fusobacteriales_Fusobacteriaceae_Cetobacterium	0.0002	0.9861
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Nitrosomonadaceae_Ellin6067	0.0002	0.9866
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Rothia	0.0002	0.9871

Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Undibacterium	0.0002	0.9876
Bacteria_Proteobacteria_Alphaproteobacteria_Micropepsales_Micropepsaceae_uncultured	0.0002	0.9880
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Janthinobacterium	0.0002	0.9885
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Sporichthyaceae_hgcIclade	0.0002	0.9889
Bacteria_Firmicutes_Bacilli_Paenibacillales_Paenibacillaceae_Paenibacillus	0.0002	0.9893
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Finegoldia	0.0002	0.9897
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Peptoniphilus	0.0002	0.9901
Bacteria_Myxococcota_Myxococcia_Myxococcales_Myxococcaceae_P3OB-42	0.0002	0.9905
Bacteria_Proteobacteria_Gammaproteobacteria_Pasteurellales_Pasteurellaceae_Haemophilus	0.0002	0.9909
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xanthomonadaceae_Luteimonas	0.0002	0.9914
Bacteria_Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae_Desemzia	0.0002	0.9917
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Blastococcus	0.0001	0.9921
Bacteria_Aquificota_Aquificae_Aquificales_Aquificaceae_Hydrogenobacter	0.0001	0.9924
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Hymenobacteraceae_Hymenobacter	0.0001	0.9927
Bacteria_Firmicutes_Bacilli_Lactobacillales_Aerococcaceae_Abiotrophia	0.0001	0.9931
Bacteria_MBNT15_MBNT15_MBNT15_MBNT15_MBNT15	0.0001	0.9934
Bacteria_Proteobacteria_Gammaproteobacteria_Diplorickettsiales_Diplorickettsiaceae_uncultured	0.0001	0.9937
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_Curtobacterium	0.0001	0.9940
Bacteria_____	0.0001	0.9943
Bacteria_Acidobacteriota_Vicinamibacteria_Vicinamibacterales_uncultured_uncultured	0.0001	0.9945
Bacteria_Actinobacteriota_Rubrobacteria_Rubrobacterales_Rubrobacteriaceae_Rubrobacter	0.0001	0.9948
Bacteria_Bacteroidota_Kapabacteria_Kapabacteriales_Kapabacteriales_Kapabacteriales	0.0001	0.9950
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Phormidiaceae_TychonemaCCAP1459-11B	0.0001	0.9953
Bacteria_Firmicutes_Clostridia_Oscillospirales_Ethanoligenenaceae_IncertaeSedis	0.0001	0.9955
Bacteria_Patescibacteria_Parcubacteria_Parcubacteria_Parcubacteria_Parcubacteria	0.0001	0.9958
Bacteria_Planctomycetota_Planctomycetes_Gemmatales_Gemmataceae_uncultured	0.0001	0.9960
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Nitrosomonadaceae_MND1	0.0001	0.9962
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Verrucomicrobiales_Rubritaleaceae_Haloferula	0.0001	0.9965
Bacteria_Bacteroidota_Bacteroidia_Flavobacteriales_Weeksellaceae_Cloacibacterium	0.0001	0.9967
Bacteria_Myxococcota_Polyangia_Polyangiales_Polyangiaceae_Pajaroellobacter	0.0001	0.9970
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_Acetobacteraceae	0.0001	0.9972
Bacteria_Actinobacteriota_Acidimicrobiia_uncultured_uncultured_uncultured	0.0001	0.9974
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Flavitalea	0.0001	0.9976
Archaea_Nanoarchaeota_Nanoarchaeia_Woesearchaeales_GW2011GWC14715_GW2011GWC14715	0.0001	0.9977
Bacteria_Actinobacteriota_Acidimicrobiia_IMCC26256_IMCC26256_IMCC26256	0.0001	0.9979
Bacteria_Actinobacteriota_MB-A2-108_MB-A2-108_MB-A2-108_MB-A2-108	0.0001	0.9981
Bacteria_Bacteroidota_Bacteroidia_Bacteroidales_Prevotellaceae_Prevotella	0.0001	0.9982
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Microscillaceae_uncultured	0.0001	0.9984
Bacteria_Chloroflexi_Chloroflexia_Kallotenuales_AKIW781_AKIW781	0.0001	0.9986
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_Gemmatimonas	0.0001	0.9987
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_T34_T34	0.0001	0.9989
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_ADurb.Bin118	0.0001	0.9991
Bacteria_Actinobacteriota_Acidimicrobiia_Actinomarinales_uncultured_uncultured	0.0001	0.9992
Bacteria_Proteobacteria_Alphaproteobacteria_Azospirillales_Azospirillaceae_Skermanella	0.0001	0.9994
Archaea_Thermoplasmatota_Thermoplasmata_uncultured_uncultured_uncultured	0.0001	0.9995
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_Acidicaldus	0.0001	0.9997
Bacteria_Proteobacteria_Alphaproteobacteria_Elsterales_uncultured_uncultured	0.0001	0.9998
Bacteria_Acidobacteriota_Vicinamibacteria_Vicinamibacterales_Vicinamibacteraceae_Vicinamibacteraceae	0.0000	0.9999

Bacteria_Planctomycetota_Planctomycetes_Pirellulales_Pirellulaceae_uncultured	0.0000	1.0000
Unassigned_____	0.0000	1.0000
Archaea_____	0.0000	1.0000
Archaea_Crenarchaeota_Nitrososphaeria_Nitrososphaerales_Nitrososphaeraceae_	0.0000	1.0000
Archaea_Crenarchaeota_Nitrososphaeria_Nitrososphaerales_Nitrososphaeraceae_CandidatusNitrocosmicus	0.0000	1.0000
Archaea_Crenarchaeota_Nitrososphaeria_Nitrososphaerales_Nitrososphaeraceae_CandidatusNitrososphaera	0.0000	1.0000
Archaea_Crenarchaeota_Nitrososphaeria_Nitrososphaerales_Nitrososphaeraceae_Nitrososphaeraceae	0.0000	1.0000
Archaea_Halobacterota_Halobacteria_Halobacterales_Haloadaptaceae_Haladaptatus	0.0000	1.0000
Archaea_Halobacterota_Halobacteria_Halobacterales_Halobacteriaceae_Halobacteriaceae	0.0000	1.0000
Archaea_Halobacterota_Halobacteria_Halobacterales_Haloferacaceae_A07HB70	0.0000	1.0000
Archaea_Halobacterota_Halobacteria_Halobacterales_Haloferacaceae_Halogranum	0.0000	1.0000
Archaea_Halobacterota_Halobacteria_Halobacterales_Haloferacaceae_Halolamina	0.0000	1.0000
Archaea_Halobacterota_Halobacteria_Halobacterales_Haloferacaceae_Halopelagius	0.0000	1.0000

Nodule vs. Root

	average	cumsum
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Frankiaceae_Frankia	0.1793	0.1929
Bacteria_Firmicutes_Bacilli_Lactobacillales__	0.0629	0.2605
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_Mitochondria_Mitochondria	0.0481	0.3123
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Psychrobacter	0.0353	0.3503
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Kocuria	0.0328	0.3855
Bacteria_Firmicutes_Bacilli_Paenibacillales_Paenibacillaceae_Paenibacillus	0.0286	0.4163
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_uncultured	0.0210	0.4389
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Rhodocyclaceae_uncultured	0.0193	0.4596
Bacteria_Actinobacteriota_Rubrobacteria_Rubrobacterales_Rubrobacteriaceae_Rubrobacter	0.0182	0.4792
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Blastococcus	0.0173	0.4979
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Corynebacterium	0.0157	0.5147
Bacteria_Actinobacteriota_Actinobacteria_Streptomycetales_Streptomycetaceae_Streptomyces	0.0151	0.5310
Bacteria_Firmicutes_Bacilli_Staphylococcales_Staphylococcaceae_Staphylococcus	0.0113	0.5431
Eukaryota_Phragmoplastophyta_Embryophyta_Magnoliophyta_Magnoliophyta_Magnoliophyta	0.0097	0.5536
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhodomicrobiaceae_Rhodomicrobium	0.0094	0.5637
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_	0.0089	0.5733
Bacteria_Proteobacteria_Gammaproteobacteria_Steroidobacterales_Steroidobacteraceae_Steroidobacter	0.0085	0.5825
Bacteria_Proteobacteria_Gammaproteobacteria_Cardiobacteriales_Wohlfahrtiimonadaceae_Ignatzschineria	0.0084	0.5916
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_	0.0081	0.6002
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Pseudomonadaceae_Pseudomonas	0.0075	0.6083
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Morganellaceae_Photorhabdus	0.0073	0.6162
Eukaryota_____	0.0073	0.6240
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Verrucomicrobiales_Verrucomicrobiaceae_uncultured	0.0061	0.6306
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_GloeocapsaPCC-7428	0.0058	0.6368
Bacteria_Firmicutes_Bacilli_Lactobacillales_Streptococcaceae_Streptococcus	0.0057	0.6430
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Brevundimonas	0.0057	0.6491
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Enterobacteriaceae_	0.0056	0.6551
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.0054	0.6609
Bacteria_Firmicutes_Bacilli_Entomoplasmatales_Entomoplasmataceae_Mesoplasma	0.0051	0.6664
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_DapisostemonumCCIBt3536	0.0050	0.6718
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Lawsonella	0.0047	0.6769
Bacteria_Proteobacteria_Gammaproteobacteria_GammaproteobacteriaIncertaeSedis_UnknownFamily_Acidibacter	0.0047	0.6819

Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_	0.0046	0.6868
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Paracoccus	0.0043	0.6915
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Tissierella	0.0041	0.6959
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Bogoriellaceae_Georgenia	0.0041	0.7003
Bacteria_Fusobacteriota_Fusobacteriia_Fusobacteriales_Fusobacteriaceae_Fusobacterium	0.0040	0.7046
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Intrasporangiaceae_Ornithinimicrobium	0.0039	0.7088
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobiaceae	0.0038	0.7129
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_uncultured_uncultured	0.0038	0.7169
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_	0.0038	0.7210
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Rubellimicrobium	0.0038	0.7250
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Polynucleobacter	0.0037	0.7291
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingomonas	0.0037	0.7330
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Geodermatophilus	0.0037	0.7370
Archaea_Crenarchaeota_Nitrososphaeria_Nitrososphaerales_Nitrososphaeraceae_	0.0033	0.7406
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Modestobacter	0.0033	0.7441
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Hydrogenophaga	0.0033	0.7476
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xanthomonadaceae_Stenotrophomonas	0.0032	0.7511
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_Aliterella	0.0032	0.7545
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Hyphomonadaceae_SWB02	0.0032	0.7580
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Acinetobacter	0.0030	0.7612
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Microscillaceae_uncultured	0.0028	0.7642
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Nocardiaceae_Rhodococcus	0.0028	0.7672
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_D05-2_D05-2	0.0028	0.7702
Bacteria_Bacteroidota_Bacteroidia_Flavobacteriales_Flavobacteriaceae_Flavobacterium	0.0028	0.7732
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_67-14_67-14	0.0028	0.7762
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales__	0.0027	0.7791
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_ChroococcidiopsisSAG2023	0.0026	0.7819
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Neisseriaceae_	0.0026	0.7847
Bacteria_Chloroflexi_Chloroflexia_Thermomicrobiales_JG30-KF-CM45_JG30-KF-CM45	0.0025	0.7874
Bacteria_Proteobacteria_Gammaproteobacteria_Cellvibrionales_Cellvibrionaceae_Cellvibrio	0.0025	0.7901
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Phenylobacterium	0.0025	0.7928
Bacteria_Bacteroidota_Bacteroidia_Bacteroidales_Dysgonomonadaceae_Dysgonomonas	0.0025	0.7955
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Rhodocyclaceae_Azoarcus	0.0024	0.7981
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_uncultured_uncultured	0.0023	0.8006
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_Blastocatella	0.0023	0.8030
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Hymenobacteraceae_Pontibacter	0.0022	0.8054
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Cellulomonadaceae_Cellulomonas	0.0022	0.8077
Bacteria_Firmicutes_Bacilli_Bacillales__	0.0021	0.8100
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Devosiaceae_Devosia	0.0021	0.8123
Bacteria_Deinococcota_Deinococci_Deinococcales_Deinococcaceae_Deinococcus	0.0021	0.8145
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Burkholderia-Caballeronia-Paraburkholderia	0.0021	0.8167
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Solirubrobacter	0.0020	0.8189
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Shewanellaceae_Shewanella	0.0019	0.8209
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Promicromonosporaceae_Cellulosimicrobium	0.0019	0.8229
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_Arcicella	0.0018	0.8249
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Alcaligenaceae_	0.0018	0.8268
Bacteria_Proteobacteria_Gammaproteobacteria_Pasteurellales_Pasteurellaceae_	0.0018	0.8287
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Massilia	0.0017	0.8306

Bacteria_Firmicutes_Bacilli_Erysipelotrichales_Erysipelotrichaceae_ZOR0006	0.0017	0.8325
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Verrucomicrobiales_Rubritaleaceae_Luteolibacter	0.0017	0.8343
Bacteria_____	0.0017	0.8360
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Niastella	0.0016	0.8378
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_	0.0016	0.8395
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Cyclobacteriaceae_Algoriphagus	0.0016	0.8412
Bacteria_Deinococcota_Deinococci_Deinococcales_Trueperaceae_Truepera	0.0016	0.8429
Bacteria_Actinobacteriota_Actinobacteria_Micromonosporales_Micromonosporaceae_Actinoplanes	0.0016	0.8446
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Sporichthyaceae_hgcIclade	0.0016	0.8462
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Tepidimicrobium	0.0015	0.8479
Bacteria_Chloroflexi_Chloroflexia_Kallotenuales_AKIW781_AKIW781	0.0015	0.8495
Bacteria_Firmicutes_Clostridia_Oscillospirales_Ruminococcaceae_CandidatusSoleaferrea	0.0015	0.8511
Bacteria_Proteobacteria_Gammaproteobacteria_Methylococcales_Methylomonadaceae_Methylomonas	0.0015	0.8527
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Dermabacteraceae_Brachybacterium	0.0015	0.8543
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Ellin6055	0.0015	0.8559
Bacteria_Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae_Dolosigranulum	0.0014	0.8574
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_	0.0014	0.8589
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_uncultured	0.0014	0.8604
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Nocardioides	0.0013	0.8618
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_uncultured	0.0013	0.8633
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_YC-ZSS-LKJ147	0.0013	0.8647
Bacteria_Firmicutes_Bacilli_Exiguobacterales_Exiguobacteraceae_Exiguobacterium	0.0013	0.8661
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_	0.0012	0.8674
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_uncultured_uncultured	0.0012	0.8687
Bacteria_Acidobacteriota_Blastocatellia_Pyrinomonadales_Pyrinomonadaceae_RB41	0.0012	0.8700
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Micrococcus	0.0011	0.8712
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_PMMR1	0.0011	0.8724
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_Sphingobacteriaceae_Pedobacter	0.0011	0.8736
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Anaerococcus	0.0011	0.8749
Bacteria_Actinobacteriota_Actinobacteria_Frankiales__	0.0011	0.8761
Bacteria_Chloroflexi_Anaerolineae_Ardenticatenales_Ardenticatenaceae_uncultured	0.0011	0.8772
Bacteria_Actinobacteriota_Actinobacteria_Euzebyales_Euzebyaceae_uncultured	0.0010	0.8784
Bacteria_Firmicutes_Bacilli_Bacillales_Planococcaceae_Planococcus	0.0010	0.8795
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Intrasporangiaceae_Ornithinicoccus	0.0010	0.8806
Bacteria_Actinobacteriota_Actinobacteria_Kineosporiales_Kineosporiaceae_	0.0010	0.8817
Bacteria_Firmicutes_Bacilli_Erysipelotrichales_Erysipelotrichaceae_	0.0010	0.8828
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobium	0.0010	0.8838
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Aquabacterium	0.0010	0.8848
Bacteria_Chloroflexi_Chloroflexia_Thermomicrobiales_AKYG1722_AKYG1722	0.0009	0.8859
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_	0.0009	0.8869
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_uncultured	0.0009	0.8878
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingopyxis	0.0009	0.8888
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_uncultured	0.0009	0.8898
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Intrasporangiaceae_	0.0009	0.8907
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Ferruginibacter	0.0009	0.8916
Bacteria_Chloroflexi_KD4-96_KD4-96_KD4-96_KD4-96	0.0009	0.8926
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_uncultured	0.0008	0.8935
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonadaceae_Rheinheimera	0.0008	0.8944

Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_	0.0008	0.8953
Bacteria_Firmicutes_Bacilli_Staphylococcales_Gemellaceae_Gemella	0.0008	0.8962
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Rhodanobacteraceae_uncultured	0.0008	0.8971
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_Pseudarcicella	0.0008	0.8979
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_ChroococcidiopsisPCC7203	0.0008	0.8988
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Sediminibacterium	0.0008	0.8996
Bacteria_Cyanobacteria_Cyanobacteriia_Thermosynechococcales_Acaryochloridaceae_AcaryochlorisMBIC11017	0.0008	0.9005
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Undibacterium	0.0008	0.9013
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Dermabacteraceae_	0.0008	0.9022
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_Craurococcus-Caldovatus	0.0007	0.9030
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Saprospiraceae_uncultured	0.0007	0.9038
Bacteria_Desulfobacterota_Desulfuromonadia_Geobacterales_Geobacteraceae_Citrifermentans	0.0007	0.9045
Bacteria_Actinobacteriota_Actinobacteria___	0.0007	0.9053
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales__	0.0007	0.9061
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_uncultured	0.0007	0.9068
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Aureimonas	0.0007	0.9076
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_CandidatusPlanktoluna	0.0007	0.9083
Bacteria_Firmicutes_Bacilli_Bacillales_Planococcaceae_	0.0007	0.9090
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Erwiniaceae_Pantoea	0.0007	0.9098
Bacteria_Myxococcota_Polyangia_Polyangiales_Sandaracinaceae_uncultured	0.0007	0.9105
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Bacillus	0.0007	0.9112
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_uncultured_uncultured	0.0007	0.9119
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Altererythrobacter	0.0007	0.9126
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Propionibacteriaceae_Cutibacterium	0.0007	0.9133
Bacteria_Proteobacteria_Alphaproteobacteria_Azospirillales_Azospirillaceae_Skermanella	0.0007	0.9141
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Rothia	0.0006	0.9147
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_	0.0006	0.9154
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Dietziaceae_Dietzia	0.0006	0.9161
Bacteria_Proteobacteria_Gammaproteobacteria_GammaproteobacteriaIncertaeSedis_UnknownFamily_CandidatusBerkiella	0.0006	0.9167
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Conexibacter	0.0006	0.9174
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_Dyadobacter	0.0006	0.9180
Bacteria_Proteobacteria_Gammaproteobacteria_EV818SWSAP88_EV818SWSAP88_EV818SWSAP88	0.0006	0.9187
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Chitinophaga	0.0006	0.9193
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Citricoccus	0.0006	0.9199
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Novosphingobium	0.0006	0.9206
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Rhizorhapis	0.0006	0.9212
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Janthinobacterium	0.0006	0.9218
Bacteria_Proteobacteria_Gammaproteobacteria_Diplorickettsiales_Diplorickettsiaceae_uncultured	0.0006	0.9224

Nodule vs. Stem

	average	cumsum
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_Mitochondria_Mitochondria	0.3705	0.3901
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Corynebacterium	0.0393	0.4315
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Psychrobacter	0.0329	0.4662
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Kocuria	0.0328	0.5007
Bacteria_Firmicutes_Bacilli_Paenibacillales_Paenibacillaceae_Paenibacillus	0.0287	0.5310
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Rhodocyclaceae_uncultured	0.0193	0.5513
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Blastococcus	0.0173	0.5695
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Acinetobacter	0.0140	0.5843

Bacteria_Firmicutes_Bacilli_Staphylococcales_Staphylococcaceae_Staphylococcus	0.0140	0.5990
Bacteria_Actinobacteriota_Rubrobacteria_Rubrobacterales_Rubrobacteriaceae_Rubrobacter	0.0095	0.6090
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Frankiaceae_Frankia	0.0094	0.6188
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Pseudomonadaceae_Pseudomonas	0.0084	0.6276
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_	0.0083	0.6363
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_uncultured	0.0080	0.6448
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Lawsonella	0.0080	0.6532
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_	0.0073	0.6609
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Enterobacteriaceae_	0.0070	0.6683
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Morganellaceae_Photorhabdus	0.0068	0.6754
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Verrucomicrobiales_Verrucomicrobiaceae_uncultured	0.0063	0.6821
Eukaryota_____	0.0062	0.6886
Bacteria_Actinobacteriota_Actinobacteria_Streptomycetales_Streptomycetaceae_Streptomyces	0.0058	0.6947
Bacteria_Firmicutes_Bacilli_Lactobacillales_Streptococcaceae_Streptococcus	0.0057	0.7007
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Brevundimonas	0.0055	0.7065
Bacteria_Firmicutes_Bacilli_Entomoplasmatales_Entomoplasmataceae_Mesoplasma	0.0049	0.7117
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.0049	0.7168
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Paracoccus	0.0043	0.7213
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_	0.0042	0.7258
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xanthomonadaceae_Stenotrophomonas	0.0042	0.7302
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Bogoriellaceae_Georgenia	0.0041	0.7345
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_	0.0040	0.7387
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Intrasporangiaceae_Ornithinimicrobium	0.0039	0.7428
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Polynucleobacter	0.0039	0.7469
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Rubellimicrobium	0.0037	0.7508
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Hydrogenophaga	0.0035	0.7545
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobiaceae	0.0033	0.7580
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Modestobacter	0.0033	0.7615
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Nocardiaceae_Rhodococcus	0.0032	0.7648
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Microscillaceae_uncultured	0.0028	0.7677
Bacteria_Bacteroidota_Bacteroidia_Flavobacteriales_Flavobacteriaceae_Flavobacterium	0.0028	0.7707
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_D05-2_D05-2	0.0028	0.7736
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Shewanellaceae_Shewanella	0.0027	0.7764
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Geodermatophilus	0.0026	0.7792
Bacteria_Chloroflexi_Chloroflexia_Thermomicrobiales_JG30-KF-CM45_JG30-KF-CM45	0.0026	0.7819
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Massilia	0.0025	0.7846
Bacteria_Proteobacteria_Gammaproteobacteria_Cellvibrionales_Cellvibrionaceae_Cellvibrio	0.0025	0.7872
Bacteria_Bacteroidota_Bacteroidia_Bacteroidales_Dysgonomonadaceae_Dysgonomonas	0.0024	0.7898
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_Aliterella	0.0024	0.7923
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Rhodocyclaceae_Azoarcus	0.0024	0.7948
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_uncultured_uncultured	0.0022	0.7972
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Hymenobacteraceae_Pontibacter	0.0022	0.7995
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Cellulomonadaceae_Cellulomonas	0.0022	0.8018
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_GloeocapsaPCC-7428	0.0021	0.8040
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Anaerococcus	0.0021	0.8063
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Devosiaceae_Devosia	0.0021	0.8085
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Bacillus	0.0020	0.8106

Bacteria_Deinococcota_Deinococci_Deinococcales_Deinococcaceae_Deinococcus	0.0020	0.8127
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Solirubrobacter	0.0020	0.8148
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_uncultured_uncultured	0.0020	0.8168
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingomonas	0.0019	0.8189
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_67-14_67-14	0.0019	0.8208
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_Arcicella	0.0018	0.8228
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_uncultured_uncultured	0.0018	0.8247
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Alcaligenaceae_	0.0018	0.8266
Bacteria_Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae_Dolosigranulum	0.0018	0.8285
Eukaryota_Phragmoplastophyta_Embryophyta_Magnoliophyta_Magnoliophyta_Magnoliophyta	0.0017	0.8303
Bacteria_____	0.0017	0.8321
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Verrucomicrobiales_Rubritaleaceae_Luteolibacter	0.0017	0.8338
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Erwiniaceae_Pantoea	0.0016	0.8355
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonadaceae_Rheinheimera	0.0016	0.8373
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Cyclobacteriaceae_Algoriphagus	0.0016	0.8389
Bacteria_Actinobacteriota_Actinobacteria_Micromonosporales_Micromonosporaceae_Actinoplanes	0.0016	0.8406
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Micrococcus	0.0016	0.8422
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Sporichthyaceae_hgcIclade	0.0016	0.8439
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Dermabacteraceae_Brachybacterium	0.0016	0.8455
Bacteria_Acidobacteriota_Acidobacteriae_Subgroup2_Subgroup2_Subgroup2	0.0016	0.8471
Bacteria_Deinococcota_Deinococci_Deinococcales_Trueperaceae_Truepera	0.0015	0.8487
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Geobacillus	0.0015	0.8502
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_DapisostemonumCCIBt3536	0.0015	0.8518
Bacteria_Proteobacteria_Gammaproteobacteria_Methylococcales_Methylomonadaceae_Methylomonas	0.0015	0.8533
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Novosphingobium	0.0014	0.8548
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_uncultured	0.0014	0.8563
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_	0.0014	0.8577
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Nocardioides	0.0014	0.8592
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_uncultured	0.0013	0.8606
Bacteria_Firmicutes_Bacilli_Exiguobacterales_Exiguobacteraceae_Exiguobacterium	0.0013	0.8619
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_uncultured	0.0013	0.8633
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Ellin6055	0.0013	0.8646
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales__	0.0013	0.8659
Bacteria_Firmicutes_Bacilli_Lactobacillales__	0.0012	0.8673
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_YC-ZSS-LKJ147	0.0012	0.8685
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_Sphingobacteriaceae_Pedobacter	0.0012	0.8698
Bacteria_Firmicutes_Bacilli_Bacillales_Planococcaceae_	0.0011	0.8710
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_PMMR1	0.0011	0.8722
Bacteria_Firmicutes_Bacilli_Bacillales_Planococcaceae_Planococcus	0.0010	0.8732
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Rhodoferax	0.0010	0.8743
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_ChroococcidiopsisSAG2023	0.0010	0.8754
Bacteria_Actinobacteriota_Actinobacteria_Frankiales__	0.0010	0.8765
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Intrasporangiaceae_Ornithinicoccus	0.0010	0.8776
Bacteria_Actinobacteriota_Actinobacteria_Kineosporiales_Kineosporiaceae_	0.0010	0.8786
Bacteria_Firmicutes_Bacilli_Staphylococcales_Gemellaceae_Gemella	0.0010	0.8797
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Halobacillus	0.0010	0.8807
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Aquabacterium	0.0010	0.8817
Bacteria_Actinobacteriota_Actinobacteria_Euzebyales_Euzebyaceae_uncultured	0.0009	0.8827

Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobium	0.0009	0.8837
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Undibacterium	0.0009	0.8846
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_uncultured_uncultured	0.0009	0.8855
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_uncultured	0.0009	0.8865
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Intrasporangiaceae_	0.0009	0.8874
Bacteria_Chloroflexi_KD4-96_KD4-96_KD4-96_KD4-96	0.0009	0.8883
Bacteria_Acidobacteriota_Acidobacteriae_Bryobacterales_Bryobacteraceae_Bryobacter	0.0009	0.8892
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Rhodanobacteraceae_uncultured	0.0008	0.8901
Bacteria_Proteobacteria_Gammaproteobacteria_B2M28_B2M28_B2M28	0.0008	0.8909
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_Pseudarcicella	0.0008	0.8918
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Niastella	0.0008	0.8926
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Sediminibacterium	0.0008	0.8935
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Dermabacteraceae_	0.0008	0.8943
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Rothia	0.0008	0.8951
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_	0.0008	0.8959
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_uncultured	0.0008	0.8967
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_Craurococcus-Caldovatus	0.0007	0.8975
Bacteria_Desulfobacterota_Desulfuromonadia_Geobacterales_Geobacteraceae_Citrifermentans	0.0007	0.8983
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Saprospiraceae_uncultured	0.0007	0.8990
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingopyxis	0.0007	0.8997
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_CandidatusPlanktoluna	0.0007	0.9005
Archaea_Crenarchaeota_Nitrososphaeria_Nitrososphaerales_Nitrososphaeraceae_	0.0007	0.9012
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Janthinobacterium	0.0007	0.9019
Bacteria_Proteobacteria_Alphaproteobacteria_Azospirillales_Azospirillaceae_Skermanella	0.0007	0.9026
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Aureimonas	0.0007	0.9033
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Altererythrobacter	0.0007	0.9040
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Propionibacteriaceae_Cutibacterium	0.0007	0.9047
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales__	0.0007	0.9054
Bacteria_Chloroflexi_Anaerolineae_Ardenticatenales_Ardenticatenaceae_uncultured	0.0006	0.9061
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Dietziaceae_Dietzia	0.0006	0.9067
Bacteria_Proteobacteria_Gammaproteobacteria_GammaproteobacteriaIncertaeSedis_UnknownFamily_CandidatusBerkiella	0.0006	0.9074
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_	0.0006	0.9080
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_uncultured	0.0006	0.9087
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Acidipila	0.0006	0.9093
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Ferruginibacter	0.0006	0.9099
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Spirosomaceae_Dyadobacter	0.0006	0.9106
Bacteria_Proteobacteria_Gammaproteobacteria_EV818SWSAP88_EV818SWSAP88_EV818SWSAP88	0.0006	0.9112
Bacteria_Proteobacteria_Gammaproteobacteria_Diplorickettsiales_Diplorickettsiaceae_uncultured	0.0006	0.9118
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Chitinophaga	0.0006	0.9124
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Citricoccus	0.0006	0.9131
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Conexibacter	0.0006	0.9137
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Rhizorhapis	0.0006	0.9143
Bacteria_Proteobacteria_Gammaproteobacteria_WD260_WD260_WD260	0.0006	0.9149
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_	0.0006	0.9155
Bacteria_Actinobacteriota_Actinobacteria___	0.0006	0.9161
Bacteria_Acidobacteriota_Thermoanaerobaculia_Thermoanaerobaculales_Thermoanaerobaculaceae_Subgroup10	0.0005	0.9167
Bacteria_Acidobacteriota_Blastocatellia_Pyrinomonadales_Pyrinomonadaceae_RB41	0.0005	0.9173
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Pseudorhodoplanes	0.0005	0.9179

Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_Phreatobacter	0.0005	0.9184
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Granulicella	0.0005	0.9190
Bacteria_Proteobacteria_Gammaproteobacteria_Oceanospirillales_Halomonadaceae_Halomonas	0.0005	0.9196
Bacteria_Firmicutes_Bacilli_Lactobacillales_Vagococcaceae_Vagococcus	0.0005	0.9201
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_	0.0005	0.9207
Bacteria_Proteobacteria_Gammaproteobacteria_Thiohalorhabdales_Thiohalorhabdaceae_uncultured	0.0005	0.9212
Bacteria_Fusobacteriota_Fusobacteriia_Fusobacteriales_Fusobacteriaceae_Fusobacterium	0.0005	0.9218
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Hyphomicrobiaceae_Hyphomicrobium	0.0005	0.9223
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Noviherbaspirillum	0.0005	0.9228
Bacteria_Actinobacteriota_Actinobacteria_Kineosporiales_Kineosporiaceae_Quadrisphaera	0.0005	0.9234
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Curvibacter	0.0005	0.9239
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xanthomonadaceae_Pseudoxanthomonas	0.0005	0.9245
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Acidothermaceae_Acidothermus	0.0005	0.9250
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Ralstonia	0.0005	0.9255
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_alphaIcluster	0.0005	0.9260

Root vs. Stem

	average	cumsum
Bacteria_Proteobacteria_Alphaproteobacteria_Rickettsiales_Mitochondria_Mitochondria	0.3370	0.3757
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Frankiaceae_Frankia	0.1793	0.5756
Bacteria_Firmicutes_Bacilli_Lactobacillales__	0.0627	0.6455
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Corynebacterium	0.0304	0.6794
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_uncultured	0.0156	0.6968
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Acinetobacter	0.0136	0.7120
Bacteria_Actinobacteriota_Actinobacteria_Streptomycetales_Streptomycetaceae_Streptomyces	0.0120	0.7253
Bacteria_Actinobacteriota_Rubrobacteria_Rubrobacterales_Rubrobacteriaceae_Rubrobacter	0.0120	0.7386
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Psychrobacter	0.0114	0.7514
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhodomicrobiaceae_Rhodomicrobium	0.0094	0.7619
Eukaryota_Phragmoplastophyta_Embryophyta_Magnoliophyta_Magnoliophyta_Magnoliophyta	0.0087	0.7716
Bacteria_Proteobacteria_Gammaproteobacteria_Steroidobacterales_Steroidobacteraceae_Steroidobacter	0.0086	0.7811
Bacteria_Proteobacteria_Gammaproteobacteria_Cardiobacteriales_Wohlfahrtiimonadaceae_Ignatzschineria	0.0084	0.7905
Bacteria_Firmicutes_Bacilli_Staphylococcales_Staphylococcaceae_Staphylococcus	0.0073	0.7987
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_	0.0064	0.8058
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Lawsonella	0.0063	0.8128
Bacteria_Proteobacteria_Gammaproteobacteria_GammaproteobacteriaIncertaeSedis_UnknownFamily_Acidibacter	0.0050	0.8184
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_GloeocapsaPCC-7428	0.0044	0.8232
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Pseudomonadaceae_Pseudomonas	0.0042	0.8279
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_DapisostemonumCCIBt3536	0.0040	0.8324
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Tissierella	0.0040	0.8369
Bacteria_Firmicutes_Bacilli_Lactobacillales_Streptococcaceae_Streptococcus	0.0038	0.8411
Bacteria_Fusobacteriota_Fusobacteriia_Fusobacteriales_Fusobacteriaceae_Fusobacterium	0.0037	0.8452
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingomonas	0.0036	0.8492
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Hyphomonadaceae_SWB02	0.0032	0.8528
Archaea_Crenarchaeota_Nitrososphaeria_Nitrososphaerales_Nitrososphaeraceae_	0.0029	0.8560
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_uncultured_uncultured	0.0026	0.8588
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Neisseriaceae_	0.0026	0.8617
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Phenylobacterium	0.0025	0.8644
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Enterobacteriaceae_	0.0023	0.8670
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_	0.0022	0.8694

Bacteria_Firmicutes_Bacilli_Bacillales__	0.0021	0.8718
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Burkholderia-Caballeronia-Paraburkholderia	0.0021	0.8741
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xanthomonadaceae_Stenotrophomonas	0.0021	0.8764
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Bacillus	0.0020	0.8786
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_Blastocatella	0.0020	0.8808
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_ChroococcidiopsisSAG2023	0.0020	0.8830
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Geodermatophilus	0.0019	0.8851
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales__	0.0019	0.8872
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Promicromonosporaceae_Cellulosimicrobium	0.0018	0.8893
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_67-14_67-14	0.0018	0.8912
Bacteria_Proteobacteria_Gammaproteobacteria_Pasteurellales_Pasteurellaceae_	0.0017	0.8932
Bacteria_Firmicutes_Bacilli_Erysipelotrichales_Erysipelotrichaceae_ZOR0006	0.0017	0.8951
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Anaerococcus	0.0017	0.8970
Bacteria_Proteobacteria_Alphaproteobacteria_Caulobacterales_Caulobacteraceae_Brevundimonas	0.0016	0.8988
Eukaryota_____	0.0016	0.9006
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_uncultured_uncultured	0.0016	0.9024
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_Aliterella	0.0016	0.9041
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcales-Tissierellales_Tepidimicrobium	0.0015	0.9058
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_Longimicrobiaceae	0.0015	0.9075
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_	0.0015	0.9092
Bacteria_Firmicutes_Clostridia_Oscillospirales_Ruminococcaceae_CandidatusSoleaferrea	0.0015	0.9109
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Geobacillus	0.0015	0.9125
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Oxalobacteraceae_Massilia	0.0014	0.9141
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Erwiniaceae_Pantoea	0.0014	0.9156
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Novosphingobium	0.0014	0.9172
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_Blastococcus	0.0014	0.9187
Bacteria_Acidobacteriota_Acidobacteriae_Subgroup2_Subgroup2_Subgroup2	0.0013	0.9202
Bacteria_Chloroflexi_Chloroflexia_Kallotenuales_AKIW781_AKIW781	0.0013	0.9217
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Shewanellaceae_Shewanella	0.0012	0.9231
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_	0.0011	0.9243
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Niastella	0.0011	0.9256
Bacteria_Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonadaceae_Rheinheimera	0.0011	0.9268
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_	0.0011	0.9280
Bacteria_Firmicutes_Bacilli_Erysipelotrichales_Erysipelotrichaceae_	0.0010	0.9291
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Rhodoferax	0.0010	0.9302
Bacteria_Firmicutes_Bacilli_Bacillales_Bacillaceae_Halobacillus	0.0010	0.9313
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_uncultured	0.0009	0.9324
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Geodermatophilaceae_	0.0009	0.9334
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_	0.0009	0.9343
Bacteria_Acidobacteriota_Acidobacteriae_Bryobacterales_Bryobacteraceae_Bryobacter	0.0009	0.9353
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Verrucomicrobiales_Verrucomicrobiaceae_uncultured	0.0008	0.9362
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.0008	0.9372
Bacteria_Deinococcota_Deinococci_Deinococcales_Deinococcaceae_Deinococcus	0.0008	0.9381
Bacteria_Acidobacteriota_Blastocatellia_Pyrinomonadales_Pyrinomonadaceae_RB41	0.0008	0.9390
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Morganellaceae_Photorhabdus	0.0008	0.9399
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Micrococcus	0.0008	0.9407
Bacteria_Actinobacteriota_Actinobacteria_Propionibacteriales_Nocardioidaceae_Nocardioides	0.0008	0.9416

Bacteria_Proteobacteria_Gammaproteobacteria_B2M28_B2M28_B2M28	0.0007	0.9424
Bacteria_Firmicutes_Bacilli_Bacillales_Planococcaceae_	0.0007	0.9432
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_Kocuria	0.0007	0.9439
Bacteria_Chloroflexi_Anaerolineae_Ardenticatenales_Ardenticatenaceae_uncultured	0.0007	0.9447
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_Polynucleobacter	0.0007	0.9454
Bacteria_Chloroflexi_Chloroflexia_Thermomicrobiales_AKYG1722_AKYG1722	0.0007	0.9462
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_uncultured_uncultured	0.0006	0.9469
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Nocardiaceae_Rhodococcus	0.0006	0.9476
Bacteria_Cyanobacteria_Cyanobacteriia_Cyanobacteriales_Chroococcidiopsaceae_ChroococcidiopsisPCC7203	0.0006	0.9483
Bacteria_Myxococcota_Polyangia_Polyangiales_Sandaracinaceae_uncultured	0.0006	0.9489
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Acidipila	0.0006	0.9495
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_	0.0005	0.9501
Bacteria_Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae_Dolosigranulum	0.0005	0.9507
Bacteria_Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae_Acidocella	0.0005	0.9513
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_RhizobialesIncertaeSedis_Phreatobacter	0.0005	0.9519
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Burkholderiaceae_	0.0005	0.9525
Bacteria_Proteobacteria_Gammaproteobacteria_Thiohalorhabdales_Thiohalorhabdaceae_uncultured	0.0005	0.9531
Bacteria_Firmicutes_Clostridia_Oscillospirales_Ruminococcaceae_uncultured	0.0005	0.9536
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Ellin6055	0.0005	0.9542
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Microvirga	0.0005	0.9548
Bacteria_Cyanobacteria_Cyanobacteriia_Thermosynechococcales_Acaryochloridaceae_AcaryochlorisMBIC11017	0.0005	0.9553
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_alphaIcluster	0.0005	0.9559
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_Pseudorhodoplanes	0.0005	0.9564
Bacteria_Acidobacteriota_Blastocatellia_Blastocatellales_Blastocatellaceae_uncultured	0.0005	0.9570
Bacteria_Deinococcota_Deinococci_Deinococcales_Trueperaceae_Truepera	0.0005	0.9575
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_Acidothermaceae_Acidothermus	0.0005	0.9580
Bacteria_Proteobacteria_Gammaproteobacteria_Chromatiales_Chromatiaceae_CandidatusThiobios	0.0005	0.9586
Bacteria_Actinobacteriota_Actinobacteria_Frankiales_uncultured_uncultured	0.0005	0.9591
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Solirubrobacter	0.0005	0.9596
Archaea_Crenarchaeota_Nitrososphaeria_Nitrososphaerales_Nitrososphaeraceae_CandidatusNitrocosmicus	0.0005	0.9601
Bacteria_Proteobacteria_Gammaproteobacteria_WD260_WD260_WD260	0.0005	0.9606
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Dinghuibacter	0.0004	0.9611
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Sutterellaceae_uncultured	0.0004	0.9616
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Conexibacter	0.0004	0.9620
Bacteria_Bacteroidota_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	0.0004	0.9625
Bacteria_Acidobacteriota_Acidobacteriae_Acidobacteriales_Acidobacteriaceae(Subgroup1)_Granulicella	0.0004	0.9630
Bacteria_Bacteroidota_Bacteroidia_Chitinophagales_Chitinophagaceae_Ferruginibacter	0.0004	0.9634
Bacteria_Gemmatimonadota_Longimicrobia_Longimicrobiales_Longimicrobiaceae_YC-ZSS-LKJ147	0.0004	0.9639
Bacteria_Firmicutes_Clostridia_Peptostreptococcales-Tissierellales_Peptostreptococcaceae_Paraclostridium	0.0004	0.9643
Bacteria_Actinobacteriota_Actinobacteria_Frankiales__	0.0004	0.9648
Unassigned_____	0.0004	0.9652
Bacteria_Actinobacteriota_Actinobacteria_Corynebacteriales_Corynebacteriaceae_Turicella	0.0004	0.9656
Bacteria_Proteobacteria_Gammaproteobacteria_KI89Aclade_KI89Aclade_KI89Aclade	0.0004	0.9660
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_	0.0004	0.9665
Bacteria_Actinobacteriota_Actinobacteria_PeM15_PeM15_PeM15	0.0004	0.9669
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Yersiniaceae_	0.0003	0.9673
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Microbacteriaceae_MWH-Ta3	0.0003	0.9676
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Comamonadaceae_Hydrogenophaga	0.0003	0.9680

Bacteria_SAR324clade(MarinegroupB)	0.0003	0.9684
Bacteria_Actinobacteriota_Actinobacteria___	0.0003	0.9688
Bacteria_Bacteroidota_Bacteroidia_Sphingobacteriales_Sphingobacteriaceae_Pedobacter	0.0003	0.9691
Bacteria_Actinobacteriota_Actinobacteria_Actinomycetales_Actinomycetaceae_Actinomyces	0.0003	0.9695
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Xanthobacteraceae_uncultured	0.0003	0.9698
Bacteria_Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae_Enhydrobacter	0.0003	0.9702
Bacteria_Firmicutes_Bacilli_Entomoplasmatales_Entomoplasmataceae_Mesoplasma	0.0003	0.9705
Bacteria_Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae_Sphingopyxis	0.0003	0.9709
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Neisseriaceae_Vitreoscilla	0.0003	0.9712
Bacteria_Proteobacteria_Gammaproteobacteria_Cardiobacteriales_Wohlfahrtiimonadaceae_	0.0003	0.9716
Bacteria_Planctomycetota_Phycisphaerae_Tepidisphaerales_WD2101soilgroup_WD2101soilgroup	0.0003	0.9719
Bacteria_Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae_Lactobacillus	0.0003	0.9722
Bacteria_Actinobacteriota_Actinobacteria_Actinomycetales_Actinomycetaceae_Actinotignum	0.0003	0.9725
Bacteria_Actinobacteriota_Actinobacteria_Kineosporiales_Kineosporiaceae_	0.0003	0.9729
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Dermabacteraceae_Brachybacterium	0.0003	0.9732
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xanthomonadaceae_Xanthomonas	0.0003	0.9735
Bacteria_____	0.0003	0.9738
Bacteria_Verrucomicrobiota_Verrucomicrobiae_Pedosphaerales_Pedosphaeraceae_Pedosphaeraceae	0.0003	0.9741
Bacteria_Firmicutes_Bacilli_Bacillales_Planococcaceae_Domibacillus	0.0003	0.9744
Bacteria_Actinobacteriota_Thermoleophilia_Solirubrobacterales_Solirubrobacteraceae_Parviterribacter	0.0003	0.9747
Bacteria_Actinobacteriota_Actinobacteria_Euzebyales_Euzebyaceae_uncultured	0.0003	0.9750
Bacteria_Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xanthomonadaceae_Vulcaniibacterium	0.0003	0.9753
Bacteria_Bacteroidota_Bacteroidia_Cytophagales_Microscillaceae_uncultured	0.0003	0.9756
Bacteria_Actinobacteriota_Actinobacteria_Micrococcales_Micrococcaceae_	0.0003	0.9759
Bacteria_Planctomycetota_Planctomycetes_Gemmatales_Gemmataceae_Fimbriiglobus	0.0003	0.9762
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_Roseiarcus	0.0003	0.9764
Bacteria_Gemmatimonadota_Gemmatimonadetes_Gemmatimonadales_Gemmatimonadaceae_uncultured	0.0003	0.9767
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Rhizobiaceae_Mesorhizobium	0.0002	0.9770
Bacteria_Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae_Granulicatella	0.0002	0.9773
Bacteria_Firmicutes_Bacilli_Staphylococcales_Gemellaceae_Gemella	0.0002	0.9775
Bacteria_Fusobacteriota_Fusobacteriia_Fusobacteriales_Leptotrichiaceae_Leptotrichia	0.0002	0.9778
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Rhodocyclaceae_	0.0002	0.9781
Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacterales_Yersiniaceae_Serratia	0.0002	0.9783
Bacteria_Proteobacteria_Gammaproteobacteria_Burkholderiales_Neisseriaceae_Neisseria	0.0002	0.9786
Bacteria_Proteobacteria_Gammaproteobacteria_Pasteurellales_Pasteurellaceae_Haemophilus	0.0002	0.9789
Bacteria_Bacteroidota_Rhodothermia_Rhodothermales_Rhodothermaceae_uncultured	0.0002	0.9791
Bacteria_Proteobacteria_Alphaproteobacteria_Rhizobiales_Beijerinckiaceae_uncultured	0.0002	0.9794
Bacteria_Chloroflexi_Chloroflexia_Thermomicrobiales_JG30-KF-CM45_JG30-KF-CM45	0.0002	0.9796
Bacteria_Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacteraceae_Rubellimicrobium	0.0002	0.9799
Bacteria_Acidobacteriota_Acidobacteriae_Solibacterales_Solibacteraceae_CandidatusSolibacter	0.0002	0.9801

Table 3.4: Phyla level Simper analysis results for the phytomicrobiome of C. myrtifolia. Taxa are listed as assigned by QIMME2 at level 2 (L2). Average and cumsum scores for each pair of sample types are listed below the labeled headers. Average refers to average contribution to dissimilarity for a given taxa and cumsum refers to the cumulative sum of dissimilarity for all taxa listed above a give row.

