Exploring drivers of leaf bacterial community dynamics across temperature-driven phenology in two temperate tree species

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In collaboration with:

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DEDICATIONS

To my family
whose unwavering love, support,
and encouragement made this
journey possible.

Vikki Wilson
Chad Wilson-Morrison

And to my cat, Indi,
for seeing me through the toughest of times.

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ABSTRACT

Leaf microbiomes are vital to host and ecosystem functions, yet their interplay with host phenology remains ill-resolved in temperate forests, where climate change is shifting phenological timing. We investigate how cumulative growing degree days (GDDs)—an index of the active, useable heat energy directing phenology—shape leaf bacterial dynamics and ecological strategies, comparing two functionally similar but phylogenetically distant trees: Grey birch (*Betula populifolia*) and trembling aspen (*Populus tremuloides*). 16S rRNA amplicon sequencing captured variation across seven GDDs from June–October 2018 and relative impacts of host identity and GDDs on bacterial diversity, taxonomic enrichment, and niche breadth were tested. Host differences in amplicon sequence variant (ASV) richness were primarily shaped by GDDs, increasing non-linearly and non-monotonically with GDDs in birch but remaining stable in aspen; Shannon diversity was unaffected by GDDs and remained consistently higher in aspen. Beta diversity diverged seasonally; birch microbiomes underwent marked restructuring at higher GDDs, while aspen exhibited compositional overlap. Overall, birch hosted more GDD-limited ASVs, with disproportionate enrichment of generalists like *Endobacter* and *1174-901-12*, whereas aspen hosted more even communities of specialists like *Nocardioides* and *Pelomonas*. The prominence of unclassified ASVs emphasizes a need to resolve microbial "dark matter". Niche analysis showed that ~81% of ASVs were thermal specialists, but species-specific patterns emerged: birch leaves supported communities with wider niches, while aspen maintained narrower niches. Though typically used to predict phenology, our results suggest that the cumulative thermal environment—as tracked by GDDs—imposes ecological filtering on leaf microbiomes based on thermal niche compatibility. Together, this study advances our understanding of microbial ecology *in situ* and expands the utility of the GDD metric.

STATEMENT OF CONTRIBUTIONS

I, Jordan Wilson-Morrison, contributed to the majority of the work conducted towards completion of this thesis. This includes the molecular DNA lab work (extractions and PCR amplifications), as well as all bioinformatic and metagenomic analyses. Sequencing was outsourced to Genome Québec. I wrote all three chapters included in this thesis, and I intend to publish Chapter 2 in the *Phytobiomes Journal*.

My M.Sc. supervisors and external collaborators also contributed to this work. Both Dr. Warren Cardinal-McTeague and Dr. Julian Starr contributed to the overall development, direction, and review of each chapter of my thesis. Dr. Subbaiah Mechanda provided invaluable laboratory training in molecular biology and contributed to the project development and data collection related to leaf specimens. Dr. Itumeleng Moroenyane, my research collaborator at Stellenbosch University, provided guidance and direction in metagenomic analyses. Dr. Etienne Laliberté, lead researcher ar the Canadian Airborne Biodiversity Observatory (CABO), and Rosalie Beauchamp-Rioux, a former M.Sc. student at the Université de Montreal, provided the project foundation and leaf samples needed to complete this metagenomic work. All contributors will be asked to provide helpful comments on the parts of this thesis that they co-authored, and for approval of the final content prior to submission to *Phytobiomes*.

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DATA AVAILABILITY

Sequence data will be submitted to public databases with the publication of Chapter 2.

All other data, code, and analyses will also be submitted to GitHub upon publication at:

https://github.com/jordan-dwm.

LIST OF ABBREVIATIONS

AIC: Akaike Information Criterion

ANOVA: Analysis of Variance

ASV: Amplicon Sequence Variant

BIC: Bayesian Information Criterion

C: Carbon

CABO: Canadian Airborne Biodiversity Observatory

DOY: Day of Year

GDD: Growing Degree Days

GDP: Gross Domestic Product

H′: Shannon Diversity

H_2O_2: Hydrogen Peroxide

LMM: Linear Mixed-Model

Log_2FC: Logarithm Base 2 of Fold Change

N: Nitrogen

OTU: Operational Taxonomic Unit

PCoA: Principal Coordinates Analysis

PERMANOVA: Permutational Multivariate Analysis of Variance

R′: Richness

R^2_c: Conditional R^2

R^2_m: Marginal R^2

RDP: Ribosomal Database Project

rRNA: Ribosomal Ribonucleic Acid

T_{base}: Base Temperature

T_{max}: Temperature Maxima

T_{min}: Temperature Minima

VOC: Volatile Organic Compound

Chapter 1
General Introduction

Microbial ecology examines the interactions between microorganisms, their hosts, and the environment, integrating microbiology, ecology, genetics, and metagenomic bioinformatics to understand microbial community dynamics. Microbes play essential roles in nutrient cycling, plant health, and ecosystem function; as rising temperatures accelerate shifts in plant phenology, investigating how leaf microbiomes respond is critical for conservation, forest management, and ecological modeling. In this thesis, I explore how bacterial dynamics—both between and within host species—are shaped in the leaf phyllosphere and endosphere microbiomes of two broadleaf deciduous trees. Focusing on temperate forests in Parc national du Mont-Saint-Bruno, Quebec, this study aims to characterize and compare general trends and patterns of variation in bacterial diversity and community composition along the seasonal progression of host phenology, measured as growing degree day (GDD; T_{base} = 5°C) accumulation. The overarching goal of my project is to build a foundational understanding of the processes influencing bacterial community dynamics in the leaf microbiomes of temperate forests.

Relevance

Widespread environmental changes are accelerating biodiversity loss, with over 60% of ecosystem services degraded since the 1950s and projected global GDP losses of 7% by 2050 (Markandya 2015). Additionally, climate change is altering plant phenology, shifting developmental events like leaf emergence and senescence (Meier et al. 2021; Piao et al. 2019). Temperate forests experience distinct dormancy and growth cycles regulated by seasonal

accumulation of thermal energy; hence, the GDD index provides a physiologically relevant metric quantifying tree phenology (McMaster and Wilhelm 1997; Prentice et al. 1992). Leaf microbiomes contribute to key biogeochemical processes—including C and N cycling, pollutant degradation, and the synthesis of compounds important for plant productivity—and exhibit reciprocal interactions with plant functional traits, both shaping and responding to them (Chaudhry et al. 2021; Lajoie and Kembel 2021; Thapa et al. 2017). Consequently, climate-driven shifts in phenology may disrupt leaf microbial dynamics, influencing plant health, ecosystem function, and forest resilience (Trivedi et al. 2020). Climate-driven shifts in temperature and precipitation are already impacting microbial networks of temperate trees (Sangiorgio et al. 2024; Wang et al. 2023), expanding pathogen ranges (Lahlali et al. 2024), and destabilizing plant-microbe interactions (Hacquard et al. 2022), yet the relation between temperature-driven phenological changes and the leaf microbiome remains virtually unexplored.

While research has expanded in tropical and agricultural systems, temperate forest leaf microbiomes remain understudied. Methodological limitations—including taxonomic biases, incomplete reference databases, and bioinformatics bottlenecks—further hinder progress in resolving plant-microbe interactions (Bharti and Grimm 2021; Leite et al. 2022; Zhang et al. 2021). Nonetheless, the economic potential of plant microbiomes in silviculture is increasingly recognized (Uroz et al. 2016), while also revealing broader implications for public health in urban and urban-adjacent areas (Hanski et al. 2012). In the face of a rapidly changing climate, addressing these gaps is essential for advancing ecological research and its practical applications. Notably, accrued data and associated results from this study will contribute to genetic databases and the improvement of assessments of biodiversity, plant health and phytopathology, ecosystem function, and climate change impacts.

Background

My research contributes to microbial ecology by investigating how host species identity and biologically active thermal energy, measured as GDD accumulation, shape bacterial diversity and community composition in temperate forest leaves, providing insight into how temperature-driven shifts in tree phenology impact the leaf microbiome, with consequences for plant functional traits, health, and ecosystem function.

Plants are not isolated organisms; they exist in association with complex microbial communities that colonize their surfaces and internal tissues (Fig. 1.1). As part of the plant holobiont, the leaf harbors microbiomes that inhabit two primary niches: the phyllosphere, comprising the leaf surface, and the endosphere, consisting of internal leaf tissues (Redford et al. 2010; Vorholt 2012). Despite the oligotrophic, nutrient-poor, and environmentally harsh conditions of the leaf, microbes play key roles in biogeochemical processes, nutrient cycling, plant health, and ecosystem function (Chaudhry et al. 2021; Lajoie and Kembel 2021; Thapa et al. 2017). For example, leaf-associated microbes influence host immunity, stress tolerance, and microbial interactions through the production of secondary metabolites, biosurfactants, and plant hormone analogs (Vorholt 2012). By enhancing their own fitness through these adaptive mechanisms, bacteria can indirectly or directly improve plant fitness. These microbial assemblages are diverse; in particular, bacteria dominate the leaf microbiome (Durand et al. 2018; Kembel et al. 2014). A summary of commonly detected bacterial taxa found in and on leaves and their known ecological functions is provided in Table A1 (Appendix).

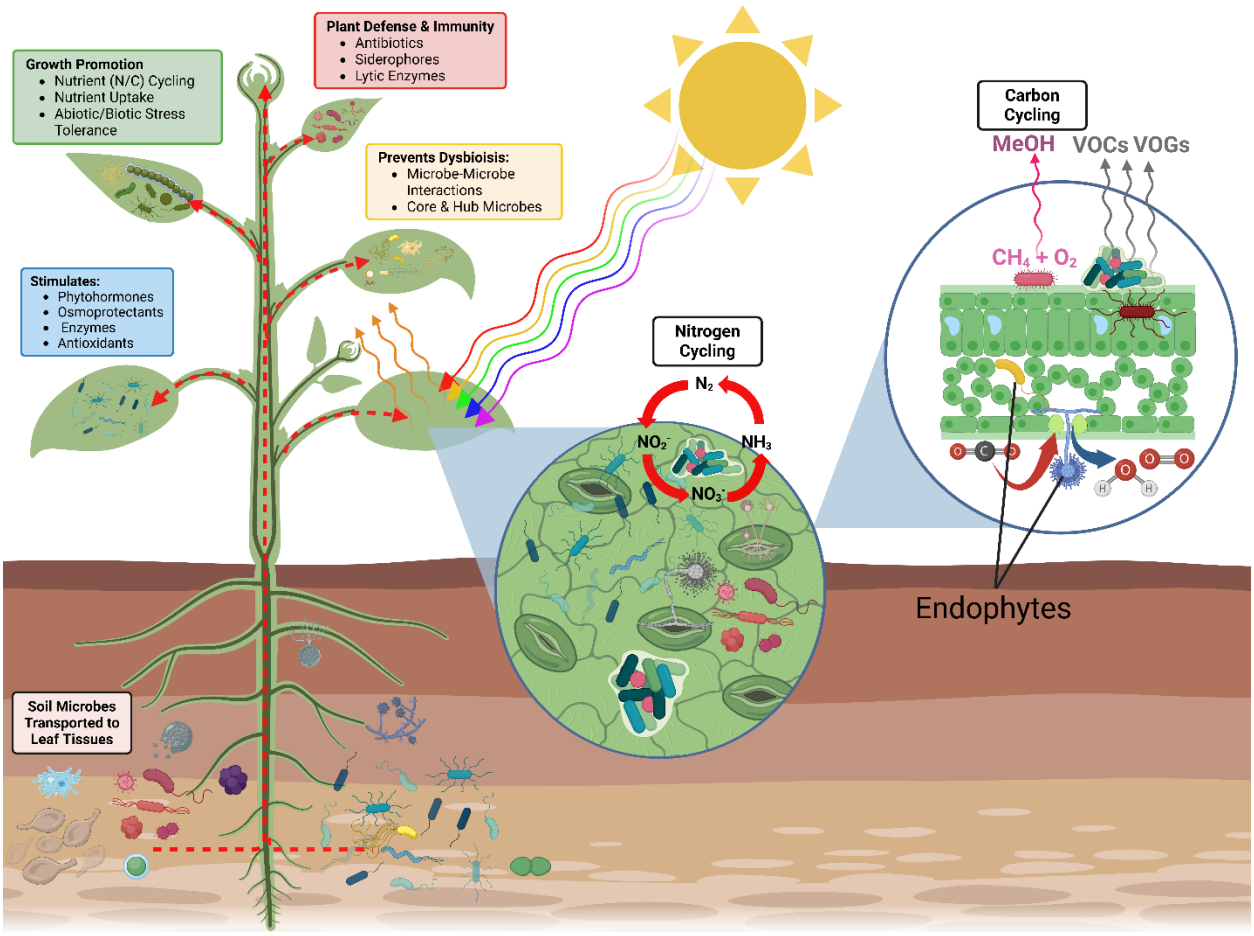

Figure 1.1. The plant associated microbiome provides benefits to the plant through various direct and indirect mechanisms that help to shape leaf functional traits. These benefits include growth promotion, stress tolerance, plant defense and immunity, phytohormone stimulation, and dysbiosis prevention. In contrast, functional traits may be altered predictably by non-beneficial, or pathogenic, microorganisms. These traits are heavily impacted by leaf microbial activity. Figure made using: https://biorender.com.

Microbial community assembly is shaped by both deterministic and stochastic processes, influencing the diversity and structure of the leaf microbiome (Moroenyane et al. 2021a,b). Deterministic processes, such as host filtering and competition, impose selective pressures that favor specific microbial taxa based on plant traits, leaf chemistry, and microenvironmental conditions. In contrast, stochastic processes, including dispersal and ecological drift, contribute to variability in microbial composition, leading to chance-based fluctuations in community structure (Chaudhry et al. 2021; Kembel et al. 2014; Moroenyane et al. 2021a,b). The relative influence of these processes remains an open question and is expected to vary drastically across

77 spatial and temporal scales, particularly in temperate forest ecosystems undergoing dramatic
78 seasonal transitions.