Fruit vs. Leaf		
	average	cumsum
Bacteria_Proteobacteria	0.1090	0.3594
Bacteria_Firmicutes	0.0674	0.5816
Bacteria_Acidobacteriota	0.0460	0.7333
Bacteria_Actinobacteriota	0.0453	0.8828
Bacteria_Bacteroidota	0.0153	0.9332
Bacteria_Verrucomicrobiota	0.0054	0.9510
Bacteria_Nitrospirota	0.0020	0.9574
Bacteria_Myxococcota	0.0019	0.9638
Bacteria_Planctomycetota	0.0018	0.9697
Bacteria_	0.0013	0.9740
Bacteria_RCP2-54	0.0012	0.9780
Bacteria_Bdellovibrionota	0.0010	0.9812
Bacteria_Patescibacteria	0.0009	0.9841
Bacteria_Chloroflexi	0.0008	0.9869
Bacteria_Gemmatimonadota	0.0008	0.9896
Bacteria_Desulfobacterota	0.0006	0.9918
Bacteria_Deinococcota	0.0006	0.9937
Bacteria_SAR324	0.0004	0.9951
Bacteria_Fusobacteriota	0.0003	0.9961
Bacteria_Aquificota	0.0003	0.9971
Bacteria_Fibrobacterota	0.0003	0.9980
Bacteria_WPS-2	0.0003	0.9989
Bacteria_Armatimonadota	0.0002	0.9997
Bacteria_MBNT15	0.0001	1.0000
Eukaryota_Basidiomycota	0.0000	1.0000
Unassigned_	0.0000	1.0000
Archaea_	0.0000	1.0000
Archaea_Crenarchaeota	0.0000	1.0000
Archaea_Halobacterota	0.0000	1.0000
Archaea_Nanoarchaeota	0.0000	1.0000
Archaea_Thermoplasmatota	0.0000	1.0000
Bacteria_Abditibacteriota	0.0000	1.0000
Bacteria_Campilobacterota	0.0000	1.0000
Bacteria_Dependentiae	0.0000	1.0000
Bacteria_Elusimicrobiota	0.0000	1.0000
Bacteria_Entotheonellaeota	0.0000	1.0000
Bacteria_FCPU426	0.0000	1.0000

Bacteria_Hydrogenedentes	0.0000	1.0000
Bacteria_Latescibacterota	0.0000	1.0000
Bacteria_Methylomirabilota	0.0000	1.0000
Bacteria_NB1-j	0.0000	1.0000
Bacteria_Spirochaetota	0.0000	1.0000
Bacteria_Sumerlaeota	0.0000	1.0000
Bacteria_WS2	0.0000	1.0000
Eukaryota_	0.0000	1.0000
Eukaryota_Ciliophora	0.0000	1.0000
Eukaryota_Phragmoplastophyta	0.0000	1.0000

Fruit vs. Nodule

	average	cumsum
Bacteria_Proteobacteria	0.1607	0.3732
Bacteria_Actinobacteriota	0.1151	0.6406
Bacteria_Firmicutes	0.0726	0.8093
Bacteria_Bacteroidota	0.0220	0.8602
Bacteria_Verrucomicrobiota	0.0112	0.8862
Bacteria_Gemmatimonadota	0.0070	0.9025
Bacteria_Chloroflexi	0.0063	0.9172
Eukaryota_	0.0062	0.9316
Bacteria_Acidobacteriota	0.0048	0.9427
Bacteria_Deinococcota	0.0036	0.9510
Bacteria_Myxococcota	0.0026	0.9570
Bacteria_	0.0025	0.9628
Bacteria_Planctomycetota	0.0024	0.9682
Eukaryota_Phragmoplastophyta	0.0021	0.9732
Bacteria_Nitrospirota	0.0020	0.9778
Bacteria_Patescibacteria	0.0017	0.9818
Bacteria_Desulfobacterota	0.0015	0.9852
Bacteria_Bdellovibrionota	0.0014	0.9884
Archaea_Crenarchaeota	0.0009	0.9905
Bacteria_Fusobacteriota	0.0008	0.9924
Archaea_Halobacterota	0.0005	0.9935
Bacteria_SAR324	0.0004	0.9945
Bacteria_Armatimonadota	0.0004	0.9954
Bacteria_Abditibacteriota	0.0003	0.9962
Bacteria_Aquificota	0.0003	0.9970
Bacteria_Fibrobacterota	0.0003	0.9977
Archaea_Nanoarchaeota	0.0002	0.9982
Bacteria_RCP2-54	0.0001	0.9985
Unassigned_	0.0001	0.9988
Archaea_Thermoplasmatota	0.0001	0.9991
Bacteria_MBNT15	0.0001	0.9993
Bacteria_Elusimicrobiota	0.0001	0.9994

Archaea_	0.0000	0.9995
Bacteria_Latescibacterota	0.0000	0.9996
Eukaryota_Basidiomycota	0.0000	0.9997
Bacteria_Sumerlaeota	0.0000	0.9998
Bacteria_WPS-2	0.0000	0.9998
Bacteria_Dependentiae	0.0000	0.9999
Bacteria_Campilobacterota	0.0000	0.9999
Bacteria_Spirochaetota	0.0000	0.9999
Bacteria_WS2	0.0000	1.0000
Bacteria_NB1-j	0.0000	1.0000
Bacteria_Hydrogenedentes	0.0000	1.0000
Bacteria_Entotheonellaeota	0.0000	1.0000
Eukaryota_Ciliophora	0.0000	1.0000
Bacteria_FCPU426	0.0000	1.0000
Bacteria_Methylomirabilota	0.0000	1.0000

Fruit vs. Root

	average	cumsum
Bacteria_Proteobacteria	0.2061	0.3435
Bacteria_Actinobacteriota	0.2036	0.6830
Bacteria_Firmicutes	0.1147	0.8743
Bacteria_Bacteroidota	0.0153	0.8998
Bacteria_Acidobacteriota	0.0103	0.9168
Eukaryota_Phragmoplastophyta	0.0087	0.9314
Archaea_Crenarchaeota	0.0058	0.9410
Bacteria_Verrucomicrobiota	0.0056	0.9504
Bacteria_Chloroflexi	0.0055	0.9594
Bacteria_Gemmatimonadota	0.0043	0.9666
Bacteria_Fusobacteriota	0.0038	0.9728
Bacteria_Myxococcota	0.0022	0.9766
Bacteria_Deinococcota	0.0021	0.9801
Bacteria_Planctomycetota	0.0020	0.9834
Bacteria_Nitrospirota	0.0019	0.9865
Eukaryota_	0.0016	0.9892
Bacteria_	0.0015	0.9918
Bacteria_Bdellovibrionota	0.0010	0.9935
Bacteria_Patescibacteria	0.0009	0.9950
Bacteria_Desulfobacterota	0.0006	0.9961
Bacteria_SAR324clade	0.0004	0.9968
Unassigned_	0.0004	0.9975
Bacteria_Aquificota	0.0003	0.9980
Bacteria_Armatimonadota	0.0003	0.9985
Bacteria_Fibrobacterota	0.0003	0.9989
Bacteria_RCP2-54	0.0001	0.9992
Bacteria_Abditibacteriota	0.0001	0.9994

Bacteria_Campilobacterota	0.0001	0.9996
Bacteria_MBNT15	0.0001	0.9997
Eukaryota_Basidiomycota	0.0001	0.9998
Bacteria_WPS-2	0.0000	0.9999
Bacteria_NB1-j	0.0000	0.9999
Bacteria_Spirochaetota	0.0000	1.0000
Bacteria_Dependentiae	0.0000	1.0000
Bacteria_Latescibacterota	0.0000	1.0000
Bacteria_Methylomirabilota	0.0000	1.0000
Archaea_	0.0000	1.0000
Archaea_Halobacterota	0.0000	1.0000
Archaea_Nanoarchaeota	0.0000	1.0000
Archaea_Thermoplasmatota	0.0000	1.0000
Bacteria_Elusimicrobiota	0.0000	1.0000
Bacteria_Entotheonellaeota	0.0000	1.0000
Bacteria_FCPU426	0.0000	1.0000
Bacteria_Hydrogenedentes	0.0000	1.0000
Bacteria_Sumerlaeota	0.0000	1.0000
Bacteria_WS2	0.0000	1.0000
Eukaryota_Ciliophora	0.0000	1.0000

Fruit vs. Stem

	average	cumsum
Bacteria_Proteobacteria	0.1425	0.4486
Bacteria_Actinobacteriota	0.0710	0.6722
Bacteria_Firmicutes	0.0621	0.8679
Bacteria_Bacteroidota	0.0153	0.9160
Bacteria_Acidobacteriota	0.0066	0.9369
Bacteria_Verrucomicrobiota	0.0058	0.9552
Bacteria_Myxococcota	0.0020	0.9616
Bacteria_Planctomycetota	0.0019	0.9676
Bacteria_Nitrospirota	0.0018	0.9733
Bacteria_	0.0014	0.9776
Bacteria_Bdellovibrionota	0.0010	0.9807
Bacteria_Patescibacteria	0.0010	0.9837
Bacteria_Gemmatimonadota	0.0009	0.9865
Bacteria_Deinococcota	0.0008	0.9892
Bacteria_Desulfobacterota	0.0006	0.9912
Bacteria_SAR324	0.0006	0.9931
Bacteria_Aquificota	0.0004	0.9944
Bacteria_Chloroflexi	0.0004	0.9955
Bacteria_Fusobacteriota	0.0003	0.9965
Bacteria_Fibrobacterota	0.0003	0.9974
Bacteria_Armatimonadota	0.0002	0.9982
Bacteria_MBNT15	0.0002	0.9988

Bacteria_RCP2-54	0.0001	0.9992
Bacteria_WPS-2	0.0001	0.9995
Archaea_Nanoarchaeota	0.0001	0.9998
Archaea_Thermoplasmatota	0.0001	1.0000
Eukaryota_Basidiomycota	0.0000	1.0000
Unassigned_	0.0000	1.0000
Archaea_	0.0000	1.0000
Archaea_Crenarchaeota	0.0000	1.0000
Archaea_Halobacterota	0.0000	1.0000
Bacteria_Abditibacteriota	0.0000	1.0000
Bacteria_Campilobacterota	0.0000	1.0000
Bacteria_Dependentiae	0.0000	1.0000
Bacteria_Elusimicrobiota	0.0000	1.0000
Bacteria_Entotheonellaeota	0.0000	1.0000
Bacteria_FCPU426	0.0000	1.0000
Bacteria_Hydrogenedentes	0.0000	1.0000
Bacteria_Latescibacterota	0.0000	1.0000
Bacteria_Methylomirabilota	0.0000	1.0000
Bacteria_NB1-j	0.0000	1.0000
Bacteria_Spirochaetota	0.0000	1.0000
Bacteria_Sumerlaeota	0.0000	1.0000
Bacteria_WS2	0.0000	1.0000
Eukaryota_	0.0000	1.0000
Eukaryota_Ciliophora	0.0000	1.0000
Eukaryota_Phragmoplastophyta	0.0000	1.0000

Leaf vs. Nodule

	average	cumsum
Bacteria_Proteobacteria	0.2265	0.4128
Bacteria_Actinobacteriota	0.1418	0.6713
Bacteria_Firmicutes	0.0568	0.7748
Bacteria_Acidobacteriota	0.0448	0.8564
Bacteria_Bacteroidota	0.0283	0.9080
Bacteria_Verrucomicrobiota	0.0101	0.9265
Bacteria_Gemmatimonadota	0.0071	0.9395
Bacteria_Chloroflexi	0.0062	0.9508
Eukaryota_	0.0062	0.9621
Bacteria_Deinococcota	0.0039	0.9693
Eukaryota_Phragmoplastophyta	0.0021	0.9732
Bacteria_	0.0018	0.9764
Bacteria_Planctomycetota	0.0017	0.9796
Bacteria_Myxococcota	0.0017	0.9826
Bacteria_Desulfobacterota	0.0013	0.9851
Bacteria_Patescibacteria	0.0012	0.9873
Bacteria_RCP2-54	0.0012	0.9895

Archaea_Crenarchaeota	0.0009	0.9911
Bacteria_Fusobacteriota	0.0009	0.9927
Bacteria_Nitrospirota	0.0009	0.9943
Bacteria_Bdellovibrionota	0.0009	0.9960
Archaea_Halobacterota	0.0005	0.9968
Bacteria_Abditibacteriota	0.0003	0.9974
Bacteria_WPS-2	0.0003	0.9979
Bacteria_Armatimonadota	0.0002	0.9983
Archaea_Nanoarchaeota	0.0002	0.9988
Unassigned_	0.0001	0.9990
Bacteria_SAR324	0.0001	0.9992
Archaea_Thermoplasmatota	0.0001	0.9994
Bacteria_Elusimicrobiota	0.0001	0.9995
Archaea_	0.0000	0.9996
Bacteria_Latescibacterota	0.0000	0.9996
Bacteria_Aquificota	0.0000	0.9997
Bacteria_Sumerlaeota	0.0000	0.9998
Eukaryota_Basidiomycota	0.0000	0.9998
Bacteria_Fibrobacterota	0.0000	0.9998
Bacteria_Dependentiae	0.0000	0.9999
Bacteria_MBNT15	0.0000	0.9999
Bacteria_Campilobacterota	0.0000	0.9999
Bacteria_Spirochaetota	0.0000	0.9999
Bacteria_WS2	0.0000	1.0000
Bacteria_NB1-j	0.0000	1.0000
Bacteria_Hydrogenedentes	0.0000	1.0000
Bacteria_Entotheonellaeota	0.0000	1.0000
Eukaryota_Ciliophora	0.0000	1.0000
Bacteria_FCPU426	0.0000	1.0000
Bacteria_Methylomirabilota	0.0000	1.0000

Leaf vs. Root

	average	cumsum
Bacteria_Proteobacteria	0.2912	0.4275
Bacteria_Actinobacteriota	0.2273	0.7612
Bacteria_Firmicutes	0.0767	0.8738
Bacteria_Acidobacteriota	0.0441	0.9385
Eukaryota_Phragmoplastophyta	0.0087	0.9513
Archaea_Crenarchaeota	0.0058	0.9598
Bacteria_Chloroflexi	0.0057	0.9681
Bacteria_Bacteroidota	0.0050	0.9755
Bacteria_Fusobacteriota	0.0038	0.9811
Bacteria_Gemmatimonadota	0.0037	0.9866
Bacteria_Deinococcota	0.0017	0.9891
Eukaryota_	0.0016	0.9915

Bacteria_RCP2-54	0.0012	0.9932
Bacteria_Myxococcota	0.0009	0.9946
Bacteria_Verrucomicrobiota	0.0008	0.9957
Bacteria_Nitrospirota	0.0007	0.9967
Bacteria_Planctomycetota	0.0006	0.9975
Unassigned_	0.0004	0.9981
Bacteria_	0.0004	0.9987
Bacteria_WPS-2	0.0003	0.9990
Bacteria_Abditibacteriota	0.0001	0.9992
Bacteria_Bdellovibrionota	0.0001	0.9994
Bacteria_Campilobacterota	0.0001	0.9996
Bacteria_Armatimonadota	0.0001	0.9997
Eukaryota_Basidiomycota	0.0001	0.9998
Bacteria_Patescibacteria	0.0000	0.9999
Bacteria_NB1-j	0.0000	0.9999
Bacteria_Spirochaetota	0.0000	0.9999
Bacteria_Dependentiae	0.0000	1.0000
Bacteria_Desulfobacterota	0.0000	1.0000
Bacteria_SAR324	0.0000	1.0000
Bacteria_Latescibacterota	0.0000	1.0000
Bacteria_Methylomirabilota	0.0000	1.0000
Archaea_	0.0000	1.0000
Archaea_Halobacterota	0.0000	1.0000
Archaea_Nanoarchaeota	0.0000	1.0000
Archaea_Thermoplasmatota	0.0000	1.0000
Bacteria_Aquificota	0.0000	1.0000
Bacteria_Elusimicrobiota	0.0000	1.0000
Bacteria_Entotheonellaeota	0.0000	1.0000
Bacteria_FCPU426	0.0000	1.0000
Bacteria_Fibrobacterota	0.0000	1.0000
Bacteria_Hydrogenedentes	0.0000	1.0000
Bacteria_MBNT15	0.0000	1.0000
Bacteria_Sumerlaeota	0.0000	1.0000
Bacteria_WS2	0.0000	1.0000
Eukaryota_Ciliophora	0.0000	1.0000

Leaf vs. Stem

	average	cumsum
Bacteria_Proteobacteria	0.0827	0.4084
Bacteria_Actinobacteriota	0.0495	0.6526
Bacteria_Acidobacteriota	0.0447	0.8735
Bacteria_Firmicutes	0.0176	0.9603
Bacteria_Bacteroidota	0.0013	0.9669
Bacteria_Verrucomicrobiota	0.0013	0.9731
Bacteria_RCP2-54	0.0012	0.9788

Bacteria_Chloroflexi	0.0007	0.9822
Bacteria_Nitrospirota	0.0005	0.9846
Bacteria_Deinococcota	0.0005	0.9868
Bacteria_Planctomycetota	0.0004	0.9889
Bacteria_Fusobacteriota	0.0004	0.9908
Bacteria_SAR324	0.0003	0.9925
Bacteria_WPS-2	0.0003	0.9941
Bacteria_Gemmatimonadota	0.0003	0.9956
Bacteria_Myxococcota	0.0003	0.9969
Bacteria_Aquificota	0.0001	0.9976
Bacteria_MBNT15	0.0001	0.9983
Bacteria_	0.0001	0.9989
Bacteria_Patescibacteria	0.0001	0.9994
Archaea_Nanoarchaeota	0.0001	0.9997
Archaea_Thermoplasmatota	0.0001	1.0000
Unassigned_	0.0000	1.0000
Archaea_	0.0000	1.0000
Archaea_Crenarchaeota	0.0000	1.0000
Archaea_Halobacterota	0.0000	1.0000
Bacteria_Abditibacteriota	0.0000	1.0000
Bacteria_Armatimonadota	0.0000	1.0000
Bacteria_Bdellovibrionota	0.0000	1.0000
Bacteria_Campilobacterota	0.0000	1.0000
Bacteria_Dependentiae	0.0000	1.0000
Bacteria_Desulfobacterota	0.0000	1.0000
Bacteria_Elusimicrobiota	0.0000	1.0000
Bacteria_Entotheonellaeota	0.0000	1.0000
Bacteria_FCPU426	0.0000	1.0000
Bacteria_Fibrobacterota	0.0000	1.0000
Bacteria_Hydrogenedentes	0.0000	1.0000
Bacteria_Latescibacterota	0.0000	1.0000
Bacteria_Methylomirabilota	0.0000	1.0000
Bacteria_NB1-j	0.0000	1.0000
Bacteria_Spirochaetota	0.0000	1.0000
Bacteria_Sumerlaeota	0.0000	1.0000
Bacteria_WS2	0.0000	1.0000
Eukaryota_	0.0000	1.0000
Eukaryota_Basidiomycota	0.0000	1.0000
Eukaryota_Ciliophora	0.0000	1.0000
Eukaryota_Phragmoplastophyta	0.0000	1.0000

Nodule vs. Root

	average	cumsum
Bacteria_Actinobacteriota	0.1678	0.3359
Bacteria_Proteobacteria	0.1171	0.5704

Bacteria_Firmicutes	0.1083	0.7872
Bacteria_Bacteroidota	0.0233	0.8339
Bacteria_Acidobacteriota	0.0112	0.8563
Eukaryota_Phragmoplastophyta	0.0100	0.8763
Bacteria_Verrucomicrobiota	0.0098	0.8960
Bacteria_Chloroflexi	0.0096	0.9153
Bacteria_Gemmatimonadota	0.0085	0.9323
Eukaryota_	0.0073	0.9468
Archaea_Crenarchaeota	0.0064	0.9595
Bacteria_Deinococcota	0.0044	0.9683
Bacteria_Fusobacteriota	0.0042	0.9767
Bacteria_	0.0017	0.9802
Bacteria_Myxococcota	0.0017	0.9836
Bacteria_Planctomycetota	0.0014	0.9865
Bacteria_Desulfobacterota	0.0013	0.9892
Bacteria_Patescibacteria	0.0012	0.9916
Bacteria_Bdellovibrionota	0.0009	0.9934
Bacteria_Nitrospirota	0.0008	0.9949
Archaea_Halobacterota	0.0005	0.9958
Unassigned_	0.0004	0.9967
Bacteria_Abditibacteriota	0.0004	0.9975
Bacteria_Armatimonadota	0.0002	0.9980
Archaea_Nanoarchaeota	0.0002	0.9985
Bacteria_Campilobacterota	0.0001	0.9987
Bacteria_SAR324clade	0.0001	0.9989
Archaea_Thermoplasmatota	0.0001	0.9991
Eukaryota_Basidiomycota	0.0001	0.9992
Bacteria_Elusimicrobiota	0.0001	0.9993
Bacteria_Latescibacterota	0.0001	0.9995
Archaea_	0.0000	0.9995
Bacteria_Aquificota	0.0000	0.9996
Bacteria_Dependentiae	0.0000	0.9997
Bacteria_Sumerlaeota	0.0000	0.9997
Bacteria_Spirochaetota	0.0000	0.9998
Bacteria_NB1-j	0.0000	0.9998
Bacteria_RCP2-54	0.0000	0.9999
Bacteria_Fibrobacterota	0.0000	0.9999
Bacteria_MBNT15	0.0000	0.9999
Bacteria_WS2	0.0000	1.0000
Bacteria_Hydrogenedentes	0.0000	1.0000
Bacteria_Methylomirabilota	0.0000	1.0000
Bacteria_Entotheonellaeota	0.0000	1.0000
Eukaryota_Ciliophora	0.0000	1.0000
Bacteria_FCPU426	0.0000	1.0000

Bacteria_WPS-2	0.0000	1.0000

Nodule vs. Stem

	average	cumsum
Bacteria_Proteobacteria	0.2370	0.4598
Bacteria_Actinobacteriota	0.1350	0.7218
Bacteria_Firmicutes	0.0595	0.8372
Bacteria_Bacteroidota	0.0273	0.8901
Bacteria_Verrucomicrobiota	0.0098	0.9092
Bacteria_Acidobacteriota	0.0077	0.9241
Bacteria_Gemmatimonadota	0.0071	0.9378
Bacteria_Chloroflexi	0.0065	0.9504
Eukaryota_	0.0062	0.9624
Bacteria_Deinococcota	0.0038	0.9698
Eukaryota_Phragmoplastophyta	0.0021	0.9739
Bacteria_	0.0017	0.9772
Bacteria_Myxococcota	0.0016	0.9804
Bacteria_Planctomycetota	0.0016	0.9834
Bacteria_Desulfobacterota	0.0013	0.9860
Bacteria_Patescibacteria	0.0012	0.9883
Bacteria_Fusobacteriota	0.0009	0.9901
Archaea_Crenarchaeota	0.0009	0.9918
Bacteria_Bdellovibrionota	0.0009	0.9935
Bacteria_Nitrospirota	0.0006	0.9947
Archaea_Halobacterota	0.0005	0.9956
Bacteria_SAR324	0.0004	0.9964
Bacteria_Abditibacteriota	0.0003	0.9971
Archaea_Nanoarchaeota	0.0003	0.9976
Bacteria_Armatimonadota	0.0002	0.9981
Bacteria_Aquificota	0.0002	0.9984
Bacteria_MBNT15	0.0002	0.9987
Unassigned_	0.0001	0.9990
Archaea_Thermoplasmatota	0.0001	0.9992
Bacteria_WPS-2	0.0001	0.9994
Bacteria_Elusimicrobiota	0.0001	0.9995
Archaea_	0.0000	0.9996
Bacteria_Latescibacterota	0.0000	0.9997
Bacteria_Sumerlaeota	0.0000	0.9998
Eukaryota_Basidiomycota	0.0000	0.9998
Bacteria_Fibrobacterota	0.0000	0.9999
Bacteria_Dependentiae	0.0000	0.9999
Bacteria_Campilobacterota	0.0000	0.9999
Bacteria_Spirochaetota	0.0000	0.9999
Bacteria_WS2	0.0000	1.0000
Bacteria_NB1-j	0.0000	1.0000

Bacteria_Hydrogenedentes	0.0000	1.0000
Bacteria_Entotheonellaeota	0.0000	1.0000
Eukaryota_Ciliophora	0.0000	1.0000
Bacteria_FCPU426	0.0000	1.0000
Bacteria_Methylomirabilota	0.0000	1.0000
Bacteria_RCP2-54	0.0000	1.0000

Root vs. Stem

	average	cumsum
Bacteria_Proteobacteria	0.2906	0.4566
Bacteria_Actinobacteriota	0.2106	0.7875
Bacteria_Firmicutes	0.0824	0.9170
Bacteria_Acidobacteriota	0.0116	0.9352
Eukaryota_Phragmoplastophyta	0.0087	0.9489
Archaea_Crenarchaeota	0.0058	0.9580
Bacteria_Chloroflexi	0.0053	0.9663
Bacteria_Bacteroidota	0.0043	0.9731
Bacteria_Gemmatimonadota	0.0039	0.9793
Bacteria_Fusobacteriota	0.0038	0.9853
Bacteria_Deinococcota	0.0020	0.9884
Eukaryota_	0.0016	0.9910
Bacteria_Verrucomicrobiota	0.0014	0.9931
Bacteria_Myxococcota	0.0010	0.9947
Bacteria_Planctomycetota	0.0007	0.9957
Bacteria_	0.0004	0.9964
Unassigned_	0.0004	0.9970
Bacteria_SAR324	0.0003	0.9975
Bacteria_Nitrospirota	0.0003	0.9980
Bacteria_Aquificota	0.0001	0.9982
Bacteria_MBNT15	0.0001	0.9984
Bacteria_Abditibacteriota	0.0001	0.9987
Bacteria_Bdellovibrionota	0.0001	0.9989
Bacteria_Patescibacteria	0.0001	0.9991
Bacteria_Campilobacterota	0.0001	0.9993
Bacteria_WPS-2	0.0001	0.9994
Bacteria_Armatimonadota	0.0001	0.9996
Archaea_Nanoarchaeota	0.0001	0.9997
Archaea_Thermoplasmatota	0.0001	0.9998
Eukaryota_Basidiomycota	0.0001	0.9998
Bacteria_NB1-j	0.0000	0.9999
Bacteria_RCP2-54	0.0000	0.9999
Bacteria_Spirochaetota	0.0000	0.9999
Bacteria_Dependentiae	0.0000	1.0000
Bacteria_Desulfobacterota	0.0000	1.0000
Bacteria_Latescibacterota	0.0000	1.0000

Bacteria_Methylomirabilota	0.0000	1.0000
Archaea_	0.0000	1.0000
Archaea_Halobacterota	0.0000	1.0000
Bacteria_Elusimicrobiota	0.0000	1.0000
Bacteria_Entotheonellaeota	0.0000	1.0000
Bacteria_FCPU426	0.0000	1.0000
Bacteria_Fibrobacterota	0.0000	1.0000
Bacteria_Hydrogenedentes	0.0000	1.0000
Bacteria_Sumerlaeota	0.0000	1.0000
Bacteria_WS2	0.0000	1.0000
Eukaryota_Ciliophora	0.0000	1.0000