79 Host species identity is a well-established driver of leaf microbiome structure, with
80 studies showing significant interspecific variation in microbial composition (Emmett et al. 2017;
81 Laforest-Lapointe et al. 2016a,b; Redford et al. 2010). Variations between plants growing in
82 proximity suggest that functional traits like leaf morphology and secondary metabolites mediate
83 leaf microbial dynamics (Kembel et al. 2014). Consequently, tree species may exert differential
84 selection pressures on leaf microbiota, affecting interspecific differences in microbiome
85 diversity, composition, and functional roles. Notably, most research has focused on highly
86 divergent taxa (e.g., angiosperms vs. gymnosperms), leaving gaps in our understanding of
87 microbial variation among functionally similar, less divergent species, broadly speaking
88 (Laforest-Lapointe et al. 2016a,b; Lajoie and Kembel 2021; Sangiorgio et al. 2024; Wang et al.
89 2023). This study investigates the leaf bacterial dynamics of two widespread deciduous broadleaf
90 tree species, grey birch (*Betula populifolia*) and trembling aspen (*Populus tremuloides*). Grey
91 birch is a stress-tolerant pioneer species native to northeastern North America. Thriving in
92 nutrient-poor, disturbed habitats, its high phenotypic plasticity and rapid growth make it an ideal
93 system for studying microbial dynamics under fluctuating conditions (Lavoie and Pellerin 2015).
94 Trembling aspen, the most widely distributed tree in North America, can form extensive clonal
95 stands; it, too, is a pioneer species but prefers drier, well-drained soils (Greer et al. 2016). Their
96 distinct ecological strategies provide a comparative framework for examining differences in
97 microbiome structure across functionally similar yet phylogenetically distant host tree species.

98 Furthermore, unlike tropical ecosystems and controlled greenhouse conditions, temperate
99 forests experience pronounced seasonal temperature fluctuations, driving distinct dormancy and

growth cycles (Piao et al. 2019). In temperate deciduous forests and high-latitude regions like Canada, tree phenology is governed by developmental thresholds that are regulated by accumulated thermal energy above a species-specific base temperature. Given that climate change is inducing shifts in plant phenology (Meier et al. 2021; Piao et al. 2019), cumulative GDDs provide a physiologically relevant metric for tracking phenological shifts by integrating thermo-temporal dynamics, improving predictions of key stages like budburst and leaf expansion over models based on static calendar-based methods despite thermo-temporal and interannual seasonal variations (McMaster and Wilhelm 1997; Prentice et al. 1992).

Distinct from broad metrics like mean annual temperature or spatial proxies such as elevation and latitude/longitude—which conflate climatic, spatial, and ecological factors—GDD accumulation represents the active, useable heat energy that an organism has received during a given period, at a finer resolution (McMaster and Wilhelm 1997; Prentice et al. 1992). Emerging evidence suggests that seasonal changes in temperature and precipitation influence tree phyllosphere bacterial communities by altering physicochemical conditions of the environment (Hacquard et al. 2022; Sangiorgio et al. 2024; Wang et al. 2023); thus, as rising temperatures accelerate GDD accumulation, altered trends in seasonal host phenology may generate disruptions to microbial colonization patterns, plant-microbe interactions, and broader ecosystem processes. To the best of our knowledge, and despite increasing recognition that host filtering and temperature shape leaf microbial communities, no studies have examined how the leaf microbiome responds to a phenology-regulating thermal metric like GDD accumulation. Yet, as climate change alters temperature regimes and extends growing seasons, temperature-driven shifts in plant phenology are increasingly recognized as a key ecological concern (Meier et al. 2021; Piao et al. 2019).

Similarly, although time, temperature, and plant developmental compartments have been shown to influence plant microbial dynamics discretely, attempts to identify a direct link to seasonal phenological change through the lens of a continuous, temperature-based framework such as GDD accumulation are lacking (Ginnan et al. 2022; Moroenyane et al. 2021a,b; Sangiorgio et al. 2024). As such, high-resolution analyses integrating these variables are needed to clarify how seasonal phenology influences bacterial diversity and community structure in temperate forest leaves and deduce the ecological mechanisms underlying plant microbial seasonal assembly and dynamics.

Research Aims and Objectives

The primary aim of this M.Sc. project is to assess how host species identity and temperature-driven phenology influence bacterial diversity and community composition in the leaf phyllosphere and endosphere of deciduous broadleaf trees in a temperate forest of Quebec. Using a metacommunity framework, this study examines microbial variations along a gradient of GDD accumulation, focusing on two co-occurring species—grey birch and trembling aspen—which share broad functional groupings (deciduousness; broadleaf leaf type) but with divergent phylogenetic histories. The specific objectives of my study are to: (1) Determine the relative influence of host species identity and GDD accumulation on seasonal patterns of leaf bacterial diversity and community composition; (2) investigate whether the microbiomes of two functionally similar but phylogenetically distinct host tree species respond similarly or divergently to GDD accumulation; (3) observe how thermal timing (GDD accumulation) structures leaf bacterial microbiomes across host seasonal phenology; and (4) ascertain whether or not leaf bacterial communities exhibit thermal niche differentiation over time, and deduce how patterns of generalist and specialist taxa vary within and between host species along phenology.

Motivation and Approach

My study is motivated by the need to improve our understanding of how climate-driven phenological shifts influence leaf phyllosphere and endosphere bacterial diversity and community structure to better predict microbial responses to environmental change and inform ecological modeling, forest management, and climate adaptation. I examine microbial persistence and community shifts across host phenology in response to GDD accumulation, assessing interspecific (between-host species) and intraspecific (within-host species) variation (Fig. 1.2). Climate change is altering phenological timing, especially in broadleaved species; yet, its impact on leaf microbiomes remains poorly understood (Meier et al. 2021; Piao et al. 2019). To address this, I applied a metacommunity framework using cumulative GDDs to quantify phenological changes in leaf bacterial microbiomes and assess deterministic versus stochastic bacterial assembly, providing a scalable, physiologically relevant approach for predicting microbial responses to climate-driven phenological shifts (McMaster and Wilhelm 1997; Prentice et al. 1992).

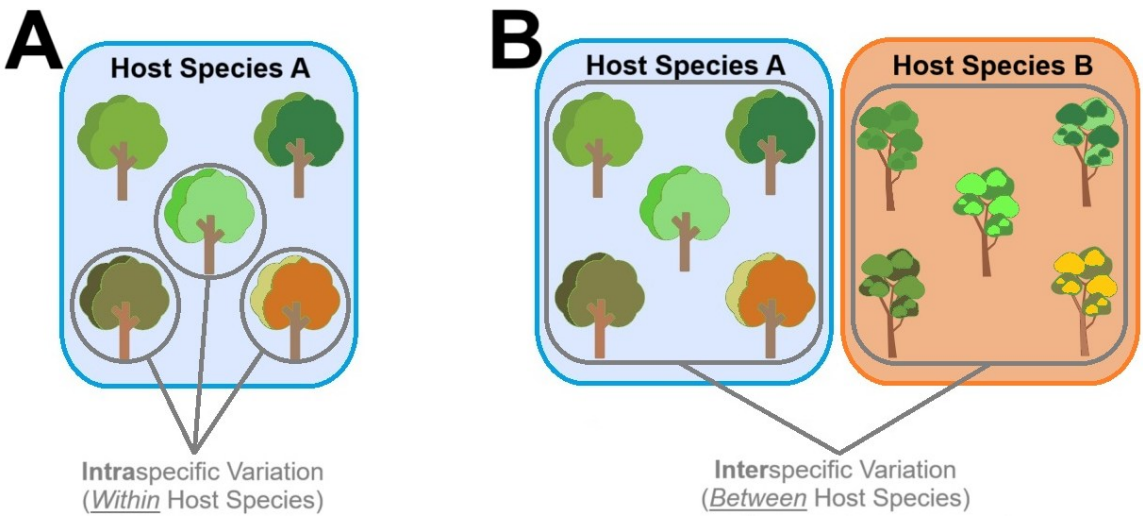

Figure 1.2. Schematic demonstrating the difference between **(A)** intraspecific variation (variation within a host species) and **(B)** interspecific variation (variation between host species). In this study, "Host Species A" and "Host Species B" represent the two host study systems, grey birch and trembling aspen.

My thesis is structured around a single main chapter (Chapter 2), which presents the primary research investigation. High-throughput 16S rRNA gene sequencing was used to characterize bacterial diversity and composition in the phyllosphere and endosphere of grey birch and trembling aspen at the ASV level. Using R, linear mixed models assessed the effects of host species, plant identity, and GDD accumulation on microbial alpha diversity, while beta diversity analyses assessed changes in community composition by employing Principal Coordinates Analysis (PCoA) and PERMANOVAs. Taxonomic profiles were generated using the SILVA reference database and differential abundance testing identified microbial shifts across phenological stages. Finally, thermal niche breadth was determined using Levin's niche width The general workflow is provided in Figure 1.3 (R Core Team, 2024).

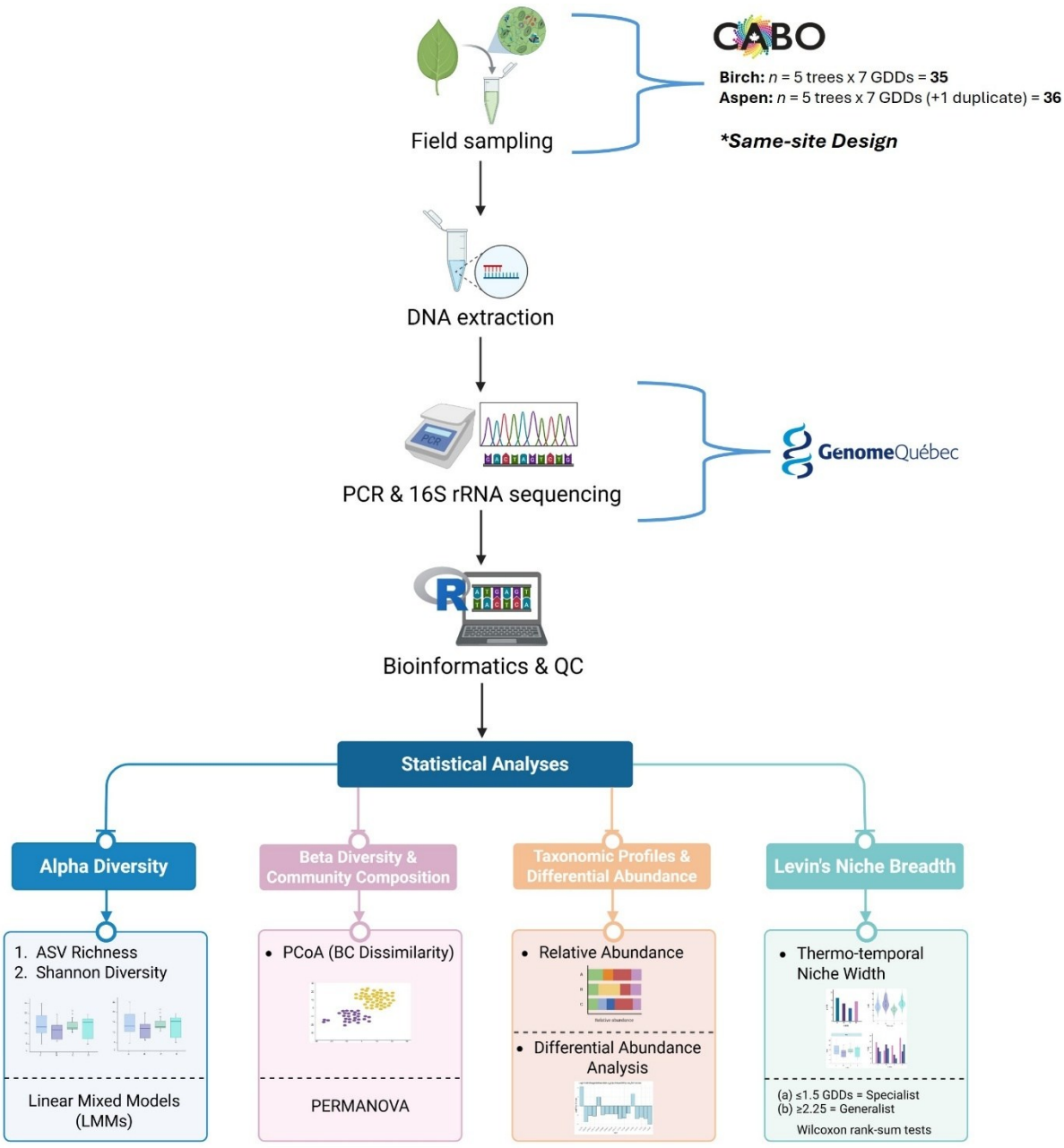

Figure 1.3. Overview of the metagenomics workflow used in this study. Raw sequencing reads were processed using the DADA2 pipeline, including quality filtering, denoising, chimera removal, and amplicon sequence variant (ASV) inference. Taxonomic classification was performed using the SILVA reference database, followed by diversity analyses (ASV richness, Shannon diversity, beta diversity), taxonomic profiling, differential abundance analysis, and assessments of Levin's niche breadth. Statistical analyses, including linear mixed models (LMMs), PERMANOVA, and differential abundance testing (DESeq2), were applied to assess the impact of host species identity, growing degree days (GDD), and individual plant factors on the leaf microbiome. Figure made using: https://biorender.com.