Appendix C

Table 3.1: *inefficax* 2x Down-regulated Genes Exposed to Biphenyl with Glucose

Name	Fold change	P-value	Product	Gene Ontology
FRA*inefficax*_RS32635	-6.34	0.01	major intrinsic protein	GO:0005215
FRA*inefficax*_RS26020	-6.31	0.04	hypothetical protein	
FRA*inefficax*_RS22065	-6.1	0.00	protein of unknown function DUF35, Formyl-CoA transferase	
FRA*inefficax*_RS15880	-6.03	0.01	major facilitator superfamily MFS_1	
FRA*inefficax*_RS32630	-5.45	0.01	Glyoxalase/bleomycin resistanceprotein/dioxygenase	
FRA*inefficax*_RS32410	-5.12	0.03	hypothetical protein, Na+/H+ antiporter subunit	GO:0005451
FRA*inefficax*_RS19815	-4.9	0.02	ferredoxin (3Fe-4S)	
FRA*inefficax*_RS20885	-4.87	0.03	cytochrome P450	GO:0004497, GO:0005506, GO:0009055, GO:0020037
FRA*inefficax*_RS35095	-4.87	0.03	GCN5-related N-acetyltransferase, protein of unknown function DUF214, ABC transporter related protein	GO:0008080, GO:0005524, GO:0016887
FRA*inefficax*_RS10095	-4.85	0.00	ChaB family protein	GO:0003715
FRA*inefficax*_RS34355	-4.55	0.01	hypothetical protein	
FRA*inefficax*_RS07330	-4.34	0.00	hypothetical protein	
FRA*inefficax*_RS16975	-4.3	0.01	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS21125	-4.25	0.00	cytochrome P450	GO:0004497, GO:0005506, GO:0009055, GO:0020037
FRA*inefficax*_RS07290	-4.19	0.05	hypothetical protein	
FRA*inefficax*_RS23650	-4.12	0.01	L-carnitine dehydratase/bile acid-inducibleprotein F	GO:0003824
FRA*inefficax*_RS12630	-3.96	0.05	Alcohol dehydrogenase GroES domain protein	GO:0008270, GO:0016491
FRA*inefficax*_RS03025	-3.96	0.02	glycosyl transferase family 2	
FRA*inefficax*_RS10090	-3.94	0.00	flavin reductase domain protein FMN-bindingprotein	
FRA*inefficax*_RS28410	-3.87	0.03	short-chain dehydrogenase/reductase SDR, ERG4/ERG24 ergosterol biosynthesis protein	GO:0016491
FRA*inefficax*_RS02155	-3.86	0.00	Transglycosylase-associated protein	
FRA*inefficax*_RS24950	-3.83	0.01	DNA binding domain protein, excisionase family	GO:0003677
FRA*inefficax*_RS12855	-3.83	0.02	Carnitine O-acetyltransferase	

FRA*inefficax*_RS09145	-3.8	0.00	hypothetical protein	
FRA*inefficax*_RS15860	-3.78	0.02	aminotransferase class I and II	GO:0016491, GO:0030170
FRA*inefficax*_RS32280	-3.7	0.00	hypothetical protein	
FRA*inefficax*_RS14965	-3.63	0.02	hypothetical protein	
FRA*inefficax*_RS20480	-3.6	0.01	hypothetical protein	
FRA*inefficax*_RS05490	-3.59	0.01	sulfate ABC transporter, inner membrane subunitCysT, sulfate ABC transporter, inner membrane subunit	GO:0015116, GO:0015563
FRA*inefficax*_RS27685	-3.56	0.00	putativeN-(5-amino-5-carboxypentanoyl)-L-cysteinyl-D-valinesynthase	
FRA*inefficax*_RS04095	-3.47	0.00	polar amino acid ABC transporter, inner membranesubunit	GO:0005215
FRA*inefficax*_RS20800	-3.43	0.04	hypothetical protein	
FRA*inefficax*_RS07295	-3.41	0.01	short-chain dehydrogenase/reductase SDR	GO:0016491
FRA*inefficax*_RS09665	-3.4	0.00	hypothetical protein	
FRA*inefficax*_RS32100	-3.4	0.01	hypothetical protein	
FRA*inefficax*_RS33240	-3.33	0.02	pyridoxamine 5'-phosphate oxidase-relatedFMN-binding protein	GO:0010181
FRA*inefficax*_RS26160	-3.24	0.01	Leucine carboxyl methyltransferase	GO:0008168
FRA*inefficax*_RS09670	-3.23	0.00	ErfK/YbiS/YcfS/YnhG family protein	
FRA*inefficax*_RS11185	-3.2	0.01	polysaccharide biosynthesis protein CapD	
FRA*inefficax*_RS26155	-3.17	0.03	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS34620	-3.13	0.03	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS34555	-3.13	0.05	hypothetical protein	
FRA*inefficax*_RS24355	-3.1	0.00	acyltransferase 3	GO:0003723
FRA*inefficax*_RS16430	-3.08	0.00	regulatory protein GntR HTH	GO:0003700
FRA*inefficax*_RS16700	-3.07	0.01	hypothetical protein	
FRA*inefficax*_RS30445	-3.07	0.00	glutamate--cysteine ligase GCS2	GO:0004357
FRA*inefficax*_RS16330	-3.05	0.02	dihydrodipicolinate reductase	GO:0008839
FRA*inefficax*_RS21710	-3.04	0.03	hypothetical protein	
FRA*inefficax*_RS12940	-3.04	0.04	nitroreductase	GO:0016491
FRA*inefficax*_RS25290	-2.98	0.00	PilT protein domain protein, prevent-host-death family protein	
FRA*inefficax*_RS13205	-2.91	0.01	hypothetical protein, MscS Mechanosensitive ion channel	
FRA*inefficax*_RS29735	-2.91	0.04	glycoside hydrolase 15-related protein	GO:0004339
FRA*inefficax*_RS16970	-2.82	0.00	Extracellular ligand-binding receptor	
FRA*inefficax*_RS32285	-2.81	0.01	anti-anti-sigma factor	GO:0045152

FRA*inefficax*_RS31950	-2.8	0.00	transcription factor WhiB, phage tail tape measure protein, TP901 family	
FRA*inefficax*_RS03830	-2.79	0.00	glutaredoxin-like protein	
FRA*inefficax*_RS21110	-2.78	0.03	monooxygenase FAD-binding protein, Beta-ketoacyl-acyl-carrier-protein synthase I	GO:0004497
FRA*inefficax*_RS19675	-2.77	0.00	hypothetical protein	
FRA*inefficax*_RS12160	-2.75	0.00	Ferritin Dps family protein	GO:0008199
FRA*inefficax*_RS35295	-2.74	0.01	periplasmic solute binding protein	GO:0046872
FRA*inefficax*_RS32420	-2.72	0.03	Na+/H+ antiporter MnhB subunit-related protein, NADH-ubiquinone oxidoreductase chain 4L	GO:0003700
FRA*inefficax*_RS32760	-2.71	0.00	NLP/P60 protein	
FRA*inefficax*_RS32530	-2.7	0.04	alpha/beta hydrolase fold protein	
FRA*inefficax*_RS26980	-2.67	0.03	cytochrome P450	GO:0004497, GO:0005506, GO:0009055, GO:0020037
FRA*inefficax*_RS15015	-2.66	0.01	2OG-Fe(II) oxygenase	GO:0016491
FRA*inefficax*_RS23475	-2.65	0.00	protein of unknown function DUF1232	
FRA*inefficax*_RS07340	-2.65	0.01	hypothetical protein, Long-chain-fatty-acyl-CoA reductase	
FRA*inefficax*_RS32120	-2.64	0.03	diguanylate cyclase/phosphodiesterase	
FRA*inefficax*_RS00195	-2.63	0.05	nitrogen regulatory protein P-II	GO:0030234
FRA*inefficax*_RS32440	-2.61	0.01	F420-dependent oxidoreductase, G6PDH family	
FRA*inefficax*_RS22865	-2.59	0.03	Alcohol dehydrogenase GroES domain protein	GO:0008270, GO:0016491
FRA*inefficax*_RS31565	-2.57	0.00	hypothetical protein, Rhodanese domain protein	
FRA*inefficax*_RS07910	-2.5	0.02	protein of unknown function DUF1211	
FRA*inefficax*_RS09280	-2.48	0.02	cytochrome P450	GO:0004497, GO:0005506, GO:0009055, GO:0020037
FRA*inefficax*_RS02770	-2.46	0.00	ferredoxin-dependent glutamate synthase	GO:0015930
FRA*inefficax*_RS24580	-2.46	0.02	O-methyltransferase family 3	GO:0008171
FRA*inefficax*_RS16370	-2.45	0.00	diguanylate cyclase/phosphodiesterase	
FRA*inefficax*_RS12360	-2.4	0.04	short-chain dehydrogenase/reductase SDR	GO:0016491
FRA*inefficax*_RS10115	-2.33	0.00	Catalase	
FRA*inefficax*_RS18365	-2.33	0.01	major facilitator superfamily MFS_1	
FRA*inefficax*_RS24555	-2.33	0.02	Methyltransferase type 11	GO:0008168
FRA*inefficax*_RS03245	-2.32	0.04	Septum formation initiator	

FRA*inefficax*_RS19955	-2.31	0.02	hypothetical protein	
FRA*inefficax*_RS23715	-2.3	0.01	amidohydrolase 2	GO:0003824
FRA*inefficax*_RS07025	-2.3	0.04	lipolytic protein G-D-S-L family	GO:0004871
FRA*inefficax*_RS02085	-2.29	0.04	hypothetical protein	
FRA*inefficax*_RS34350	-2.24	0.02	hypothetical protein	
FRA*inefficax*_RS17460	-2.23	0.01	Xanthine/uracil/vitamin C permease	GO:0005215
FRA*inefficax*_RS21210	-2.21	0.01	putative transcriptional regulator, TetR family	
FRA*inefficax*_RS19990	-2.2	0.03	drug resistance transporter, EmrB/QacAsubfamily	
FRA*inefficax*_RS04270	-2.19	0.01	hypothetical protein	
FRA*inefficax*_RS34375	-2.19	0.01	hypothetical protein	
FRA*inefficax*_RS06110	-2.19	0.02	hypothetical protein	
FRA*inefficax*_RS02955	-2.18	0.03	glycosyl transferase family 2, NAD-dependent epimerase/dehydratase	GO:0003824, GO:0050662
FRA*inefficax*_RS10855	-2.18	0.02	regulatory protein TetR, Alkane 1-monooxygenase	GO:0003700
FRA*inefficax*_RS33860	-2.17	0.03	oxidoreductase molybdopterin binding protein	GO:0009055
FRA*inefficax*_RS09905	-2.15	0.03	amidohydrolase 2	GO:0003824
FRA*inefficax*_RS28535	-2.14	0.01	putative F420-dependent enzyme	
FRA*inefficax*_RS05915	-2.14	0.02	major facilitator superfamily MFS_1	
FRA*inefficax*_RS15660	-2.13	0.02	hypothetical protein	
FRA*inefficax*_RS14730	-2.13	0.03	acyltransferase 3	GO:0005524
FRA*inefficax*_RS08265	-2.12	0.04	aminodeoxychorismate lyase	
FRA*inefficax*_RS01760	-2.11	0.03	hypothetical protein	
FRA*inefficax*_RS01835	-2.11	0.01	phosphate ABC transporter, periplasmicphosphate-binding protein	GO:0005315, GO:0015114
FRA*inefficax*_RS11000	-2.11	0.01	protein of unknown function DUF1486	
FRA*inefficax*_RS01145	-2.11	0.02	beta-phosphoglucomutase family hydrolase, glycoside hydrolase family 65 central catalytic	GO:0003824, GO:0030246
FRA*inefficax*_RS06665	-2.1	0.02	Phosphoglycerate mutase	
FRA*inefficax*_RS13410	-2.1	0.04	undecaprenol kinase	GO:0050380
FRA*inefficax*_RS07280	-2.07	0.01	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS03920	-2.07	0.03	aminotransferase class-III	GO:0008483, GO:0030170
FRA*inefficax*_RS24030	-2.06	0.02	protein of unknown function DUF403, protein of unknown function DUF404	
FRA*inefficax*_RS12170	-2.06	0.03	protein of unknown function zincmetallopeptidase	
FRA*inefficax*_RS01210	-2.05	0.03	ABC transporter transmembrane region	GO:0005524, GO:0016887

FRA*inefficax*_RS23705	-2.05	0.03	Enoyl-CoA hydratase/isomerase	GO:0003824
FRA*inefficax*_RS33805	-2.05	0.02	regulatory protein TetR, amidohydrolase 2	GO:0003700, GO:0003824
FRA*inefficax*_RS04100	-2.05	0.02	polar amino acid ABC transporter, inner membranesubunit, extracellular solute-binding protein family 3	GO:0005215
FRA*inefficax*_RS30830	-2.04	0.03	translation initiation factor IF-1	GO:0003743
FRA*inefficax*_RS07855	-2.03	0.04	peptidase S15	
FRA*inefficax*_RS07925	-2.03	0.01	Glyoxalase/bleomycin resistanceprotein/dioxygenase, protein of unknown function DUF6 transmembrane	
FRA*inefficax*_RS33135	-2.03	0.05	type I phosphodiesterase/nucleotidepyrophosphatase	GO:0003824
FRA*inefficax*_RS29475	-2.03	0.02	WD40 repeat, subgroup	
FRA*inefficax*_RS23820	-2	0.04	urate oxidase	GO:0016491

Table 3.2: inefficax 2x Up-Regulated Genes with Biphenyl as Sole Carbon Source

Name	Fold change	P-value	Product	Gene Ontology
FRA*inefficax*_RS03520	27.28	0.04	NUDIX hydrolase	GO:0016787
FRA*inefficax*_RS01715	25.43	0.04	Endoribonuclease L-PSP	
FRA*inefficax*_RS25175	25.05	0.04	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS33795	11.53	0.01	multi-sensor signal transduction histidinekinase, ABC transporter related protein	GO:0000155, GO:0005524, GO:0046983, GO:0016887
FRA*inefficax*_RS14945	10.63	0.01	hypothetical protein	
FRA*inefficax*_RS21575	10.54	0.01	hypothetical protein	
FRA*inefficax*_RS24405	10.36	0.01	thioesterase superfamily protein	
FRA*inefficax*_RS17490	8.82	0.02	L-carnitine dehydratase/bile acid-inducibleprotein F	GO:0003824
FRA*inefficax*_RS02820	7.64	0.00	transposase IS116/IS110/IS902 family protein	GO:0003677, GO:0004803
FRA*inefficax*_RS20715	7.48	0.05	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS35395	7.15	0.03	hypothetical protein	
FRA*inefficax*_RS15505	7.03	0.04	luciferase family oxidoreductase, group 1	
FRA*inefficax*_RS10675	7.01	0.04	Glyoxalase/bleomycin resistanceprotein/dioxygenase	
FRA*inefficax*_RS04080	6.88	0.01	Peptidase S24/S26A/S26B, conserved region, dTDP-4-dehydrorhamnose 3,5-epimerase	GO:0008830
FRA*inefficax*_RS31470	6.87	0.04	aminotransferase class IV	GO:0003824

FRA*inefficax*_RS29225	6.58	0.01	hypothetical protein	
FRA*inefficax*_RS05405	6.49	0.05	Uncharacterized protein family UPF0102, Mg chelatase, subunit ChlI, DNA protecting protein DprA	
FRA*inefficax*_RS02310	6.42	0.01	hypothetical protein	
FRA*inefficax*_RS34550	6.4	0.05	hypothetical protein	
FRA*inefficax*_RS20195	6.39	0.05	Carboxymuconolactone decarboxylase	
FRA*inefficax*_RS27550	5.79	0.00	transcriptional regulator, AraC family, methylated-DNA/protein-cysteinemethyltransferase	GO:0003677, GO:0003700, GO:0008168, GO:0008270, GO:0043565, GO:0003824
FRA*inefficax*_RS24605	5.67	0.00	Aldehyde Dehydrogenase	GO:0016491
FRA*inefficax*_RS29345	5.58	0.02	hypothetical protein	
FRA*inefficax*_RS18185	5.49	0.02	hypothetical protein	
FRA*inefficax*_RS29740	5.36	0.03	integral membrane protein	
FRA*inefficax*_RS07810	5.11	0.00	Methyltransferase type 11	GO:0008168
FRA*inefficax*_RS10805	5.06	0.01	putative RNA polymerase, sigma-24 subunit, ECFsubfamily	GO:0003677, GO:0003700, GO:0016987
FRA*inefficax*_RS13070	5.05	0.03	binding-protein-dependent transport systemsinner membrane component, ABC transporter related protein	GO:0005215, GO:0005524, GO:0016887
FRA*inefficax*_RS14355	5.03	0.03	Enoyl-CoA hydratase/isomerase	GO:0003824
FRA*inefficax*_RS30740	5.01	0.03	ribosomal-protein-alanine acetyltransferase, peptidase M22 glycoprotease	GO:0016407, GO:0004222
FRA*inefficax*_RS08200	5	0.00	protein of unknown function DUF202	
FRA*inefficax*_RS21265	4.81	0.00	hypothetical protein	
FRA*inefficax*_RS05705	4.78	0.02	regulatory protein RecX	
FRA*inefficax*_RS00750	4.57	0.02	hypothetical protein	
FRA*inefficax*_RS30010	4.55	0.04	hypothetical protein	
FRA*inefficax*_RS33790	4.49	0.02	multi-sensor signal transduction histidinekinase	GO:0000155, GO:0005524, GO:0046983
FRA*inefficax*_RS09020	4.49	0.00	hypothetical protein	
FRA*inefficax*_RS24610	4.42	0.01	protein of unknown function DUF779	
FRA*inefficax*_RS04650	4.41	0.03	peptide chain release factor 1, protein-(glutamine-N5) methyltransferase,release factor-specific	GO:0003735, GO:0008276
FRA*inefficax*_RS23245	4.4	0.05	Protein of unknown function DUF2889	
FRA*inefficax*_RS00715	4.36	0.00	trehalose-phosphatase	GO:0003824

FRA*inefficax*_RS11380	4.36	0.02	hypothetical protein	
FRA*inefficax*_RS33785	4.31	0.00	protein of unknown function DUF214	
FRA*inefficax*_RS09615	4.31	0.03	Amidohydrolase 3	GO:0008270
FRA*inefficax*_RS22560	4.28	0.00	acetyl-CoA acetyltransferase	GO:0016887
FRA*inefficax*_RS07800	4.24	0.00	hypothetical protein, translation initiation factor IF-2	
FRA*inefficax*_RS20685	4.2	0.03	hypothetical protein	
FRA*inefficax*_RS32920	4.13	0.01	regulatory protein MarR	GO:0003700
FRA*inefficax*_RS08370	4.12	0.03	primosome assembly protein PriA	
FRA*inefficax*_RS04820	4.1	0.00	protein of unknown function DUF77	
FRA*inefficax*_RS22495	4.09	0.00	amino acid adenylation domain protein, MbtH domain protein	GO:0016874
FRA*inefficax*_RS04035	4.08	0.00		
FRA*inefficax*_RS05120	4.02	0.00	hypothetical protein	
FRA*inefficax*_RS05660	3.94	0.00	CDP-diacylglycerol/glycerol-3-phosphate3-phosphatidyltransferase, competence/damage-inducible protein CinA	GO:0008444
FRA*inefficax*_RS14290	3.93	0.04	Enoyl-CoA hydratase/isomerase	GO:0003824
FRA*inefficax*_RS00545	3.88	0.02	SEC-C motif domain protein	
FRA*inefficax*_RS15220	3.85	0.02		
FRA*inefficax*_RS31675	3.84	0.00	peptidase M20	GO:0005515, GO:0016787
FRA*inefficax*_RS13905	3.7	0.04	Enoyl-CoA hydratase/isomerase	GO:0003824
FRA*inefficax*_RS34450	3.68	0.03	hypothetical protein, Lanthionine synthetase C family protein	
FRA*inefficax*_RS30250	3.65	0.03	hypothetical protein	
FRA*inefficax*_RS24835	3.64	0.04	protein of unknown function DUF6 transmembrane	
FRA*inefficax*_RS22670	3.64	0.04	Roadblock/LC7 family protein, integral membrane sensor signal transductionhistidine kinase	GO:0004871, GO:0005524
FRA*inefficax*_RS29470	3.62	0.03	transcriptional regulator, GntR family withaminotransferase domain	GO:0003700, GO:0030170
FRA*inefficax*_RS00580	3.6	0.03	GCN5-related N-acetyltransferase, dihydropteroate synthase	GO:0008080, GO:0004156
FRA*inefficax*_RS18175	3.49	0.01	phospholipid/glycerol acyltransferase	GO:0008415
FRA*inefficax*_RS15380	3.37	0.01	Beta-ketoacyl synthase	GO:0016491, GO:0016740, GO:0048037
FRA*inefficax*_RS29995	3.36	0.00	hypothetical protein, SAF domain protein	
FRA*inefficax*_RS35275	3.34	0.00	copper resistance protein CopC	GO:0005507

FRA*inefficax*_RS30120	3.33	0.01	putative signal peptide-containing protein	
FRA*inefficax*_RS34295	3.3	0.04	FAD dependent oxidoreductase, glycosyl transferase group 1	GO:0016491
FRA*inefficax*_RS28525	3.28	0.00	serine/threonine protein kinase	GO:0004672, GO:0005524
FRA*inefficax*_RS05515	3.28	0.00	protein of unknown function DUF150, transcription termination factor NusA	GO:0003723, GO:0030528
FRA*inefficax*_RS21790	3.19	0.04	Carboxymuconolactone decarboxylase	
FRA*inefficax*_RS29510	3.18	0.02	protein of unknown function DUF397	
FRA*inefficax*_RS01045	3.18	0.03	NAD-dependent epimerase/dehydratase	GO:0003824, GO:0050662
FRA*inefficax*_RS13975	3.16	0.02	hypothetical protein	
FRA*inefficax*_RS34925	3.08	0.04	xylulokinase	GO:0004856
FRA*inefficax*_RS09785	3.04	0.00	hypothetical protein	
FRA*inefficax*_RS08505	3.03	0.02	arginine repressor, ArgR	GO:0003700
FRA*inefficax*_RS27400	3.03	0.01	Desulfoferrodoxin Dfx domain protein	GO:0005506
FRA*inefficax*_RS23270	3.01	0.01	transcriptional regulator, MarR family	GO:0003700
FRA*inefficax*_RS29385	2.98	0.04	transcriptional regulator, HxlR family	
FRA*inefficax*_RS33430	2.95	0.02	putative two-component sensor	
FRA*inefficax*_RS01155	2.93	0.04	hypothetical protein	
FRA*inefficax*_RS06265	2.93	0.05	acetyl-CoA acetyltransferase	GO:0030429
FRA*inefficax*_RS00385	2.92	0.00	protein of unknown function DUF574	
FRA*inefficax*_RS14270	2.91	0.00	hypothetical protein	
FRA*inefficax*_RS10255	2.9	0.04	hypothetical protein	
FRA*inefficax*_RS35225	2.89	0.03	hypothetical protein	
FRA*inefficax*_RS13055	2.88	0.02	beta-lactamase domain protein, extracellular solute-binding protein family 1	GO:0005215
FRA*inefficax*_RS22220	2.85	0.04	hypothetical protein	
FRA*inefficax*_RS34435	2.84	0.01	hypothetical protein	
FRA*inefficax*_RS03020	2.84	0.02	hypothetical protein	
FRA*inefficax*_RS26405	2.81	0.00	protein of unknown function DUF35	
FRA*inefficax*_RS02515	2.81	0.02	hypothetical protein	
FRA*inefficax*_RS17580	2.8	0.02	protein of unknown function DUF1486	
FRA*inefficax*_RS16205	2.8	0.03	short-chain dehydrogenase/reductase SDR	GO:0016491
FRA*inefficax*_RS29940	2.78	0.04	TadE family protein	
FRA*inefficax*_RS27385	2.74	0.03	hypothetical protein, oxidoreductase, short chaindehydrogenase/reductase family protein	

FRA*inefficax*_RS33460	2.74	0.00	adenylate/guanylate cyclase, short-chain dehydrogenase/reductase SDR	GO:0000156, GO:0016849, GO:0016491
FRA*inefficax*_RS35730	2.65	0.02	HNH endonuclease	GO:0003676, GO:0004519
FRA*inefficax*_RS24790	2.63	0.04	protein of unknown function DUF43	
FRA*inefficax*_RS30050	2.62	0.04	putative integral membrane protein, hypothetical protein	
FRA*inefficax*_RS22705	2.61	0.00	drug resistance transporter, EmrB/QacAsubfamily	
FRA*inefficax*_RS26445	2.6	0.04	Carboxylesterase type B	
FRA*inefficax*_RS16630	2.58	0.01	putative F420-dependent oxidoreductase	
FRA*inefficax*_RS12400	2.57	0.01	hypothetical protein	
FRA*inefficax*_RS25340	2.56	0.00	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS33745	2.55	0.02	transglutaminase domain-containing protein	
FRA*inefficax*_RS01910	2.54	0.00	2-C-methyl-D-erythritol 4-phosphatecytidylyltransferase, 2C-methyl-D-erythritol 2,4-cyclodiphosphatesynthase	GO:0003824, GO:0008685
FRA*inefficax*_RS30055	2.52	0.01	putative integral membrane protein, hypothetical protein, ATPase associated with various cellularactivities AAA_3	GO:0005524, GO:0016887
FRA*inefficax*_RS24235	2.51	0.00	sporulation and cell division protein SsgA	
FRA*inefficax*_RS06415	2.5	0.04	replication initiator protein	
FRA*inefficax*_RS34285	2.5	0.03	AIR synthase related protein	GO:0003824, GO:0008080
FRA*inefficax*_RS08495	2.49	0.04	acetylornithine and succinylornithineaminotransferase	GO:0008483
FRA*inefficax*_RS23805	2.48	0.04	OmpA/MotB domain protein	
FRA*inefficax*_RS34705	2.46	0.01	hypothetical protein	
FRA*inefficax*_RS30715	2.45	0.01	alpha/beta hydrolase fold protein	
FRA*inefficax*_RS22540	2.43	0.00	serine/threonine protein kinase	GO:0004672, GO:0005524
FRA*inefficax*_RS17225	2.43	0.01	transcriptional regulator, LacI family	GO:0003700
FRA*inefficax*_RS05575	2.42	0.01	hypothetical protein	
FRA*inefficax*_RS03965	2.4	0.04	GTPase EngC	GO:0003924, GO:0005525
FRA*inefficax*_RS03180	2.38	0.00	glycosyl transferase group 1	
FRA*inefficax*_RS03470	2.38	0.01	exodeoxyribonuclease VII, large subunit	GO:0008855
FRA*inefficax*_RS24820	2.36	0.05	short-chain dehydrogenase/reductase SDR	GO:0016491
FRA*inefficax*_RS11395	2.36	0.04	protoporphyrinogen oxidase	GO:0004729
FRA*inefficax*_RS31485	2.35	0.01	putative transcriptional regulator	
FRA*inefficax*_RS03875	2.34	0.02	hypothetical protein	