Chapter 2
Growing degree days shape host-specific leaf bacterial community dynamics and thermal niche strategies in two functionally similar temperate tree species*

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1.0 INTRODUCTION

The phyllosphere—the total aboveground surface of plants—hosts a vast and dynamic assemblage of microorganisms that influence plant function, fitness, and ecosystem processes (Chaudhry et al. 2021; Vorholt 2012). Among these, leaf-associated bacteria play a central role in nutrient cycling, atmospheric interactions, and protection against pathogens, making them critical ecological actors (Kembel et al. 2014; Compant et al. 2019). Although the diversity and structure of phyllosphere microbiomes vary within and between host species, they often exhibit stable core assemblages shaped by their host species, environmental conditions, and spatiotemporal processes (Grady et al. 2019; Kembel et al. 2014). Yet, the mechanisms governing the seasonal assembly and turnover of these communities remain incompletely understood, particularly with respect to temperature-mediated processes and their interplay with host phenology (i.e., the seasonal timing of plant processes and development).

In temperate ecosystems, the timing of plant growth and development (i.e., phenology) unfolds gradually and sequentially through the growing season, strongly directed by the accumulation of heat units (McMaster and Wilhelm 1997; Prentice et al. 1992). Since phenology follows temperature-driven schedules, growing degree days (GDDs) are a well-established, biologically meaningful metric that captures this progression by quantifying the accumulation of daily thermal energy above a species- or process-specific baseline temperature, below which development is assumed negligible (McMaster and Wilhelm 1997; Prentice et al. 1992). Widely used in agronomy and ecological modeling, GDDs have proven particularly valuable in predicting the pace of plant maturity, regardless of annual temperature fluctuations. Thus, GDDs serve as a standardized physiological clock that often tracks phenology more reliably than Julian date and enable high-resolution comparisons across years, individuals, and ecosystems. Indeed,

206 microbial taxa with distinct thermal preferences or phenological associations may exhibit
207 seasonal turnover along the GDD continuum, paralleling classical theories of trait-based
208 environmental filtering and niche partitioning, with thermal accumulation acting as a seasonal
209 environmental filter that constrains bacterial persistence, recruitment, and turnover in the leaf
210 phyllosphere and endosphere (Weiher et al. 1998; Chase and Leibold 2003).

211 While recent studies have begun to infer plant microbial responses to temperature from
212 experimental warming (Faticov et al. 2021), elevational gradients (Huang et al. 2023; Wang et al.
213 2023), mean annual temperature, and continental-scale climate gradients (Sangiorgio et al. 2024),
214 these studies mainly focus on the rhizosphere and/or fungi; moreover, these approaches can
215 obscure fine-scale seasonal ecological dynamics and conflate temperature effects with other
216 climate variables or long-range microbial dispersal. In contrast, this study examines thermal
217 accumulation under shared environmental conditions *in situ*, allowing clearer attribution of
218 microbial responses to thermal-time dynamics in natural forest ecosystems. GDDs offer a
219 continuous metric that integrates temperature-regulated host phenology with the ecological
220 context in which leaf microbiomes assemble and shift temporally. Additionally, while host
221 species identity is widely acknowledged as a dominant—if not the primary—factor shaping the
222 leaf microbiome (Laforest-Lapointe et al. 2016a,b; Lajoie and Kembel 2021), its role relative to
223 seasonal thermal accumulation, and how these effects interact, remains underexplored, especially
224 within functionally similar host groups.

225 To address these gaps, we investigated how temperature accumulation, expressed as
226 GDDs, influences the diversity, composition, and ecological structure of bacterial communities
227 inhabiting the leaf phyllosphere and endosphere of two temperate tree species: Grey birch
228 (*Betula populifolia* Marshall; Betulaceae, Fagales) and trembling aspen (*Populus tremuloides*

Michx.; Salicaceae, Malpighiales). Belonging to different orders, these Rosids are functionally similar (fast-growing, early-successional, deciduous broadleaf species), yet phylogenetically distant, enabling us to assess microbial responses within a shared environment while providing a unique opportunity to disentangle host functional similarity from phylogenetic relatedness in microbiome responses. By sampling host leaves from naturally co-occurring trees growing in the same forest site in Québec at seven points along the seasonal GDD gradient, we minimized environmental confounders and isolated the effects of cumulative thermal-time (GDDs), host species identity, and their two-way interaction. My primary objective is to describe general patterns of seasonal phenological variation in leaf bacterial phyllosphere and endosphere microbiomes of grey birch and trembling aspen across a gradient of GDD accumulation. Specifically, I seek to address the following research questions:

1. Do the microbiomes of two functionally similar but phylogenetically distinct host tree species—birch and aspen—respond similarly or divergently to GDD accumulation?
2. How does thermal timing (GDD accumulation) structure the diversity and composition of leaf bacterial communities across host seasonal phenology?
3. Do bacterial communities exhibit thermal niche differentiation over time, and how do patterns of generalism and specialization vary within and between host species?

I hypothesized that (1) host species identity is the primary driver of leaf microbial community turnover, shaping presence, abundance, and diversity; (2) despite shared functional type, grey birch and trembling aspen will host distinct microbiomes with divergent temperature-driven seasonal dynamics, but that there will be a lesser degree of interspecific variation compared to other studies due to functional similarity; (3) GDD accumulation will have a significant indirect impact on shaping leaf microbial dynamics through the interaction between

host biotic attributes (i.e., host identity) and thermally-regulated phenology, reflecting species-specific interactions with GDD accumulation; and (4) bacterial taxa and ASVs will exhibit thermal niche differentiation along the GDD gradient, with each species hosting leaf microbiomes that exhibit distinct ecological strategies.

By focusing on continuous thermal accumulation as both a proxy for phenology and an ecological gradient in its own right, this study advances understanding of plant-microbe interactions in temperate forests. This study extends phenological modeling into the microbial domain, where cumulative temperature not only influences host phenology but also drives microbiome diversity, structure, and potential ecological consequences. Furthermore, this work offers novel insights into how microbiomes respond to seasonal thermal dynamics and underscores the importance of integrating microbial ecology with climate-sensitive phenological frameworks in a rapidly warming world. In doing so, we explore the potential of leaf microbiomes to act as biosensors of active heat accumulation related to host phenological change, revealing possible unrealized applications of the GDD index to microbial ecology.

2.0 MATERIALS AND METHODS

All data processing and statistical analyses were performed using R v.2024.09.0 (R Core Team 2024). An $\alpha = 0.05$ was used as the significance threshold.

2.1 Host Leaf Sampling and Estimating Seasonal Phenology (Growing Degree Days)—To assess the leaf bacteriome over host phenology, 36 leaf disk samples of trembling aspen (*Populus tremuloides* Michx., Salicaceae, Malpighiales) and 35 leaf samples of grey birch (*Betula populifolia* Marshall, Betulaceae, Fagales) were provided by my collaborators at the Canadian Airborne Biodiversity Observatory (CABO), found at https://www.caboscience.org

and at the Université de Montréal. Alongside the samples, sample data were also provided by my CABO colleagues (Kothari et al. 2023). Upon receipt, all leaf disk samples were stored in a -80°C freezer. These leaf disks were collected along a six-month chronosequence spanning the months of June 2018 to October 2018; roughly, specimens were sampled biweekly (Table 1). For each sample, a large group of sunlit leaves (>3 h estimated sun exposure per day) were collected at the same vertical position; for each tree, the same branch or neighboring branches from the same individual were sampled. Leaves with noticeable damage were avoided.

Table 2.1. Cumulative growing degree days (GDDs) at a base temperature of 5°C and their corresponding sampling dates classified into generalized phenological periods for temperate trees in the Northern Hemisphere.

Cumulative Growing Degree Days (T_{base} = 5°C)	Sampling Date	General Phenological Period
437	June 8, 2018	Early-Mid
605	June 21, 2018	Early-Mid
1087	July 19, 2018	Mid
1606	August 16, 2018	Mid-Late
1992	September 11, 2018	Late
2140	September 24, 2018	Late
2219	October 8, 2018	Late-Early Senescence

Since this study seeks to evaluate phenology as a continuous response variable that encompasses both thermal and temporal dimensions, sampling dates were converted to cumulative growing degree days (GDDs) using 2018 temperature data from the Montréal/Saint-Hubert weather station in Québec. To calculate cumulative GDDs at a base temperature of 5°C from the first day of the year (j = 1) to a given sampling day of the year (DOY) i, the following equation was employed, as described by McMaster and Wilhelm (1997):

$$Cumulative\ GDD\ on\ DOY\ i = \sum_{j=1}^{i}\left[\frac{\left(T_{max,j} + T_{min,j}\right)}{2}\right] - T_{base}$$

Where $T_{max,j}$ is the temperature maxima on sampling day j, $T_{min,j}$ is the temperature minima on sampling day j, and T_{base} is the chosen base temperature of 5°C. Thus, GDDs 437, 605, 1087, 1606, 1992, 2140, and 2219 represent the cumulative GDD sampling points along the continuum of host phenology (Table 1). For each of the two host species, five individual plants were sampled at each of the seven GDDs (N = 10), with the exception of an inadvertently repeated sample taken from the same aspen individual at GDD = 1087, resulting in N = 11 (Kothari et al. 2023). The additional aspen sample was retained to avoid omitting potentially valuable microbiome data, resulting in a total sample size of n = 71 samples, with 35 samples for birch and 36 samples for aspen. Each individual serves as a biological replicate, and the same individuals are resampled at each GDD point, providing temporal resolution across the seven GDD points.

***2.2 DNA Extraction*—**To isolate microbial DNA from leaf disks, the Qiagen DNeasy® PowerLyzer® PowerSoil® kit was used according to the manufacturer's instructions, with some procedural adjustments. Although the extraction protocol calls for up to 0.25 g of sample, only 20 mg of leaf tissue was used due to limited leaf material. To account for microbial "kitome" effects exerted by the three DNA extraction kits used, a negative control was performed; additionally, there were two positive controls prepared using the ZymoBIOMICS™ Microbial Community Standard (Catalog No. D6300, Zymo Research Corp., Irvine, CA, USA).

***2.3 Amplification and Sequencing of 16S rRNA Gene*—**To conduct microbiome profiling, PCR amplification and sequencing targeted the V3-V4 hypervariable regions of the bacterial 16S rRNA gene. All PCRs and sequencing were conducted at the Genome Québec Innovation Centre. To amplify 16S rRNA regions, the Illumina primer pair 520F

(AGCAGCCGCGGTAAT)/799R2 (CAGGGTATCTAATCCTGTT) was used to exclude chloroplast sequences, targeting an amplicon length of approximately 280 bp (Edwards et al. 2007). All primers were fitted with adapter sequences for multiplex sequencing. Extracted DNA was organized and submitted on the Genome Québec Innovation Centre's sequencing submission portal, Nanuq. Sequencing libraries were constructed with this DNA using paired-end reads on the Illumina MiSeq platform (Moroenyane et al. 2021a; Moroenyane et al. 2021b; Zhou et al. 2011).

2.4 Sequence Quality Control, Filtering, and Taxonomic Assignment of ASVs—Reads were processed using the *DADA2* pipeline in R (Callahan et al. 2016; Lajoie and Kembel 2021; R Core Team 2024). Next, an amplicon sequence variant (ASV) table was generated from the merged sequences. Chimeric sequences were identified and removed using the 'removeBimeraDenovo()' function, which reconstructs chimeras from segments of abundant parent sequences (Callahan et al. 2017). In this dataset, approximately 97.74% of sequences were non-chimeric. Reads identified as mitochondria and chloroplasts were removed, and samples from GDD 323 were excluded due to missing data for *P. tremuloides*. Altogether, these adjustments reduced the total number of reads to 133015 and resulted in 1731 ASVs.

2.5 Statistical Analyses—All statistical analyses were conducted using R v.2024.09.0 (R Core Team, 2024). The bacterial ASV abundance data were normalized such that the summed relative abundance of all ASVs of each sample was equal to one. All analyses were repeated to assess both interspecific and intraspecific variation in host tree microbiomes, with specific adjustments that will be described in the following sections.

2.5.1 Bacterial Alpha Diversity Patterns—**Sampling Effort and ASV Diversity:** ASV accumulation curves were generated for all samples and for the positive control using the 'specaccum()' function from the *vegan* package to determine if the sampling effort was sufficient to recover the majority of ASV diversity (Oksanen et al. 2022; Moroenyane et al. 2021a; Moroenyane et al. 2021b). In this study, the curve asymptotes in both cases, indicating that the sampling effort captured the majority of detectable ASV diversity (Supplementary Fig. S1). To evaluate the estimated richness and occurrence of both abundant and rare taxa, Preston log-normal curves were generated using the 'prestondistr()' function in *vegan*. The observed data fitted well to the normal distribution, suggesting a high probability that both abundant and rare ASVs were captured in this study (Supplementary Fig. S2).

Alpha Diversity Calculations: From the *vegan* package, ASV richness (the total number of unique ASVs per sample) was calculated using the 'specnumber()' function, and Shannon diversity was calculated using the 'diversity()' function with the index parameter set to "shannon" (Oksanen et al. 2022; Moroenyane et al. 2021a; Moroenyane et al. 2021b). To visualize diversity patterns, raw data for both metrics were plotted as a function of GDD accumulation at T_{base} = 5°C and their associated months for both host species.

Alpha Diversity Modelling and Statistical Analysis: To evaluate the effects of accumulated thermal energy (GDDs), host identity, and their interaction on bacterial alpha diversity, ASV richness and Shannon diversity were modeled using linear mixed models (LMMs) using the 'lmer()' function from *lme4* (Bates et al. 2015). Separate models were fit for inter- and intraspecific comparisons according to model assumptions and diagnostics. For interspecific models, ASV richness was log-transformed, and Shannon diversity was square-root transformed. Fixed effects included host species identity, GDDs (T_{base} = 5°C), and their interaction, with

357 'Plant_ID' included as a random effect to account for repeated measures. Intraspecific models
358 were constructed separately for each host species, with appropriate transformations applied to
359 meet model assumptions (Supplemental Methods S2.5.1). To assess post-hoc contrasts, estimated
360 marginal means were generated using the *emmeans* package, and both marginal (R^2_m) and
361 conditional (R^2_c) R^2 values were calculated to quantify explanatory power of the models and
362 fixed effects (Lenth 2024). Final model structures, full model diagnostics, pairwise comparisons,
363 and methodological details are presented in the *Supplementary Methods*.