FRA*inefficax*_RS00505	2.33	0.03	hypothetical protein	
FRA*inefficax*_RS18700	2.31	0.02	Exodeoxyribonuclease V, hypothetical protein	
FRA*inefficax*_RS02960	2.29	0.02	Fusaric acid resistance protein conservedregion	
FRA*inefficax*_RS30765	2.26	0.02	hypothetical protein	
FRA*inefficax*_RS33310	2.25	0.00	hypothetical protein	
FRA*inefficax*_RS29930	2.25	0.04	hypothetical protein	
FRA*inefficax*_RS15850	2.24	0.02	molybdopterin oxidoreductase	GO:0010181, GO:0016491, GO:0030151
FRA*inefficax*_RS23260	2.23	0.02	short-chain dehydrogenase/reductase SDR	GO:0016491
FRA*inefficax*_RS08485	2.23	0.02	arginine biosynthesis bifunctional protein ArgJ, acetylglutamate kinase	GO:0004358, GO:0003991
FRA*inefficax*_RS35255	2.23	0.02	two component transcriptional regulator, LuxRfamily	GO:0000156, GO:0003700, GO:0043565
FRA*inefficax*_RS03970	2.23	0.01	3-phosphoshikimate 1-carboxyvinyltransferase	GO:0003866
FRA*inefficax*_RS12980	2.22	0.03	alpha/beta hydrolase fold protein, hypothetical protein	
FRA*inefficax*_RS00485	2.22	0.02	haloacid dehalogenase domain protein hydrolase	
FRA*inefficax*_RS08645	2.19	0.00	3-methyl-2-oxobutanoatehydroxymethyltransferase	GO:0003864
FRA*inefficax*_RS15260	2.19	0.05	helix-turn-helix domain protein	GO:0043565
FRA*inefficax*_RS08510	2.17	0.01	argininosuccinate lyase, DNA-3-methyladenine glycosylase	GO:0004056, GO:0003677, GO:0003905
FRA*inefficax*_RS03865	2.12	0.01	conserved hypothetical protein	
FRA*inefficax*_RS26110	2.12	0.02	acetyl-CoA acetyltransferase	GO:0016491
FRA*inefficax*_RS05690	2.11	0.04	DEAD/H associated domain protein	GO:0003676, GO:0004386, GO:0005524, GO:0008026
FRA*inefficax*_RS08275	2.1	0.03	chorismate synthase, Shikimate kinase	GO:0004107
FRA*inefficax*_RS17045	2.09	0.04	hypothetical protein	
FRA*inefficax*_RS23960	2.09	0.03	expression regulator	
FRA*inefficax*_RS19770	2.08	0.02	Glyoxalase/bleomycin resistanceprotein/dioxygenase	
FRA*inefficax*_RS05740	2.08	0.02	methionine aminopeptidase, type I	GO:0004177, GO:0008235
FRA*inefficax*_RS04230	2.07	0.02	ATPase-like protein	
FRA*inefficax*_RS21845	2.07	0.03	beta-lactamase domain-containing protein, hypothetical protein, short-chain dehydrogenase/reductase SDR	GO:0016491
FRA*inefficax*_RS08360	2.06	0.02	phosphopantothenoylcysteinedecarboxylase/	GO:0004632,

			phosphopantothenate/cysteine ligase	GO:0004633, GO:0010181
FRA*inefficax*_RS07090	2.04	0.01	GntR domain protein	GO:0003700
FRA*inefficax*_RS30865	2.04	0.02	ribosomal protein L18	GO:0003735
FRA*inefficax*_RS24615	2.02	0.04	protein of unknown function DUF81	
FRA*inefficax*_RS35145	2.01	0.02	phosphoribosylformylglycinamidine cyclo-ligase, amidophosphoribosyltransferase	GO:0004641, GO:0004044

Table 3.3: inefficax 10x Differentially Regulated Genes Under Biphenyl Stress with Glucose

Name	Fold change	P-value	Product	Gene Ontology
FRA*inefficax*_RS03520	27.28	0.04	NUDIX hydrolase	GO:0016787
FRA*inefficax*_RS01715	25.43	0.04	Endoribonuclease L-PSP	
FRA*inefficax*_RS25175	25.05	0.04	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS33795	11.53	0.01	multi-sensor signal transduction histidinekinase, ABC transporter related protein	GO:0000155, GO:0005524, GO:0046983, GO:0016887
FRA*inefficax*_RS14945	10.63	0.01	hypothetical protein	
FRA*inefficax*_RS21575	10.54	0.01	hypothetical protein	
FRA*inefficax*_RS24405	10.36	0.01	thioesterase superfamily protein	

Table 3.4: inefficax 10x Differentially Regulated Genes with Biphenyl as Sole Carbon Source

Name	Fold change	P-value	Product	Gene Ontology
FRA*inefficax*_RS29675	57.01	0.01	ABC transporter related protein, hypothetical protein	GO:0005524, GO:0016887
FRA*inefficax*_RS01715	35.03	0.02	Endoribonuclease L-PSP	
FRA*inefficax*_RS09955	27.57	0.04	HhH-GPD family protein, regulatory protein MarR	GO:0003700
FRA*inefficax*_RS16095	23.68	0.04	acyl-CoA dehydrogenase domain-containingprotein	GO:0003995
FRA*inefficax*_RS32965	22.17	0.05	NB-ARC domain protein	GO:0005524
FRA*inefficax*_RS25115	21.58	0.05	amidohydrolase 2, AMP-dependent synthetase and ligase	GO:0003824
FRA*inefficax*_RS17490	14.83	0.00	L-carnitine dehydratase/bile acid-inducibleprotein F	GO:0003824
FRA*inefficax*_RS14945	14.66	0.00	hypothetical protein	

FRA*inefficax*_RS17125	13.64	0.00	Carboxymuconolactone decarboxylase	
FRA*inefficax*_RS17100	10.83	0.01	oxidoreductase domain protein	GO:0016491
FRA*inefficax*_RS10095	-10.28	0.00	ChaB family protein	GO:0003715
FRA*inefficax*_RS09665	-11.26	0.00	hypothetical protein	
FRA*inefficax*_RS02155	-19.94	0.00	Transglycosylase-associated protein	

Table 3.5: inefficax 2x Down Regulated Genes with Biphenyl as a Sole Carbon Source

Name	Fold change	P-value	Product	Gene Ontology
FRA*inefficax*_RS02155	-19.94	0.00	Transglycosylase-associated protein	
FRA*inefficax*_RS09665	-11.26	0.00	hypothetical protein	
FRA*inefficax*_RS10095	-10.28	0.00	ChaB family protein	GO:0003715
FRA*inefficax*_RS35140	-7.56	0.00	Protein of unknown function DUF3073	
FRA*inefficax*_RS02785	-7.42	0.00	hypothetical protein	
FRA*inefficax*_RS16080	-7.37	0.04	short-chain dehydrogenase/reductase SDR	GO:0016491
FRA*inefficax*_RS02975	-7.10	0.00	filamentation induced by cAMP protein Fic, hypothetical protein	
FRA*inefficax*_RS21050	-7.04	0.00	Polyketide cyclase/dehydrase	
FRA*inefficax*_RS26150	-7.03	0.00	hypothetical protein	
FRA*inefficax*_RS15660	-7.02	0.00	hypothetical protein	
FRA*inefficax*_RS34620	-6.83	0.00	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS32375	-6.77	0.00	hypothetical protein	
FRA*inefficax*_RS27910	-6.22	0.00	flavin reductase domain protein FMN-bindingprotein	
FRA*inefficax*_RS04270	-6.10	0.00	hypothetical protein	
FRA*inefficax*_RS03600	-6.01	0.00	hypothetical protein	
FRA*inefficax*_RS09370	-5.58	0.00	high-affinity nickel-transporter	GO:0015099
FRA*inefficax*_RS04950	-5.41	0.02	hypothetical protein	
FRA*inefficax*_RS13210	-5.40	0.00	putative transglycosylase associated protein	
FRA*inefficax*_RS28535	-5.21	0.00	putative F420-dependent enzyme	
FRA*inefficax*_RS10115	-5.16	0.00	Catalase	
FRA*inefficax*_RS17455	-5.05	0.01	isochorismatase hydrolase	GO:0003824
FRA*inefficax*_RS34135	-4.93	0.00	cold-shock DNA-binding domain protein	GO:0003677
FRA*inefficax*_RS07755	-4.93	0.00	hypothetical protein	
FRA*inefficax*_RS31215	-4.90	0.00	hypothetical protein	

FRA*inefficax*_RS10090	-4.86	0.00	flavin reductase domain protein FMN-bindingprotein	
FRA*inefficax*_RS02020	-4.85	0.00	short-chain dehydrogenase/reductase SDR	GO:0016491
FRA*inefficax*_RS28325	-4.81	0.00	amidohydrolase	GO:0016787
FRA*inefficax*_RS31245	-4.79	0.00	Insertion element protein, nitrite and sulphite reductase 4Fe-4S region	GO:0016491, GO:0020037, GO:0051536
FRA*inefficax*_RS07000	-4.69	0.04	serine/threonine protein kinase-like protein, diguanylate cyclase/phosphodiesterase withPAS/PAC and GAF sensor(s)	GO:0004871
FRA*inefficax*_RS03740	-4.69	0.00	DEAD/DEAH box helicase domain protein	GO:0003676, GO:0004386, GO:0005524, GO:0008026
FRA*inefficax*_RS23475	-4.62	0.00	protein of unknown function DUF1232	
FRA*inefficax*_RS31565	-4.56	0.00	hypothetical protein, Rhodanese domain protein	
FRA*inefficax*_RS09670	-4.47	0.00	ErfK/YbiS/YcfS/YnhG family protein	
FRA*inefficax*_RS19305	-4.33	0.00	alpha/beta hydrolase fold protein	
FRA*inefficax*_RS35315	-4.32	0.00	ABC-3 protein, ferric uptake regulator, Fur family	GO:0005524, GO:0003700
FRA*inefficax*_RS19420	-4.25	0.00	hypothetical protein	
FRA*inefficax*_RS33375	-4.14	0.00	protein of unknown function DUF397, hypothetical protein	
FRA*inefficax*_RS25290	-4.11	0.00	PilT protein domain protein, prevent-host-death family protein	
FRA*inefficax*_RS35365	-4.08	0.00	hypothetical protein	
FRA*inefficax*_RS19675	-4.04	0.00	hypothetical protein	
FRA*inefficax*_RS05305	-4.02	0.00	protein of unknown function DUF177, ribosomal protein L32	GO:0003735
FRA*inefficax*_RS21480	-3.99	0.00	magnesium transporter accessory protein	
FRA*inefficax*_RS29065	-3.93	0.00	thiamineS protein	
FRA*inefficax*_RS04680	-3.91	0.00	H+transporting two-sector ATPase C subunit	GO:0015078
FRA*inefficax*_RS02475	-3.90	0.00	pyridoxamine 5'-phosphate oxidase-relatedFMN-binding protein	GO:0010181
FRA*inefficax*_RS17795	-3.90	0.00	hypothetical protein	
FRA*inefficax*_RS13245	-3.89	0.00	two component transcriptional regulator, LuxRfamily	GO:0000156, GO:0003700, GO:0043565
FRA*inefficax*_RS21120	-3.89	0.00	Methyltransferase type 11	GO:0008168
FRA*inefficax*_RS04275	-3.88	0.00	hypothetical protein	
FRA*inefficax*_RS32280	-3.88	0.00	hypothetical protein	

FRA*inefficax*_RS08300	-3.85	0.00	translation elongation factor P, NusB antitermination factor	GO:0003746, GO:0003715
FRA*inefficax*_RS22385	-3.82	0.00	hypothetical protein	
FRA*inefficax*_RS04640	-3.81	0.00	ribosomal protein L31	GO:0003735
FRA*inefficax*_RS11400	-3.78	0.00	Chlorite dismutase	
FRA*inefficax*_RS04675	-3.77	0.00	ATP synthase F0, A subunit	GO:0015078
FRA*inefficax*_RS10770	-3.75	0.00	Alcohol dehydrogenase zinc-binding domainprotein, hypothetical protein	GO:0008270, GO:0016491
FRA*inefficax*_RS11000	-3.71	0.00	protein of unknown function DUF1486	
FRA*inefficax*_RS12160	-3.70	0.00	Ferritin Dps family protein	GO:0008199
FRA*inefficax*_RS22065	-3.67	0.00	protein of unknown function DUF35, Formyl-CoA transferase	
FRA*inefficax*_RS19440	-3.63	0.04	Methyltransferase type 11	GO:0008168
FRA*inefficax*_RS31035	-3.60	0.00	ribosomal protein L33	GO:0003735
FRA*inefficax*_RS14965	-3.59	0.01	hypothetical protein	
FRA*inefficax*_RS01030	-3.57	0.02	Transglycosylase-like domain protein	
FRA*inefficax*_RS32405	-3.52	0.03	hypothetical protein, Na+/H+ antiporter subunit	GO:0005451
FRA*inefficax*_RS24950	-3.49	0.00	DNA binding domain protein, excisionase family	GO:0003677
FRA*inefficax*_RS07280	-3.47	0.00	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS32100	-3.44	0.00	hypothetical protein	
FRA*inefficax*_RS12170	-3.40	0.00	protein of unknown function zincmetallopeptidase	
FRA*inefficax*_RS07285	-3.40	0.00	short-chain dehydrogenase/reductase SDR	GO:0016491
FRA*inefficax*_RS17870	-3.39	0.00	alkylhydroperoxidase like protein, AhpD family	
FRA*inefficax*_RS02805	-3.39	0.02	Glyoxalase/bleomycin resistanceprotein/dioxygenase	
FRA*inefficax*_RS31840	-3.37	0.00	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS21260	-3.36	0.00	hypothetical protein	
FRA*inefficax*_RS27470	-3.36	0.01	hypothetical protein	
FRA*inefficax*_RS08855	-3.36	0.00	Protein of unknown function DUF3043, quinolinate synthetase complex, A subunit	GO:0008987
FRA*inefficax*_RS03370	-3.27	0.00	peptide methionine sulfoxide reductase	GO:0005524
FRA*inefficax*_RS09790	-3.25	0.00	ribosomal protein L21	GO:0003723, GO:0003735
FRA*inefficax*_RS32290	-3.24	0.02	hypothetical protein	
FRA*inefficax*_RS24345	-3.24	0.00	hypothetical protein	
FRA*inefficax*_RS31360	-3.24	0.00	copper-translocating P-type ATPase	GO:0004008, GO:0005524, GO:0046873

FRA*inefficax*_RS07020	-3.23	0.01	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS30950	-3.22	0.00	ribosomal protein S10	GO:0003735
FRA*inefficax*_RS05265	-3.22	0.01	Transcription regulator AsnC-type-like protein	GO:0003700, GO:0043565
FRA*inefficax*_RS31325	-3.17	0.00	Redoxin domain protein	GO:0016491
FRA*inefficax*_RS24330	-3.17	0.00	protein of unknown function UPF0027	
FRA*inefficax*_RS15285	-3.15	0.00	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS02165	-3.13	0.00	hypothetical protein	
FRA*inefficax*_RS03985	-3.12	0.00	RNA polymerase, sigma-24 subunit, ECF subfamily, anti-sigma factor	GO:0003677, GO:0003700, GO:0016987
FRA*inefficax*_RS06015	-3.09	0.00	ATP-binding region ATPase domain protein	GO:0005524
FRA*inefficax*_RS15290	-3.09	0.00	isochorismatase hydrolase	GO:0003824
FRA*inefficax*_RS32760	-3.06	0.00	NLP/P60 protein	
FRA*inefficax*_RS24805	-3.06	0.01	hypothetical protein	
FRA*inefficax*_RS26040	-3.03	0.01	fatty acid hydroxylase	GO:0005506, GO:0016491
FRA*inefficax*_RS01625	-3.02	0.00	hypothetical protein	
FRA*inefficax*_RS33805	-3.02	0.00	regulatory protein TetR, amidohydrolase 2	GO:0003700, GO:0003824
FRA*inefficax*_RS30585	-3.01	0.00	hypothetical protein	
FRA*inefficax*_RS06395	-2.98	0.00	transcriptional regulator, HxlR family	
FRA*inefficax*_RS32200	-2.96	0.00	Hemerythrin HHE cation binding domain protein	
FRA*inefficax*_RS10220	-2.96	0.00	putative signal peptide-containing protein	
FRA*inefficax*_RS15675	-2.95	0.00	transcriptional regulator, GntR family	GO:0003700
FRA*inefficax*_RS26815	-2.94	0.02	acyl-CoA dehydrogenase domain-containingprotein, hypothetical protein	GO:0003995
FRA*inefficax*_RS02215	-2.94	0.00	ribonucleoside-diphosphate reductase,adenosylcobalamin-dependent	
FRA*inefficax*_RS29365	-2.93	0.00	urease accessory protein UreG	GO:0005524, GO:0016151
FRA*inefficax*_RS21220	-2.93	0.00	GCN5-related N-acetyltransferase	GO:0003700, GO:0008080
FRA*inefficax*_RS28855	-2.92	0.00	hypothetical protein, glutamate racemase	GO:0008881
FRA*inefficax*_RS17415	-2.92	0.04	hypothetical protein, transcriptional regulator, XRE family	GO:0043565
FRA*inefficax*_RS31765	-2.92	0.00	UspA domain-containing protein	
FRA*inefficax*_RS33925	-2.92	0.00	NLP/P60 protein	

FRA*inefficax*_RS30830	-2.91	0.00	translation initiation factor IF-1	GO:0003743
FRA*inefficax*_RS17755	-2.91	0.00	hypothetical protein	
FRA*inefficax*_RS21635	-2.90	0.00	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS18080	-2.90	0.00	NAD(P)H dehydrogenase (quinone)	GO:0009055, GO:0016491, GO:0050662
FRA*inefficax*_RS11785	-2.89	0.00	MraZ protein	
FRA*inefficax*_RS26930	-2.86	0.00	amidohydrolase 2	GO:0003824
FRA*inefficax*_RS30935	-2.86	0.00	Ribosomal protein L25/L23, ribosomal protein L4/L1e	GO:0003735
FRA*inefficax*_RS32330	-2.86	0.04	gas vesicle protein GVPa	GO:0005198
FRA*inefficax*_RS31570	-2.85	0.00	hypothetical protein, Rhodanese domain protein	
FRA*inefficax*_RS10765	-2.85	0.00	Alcohol dehydrogenase zinc-binding domainprotein, hypothetical protein	GO:0008270, GO:0016491
FRA*inefficax*_RS07925	-2.84	0.00	Glyoxalase/bleomycin resistanceprotein/dioxygenase, protein of unknown function DUF6 transmembrane	
FRA*inefficax*_RS34275	-2.84	0.00	DsrE family protein, Radical SAM domain protein	GO:0003824, GO:0051536
FRA*inefficax*_RS04760	-2.82	0.01	hypothetical protein	
FRA*inefficax*_RS23210	-2.82	0.05	hypothetical protein	
FRA*inefficax*_RS18965	-2.82	0.00	Rieske (2Fe-2S) iron-sulfur domain protein	GO:0016491
FRA*inefficax*_RS10865	-2.82	0.00	adenosine deaminase	GO:0004000
FRA*inefficax*_RS18205	-2.81	0.00	WD40 repeat, subgroup	
FRA*inefficax*_RS02970	-2.80	0.00	filamentation induced by cAMP protein Fic	
FRA*inefficax*_RS28560	-2.80	0.00	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS19800	-2.80	0.00	putative secreted protein	
FRA*inefficax*_RS21030	-2.80	0.00	transcriptional regulator, SARP family, 4'-phosphopantetheinyl transferase	GO:0000156, GO:0003677, GO:0000287, GO:0008897
FRA*inefficax*_RS25370	-2.80	0.00	putative secreted protein	
FRA*inefficax*_RS23345	-2.79	0.01	transcriptional regulator, AsnC family	GO:0003700, GO:0043565
FRA*inefficax*_RS15060	-2.79	0.03	binding-protein-dependent transport systemsinner membrane component, ROK family protein	GO:0005215, GO:0003700
FRA*inefficax*_RS10925	-2.78	0.01	ribosomal protein S20	GO:0003723, GO:0003735
FRA*inefficax*_RS33875	-2.77	0.03	transcriptional regulator, PadR-like family	
FRA*inefficax*_RS02085	-2.77	0.01	hypothetical protein	
FRA*inefficax*_RS27840	-2.76	0.00	filamentation induced by cAMP protein Fic	

FRA*inefficax*_RS32610	-2.74	0.01	transcriptional regulator, TetR family	GO:0003700
FRA*inefficax*_RS08430	-2.74	0.00	ribosomal protein L35	GO:0003735
FRA*inefficax*_RS00335	-2.74	0.00	adenosylhomocysteinase	GO:0004013
FRA*inefficax*_RS09255	-2.73	0.03	hypothetical protein	
FRA*inefficax*_RS26140	-2.72	0.01	MaoC domain protein dehydratase	GO:0016491
FRA*inefficax*_RS07275	-2.71	0.00	cytochrome P450	GO:0004497, GO:0005506, GO:0009055, GO:0020037
FRA*inefficax*_RS07435	-2.71	0.02	hypothetical protein	
FRA*inefficax*_RS14375	-2.71	0.00	transcriptional regulator, GntR family	GO:0003700
FRA*inefficax*_RS16700	-2.71	0.01	hypothetical protein	
FRA*inefficax*_RS30355	-2.70	0.00	cell envelope-related transcriptionalattenuator	
FRA*inefficax*_RS31575	-2.70	0.00	protein of unknown function DUF1416	
FRA*inefficax*_RS01145	-2.70	0.00	beta-phosphoglucomutase family hydrolase, glycoside hydrolase family 65 central catalytic	GO:0003824, GO:0030246
FRA*inefficax*_RS31655	-2.69	0.00	Peptidase M75, Imelysin	
FRA*inefficax*_RS03605	-2.68	0.00	PGRS family protein	
FRA*inefficax*_RS08865	-2.68	0.00	iron-sulfur cluster assembly accessory protein	GO:0005198, GO:0051536
FRA*inefficax*_RS22090	-2.68	0.00	drug resistance transporter, EmrB/QacAsubfamily	
FRA*inefficax*_RS03555	-2.67	0.00	ferredoxin	
FRA*inefficax*_RS06665	-2.67	0.00	Phosphoglycerate mutase	
FRA*inefficax*_RS05605	-2.66	0.00	Phosphoketolase	
FRA*inefficax*_RS10880	-2.66	0.00	protein of unknown function DUF159	
FRA*inefficax*_RS31620	-2.66	0.00	anti-anti-sigma factor	GO:0045152
FRA*inefficax*_RS35360	-2.66	0.00	hypothetical protein	
FRA*inefficax*_RS20090	-2.66	0.00	binding-protein-dependent transport systemsinner membrane component	GO:0005215
FRA*inefficax*_RS02245	-2.65	0.01	ribonuclease BN	GO:0004540
FRA*inefficax*_RS33125	-2.64	0.02	twin-arginine translocation protein, TatA/Efamily subunit	GO:0008565
FRA*inefficax*_RS15830	-2.64	0.03	transcriptional regulator, ArsR family	GO:0003700
FRA*inefficax*_RS01230	-2.63	0.00	transcriptional regulator, SARP family	GO:0000156, GO:0003677
FRA*inefficax*_RS34625	-2.63	0.00	amidohydrolase 2	GO:0003824
FRA*inefficax*_RS21685	-2.62	0.05	hypothetical protein	
FRA*inefficax*_RS15040	-2.62	0.02	hypothetical protein	