364 ***2.5.2 Bacterial Community Structure (Beta Diversity)—*** To assess beta diversity, a
365 Bray-Curtis dissimilarity matrix was generated using 'vegdist()' in *vegan*, and principal
366 coordinate analysis (PCoA) was conducted using 'pcoa()' from *ape* to visualize inter- and
367 intraspecific differences in leaf bacterial communities along a GDD accumulation gradient
368 (Moroenyane et al. 2021a; Oksanen et al. 2022; Paradis and Schliep 2019). Multivariate
369 dispersion was evaluated using 'betadisper()' followed by 'permutest()', employing ANOVA
370 with 999 permutations (Moroenyane et al. 2021a; Oksanen et al. 2022). Next, post-hoc pairwise
371 comparisons of all variable groupings were assessed via 'TukeyHSD()' (R Core Team 2024).
372 Finally, the 95% confidence intervals for the Tukey HSD results of each variable grouping were
373 plotted (Moroenyane et al. 2021a). For interspecific comparisons, groupings included host
374 'Species', 'GDD_5C', and their two-way interaction. For intraspecific comparisons, groupings
375 included 'GDD_5C' and 'Plant_ID'. These steps evaluated whether significant differences in
376 beta diversity detected in subsequent PERMANOVA analyses could be influenced by unequal
377 within-group variability.

378 To determine the drivers of variation in community composition and quantify their
379 explanatory power, PERMANOVA was performed with 999 permutations using the 'adonis2()'

function in *vegan*, to model the effects of host species ('Species'), cumulative growing degree days at a base temperature of 5°C ('GDD_5C'), and their two-way interaction on leaf bacterial community composition and turnover (Faticov et al. 2021; Moroenyane et al. 2021a; Oksanen et al. 2022). For intraspecific comparisons, the same method was applied, but PERMANOVA was used to model the effects of 'GDD_5C', 'Plant_ID', and their two-way interaction on leaf bacterial community composition. All models here were run using absolute ASV count data.

2.5.3 Relative Abundance and Taxonomic Profiles—Using the 'tax_glom()' and 'transform_sample_counts()' functions from the *phyloseq* package in R, the relative abundances of leaf bacterial taxa were calculated and then plotted at the phylum and genus levels for birch and aspen across GDDs to evaluate and compare general phenological patterns in taxonomic shifts within and between host species (McMurdie and Holmes 2013). All recovered bacterial phyla were presented, but only the top 20 genera by relative abundance were visualized, as the large number of genera—particularly those with lower abundances—made comprehensive visualization impractical. Relative abundances were calculated within each sample by dividing ASV counts by the sample's total read count, yielding proportions that sum to 1. This transformation standardizes for sequencing depth while preserving sample-specific community composition. Taxonomic profiles of leaf bacterial relative abundances were generated as a preliminary analysis to evaluate general phenological patterns in taxonomic shifts and identify dominant bacterial taxa associated with each host tree species and phenological stage.

2.5.4 Differential Abundance Analysis—To assess how leaf bacterial ASVs (and their associated taxonomic assignments) responded to seasonal GDD accumulation, differential abundance analysis was performed using the *DESeq2* package in conjunction with the *phyloseq* package (Faticov et al. 2021; Love et al. 2014; McMurdie and Holmes 2013). Analyses were

conducted separately for each host species (grey birch and trembling aspen) to identify ASVs whose relative abundance changed significantly across the seasonal gradient of thermal accumulation, measured as continuous GDDs. Starting with the filtered *phyloseq* object, the abundance data was converted into a *DESeq2* object using the 'phyloseq_to_deseq2()' function. For each species, the model formula "~ GDD_5C" was used, treating GDD as a continuous numeric predictor. This allowed testing for log2 fold changes in ASV abundance per unit increase in cumulative GDD, effectively modeling temperature-driven phenological progression without discretizing the thermal gradient. Size factors were estimated internally using *DESeq2*'s default method, which applies median-of-ratios normalization to account for library size differences. Dispersion estimates and shrinkage of log2 fold changes were calculated using the default *DESeq2* pipeline. *P*-values were adjusted for multiple testing using the Benjamini–Hochberg false discovery rate (FDR) method (Faticov et al. 2021; Love et al. 2014). ASVs were considered significantly differentially abundant across GDD when FDR-adjusted $p < 0.05$.

To facilitate ecological interpretation, we annotated differentially abundant ASVs to the genus level and visualized patterns of log2 fold change across the GDD gradient. Positive log2 fold changes indicate increased abundance with thermal accumulation, while negative values denote declines with increased heat accumulation. This approach enabled us to identify thermally limited taxa within each host species and relate their seasonal enrichment or depletion to broader patterns of microbial succession and niche differentiation. For species-specific seasonal differential abundance analyses, please see *S2.5.4 Differential Abundance Analysis* in the Supplemental Materials and Methods.

***2.5.5 Niche Width Analysis*—**To assess bacterial thermal niche breadth across GDD accumulation, Levins' niche width index was calculated for each ASV using the 'niche.width()'

function from the *spaa* package in R. Input data consisted of scaled relative abundances of ASVs across continuous GDD values to standardize across sequencing depth, summed within each unique GDD value, thus capturing microbial distribution across thermal time. This formulation incorporates both the presence and evenness of an ASV's abundance across thermal conditions. Notably, ASVs were retained only if they exhibited non-zero relative abundance across at least two distinct GDD values, to avoid inflating niche width estimates with single-point occurrences. To classify ecological strategies, we applied fixed thresholds: ASVs with niche width ≤ 1.5 were designated thermal specialists, those with ≥ 2.25 as generalists, and those in between as intermediate. These thresholds were selected to reflect strongly concentrated distributions (≥2 GDDs) versus moderate-to-even distributions across ≥3 GDDs, while excluding transient or ambiguously distributed taxa.

Distribution of ASV niche breadth were visualized using histograms and proportional bar plots of specialist, intermediate, and generalist classifications. Classification distributions were also compared between host species using faceted bar plots. To assess temporal patterns, we generated boxplots of ASV niche width across cumulative GDD values, subset by host species. To evaluate taxonomic variation, we plotted niche width by bacterial genus (focal genera only) and by individual ASV. Total ASV proportion plots (Supplementary Fig. S23) and violin plots of ASV niche widths by host species (Supplementary Fig. S24) were additionally produced and included to illustrate distributional spread. Differences in niche width distributions between host species were tested using Wilcoxon rank-sum tests.