FRA*inefficax*_RS06275	-2.61	0.02	ATP-dependent protease Clp ATPase subunit-likeprotein	
FRA*inefficax*_RS34355	-2.60	0.05	hypothetical protein	
FRA*inefficax*_RS00660	-2.60	0.00	glycoside hydrolase family 16	GO:0004315
FRA*inefficax*_RS32395	-2.60	0.00	protein of unknown function DUF1360	
FRA*inefficax*_RS31660	-2.60	0.00	iron permease FTR1	
FRA*inefficax*_RS35555	-2.59	0.00	ribosomal protein S6	GO:0003735, GO:0019843
FRA*inefficax*_RS15050	-2.59	0.00	extracellular solute-binding protein family 1	GO:0005215
FRA*inefficax*_RS19670	-2.58	0.02	glycosyl transferase family 2	
FRA*inefficax*_RS20480	-2.58	0.01	hypothetical protein	
FRA*inefficax*_RS13220	-2.58	0.03	protein of unknown function DUF1003	
FRA*inefficax*_RS24130	-2.57	0.00	protoheme IX farnesyltransferase	GO:0008495
FRA*inefficax*_RS30920	-2.57	0.01	ribosomal protein S3, ribosomal protein L22, ribosomal protein S19	GO:0003735
FRA*inefficax*_RS08930	-2.56	0.00	Cytochrome-c oxidase	
FRA*inefficax*_RS14925	-2.56	0.00	hypothetical protein	
FRA*inefficax*_RS25800	-2.56	0.00	Peroxiredoxin	
FRA*inefficax*_RS35700	-2.56	0.00	thioredoxin	GO:0009055, GO:0015035
FRA*inefficax*_RS19465	-2.56	0.01	ABC transporter related protein, transcriptional regulator PadR family protein	GO:0005524, GO:0016887
FRA*inefficax*_RS32285	-2.56	0.00	anti-anti-sigma factor	GO:0045152
FRA*inefficax*_RS09420	-2.56	0.00	Propanoyl-CoA C-acyltransferase, acetyl-CoA acetyltransferase-like protein	
FRA*inefficax*_RS21640	-2.55	0.02	Carboxymuconolactone decarboxylase	
FRA*inefficax*_RS28320	-2.55	0.00	ABC transporter related protein, hypothetical protein	GO:0005524, GO:0016887
FRA*inefficax*_RS19310	-2.54	0.01	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS30845	-2.54	0.00	adenylate kinase, preprotein translocase, SecY subunit	GO:0005524, GO:0019201, GO:0015450
FRA*inefficax*_RS04100	-2.54	0.00	polar amino acid ABC transporter, inner membranesubunit, extracellular solute-binding protein family 3	GO:0005215
FRA*inefficax*_RS07185	-2.53	0.00	hypothetical protein	
FRA*inefficax*_RS35545	-2.53	0.00	ribosomal protein S18	GO:0003735
FRA*inefficax*_RS31925	-2.53	0.02	hypothetical protein	
FRA*inefficax*_RS19785	-2.52	0.01	hypothetical protein	

FRA*inefficax*_RS32440	-2.52	0.00	F420-dependent oxidoreductase, G6PDH family	
FRA*inefficax*_RS34240	-2.52	0.00	hypothetical protein, band 7 protein	
FRA*inefficax*_RS18225	-2.52	0.00	ABC transporter transmembrane region	GO:0005524, GO:0016887
FRA*inefficax*_RS15795	-2.51	0.00	hypothetical protein	
FRA*inefficax*_RS11620	-2.51	0.00	protein-export membrane protein SecF	GO:0008565, GO:0015450
FRA*inefficax*_RS33480	-2.51	0.00	YVTN beta-propeller repeat-containing protein	
FRA*inefficax*_RS16005	-2.51	0.00	diguanylate cyclase	
FRA*inefficax*_RS08890	-2.50	0.00	cytochrome c oxidase, subunit II, cytochrome c oxidase, subunit I, Cytochrome c oxidase subunit IV	GO:0004129, GO:0005507
FRA*inefficax*_RS22390	-2.50	0.00	protein of unknown function UCP012641	
FRA*inefficax*_RS23650	-2.50	0.03	L-carnitine dehydratase/bile acid-inducibleprotein F	GO:0003824
FRA*inefficax*_RS21655	-2.49	0.00	cytochrome P450	GO:0004497, GO:0005506, GO:0009055, GO:0020037
FRA*inefficax*_RS11390	-2.49	0.00	uroporphyrinogen decarboxylase	GO:0004853
FRA*inefficax*_RS03100	-2.49	0.01	ribosomal 5S rRNA E-loop binding proteinCtc/L25/TL5	GO:0003735, GO:0008097
FRA*inefficax*_RS10345	-2.48	0.01	succinate dehydrogenase (or fumarate reductase)cytochrome b subunit, b558 family	
FRA*inefficax*_RS35600	-2.47	0.05	hypothetical protein	
FRA*inefficax*_RS08850	-2.47	0.00	Protein of unknown function DUF3043, quinolinate synthetase complex, A subunit	GO:0008987
FRA*inefficax*_RS08935	-2.47	0.01	cytochrome c class I, Rieske (2Fe-2S) iron-sulfur domain protein	GO:0005506, GO:0009055, GO:0020037, GO:0016491
FRA*inefficax*_RS31815	-2.47	0.05	PKD domain containing protein	
FRA*inefficax*_RS31155	-2.47	0.00	NADH-ubiquinone/plastoquinone oxidoreductasechain 6, NADH-quinone oxidoreductase, chain I	GO:0008137, GO:0051536
FRA*inefficax*_RS20080	-2.47	0.00	extracellular solute-binding protein family 1, binding-protein-dependent transport systemsinner membrane component	GO:0005215
FRA*inefficax*_RS04840	-2.46	0.00	trehalose synthase, Protein of unknown function DUF3416	GO:0003824, GO:0043169
FRA*inefficax*_RS04540	-2.45	0.00	protein of unknown function DUF574	
FRA*inefficax*_RS32535	-2.45	0.01	hypothetical protein	
FRA*inefficax*_RS02015	-2.44	0.00	hypothetical protein	

FRA*inefficax*_RS02025	-2.44	0.01	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS24635	-2.43	0.01	hypothetical protein	
FRA*inefficax*_RS28330	-2.42	0.00	Aldehyde Dehydrogenase	GO:0016491
FRA*inefficax*_RS32450	-2.42	0.00	Rieske (2Fe-2S) iron-sulfur domain protein	GO:0016491
FRA*inefficax*_RS34350	-2.42	0.00	hypothetical protein	
FRA*inefficax*_RS27900	-2.42	0.01	protein of unknown function DUF1469, Protein of unknown function DUF3618	
FRA*inefficax*_RS32765	-2.41	0.00	protein of unknown function DUF305	
FRA*inefficax*_RS30820	-2.41	0.01	30S ribosomal protein S13	GO:0003723, GO:0003735
FRA*inefficax*_RS22330	-2.41	0.01	protein of unknown function DUF1206	
FRA*inefficax*_RS20005	-2.41	0.00	putative exporter of polyketide antibiotics-likeprotein, ABC transporter related protein	GO:0005524, GO:0016887
FRA*inefficax*_RS02615	-2.41	0.01	ATP-binding region ATPase domain protein	GO:0005524
FRA*inefficax*_RS35195	-2.40	0.00	citrate synthase I	GO:0004108
FRA*inefficax*_RS10135	-2.39	0.00	cytochrome P450	GO:0004497, GO:0005506, GO:0009055, GO:0020037
FRA*inefficax*_RS28335	-2.39	0.00	amidohydrolase 2	GO:0003824
FRA*inefficax*_RS12440	-2.38	0.01	aldo/keto reductase, flavoprotein	GO:0016491, GO:0003824
FRA*inefficax*_RS01150	-2.38	0.00	beta-phosphoglucomutase family hydrolase, glycoside hydrolase family 65 central catalytic	GO:0003824, GO:0030246
FRA*inefficax*_RS22315	-2.38	0.02	transcriptional regulator	
FRA*inefficax*_RS10855	-2.38	0.00	regulatory protein TetR, Alkane 1-monooxygenase	GO:0003700
FRA*inefficax*_RS04370	-2.37	0.05		
FRA*inefficax*_RS26060	-2.37	0.02	hypothetical protein	
FRA*inefficax*_RS20025	-2.37	0.00		
FRA*inefficax*_RS18375	-2.37	0.05	short-chain dehydrogenase/reductase SDR	GO:0016491
FRA*inefficax*_RS02010	-2.36	0.01	hypothetical protein	
FRA*inefficax*_RS16970	-2.36	0.00	Extracellular ligand-binding receptor	
FRA*inefficax*_RS27040	-2.36	0.00	acetyl-CoA acetyltransferase	GO:0016491
FRA*inefficax*_RS31610	-2.36	0.00	putative two component transcriptionalregulator, winged helix family	GO:0000156, GO:0003677
FRA*inefficax*_RS07270	-2.35	0.03	Carboxymuconolactone decarboxylase, regulatory protein TetR	GO:0003700
FRA*inefficax*_RS27925	-2.35	0.00	Glyoxalase/bleomycin resistanceprotein/dioxygenase	

FRA*inefficax*_RS11790	-2.34	0.02	S-adenosyl-methyltransferase MraW, hypothetical protein	GO:0008168
FRA*inefficax*_RS02480	-2.34	0.03	protein of unknown function DUF35	
FRA*inefficax*_RS32310	-2.34	0.03	gas vesicle protein GVPa	GO:0005198
FRA*inefficax*_RS11055	-2.34	0.00	DNA primase	GO:0003896
FRA*inefficax*_RS32685	-2.33	0.04	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS30090	-2.33	0.00	adenosylhomocysteinase	GO:0004013
FRA*inefficax*_RS31195	-2.33	0.02	NADH-quinone oxidoreductase, B subunit, NADH-ubiquinone/plastoquinone oxidoreductasechain 3	GO:0008137, GO:0048038
FRA*inefficax*_RS35450	-2.33	0.00	hypothetical protein	
FRA*inefficax*_RS13250	-2.33	0.01	tellurium resistance protein	
FRA*inefficax*_RS12940	-2.32	0.04	nitroreductase	GO:0016491
FRA*inefficax*_RS04795	-2.32	0.00	FG-GAP repeat protein	
FRA*inefficax*_RS26155	-2.32	0.04	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS20465	-2.31	0.04	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS15250	-2.31	0.00	ribose-phosphate pyrophosphokinase	GO:0000287, GO:0004749
FRA*inefficax*_RS28555	-2.30	0.03	short-chain dehydrogenase/reductase SDR	GO:0016491
FRA*inefficax*_RS31940	-2.30	0.03	hypothetical protein, transcription factor WhiB	
FRA*inefficax*_RS08305	-2.29	0.01	helix-turn-helix domain protein	GO:0043565
FRA*inefficax*_RS00205	-2.29	0.03	NADPH-dependent FMN reductase	
FRA*inefficax*_RS27350	-2.29	0.01	hypothetical protein	
FRA*inefficax*_RS03265	-2.29	0.03	FAD-dependent pyridine nucleotide-disulfideoxidoreductase	
FRA*inefficax*_RS01435	-2.29	0.01	hypothetical protein	
FRA*inefficax*_RS23945	-2.29	0.05	hypothetical protein	
FRA*inefficax*_RS31400	-2.28	0.01	HAD-superfamily subfamily IB hydrolase,TIGR01490	GO:0016791
FRA*inefficax*_RS32215	-2.27	0.00	Alcohol dehydrogenase GroES domain protein, hypothetical protein	GO:0016491
FRA*inefficax*_RS30595	-2.27	0.01	phosphoribosylglycinamide formyltransferase	GO:0004644
FRA*inefficax*_RS15680	-2.27	0.00	drug resistance transporter, EmrB/QacAsubfamily	
FRA*inefficax*_RS24120	-2.25	0.04	hypothetical protein, PemK family protein	GO:0003677
FRA*inefficax*_RS17700	-2.25	0.00	hypothetical protein	
FRA*inefficax*_RS35595	-2.25	0.01	hypothetical protein	
FRA*inefficax*_RS30925	-2.25	0.01	ribosomal protein L22, ribosomal protein S19	GO:0003735
FRA*inefficax*_RS08435	-2.24	0.01	ribosomal protein L20	GO:0003735, GO:0019843

FRA*inefficax*_RS09415	-2.24	0.04	Propanoyl-CoA C-acyltransferase, acetyl-CoA acetyltransferase-like protein	
FRA*inefficax*_RS33070	-2.24	0.01	Peptidylprolyl isomerase	
FRA*inefficax*_RS30445	-2.24	0.00	glutamate--cysteine ligase GCS2	GO:0004357
FRA*inefficax*_RS03030	-2.23	0.02	tryptophanyl-tRNA synthetase	GO:0000166, GO:0004830, GO:0005524
FRA*inefficax*_RS18630	-2.22	0.00	protein of unknown function DUF245 domainprotein	
FRA*inefficax*_RS01140	-2.22	0.00	deoxycytidine triphosphate deaminase	GO:0005515, GO:0008829
FRA*inefficax*_RS17725	-2.21	0.01	methylmalonyl-CoA epimerase	
FRA*inefficax*_RS26920	-2.21	0.01	L-carnitine dehydratase/bile acid-inducibleprotein F, Aldehyde Dehydrogenase	GO:0003824, GO:0016491
FRA*inefficax*_RS03700	-2.21	0.00	Chorismate mutase	
FRA*inefficax*_RS21210	-2.21	0.01	putative transcriptional regulator, TetR family	
FRA*inefficax*_RS06955	-2.21	0.03	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS19210	-2.20	0.00	Integral membrane protein TerC	
FRA*inefficax*_RS03940	-2.20	0.01	Aldehyde Dehydrogenase	GO:0016491
FRA*inefficax*_RS06420	-2.20	0.03	hypothetical protein	
FRA*inefficax*_RS08945	-2.20	0.01	Rieske (2Fe-2S) iron-sulfur domain protein, ubiquinol-cytochrome c reductase cytochrome bsubunit	GO:0016491
FRA*inefficax*_RS12860	-2.20	0.04	hypothetical protein	
FRA*inefficax*_RS05915	-2.19	0.01	major facilitator superfamily MFS_1	
FRA*inefficax*_RS01135	-2.19	0.01	ATP-dependent chaperone ClpB	
FRA*inefficax*_RS24655	-2.19	0.01	Glutamate synthase (ferredoxin)	
FRA*inefficax*_RS02790	-2.19	0.00	fumarate reductase/succinate dehydrogenaseflavoprotein domain protein	GO:0009055, GO:0016491
FRA*inefficax*_RS08700	-2.19	0.01	glutamine synthetase, type I	GO:0004356
FRA*inefficax*_RS31860	-2.19	0.01	hypothetical protein	
FRA*inefficax*_RS00465	-2.19	0.01	Rhodanese domain protein	
FRA*inefficax*_RS08630	-2.18	0.01	NADPH-dependent F420 reductase	
FRA*inefficax*_RS03830	-2.18	0.00	glutaredoxin-like protein	
FRA*inefficax*_RS11035	-2.18	0.01	protein of unknown function DUF218	
FRA*inefficax*_RS00960	-2.17	0.03	hypothetical protein	
FRA*inefficax*_RS24665	-2.17	0.01	protein of unknown function DUF125transmembrane, prolipoprotein diacylglyceryl transferase	GO:0005524
FRA*inefficax*_RS18075	-2.17	0.01	two component transcriptional regulator, LuxRfamily	GO:0000156, GO:0003700,

				GO:0043565
FRA*inefficax*_RS18525	-2.17	0.02	hypothetical protein	
FRA*inefficax*_RS18925	-2.17	0.02	transcriptional regulator, PadR-like family	
FRA*inefficax*_RS31735	-2.17	0.01	Protein of unknown function DUF3039	
FRA*inefficax*_RS02130	-2.16	0.00	band 7 protein	
FRA*inefficax*_RS33490	-2.16	0.01	Luciferase-like, subgroup	
FRA*inefficax*_RS19890	-2.16	0.02	hypothetical protein	
FRA*inefficax*_RS18110	-2.15	0.01	methionine-R-sulfoxide reductase	GO:0008113
FRA*inefficax*_RS02160	-2.15	0.01	hypothetical protein	
FRA*inefficax*_RS18565	-2.15	0.00	Sec-independent protein translocase, TatCsubunit	
FRA*inefficax*_RS07095	-2.15	0.01	Taurine catabolism dioxygenase TauD/TfdA	GO:0016491
FRA*inefficax*_RS09065	-2.14	0.02	Lytic transglycosylase catalytic	
FRA*inefficax*_RS30855	-2.14	0.02	ribosomal protein L30, ribosomal protein S5	GO:0003735
FRA*inefficax*_RS26980	-2.14	0.04	cytochrome P450	GO:0004497, GO:0005506, GO:0009055, GO:0020037
FRA*inefficax*_RS27725	-2.14	0.01	hypothetical protein	
FRA*inefficax*_RS00700	-2.14	0.01	threonine synthase	GO:0004795
FRA*inefficax*_RS28185	-2.14	0.01	hypothetical protein	
FRA*inefficax*_RS22750	-2.14	0.02	hypothetical protein	
FRA*inefficax*_RS30110	-2.14	0.02	protein of unknown function DUF343	
FRA*inefficax*_RS00235	-2.13	0.05	protein of unknown function DUF308 membrane	
FRA*inefficax*_RS31720	-2.13	0.02	nitrogen regulatory protein P-II	GO:0030234
FRA*inefficax*_RS05715	-2.13	0.02	RNA modification enzyme, MiaB family	GO:0003824, GO:0016740
FRA*inefficax*_RS10780	-2.13	0.01	putative integral membrane export protein	
FRA*inefficax*_RS32300	-2.13	0.03	transcriptional regulator, MerR family	GO:0003700
FRA*inefficax*_RS26520	-2.13	0.01	amidohydrolase 2	GO:0003824
FRA*inefficax*_RS15025	-2.13	0.01	Citrate (Si)-synthase	
FRA*inefficax*_RS31865	-2.12	0.02	protein of unknown function DUF72	
FRA*inefficax*_RS26160	-2.12	0.03	Leucine carboxyl methyltransferase	GO:0008168
FRA*inefficax*_RS02150	-2.12	0.05	ATP-binding region ATPase domain protein	GO:0005524
FRA*inefficax*_RS10955	-2.12	0.01	PhoH family protein	GO:0005524
FRA*inefficax*_RS16305	-2.12	0.01	dihydrodipicolinate reductase, regulatory protein TetR	GO:0008839, GO:0003700

FRA*inefficax*_RS31545	-2.12	0.01	Protein of unknown function DUF2596	
FRA*inefficax*_RS26800	-2.11	0.01	Enoyl-CoA hydratase/isomerase	GO:0003824
FRA*inefficax*_RS16395	-2.11	0.04	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS03565	-2.11	0.02	2,3,4,5-tetrahydropyridine-2,6-carboxylateN-succinyltransferase	
FRA*inefficax*_RS05045	-2.11	0.00	glutamyl-tRNA(Gln) amidotransferase, C subunit	
FRA*inefficax*_RS20010	-2.10	0.00	putative exporter of polyketide antibiotics-likeprotein, ABC transporter related protein	GO:0005524, GO:0016887
FRA*inefficax*_RS04665	-2.10	0.03	hypothetical protein	
FRA*inefficax*_RS24125	-2.10	0.04	hypothetical protein, PemK family protein	GO:0003677
FRA*inefficax*_RS08895	-2.10	0.01	cytochrome c oxidase, subunit I, Cytochrome c oxidase subunit IV	GO:0004129, GO:0005507
FRA*inefficax*_RS13810	-2.10	0.00	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS24085	-2.10	0.02	FeS assembly protein SufD, FeS assembly protein SufB, putative transcriptional regulator	GO:0005515, GO:0003700
FRA*inefficax*_RS35290	-2.09	0.03	hypothetical protein	
FRA*inefficax*_RS28340	-2.09	0.00	transcriptional regulator, GntR family	GO:0003700
FRA*inefficax*_RS08885	-2.09	0.02	cytochrome c oxidase, subunit II, cytochrome c oxidase, subunit I	GO:0004129, GO:0005507
FRA*inefficax*_RS33035	-2.09	0.02	cold-shock DNA-binding domain protein	GO:0003677
FRA*inefficax*_RS05330	-2.09	0.02	hypothetical protein	
FRA*inefficax*_RS13260	-2.08	0.03	putative F420-dependent oxidoreductase	
FRA*inefficax*_RS31730	-2.08	0.01	NLP/P60 protein	
FRA*inefficax*_RS30610	-2.08	0.01	hypothetical protein	
FRA*inefficax*_RS23595	-2.08	0.01	Cupin 2 conserved barrel domain protein, cyclase/dehydrase	
FRA*inefficax*_RS11260	-2.08	0.02	hypothetical protein	
FRA*inefficax*_RS01315	-2.07	0.01	hypothetical protein	
FRA*inefficax*_RS27475	-2.07	0.01	Rieske (2Fe-2S) iron-sulfur domain protein	GO:0016491
FRA*inefficax*_RS28710	-2.07	0.03	FAD-dependent pyridine nucleotide-disulfideoxidoreductase	
FRA*inefficax*_RS27495	-2.07	0.02	carbon monoxide dehydrogenase subunit G	
FRA*inefficax*_RS09075	-2.06	0.01	thiazole biosynthesis family protein, biotin and thiamin synthesis associated	GO:0003824, GO:0051536
FRA*inefficax*_RS00400	-2.06	0.03	protein of unknown function UPF0233	
FRA*inefficax*_RS26475	-2.06	0.03	hypothetical protein	
FRA*inefficax*_RS05785	-2.05	0.03	RDD domain containing protein	

FRA*inefficax*_RS03760	-2.05	0.02	hypothetical protein	
FRA*inefficax*_RS07170	-2.05	0.02	two component transcriptional regulator, wingedhelix family	GO:0000156, GO:0003677
FRA*inefficax*_RS32385	-2.05	0.01	alpha/beta hydrolase fold protein	
FRA*inefficax*_RS03400	-2.05	0.05	class II aldolase/adducin family protein	GO:0046872
FRA*inefficax*_RS15175	-2.05	0.04	hypothetical protein	
FRA*inefficax*_RS08915	-2.05	0.01	ferric uptake regulator, Fur family	GO:0003700
FRA*inefficax*_RS24960	-2.05	0.01	amidohydrolase 2	GO:0003824
FRA*inefficax*_RS09715	-2.05	0.03	Endopeptidase Clp	
FRA*inefficax*_RS34920	-2.04	0.01	xylose isomerase	GO:0009045
FRA*inefficax*_RS10895	-2.04	0.02	YceI family protein	
FRA*inefficax*_RS05395	-2.04	0.02	Ribonuclease H, Protein of unknown function DUF2469	
FRA*inefficax*_RS23555	-2.04	0.02	O-methyltransferase family 2	GO:0008171
FRA*inefficax*_RS05935	-2.04	0.03	3-oxoacyl-(acyl-carrier-protein) synthase 2, acyl carrier protein	GO:0046872, GO:0000036
FRA*inefficax*_RS03480	-2.04	0.01	hypothetical protein	
FRA*inefficax*_RS33360	-2.03	0.01	peptidyl-prolyl cis-trans isomerase cyclophilintype	GO:0003755
FRA*inefficax*_RS09590	-2.03	0.01	Luciferase-like, subgroup	
FRA*inefficax*_RS31315	-2.03	0.00	cytochrome c-type biogenesis protein CcsB, putative cytochrome c biogenesis membraneprotein, cytochrome c biogenesis protein transmembraneregion	
FRA*inefficax*_RS07695	-2.03	0.03	short-chain dehydrogenase/reductase SDR	GO:0016491
FRA*inefficax*_RS18620	-2.03	0.01	Recombination endonuclease VII	GO:0004519
FRA*inefficax*_RS10610	-2.03	0.02	Polymorphic membrane protein Chlamydia	
FRA*inefficax*_RS24210	-2.03	0.03	glyceraldehyde-3-phosphate dehydrogenase, typeI	GO:0008943, GO:0051287
FRA*inefficax*_RS24280	-2.03	0.00	peptidase M50	GO:0004222
FRA*inefficax*_RS04830	-2.03	0.01	1,4-alpha-glucan branching enzyme	GO:0003844
FRA*inefficax*_RS09395	-2.03	0.02	transcriptional regulator, GntR family withaminotransferase domain	GO:0003700, GO:0030170
FRA*inefficax*_RS23155	-2.03	0.01	Proteasome assembly chaperone 2	
FRA*inefficax*_RS22945	-2.03	0.02	hypothetical protein	
FRA*inefficax*_RS24580	-2.03	0.03	O-methyltransferase family 3	GO:0008171
FRA*inefficax*_RS11580	-2.02	0.02	pyridoxine biosynthesis protein	
FRA*inefficax*_RS05875	-2.02	0.03	hypothetical protein	
FRA*inefficax*_RS23465	-2.02	0.01	Heat shock protein 70	
FRA*inefficax*_RS11470	-2.02	0.01	protein of unknown function DUF107, band 7 protein	

FRA*inefficax*_RS14670	-2.02	0.01	protein of unknown function DUF151	
FRA*inefficax*_RS11550	-2.02	0.03	histidine triad (HIT) protein	
FRA*inefficax*_RS05295	-2.02	0.01	methyltransferase, pantetheine-phosphate adenylyltransferase	GO:0003824, GO:0004595
FRA*inefficax*_RS31140	-2.02	0.01	proton-translocating NADH-quinoneoxidoreductase, chain L	GO:0008137
FRA*inefficax*_RS02685	-2.01	0.02	regulatory protein, FmdB family	
FRA*inefficax*_RS33810	-2.01	0.05	regulatory protein TetR, amidohydrolase 2	GO:0003700, GO:0003824
FRA*inefficax*_RS35675	-2.01	0.01	serine/threonine protein kinase	GO:0004674, GO:0005524
FRA*inefficax*_RS24090	-2.01	0.02	FeS assembly protein SufB, putative transcriptional regulator	GO:0005515, GO:0003700
FRA*inefficax*_RS01090	-2.01	0.02	protein of unknown function DUF224 cysteine-richregion domain protein	
FRA*inefficax*_RS30185	-2.00	0.01	Nucleotidyl transferase	GO:0016779

Table 3.6: inefficax Up-Regulated Genes with Biphenyl as Sole Carbon Source

Name	Fold change	P-value	product (CP002299 *inefficax*) (CDS)	Gene Ontology
FRA*inefficax*_RS29675	57.01	0.01	ABC transporter related protein, hypothetical protein	GO:0005524, GO:0016887
FRA*inefficax*_RS01715	35.03	0.02	Endoribonuclease L-PSP	
FRA*inefficax*_RS09955	27.57	0.04	HhH-GPD family protein, regulatory protein MarR	GO:0003700
FRA*inefficax*_RS16095	23.68	0.04	acyl-CoA dehydrogenase domain-containingprotein	GO:0003995
FRA*inefficax*_RS32965	22.17	0.05	NB-ARC domain protein	GO:0005524
FRA*inefficax*_RS25115	21.58	0.05	amidohydrolase 2, AMP-dependent synthetase and ligase	GO:0003824
FRA*inefficax*_RS17490	14.83	0.00	L-carnitine dehydratase/bile acid-inducibleprotein F	GO:0003824
FRA*inefficax*_RS14945	14.66	0.00	hypothetical protein	
FRA*inefficax*_RS17125	13.64	0.00	Carboxymuconolactone decarboxylase	
FRA*inefficax*_RS17100	10.83	0.01	oxidoreductase domain protein	GO:0016491
FRA*inefficax*_RS22645	8.48	0.02	Thioesterase, hypothetical protein	GO:0020037
FRA*inefficax*_RS05405	8.47	0.02	Uncharacterized protein family UPF0102, Mg chelatase, subunit ChlI, DNA protecting protein DprA	
FRA*inefficax*_RS21310	8.26	0.00	ABC transporter related protein	GO:0005524, GO:0016887
FRA*inefficax*_RS28935	8.10	0.02	hypothetical protein, Lytic transglycosylase catalytic	

FRA*inefficax*_RS15505	8.01	0.02	luciferase family oxidoreductase, group 1	
FRA*inefficax*_RS06315	7.99	0.02	Enoyl-CoA hydratase/isomerase, acyl-CoA dehydrogenase domain-containingprotein	GO:0003824
FRA*inefficax*_RS33795	7.96	0.02	multi-sensor signal transduction histidinekinase, ABC transporter related protein	GO:0000155, GO:0005524, GO:0046983, GO:0016887
FRA*inefficax*_RS15375	7.86	0.02	6-deoxyerythronolide-B synthase	
FRA*inefficax*_RS29740	7.74	0.00	integral membrane protein	
FRA*inefficax*_RS15510	7.68	0.02	Luciferase-like, subgroup	
FRA*inefficax*_RS28985	7.57	0.02	hypothetical protein, transcription factor WhiB	
FRA*inefficax*_RS21815	7.27	0.01	inositol monophosphatase	GO:0004437
FRA*inefficax*_RS34550	7.11	0.03	hypothetical protein	
FRA*inefficax*_RS18135	6.97	0.03	RNA polymerase, sigma-24 subunit, ECF subfamily, hypothetical protein	GO:0003677, GO:0003700, GO:0016987
FRA*inefficax*_RS22525	6.80	0.01	ABC transporter related protein	GO:0005524, GO:0016887
FRA*inefficax*_RS29845	6.77	0.03	short-chain dehydrogenase/reductase SDR	GO:0016491
FRA*inefficax*_RS17300	6.75	0.01	Alcohol dehydrogenase zinc-binding domainprotein	GO:0008270, GO:0016491
FRA*inefficax*_RS21160	6.58	0.00	hypothetical protein	
FRA*inefficax*_RS13080	6.58	0.00	cytochrome P450	GO:0004497, GO:0005506, GO:0009055, GO:0020037
FRA*inefficax*_RS31470	6.45	0.04	aminotransferase class IV	GO:0003824
FRA*inefficax*_RS25240	6.24	0.05	major facilitator superfamily MFS_1	
FRA*inefficax*_RS13905	6.21	0.00	Enoyl-CoA hydratase/isomerase	GO:0003824
FRA*inefficax*_RS25910	6.13	0.05	nicotinate-nucleotide/ dimethylbenzimidazolephosphoribosyltransferase	GO:0008939
FRA*inefficax*_RS34485	6.06	0.00	helix-turn-helix domain protein, flavoprotein	GO:0043565, GO:0003824
FRA*inefficax*_RS24250	6.03	0.05	hypothetical protein	
FRA*inefficax*_RS07680	6.00	0.01	hypothetical protein	
FRA*inefficax*_RS13950	5.98	0.05	short-chain dehydrogenase/reductase SDR	GO:0016491
FRA*inefficax*_RS33790	5.88	0.00	multi-sensor signal transduction histidinekinase	GO:0000155, GO:0005524, GO:0046983
FRA*inefficax*_RS15380	5.79	0.00	Beta-ketoacyl synthase	GO:0016491,

				GO:0016740, GO:0048037
FRA*inefficax*_RS20655	5.78	0.01	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS18175	5.74	0.00	phospholipid/glycerol acyltransferase	GO:0008415
FRA*inefficax*_RS33300	5.70	0.01	Peptidoglycan-binding domain 1 protein	
FRA*inefficax*_RS14085	5.68	0.00	AMP-dependent synthetase and ligase	GO:0003824
FRA*inefficax*_RS17210	5.67	0.02	class II aldolase/adducin family protein, L-ribulokinase	GO:0046872, GO:0008741
FRA*inefficax*_RS23750	5.62	0.02	hypothetical protein	
FRA*inefficax*_RS06365	5.60	0.01	glycine cleavage T protein (aminomethyltransferase)	GO:0004047, GO:0016491
FRA*inefficax*_RS30010	5.57	0.02	hypothetical protein	
FRA*inefficax*_RS16800	5.54	0.00	ABC transporter related protein, inner-membrane translocator	GO:0005524, GO:0016887, GO:0005215
FRA*inefficax*_RS13790	5.54	0.02	acetyl-CoA acetyltransferase, acyl-CoA dehydrogenase domain-containingprotein	GO:0003700, GO:0003995
FRA*inefficax*_RS03980	5.51	0.02	hypothetical protein	
FRA*inefficax*_RS28925	5.43	0.01	hypothetical protein	
FRA*inefficax*_RS09450	5.39	0.01	hypothetical protein	
FRA*inefficax*_RS13070	5.33	0.02	binding-protein-dependent transport systemsinner membrane component, ABC transporter related protein	GO:0005215, GO:0005524, GO:0016887
FRA*inefficax*_RS29145	5.29	0.00	ABC transporter related protein	GO:0005524, GO:0016887
FRA*inefficax*_RS20440	5.24	0.02	short-chain dehydrogenase/reductase SDR, Enoyl-CoA hydratase/isomerase	GO:0016491, GO:0003824
FRA*inefficax*_RS29345	5.21	0.03	hypothetical protein	
FRA*inefficax*_RS10805	5.20	0.01	putative RNA polymerase, sigma-24 subunit, ECFsubfamily	GO:0003677, GO:0003700, GO:0016987
FRA*inefficax*_RS17995	5.16	0.01	polysaccharide deacetylase, amidohydrolase	GO:0016887, GO:0016787
FRA*inefficax*_RS27860	5.15	0.01	low temperature requirement A, two component transcriptional regulator, LuxRfamily	GO:0000156, GO:0003700, GO:0043565
FRA*inefficax*_RS02820	5.14	0.00	transposase IS116/IS110/IS902 family protein	GO:0003677, GO:0004803
FRA*inefficax*_RS07420	5.07	0.03	hypothetical protein	
FRA*inefficax*_RS00590	5.05	0.02	dihydroneopterin aldolase, 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	GO:0004150, GO:0003848

FRA*inefficax*_RS19195	4.99	0.00	cytochrome P450	GO:0004497, GO:0005506, GO:0009055, GO:0020037
FRA*inefficax*_RS29020	4.93	0.00	Integrase catalytic region	GO:0003677
FRA*inefficax*_RS18325	4.92	0.04	ABC-2 type transporter, ABC transporter related protein	GO:0005524, GO:0016887
FRA*inefficax*_RS20180	4.92	0.02	dihydrodipicolinate reductase, L-carnitine dehydratase/bile acid-inducibleprotein F	GO:0008839, GO:0003824
FRA*inefficax*_RS02875	4.85	0.00	Dyp-type peroxidase family	
FRA*inefficax*_RS12330	4.82	0.01	class II aldolase/adducin family protein	GO:0046872
FRA*inefficax*_RS18730	4.81	0.05	helix-turn-helix domain protein	GO:0043565
FRA*inefficax*_RS25295	4.76	0.00	hypothetical protein	
FRA*inefficax*_RS19250	4.74	0.03	superoxide dismutase copper/zinc bindingprotein	GO:0046872
FRA*inefficax*_RS11195	4.74	0.05	glycosyl transferase group 1, NAD-dependent epimerase/dehydratase	GO:0003824, GO:0050662
FRA*inefficax*_RS18855	4.73	0.01	ABC transporter related protein	GO:0005524, GO:0016887
FRA*inefficax*_RS18820	4.66	0.03	Taurine dioxygenase, binding-protein-dependent transport systemsinner membrane component, ABC transporter related protein	GO:0005215, GO:0005524, GO:0016887
FRA*inefficax*_RS15755	4.62	0.01	RNA polymerase, sigma-24 subunit, ECF subfamily	GO:0003677, GO:0003700, GO:0016987
FRA*inefficax*_RS18810	4.60	0.01	extracellular solute-binding protein family 3, Taurine dioxygenase	GO:0005215
livG	4.56	0.03	ABC transporter related protein	GO:0005524, GO:0016887
FRA*inefficax*_RS18465	4.55	0.04	hypothetical protein	
FRA*inefficax*_RS29445	4.55	0.01	binding-protein-dependent transport systemsinner membrane component	GO:0005215
FRA*inefficax*_RS20340	4.54	0.05	aromatic-ring-hydroxylating dioxygenase betasubunit	GO:0003824
FRA*inefficax*_RS29370	4.53	0.00	major facilitator superfamily MFS_1	
FRA*inefficax*_RS16915	4.51	0.02	regulatory protein TetR	GO:0003700
FRA*inefficax*_RS01955	4.46	0.00	hypothetical protein	
FRA*inefficax*_RS15480	4.45	0.04	binding-protein-dependent transport systemsinner membrane component, ABC transporter related protein	GO:0005215, GO:0000166, GO:0005524, GO:0016887
FRA*inefficax*_RS21255	4.41	0.01	alpha/beta hydrolase fold protein	
FRA*inefficax*_RS27245	4.39	0.02	putative F420-dependent oxidoreductase	

FRA*inefficax*_RS11200	4.39	0.01	glycosyl transferase group 1, NAD-dependent epimerase/dehydratase	GO:0003824, GO:0050662
FRA*inefficax*_RS05705	4.38	0.02	regulatory protein RecX	
FRA*inefficax*_RS15790	4.36	0.04	hypothetical protein	
FRA*inefficax*_RS20585	4.36	0.05	hypothetical protein, Methyltransferase type 11	GO:0008168
FRA*inefficax*_RS17895	4.30	0.01	major facilitator superfamily MFS_1	
FRA*inefficax*_RS02310	4.27	0.04	hypothetical protein	
FRA*inefficax*_RS11105	4.27	0.00	diguanylate cyclase/phosphodiesterase	
FRA*inefficax*_RS06460	4.26	0.02		
FRA*inefficax*_RS17975	4.25	0.03	binding-protein-dependent transport systemsinner membrane component	GO:0005215
FRA*inefficax*_RS00105	4.24	0.05	hypothetical protein	
FRA*inefficax*_RS13350	4.24	0.03	dihydrodipicolinate reductase	GO:0008839
FRA*inefficax*_RS15340	4.23	0.02	crotonyl-CoA reductase	
FRA*inefficax*_RS20790	4.23	0.04	protein of unknown function DUF35, lipid-transfer protein	
FRA*inefficax*_RS32845	4.23	0.00	regulatory protein LuxR	
FRA*inefficax*_RS22775	4.21	0.01	transcriptional regulator, SARP family	
FRA*inefficax*_RS14800	4.21	0.02	major facilitator superfamily MFS_1	
FRA*inefficax*_RS18185	4.15	0.05	hypothetical protein	
FRA*inefficax*_RS14045	4.14	0.00	sulfate adenylyltransferase, small subunit, sulfate adenylyltransferase, large subunit	GO:0004781, GO:0005524, GO:0016301
FRA*inefficax*_RS28955	4.11	0.00	hypothetical protein	
FRA*inefficax*_RS14055	4.09	0.02	hypothetical protein	
FRA*inefficax*_RS01155	4.09	0.00	hypothetical protein	
FRA*inefficax*_RS06425	4.04	0.04	hypothetical protein	
FRA*inefficax*_RS17705	4.02	0.04	beta-lactamase	
FRA*inefficax*_RS32165	4.01	0.02	WD40 repeat, subgroup, PE-PGRS family protein	
FRA*inefficax*_RS16280	4.01	0.00	Carbamoyl-phosphate synthase L chain ATP-bindingprotein, Wyosine base formation domain-containingprotein	GO:0003824, GO:0005524, GO:0016874
FRA*inefficax*_RS16940	3.99	0.02	hydrolase CocE/NonD family protein	GO:0016787
FRA*inefficax*_RS17000	3.97	0.00	glycoside hydrolase family 3 domain protein	GO:0016887
FRA*inefficax*_RS21865	3.92	0.00	hypothetical protein	
FRA*inefficax*_RS27065	3.87	0.03	DitF protein	
FRA*inefficax*_RS34285	3.87	0.00	AIR synthase related protein	GO:0003824,

				GO:0008080
FRA*inefficax*_RS32115	3.82	0.02	protein of unknown function DUF81	
FRA*inefficax*_RS29665	3.81	0.00	integral membrane sensor signal transductionhistidine kinase	GO:0000155, GO:0004871, GO:0005524
FRA*inefficax*_RS23805	3.79	0.00	OmpA/MotB domain protein	
FRA*inefficax*_RS03020	3.78	0.00	hypothetical protein	
FRA*inefficax*_RS04320	3.78	0.01	hypothetical protein	
FRA*inefficax*_RS07865	3.77	0.03	hypothetical protein	
FRA*inefficax*_RS15365	3.73	0.03	protein of unknown function DUF1486	
FRA*inefficax*_RS15370	3.73	0.03	short-chain dehydrogenase/reductase SDR, 6-deoxyerythronolide-B synthase	GO:0016491
FRA*inefficax*_RS21325	3.70	0.01	polar amino acid ABC transporter, inner membranesubunit	GO:0005215
FRA*inefficax*_RS10060	3.69	0.00	binding-protein-dependent transport systemsinner membrane component	GO:0005215
FRA*inefficax*_RS21265	3.68	0.01	hypothetical protein	
FRA*inefficax*_RS20380	3.65	0.00	2-oxopent-4-enoate hydratase, acetaldehyde dehydrogenase (acetylating), 4-hydroxy-2-oxovalerate aldolase	GO:0008774, GO:0008701
FRA*inefficax*_RS13035	3.64	0.02	cytochrome P450	GO:0004497, GO:0005506, GO:0009055, GO:0020037
FRA*inefficax*_RS00305	3.59	0.02	major facilitator superfamily MFS_1	
FRA*inefficax*_RS26705	3.59	0.02	L-carnitine dehydratase/bile acid-inducibleprotein F	GO:0003824
FRA*inefficax*_RS14610	3.59	0.02	hypothetical protein	
FRA*inefficax*_RS07830	3.59	0.01	hypothetical protein	
FRA*inefficax*_RS09615	3.57	0.05	Amidohydrolase 3	GO:0008270
FRA*inefficax*_RS31290	3.56	0.04	hypothetical protein, 3-octaprenyl-4-hydroxybenzoate carboxy-lyase, 4-hydroxybenzoate polyprenyltransferase	GO:0016831
FRA*inefficax*_RS25585	3.56	0.05	transcriptional regulator, ArgP, LysR family	
FRA*inefficax*_RS34430	3.55	0.00	TrwC relaxase	
FRA*inefficax*_RS34450	3.55	0.02	hypothetical protein, Lanthionine synthetase C family protein	
FRA*inefficax*_RS30650	3.54	0.03	transcription factor WhiB	
FRA*inefficax*_RS09235	3.51	0.00		
FRA*inefficax*_RS16175	3.50	0.01	inner-membrane translocator	GO:0005215
FRA*inefficax*_RS13975	3.50	0.01	hypothetical protein	

FRA*inefficax*_RS23110	3.48	0.00	lipoprotein	
FRA*inefficax*_RS16165	3.48	0.04	ABC transporter related protein	GO:0005524, GO:0016887
FRA*inefficax*_RS27780	3.47	0.00	glycoside hydrolase family 4	GO:0005529
FRA*inefficax*_RS32830	3.43	0.02	putative arylesterase-like protein	
FRA*inefficax*_RS07255	3.43	0.04	Aldehyde Dehydrogenase, short-chain dehydrogenase/reductase SDR, 6-phosphogluconate dehydrogenase NAD-bindingprotein	GO:0016491, GO:0004616
FRA*inefficax*_RS21340	3.42	0.03	AMP-dependent synthetase and ligase	GO:0003824
FRA*inefficax*_RS18495	3.42	0.00	RNA polymerase, sigma-24 subunit, ECF subfamily, hypothetical protein	GO:0003677, GO:0003700, GO:0016987
FRA*inefficax*_RS15235	3.41	0.02	coenzyme F420-dependent N5 N10-methylenetetrahydromethanopterin reductase-like protein	
FRA*inefficax*_RS17260	3.41	0.03	Rhodanese domain protein	
FRA*inefficax*_RS00545	3.41	0.03	SEC-C motif domain protein	
FRA*inefficax*_RS07575	3.40	0.01	integral membrane sensor signal transductionhistidine kinase, two component transcriptional regulator, wingedhelix family	GO:0000155, GO:0004871, GO:0005524, GO:0000156, GO:0003677
FRA*inefficax*_RS35730	3.39	0.00	HNH endonuclease	GO:0003676, GO:0004519
FRA*inefficax*_RS25085	3.38	0.01	Enoyl-CoA hydratase/isomerase	GO:0003824
FRA*inefficax*_RS16510	3.37	0.02	protein of unknown function DUF35	
FRA*inefficax*_RS06825	3.36	0.02	acyl-CoA dehydrogenase domain-containingprotein, Enoyl-CoA hydratase/isomerase	GO:0003995, GO:0003824
FRA*inefficax*_RS12325	3.33	0.01	amidohydrolase 2	GO:0003824
FRA*inefficax*_RS13060	3.32	0.00	beta-lactamase domain protein, extracellular solute-binding protein family 1	GO:0005215
FRA*inefficax*_RS33560	3.31	0.03	esterase	
FRA*inefficax*_RS00260	3.31	0.01	UDP-N-acetylglucosamine 2-epimerase	GO:0008761
FRA*inefficax*_RS19645	3.31	0.03	aminoglycoside phosphotransferase	
FRA*inefficax*_RS17040	3.26	0.00	ABC transporter transmembrane region, ABC transporter related protein	GO:0005524, GO:0016887
FRA*inefficax*_RS08000	3.26	0.01	hypothetical protein	
FRA*inefficax*_RS34035	3.24	0.01	single-strand binding protein	GO:0003697
FRA*inefficax*_RS12785	3.23	0.03	transcriptional regulator, MarR family	GO:0003700
FRA*inefficax*_RS29995	3.23	0.00	hypothetical protein, SAF domain protein	
FRA*inefficax*_RS28820	3.22	0.01	polysaccharide biosynthesis protein CapD	

FRA*inefficax*_RS28015	3.22	0.01	Enoyl-CoA hydratase/isomerase, L-carnitine dehydratase/bile acid-inducibleprotein F	GO:0003824
FRA*inefficax*_RS17570	3.21	0.03		
FRA*inefficax*_RS22220	3.20	0.01	hypothetical protein	
FRA*inefficax*_RS34710	3.20	0.02	HNH endonuclease	GO:0003676, GO:0004519
FRA*inefficax*_RS20385	3.20	0.01	4-hydroxy-2-oxovalerate aldolase	GO:0008701
FRA*inefficax*_RS21880	3.20	0.03	aldo/keto reductase	GO:0016491
FRA*inefficax*_RS06265	3.19	0.02	acetyl-CoA acetyltransferase	GO:0030429
FRA*inefficax*_RS19175	3.18	0.01	putative lipase	
FRA*inefficax*_RS16170	3.18	0.01	inner-membrane translocator	GO:0005215
FRA*inefficax*_RS01590	3.18	0.01	monooxygenase FAD-binding protein, AAA ATPase central domain protein, protein of unknown function DUF894 DitE	GO:0004497, GO:0005524
FRA*inefficax*_RS28375	3.18	0.04	ATP-dependent helicase HrpB	
FRA*inefficax*_RS12955	3.18	0.02	hypothetical protein	
FRA*inefficax*_RS18505	3.18	0.02	serine/threonine protein kinase	GO:0004672, GO:0005524
FRA*inefficax*_RS28475	3.18	0.03	RNA polymerase, sigma-24 subunit, ECF subfamily	GO:0003677, GO:0003700, GO:0016987
FRA*inefficax*_RS00715	3.16	0.02	trehalose-phosphatase	GO:0003824
FRA*inefficax*_RS18155	3.16	0.04	5'-3' exonuclease, N-terminal resolvase-likedomain protein	GO:0003677, GO:0008409
FRA*inefficax*_RS00385	3.16	0.00	protein of unknown function DUF574	
FRA*inefficax*_RS15775	3.15	0.00		
FRA*inefficax*_RS10205	3.14	0.04	limonene-1,2-epoxide hydrolase	
FRA*inefficax*_RS32550	3.13	0.03	Integrase catalytic region	GO:0003677
FRA*inefficax*_RS25170	3.13	0.05	short-chain dehydrogenase/reductase SDR	GO:0016491
FRA*inefficax*_RS14080	3.13	0.04	Enoyl-CoA hydratase/isomerase	GO:0003824
FRA*inefficax*_RS27385	3.12	0.01	hypothetical protein, oxidoreductase, short chaindehydrogenase/reductase family protein	
FRA*inefficax*_RS15325	3.11	0.03	binding-protein-dependent transport systemsinner membrane component, hypothetical protein	GO:0005215
FRA*inefficax*_RS24605	3.10	0.00	Aldehyde Dehydrogenase	GO:0016491
FRA*inefficax*_RS04295	3.09	0.01	hypothetical protein	
FRA*inefficax*_RS35275	3.08	0.00	copper resistance protein CopC	GO:0005507
FRA*inefficax*_RS03435	3.08	0.03	hypothetical protein	

FRA*inefficax*_RS28135	3.07	0.04	hypothetical protein	
FRA*inefficax*_RS17215	3.07	0.02	L-ribulokinase	GO:0008741
FRA*inefficax*_RS24415	3.07	0.03	inner-membrane translocator	GO:0005215
FRA*inefficax*_RS27675	3.06	0.00	AMP-dependent synthetase and ligase	GO:0003824
FRA*inefficax*_RS05515	3.03	0.00	protein of unknown function DUF150, transcription termination factor NusA	GO:0003723, GO:0030528
FRA*inefficax*_RS14130	3.03	0.01	amidohydrolase 2	GO:0003824
FRA*inefficax*_RS07965	3.03	0.00	cell division protein FtsK/SpoIIIE	GO:0000166, GO:0003677, GO:0005524
FRA*inefficax*_RS25640	3.02	0.02	helix-turn-helix domain protein	GO:0043565
FRA*inefficax*_RS31675	3.01	0.00	peptidase M20	GO:0005515, GO:0016787
FRA*inefficax*_RS29940	3.01	0.02	TadE family protein	
FRA*inefficax*_RS03295	3.00	0.05	membrane bound O-acyl transferase MBOAT familyprotein	
FRA*inefficax*_RS15385	3.00	0.00	6-deoxyerythronolide-B synthase	
FRA*inefficax*_RS04330	2.99	0.03	major facilitator superfamily MFS_1	
FRA*inefficax*_RS20160	2.99	0.01	esterase/lipase/thioesterase	
FRA*inefficax*_RS13095	2.99	0.01	ferritin/ribonucleotide reductase-like protein, thioesterase superfamily protein	
FRA*inefficax*_RS06310	2.99	0.02	Enoyl-CoA hydratase/isomerase	GO:0003824
FRA*inefficax*_RS29385	2.99	0.03	transcriptional regulator, HxlR family	
FRA*inefficax*_RS31705	2.99	0.03	helix-turn-helix domain protein	GO:0043565
FRA*inefficax*_RS27200	2.98	0.00	short-chain dehydrogenase/reductase SDR, Rieske (2Fe-2S) iron-sulfur domain protein	GO:0016491
FRA*inefficax*_RS20850	2.98	0.02	acetyl-CoA acetyltransferase	GO:0003824
FRA*inefficax*_RS21965	2.98	0.00	NADH:flavin oxidoreductase/NADH oxidase	GO:0010181, GO:0016491
FRA*inefficax*_RS04035	2.97	0.00		
FRA*inefficax*_RS15485	2.97	0.02	polar amino acid ABC transporter, inner membranesubunit, ABC transporter related protein	GO:0005215, GO:0005524, GO:0016887
FRA*inefficax*_RS15210	2.96	0.04	Taurine dioxygenase	
FRA*inefficax*_RS33085	2.96	0.01	protein of unknown function UPF0089	
FRA*inefficax*_RS27145	2.95	0.02	Alcohol dehydrogenase zinc-binding domainprotein	GO:0008270, GO:0016491
FRA*inefficax*_RS28485	2.95	0.02	GTP-binding protein HSR1-related protein, GrpE protein	GO:0000774, GO:0042803,

				GO:0051087
FRA*inefficax*_RS15085	2.95	0.04	major facilitator superfamily MFS_1	
FRA*inefficax*_RS13440	2.93	0.02	(NiFe) hydrogenase maturation protein HypF	GO:0030528
FRA*inefficax*_RS21740	2.93	0.01	transcriptional regulator, CdaR	
FRA*inefficax*_RS34925	2.92	0.04	xylulokinase	GO:0004856
FRA*inefficax*_RS20300	2.90	0.01	hypothetical protein	
FRA*inefficax*_RS21410	2.90	0.04	AMP-dependent synthetase and ligase	GO:0003824
FRA*inefficax*_RS09785	2.90	0.00	hypothetical protein	
FRA*inefficax*_RS05120	2.89	0.02	hypothetical protein	
FRA*inefficax*_RS20330	2.89	0.00	Aromatic-ring-hydroxylating dioxygenase, alphasubunit-like protein, Rieske (2Fe-2S) iron-sulfur domain protein	GO:0005506, GO:0016491
FRA*inefficax*_RS09605	2.88	0.01		
FRA*inefficax*_RS15390	2.87	0.00	6-deoxyerythronolide-B synthase	
FRA*inefficax*_RS27550	2.86	0.05	transcriptional regulator, AraC family, methylated-DNA/protein-cysteinemethyltransferase	GO:0003677, GO:0003700, GO:0008168, GO:0008270, GO:0043565, GO:0003824
FRA*inefficax*_RS21690	2.86	0.02	protein of unknown function DUF214	
FRA*inefficax*_RS11750	2.84	0.00	DNA polymerase III, alpha subunit	GO:0008408
FRA*inefficax*_RS16660	2.84	0.03	NB-ARC domain protein	GO:0005524
FRA*inefficax*_RS16745	2.82	0.00	6-deoxyerythronolide-B synthase	
FRA*inefficax*_RS33780	2.82	0.00	hypothetical protein	
FRA*inefficax*_RS16830	2.82	0.02	protein of unknown function DUF35, L-carnitine dehydratase/bile acid-inducibleprotein F	GO:0003824
FRA*inefficax*_RS15185	2.81	0.00	K+-transporting ATPase, B subunit	GO:0000287, GO:0005524, GO:0008556
FRA*inefficax*_RS08070	2.78	0.03	hopanoid biosynthesis associated radical SAMprotein HpnH	
FRA*inefficax*_RS16945	2.78	0.04	serine/threonine protein kinase	GO:0004672, GO:0005524
FRA*inefficax*_RS15410	2.78	0.00	extracellular solute-binding protein family 5, binding-protein-dependent transport systemsinner membrane component	GO:0005215
FRA*inefficax*_RS28115	2.75	0.02	Mannitol dehydrogenase domain protein, Glucuronate isomerase	GO:0016491, GO:0050662
FRA*inefficax*_RS35075	2.75	0.01	Alcohol dehydrogenase GroES domain protein	GO:0008270, GO:0016491

FRA*inefficax*_RS11160	2.74	0.02	hypothetical protein	
FRA*inefficax*_RS27080	2.73	0.02	Luciferase-like, subgroup, L-carnitine dehydratase/bile acid-inducibleprotein F	GO:0003824
FRA*inefficax*_RS22135	2.71	0.04	drug resistance transporter, EmrB/QacAsubfamily	
FRA*inefficax*_RS22735	2.71	0.04	hypothetical protein	
FRA*inefficax*_RS29510	2.70	0.04	protein of unknown function DUF397	
FRA*inefficax*_RS33785	2.70	0.03	protein of unknown function DUF214	
FRA*inefficax*_RS25705	2.70	0.01	protein of unknown function DUF347	
FRA*inefficax*_RS20450	2.70	0.03	Enoyl-CoA hydratase/isomerase, AMP-dependent synthetase and ligase	GO:0003824
FRA*inefficax*_RS15240	2.69	0.00	HNH endonuclease	GO:0003676, GO:0004519
FRA*inefficax*_RS12500	2.69	0.04	regulatory protein LuxR	GO:0003700, GO:0043565
FRA*inefficax*_RS15730	2.69	0.00	methylamine utilization MauE	
FRA*inefficax*_RS02965	2.68	0.00	protein of unknown function DUF1006	
FRA*inefficax*_RS06645	2.68	0.03	binding-protein-dependent transport systemsinner membrane component, oligopeptide/dipeptide ABC transporter, ATPasesubunit	GO:0005215, GO:0005524, GO:0015197
FRA*inefficax*_RS08760	2.67	0.01	inner-membrane translocator	GO:0005215
FRA*inefficax*_RS16090	2.67	0.03	acyl-CoA dehydrogenase domain-containingprotein	GO:0003995
FRA*inefficax*_RS23660	2.66	0.01	hypothetical protein	
FRA*inefficax*_RS09930	2.66	0.00	hypothetical protein	
FRA*inefficax*_RS15260	2.66	0.01	helix-turn-helix domain protein	GO:0043565
FRA*inefficax*_RS16260	2.65	0.02	Enoyl-CoA hydratase/isomerase	GO:0003824
FRA*inefficax*_RS08490	2.65	0.00	acetylglutamate kinase	GO:0003991
FRA*inefficax*_RS32880	2.64	0.04	putative transmembrane anti-sigma factor, RNA polymerase, sigma-24 subunit, ECF subfamily	GO:0003677, GO:0003700, GO:0016987
FRA*inefficax*_RS22985	2.64	0.04	FAD dependent oxidoreductase, Creatininase	GO:0016491
FRA*inefficax*_RS35255	2.64	0.00	two component transcriptional regulator, LuxRfamily	GO:0000156, GO:0003700, GO:0043565
FRA*inefficax*_RS13345	2.64	0.01	Enoyl-CoA hydratase/isomerase	GO:0003824
FRA*inefficax*_RS01420	2.63	0.03	putative integral membrane sensor protein	
FRA*inefficax*_RS11170	2.63	0.04	two component transcriptional regulator, LuxRfamily, integral membrane sensor signal transductionhistidine kinase	GO:0000156, GO:0003700, GO:0043565, GO:0000155, GO:0005524,

				GO:0046983
FRA*inefficax*_RS11180	2.63	0.00	hypothetical protein	
FRA*inefficax*_RS20400	2.61	0.03	AMP-dependent synthetase and ligase, hypothetical protein	GO:0003824
FRA*inefficax*_RS09315	2.61	0.03	cytochrome P450	GO:0004497, GO:0005506, GO:0009055, GO:0020037
FRA*inefficax*_RS24980	2.60	0.01	glutamate 5-kinase	GO:0004349
FRA*inefficax*_RS25930	2.60	0.03	Choloyl-CoA hydrolase, FAD dependent oxidoreductase	GO:0004499, GO:0016491, GO:0050660, GO:0050661
FRA*inefficax*_RS10360	2.59	0.05	GCN5-related N-acetyltransferase	GO:0008080
FRA*inefficax*_RS17035	2.59	0.01	ABC transporter transmembrane region, ABC transporter related protein	GO:0005524, GO:0016887
FRA*inefficax*_RS03725	2.59	0.01	hypothetical protein	
FRA*inefficax*_RS21945	2.58	0.02	short-chain dehydrogenase/reductase SDR, Taurine catabolism dioxygenase TauD/TfdA	GO:0016491
FRA*inefficax*_RS13715	2.58	0.01	Extracellular ligand-binding receptor	
FRA*inefficax*_RS06415	2.57	0.02	replication initiator protein	
FRA*inefficax*_RS28495	2.57	0.05	Heat shock protein 70	
FRA*inefficax*_RS27235	2.56	0.04	short-chain dehydrogenase/reductase SDR	GO:0016491
FRA*inefficax*_RS17485	2.56	0.03	ABC-type branched-chain amino acid transportsystems periplasmic component-like protein	
FRA*inefficax*_RS20975	2.55	0.03	binding-protein-dependent transport systemsinner membrane component	GO:0005215
FRA*inefficax*_RS20540	2.55	0.01	inner-membrane translocator	GO:0005215, GO:0005524, GO:0016887
FRA*inefficax*_RS30055	2.54	0.00	putative integral membrane protein, hypothetical protein, ATPase associated with various cellularactivities AAA_3	GO:0005524, GO:0016887
FRA*inefficax*_RS00115	2.53	0.04	replication initiator protein	
FRA*inefficax*_RS13840	2.52	0.03	short-chain dehydrogenase/reductase SDR	GO:0016491
FRA*inefficax*_RS20050	2.52	0.01	integral membrane sensor signal transductionhistidine kinase	GO:0000155, GO:0004871, GO:0005524
FRA*inefficax*_RS15620	2.52	0.03	binding-protein-dependent transport systemsinner membrane component, ABC transporter related protein, ABC transporter substrate-binding protein	GO:0005215, GO:0005524, GO:0016887
FRA*inefficax*_RS08475	2.52	0.03	cellulose-binding family II	GO:0030246

FRA*inefficax*_RS13740	2.51	0.01	hypothetical protein	
FRA*inefficax*_RS31435	2.51	0.03	Methyltransferase type 11	GO:0008168
FRA*inefficax*_RS06845	2.51	0.00	multi-sensor signal transduction histidinekinase	GO:0000155, GO:0005524, GO:0046983
FRA*inefficax*_RS20285	2.51	0.03	hypothetical protein	
FRA*inefficax*_RS14960	2.50	0.00	hypothetical protein	
FRA*inefficax*_RS11335	2.50	0.01	hypothetical protein	
FRA*inefficax*_RS16275	2.50	0.00	carboxyl transferase	GO:0016874
FRA*inefficax*_RS01310	2.50	0.00	hypothetical protein	
FRA*inefficax*_RS18990	2.50	0.02	phosphonate ABC transporter, ATPase subunit, binding-protein-dependent transport systemsinner membrane component	GO:0005524, GO:0015416, GO:0005215
FRA*inefficax*_RS21540	2.49	0.02	hypothetical protein	
FRA*inefficax*_RS22665	2.49	0.04	protein of unknown function ATP binding protein, protein of unknown function DUF742	GO:0000166
FRA*inefficax*_RS33170	2.49	0.03	glycosyl transferase family 39	GO:0000030
FRA*inefficax*_RS08465	2.48	0.02	hypothetical protein, protein of unknown function DUF692	
FRA*inefficax*_RS16425	2.48	0.01	acyl-CoA dehydrogenase domain-containingprotein, amidohydrolase 2	GO:0003995, GO:0003824
FRA*inefficax*_RS20200	2.48	0.04	short-chain dehydrogenase/reductase SDR	GO:0016491
FRA*inefficax*_RS13450	2.48	0.02	putative signal transduction protein with Nachtdomain	
FRA*inefficax*_RS12795	2.47	0.03	Enoyl-CoA hydratase/isomerase, acetoacetyl-CoA synthase	GO:0003824, GO:0030729
FRA*inefficax*_RS12000	2.47	0.03	peptidase M20, cysteine desulfurase family protein	GO:0005515, GO:0016787
FRA*inefficax*_RS16470	2.47	0.01	hypothetical protein	
FRA*inefficax*_RS15850	2.46	0.00	molybdopterin oxidoreductase	GO:0010181, GO:0016491, GO:0030151
FRA*inefficax*_RS16505	2.46	0.02	cytochrome P450, Aldehyde Dehydrogenase, protein of unknown function DUF35	GO:0004497, GO:0005506, GO:0009055, GO:0020037, GO:0016491
FRA*inefficax*_RS21725	2.45	0.04	AMP-dependent synthetase and ligase, Beta-ketoacyl synthase	GO:0003824, GO:0048037
FRA*inefficax*_RS08990	2.45	0.05	glucokinase, ROK family, hypothetical protein	GO:0004340
FRA*inefficax*_RS02795	2.45	0.05	cutinase	GO:0016787

FRA*inefficax*_RS33285	2.44	0.00	osmosensitive K channel signal transductionhistidine kinase	GO:0000155, GO:0004673, GO:0005524
FRA*inefficax*_RS06650	2.44	0.03	oligopeptide/dipeptide ABC transporter, ATPasesubunit, Taurine dioxygenase	GO:0005524, GO:0015197
FRA*inefficax*_RS27435	2.44	0.02	Long-chain-fatty-acyl-CoA reductase, aldo/keto reductase	GO:0016491
FRA*inefficax*_RS18515	2.44	0.01	putative ABC transporter	
FRA*inefficax*_RS12930	2.44	0.05	low temperature requirement A	
FRA*inefficax*_RS07410	2.43	0.00	cell division protein FtsK/SpoIIIE	GO:0000166, GO:0003677, GO:0005524
FRA*inefficax*_RS28510	2.43	0.02	ABC transporter related protein	GO:0005524, GO:0016887
FRA*inefficax*_RS30765	2.42	0.01	hypothetical protein	
FRA*inefficax*_RS27560	2.42	0.01	AMP-dependent synthetase and ligase	GO:0003824
FRA*inefficax*_RS25870	2.42	0.00	Polyketide cyclase/dehydrase	
FRA*inefficax*_RS28105	2.41	0.01	glycoside hydrolase family 2 TIM barrel	GO:0004565
FRA*inefficax*_RS28500	2.41	0.04	Heat shock protein 70, hypothetical protein	
FRA*inefficax*_RS29735	2.40	0.01	glycoside hydrolase 15-related protein	GO:0004339
FRA*inefficax*_RS07545	2.38	0.02	MmgE/PrpD family protein	GO:0047547
FRA*inefficax*_RS13015	2.38	0.01	HNH endonuclease	GO:0003676, GO:0004519
FRA*inefficax*_RS00290	2.38	0.01	band 7 protein	
FRA*inefficax*_RS08035	2.37	0.04	amidohydrolase 2	GO:0003824
FRA*inefficax*_RS15035	2.37	0.01	FAD linked oxidase domain protein	GO:0016491, GO:0050660
FRA*inefficax*_RS14250	2.36	0.04	MmpL domain-containing protein	
FRA*inefficax*_RS14005	2.35	0.03	Luciferase-like, subgroup	
FRA*inefficax*_RS12020	2.35	0.03	hypothetical protein	
FRA*inefficax*_RS29930	2.35	0.02	hypothetical protein	
ppnK	2.34	0.00	RNA-binding S4 domain protein, ATP-NAD/AcoX kinase	GO:0003676, GO:0003723, GO:0008168, GO:0003951
FRA*inefficax*_RS09365	2.34	0.01	NUDIX hydrolase	GO:0016787
FRA*inefficax*_RS25750	2.34	0.02	binding-protein-dependent transport systemsinner membrane component, ABC transporter related protein	GO:0005215, GO:0005524, GO:0016887
FRA*inefficax*_RS17055	2.33	0.04	regulatory protein TetR	GO:0003700

FRA*inefficax*_RS29775	2.33	0.03	diaminopimelate decarboxylase	GO:0008836
FRA*inefficax*_RS07150	2.33	0.01	protein of unknown function DUF214, ABC transporter related protein	GO:0005524, GO:0016887
FRA*inefficax*_RS17085	2.33	0.01	Xylan 1,4-beta-xylosidase	
FRA*inefficax*_RS16020	2.32	0.01	hypothetical protein, CoA-binding domain protein	
FRA*inefficax*_RS18895	2.32	0.04	Nitrilotriacetate monooxygenase componentA/pristinamycin IIA synthase subunit A	GO:0004497
FRA*inefficax*_RS21870	2.32	0.05	integral membrane sensor signal transductionhistidine kinase, two component transcriptional regulator, wingedhelix family	GO:0000155, GO:0004871, GO:0005524, GO:0000156, GO:0003677
FRA*inefficax*_RS33870	2.31	0.03	putative formate dehydrogenase, acetyltransferase	
FRA*inefficax*_RS19370	2.31	0.01	L-fucose isomerase-like protein	GO:0008736
FRA*inefficax*_RS20265	2.31	0.03	dihydrodipicolinate reductase	GO:0008839
FRA*inefficax*_RS33160	2.31	0.01	transcriptional regulator, LysR family	GO:0003700
FRA*inefficax*_RS11555	2.30	0.02	small GTP-binding protein	GO:0005525
FRA*inefficax*_RS22480	2.29	0.00	amino acid adenylation domain protein	GO:0016874
FRA*inefficax*_RS20320	2.29	0.04	3-carboxyethylcatechol 2,3-dioxygenase, Alcohol dehydrogenase zinc-binding domainprotein	GO:0008270, GO:0016491
FRA*inefficax*_RS19720	2.29	0.05	undecaprenol kinase	GO:0050380
FRA*inefficax*_RS07800	2.29	0.02	hypothetical protein, translation initiation factor IF-2	
FRA*inefficax*_RS33840	2.29	0.04	integral membrane sensor signal transductionhistidine kinase, two component transcriptional regulator, LuxRfamily	GO:0000155, GO:0005524, GO:0046983, GO:0000156, GO:0003700, GO:0043565
FRA*inefficax*_RS07030	2.28	0.00	Aldehyde Dehydrogenase	GO:0016491
FRA*inefficax*_RS22145	2.28	0.04	hypothetical protein	
FRA*inefficax*_RS26695	2.27	0.04	putative F420-dependent oxidoreductase	
FRA*inefficax*_RS32575	2.27	0.01	hypothetical protein	
FRA*inefficax*_RS12740	2.26	0.04	integral membrane sensor signal transductionhistidine kinase, two component transcriptional regulator, LuxRfamily	GO:0000155, GO:0005524, GO:0046983, GO:0000156, GO:0003700, GO:0043565
FRA*inefficax*_RS10590	2.25	0.03	hypothetical protein	
FRA*inefficax*_RS20670	2.25	0.00	WD40 repeat, subgroup	
FRA*inefficax*_RS06995	2.24	0.02	PKD domain containing protein	

FRA*inefficax*_RS07585	2.24	0.05	transcriptional regulator, LuxR family	GO:0003700, GO:0043565
FRA*inefficax*_RS28190	2.24	0.03	glycosyl transferase family 2	
FRA*inefficax*_RS02905	2.24	0.04	amino acid permease-associated region	
FRA*inefficax*_RS06630	2.24	0.05	extracellular solute-binding protein family 5	GO:0005215
FRA*inefficax*_RS08165	2.23	0.03	hypothetical protein	
FRA*inefficax*_RS29580	2.23	0.04	Glyoxalase/bleomycin resistanceprotein/dioxygenase, Phosphosulfolactate synthase	
FRA*inefficax*_RS28020	2.23	0.03	L-carnitine dehydratase/bile acid-inducibleprotein F	GO:0003824
FRA*inefficax*_RS11705	2.23	0.03	phytoene desaturase	
FRA*inefficax*_RS10430	2.21	0.03	hypothetical protein	
FRA*inefficax*_RS08625	2.21	0.05	hypothetical protein	
FRA*inefficax*_RS32930	2.21	0.03	beta-lactamase domain protein	GO:0016787
FRA*inefficax*_RS19110	2.21	0.00	major facilitator superfamily MFS_1	
FRA*inefficax*_RS20755	2.20	0.05	regulatory protein TetR, amidohydrolase 2	GO:0003700, GO:0003824
FRA*inefficax*_RS01910	2.19	0.02	2-C-methyl-D-erythritol 4-phosphatecytidylyltransferase, 2C-methyl-D-erythritol 2,4-cyclodiphosphatesynthase	GO:0003824, GO:0008685
FRA*inefficax*_RS02885	2.19	0.03	(R)-6-hydroxynicotine oxidase	
FRA*inefficax*_RS07880	2.19	0.04	Methyltransferase type 11	GO:0008168
FRA*inefficax*_RS16680	2.18	0.02	hypothetical protein	
FRA*inefficax*_RS06725	2.18	0.00	YD repeat-containing protein	
FRA*inefficax*_RS05690	2.18	0.02	DEAD/H associated domain protein	GO:0003676, GO:0004386, GO:0005524, GO:0008026
FRA*inefficax*_RS33270	2.18	0.03	Mg2 transporter protein CorA family protein	GO:0046873
FRA*inefficax*_RS12005	2.17	0.04	hypothetical protein	
FRA*inefficax*_RS28220	2.17	0.01	Ribonuclease H	
FRA*inefficax*_RS17495	2.16	0.03	amidohydrolase 2	GO:0003824
FRA*inefficax*_RS25140	2.16	0.01	Enoyl-CoA hydratase/isomerase	GO:0003824
FRA*inefficax*_RS20355	2.16	0.01	AMP-dependent synthetase and ligase	GO:0003824
FRA*inefficax*_RS29270	2.16	0.01	putative transcriptional regulator	
FRA*inefficax*_RS14050	2.16	0.01	sulfate adenylyltransferase, small subunit, sulfate adenylyltransferase, large subunit	GO:0004781, GO:0005524, GO:0016301
FRA*inefficax*_RS15725	2.16	0.01	conserved repeat domain protein	
FRA*inefficax*_RS20390	2.15	0.02	hydrolase CocE/NonD family protein	GO:0016787

FRA*inefficax*_RS07330	2.15	0.00	hypothetical protein	
FRA*inefficax*_RS27325	2.15	0.04	ABC transporter related protein	GO:0005215, GO:0005524, GO:0016887
FRA*inefficax*_RS16910	2.14	0.02	short-chain dehydrogenase/reductase SDR	GO:0016491
FRA*inefficax*_RS07665	2.14	0.04	RNA polymerase, sigma-24 subunit, ECF subfamily, hypothetical protein	GO:0003677, GO:0003700, GO:0016987
FRA*inefficax*_RS10600	2.14	0.02	protein of unknown function DUF1557	
FRA*inefficax*_RS10305	2.14	0.03	Roadblock/LC7 family protein, protein of unknown function DUF742, protein of unknown function ATP binding protein	GO:0000166
FRA*inefficax*_RS00110	2.14	0.04	cell division protein FtsK/SpoIIIE	GO:0000166, GO:0003677, GO:0005524
FRA*inefficax*_RS08325	2.14	0.04	dihydroorotase, multifunctional complex type, hypothetical protein	
FRA*inefficax*_RS17360	2.13	0.01	Phospholipase C	
FRA*inefficax*_RS07005	2.13	0.02	serine/threonine protein kinase-like protein, diguanylate cyclase/phosphodiesterase withPAS/PAC and GAF sensor(s)	GO:0004871
FRA*inefficax*_RS06715	2.12	0.00	FHA domain containing protein	GO:0000166, GO:0003677, GO:0005524
FRA*inefficax*_RS26345	2.12	0.02	L-carnitine dehydratase/bile acid-inducibleprotein F	GO:0003824
FRA*inefficax*_RS14135	2.11	0.03	amidohydrolase 2	GO:0003824
FRA*inefficax*_RS15120	2.11	0.03	sulfotransferase	GO:0008146
FRA*inefficax*_RS24560	2.10	0.04	HNH endonuclease	GO:0003676, GO:0004519
FRA*inefficax*_RS09960	2.10	0.02	Polyketide cyclase/dehydrase	
FRA*inefficax*_RS03715	2.09	0.04	hypothetical protein	
FRA*inefficax*_RS21990	2.07	0.02	Rieske (2Fe-2S) iron-sulfur domain protein	GO:0005506, GO:0016491
FRA*inefficax*_RS07730	2.05	0.02	phosphopantetheine-binding protein, Beta-ketoacyl synthase	GO:0048037
FRA*inefficax*_RS04935	2.05	0.02	putative transcriptional regulator	
FRA*inefficax*_RS14210	2.04	0.02	Aldehyde Dehydrogenase	GO:0016491
FRA*inefficax*_RS21875	2.04	0.03	integral membrane sensor signal transductionhistidine kinase, two component transcriptional regulator, wingedhelix family	GO:0000155, GO:0004871, GO:0005524, GO:0000156, GO:0003677

FRA*inefficax*_RS01970	2.04	0.03	protein of unknown function UPF0089	
FRA*inefficax*_RS28100	2.03	0.03	major facilitator superfamily MFS_1	GO:0005524, GO:0016887
FRA*inefficax*_RS29235	2.03	0.04	regulatory protein LuxR	GO:0003700, GO:0043565
FRA*inefficax*_RS26095	2.02	0.03	Enoyl-CoA hydratase/isomerase	GO:0003824
FRA*inefficax*_RS31820	2.01	0.04	SNARE associated Golgi protein-like protein	
FRA*inefficax*_RS16670	2.01	0.05	cation diffusion facilitator family transporter	GO:0008324
FRA*inefficax*_RS12980	2.01	0.04	alpha/beta hydrolase fold protein, hypothetical protein	
FRA*inefficax*_RS16445	2.01	0.05	amidohydrolase 2	GO:0003824
FRA*inefficax*_RS02915	2.00	0.02	metallophosphoesterase	

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