3.0 RESULTS

Across the 2018 growing season, the growing degree day (GDD; T_{base} = 5°C) accumulation curve increased in a sigmoidal fashion, with the highest rates observed during mid-phenology—occurring between mid-July and the end of August. This pattern of GDD accumulation offers a cumulative measure of thermal exposure and seasonal progression for both host species (Fig. 2.1). Sampling dates spanned a cumulative GDD range of 437 to 2219, capturing early leaf expansion through senescence. This GDD trajectory served as the primary ecological axis for analyzing temporal shifts in microbial diversity, community composition, and thermal niche breadth.

The amplicon sequence variant (ASV) accumulation curve reveals that sampling recovered a considerable number of bacterial ASVs, and its asymptote demonstrates saturation or near-saturation, indicating that sampling effort was comprehensive enough (Supplementary Fig. S1). Additionally, the Preston log-normal curve is bell-shaped and exhibits practically perfect overlap with the expected normal distribution; this communicates that sequencing was deep enough to detect rare and low-abundance bacterial taxa (Supplementary Fig. S2). Taken together, these figures demonstrate that sampling effort not only recovered the most abundant taxa but also rare taxa, permitting a more complete insight into the leaf bacterial communities (Moroenyane et al. 2021a).

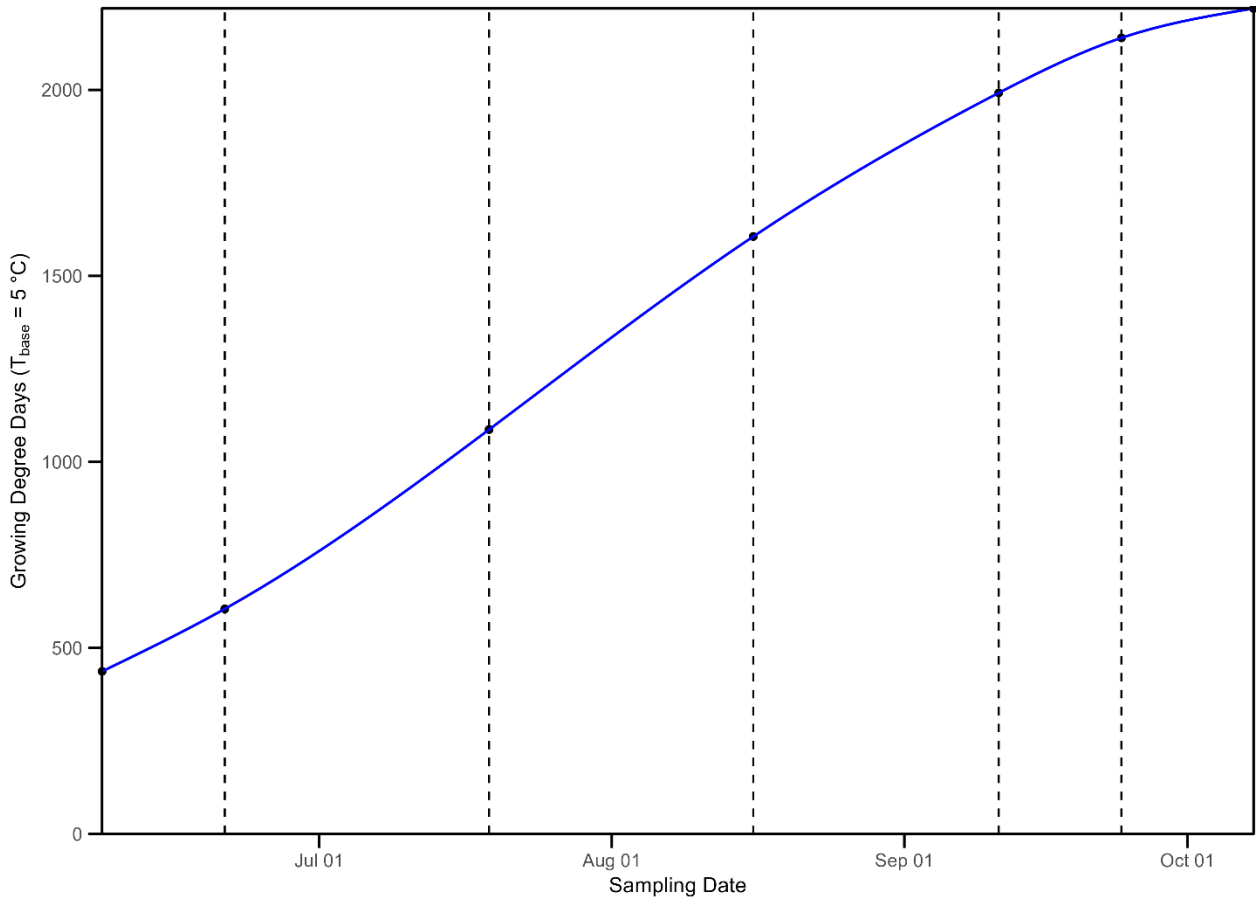

Figure 2.1. Cumulative growing degree days (GDDs; T_{base} = 5°C) across the 2018 growing season at the study site in Québec. Cumulative GDDs were calculated as the daily mean temperature minus the 5°C base threshold, summed across all days with positive values. Vertical dashed lines represent leaf sampling dates. This curve reflects the seasonal progression of thermal energy accumulation—a physiologically relevant metric for predicting plant phenology and a key environmental driver of microbiome dynamics in this study.

3.1 Seasonal GDD accumulation drives bacterial richness more than species identity and shapes community composition in functionally similar hosts—Alpha diversity patterns revealed distinct species-specific trajectories over phenology (Fig. 2.2A). Trembling aspen consistently exhibited higher Shannon diversity than grey birch, regardless of GDD (P = 0.0413), suggesting stable and more even microbial communities in aspen across the season. In contrast, ASV richness was more dynamic and sensitive to GDD accumulation, particularly in birch. Linear mixed models showed significant effects of host species (P = 0.0086), GDD (P = 0.0004), and their interaction (P = 0.0053) on ASV richness (Table 2.2). Notably, the interaction (Species

x GDD) explained ~32.6% of the variance via fixed effects (R^2_c = 0.326) and ~9.94% (R^2_m = 0.0994) when accounting for plant-level random effects. While aspen maintained relative overall stability across GDDs with modest seasonal variation, birch exhibited a general increase in richness. However, this pattern was not strictly linear or monotonic: richness rose early, dipped at mid-season, and rebounded in late phenology, suggesting a multi-phase or non-linear response (Fig. 2.2A; Supplementary Fig. S3A). Post-hoc pairwise comparisons at specific GDDs (Supplementary Table S1) found no significant interspecific differences, suggesting the interaction reflects cumulative patterns rather than sharp divergence at individual time points.

While host species explained the most variance in Shannon diversity (R^2_c = 34.1%; R^2_m = 26.1%), highlighting its role in shaping microbial evenness, it contributed minimally to ASV richness (R^2_c = 14.4%; R^2_m = 1.33%), where cumulative GDDs played a larger role (R^2_c = 19.2%; R^2_m = 6.17%). This suggests host species differences influence evenness and relative abundance more strongly, while environmental factors like cumulative GDDs shape the total number of unique ASVs present; in fact, its influence on ASV richness diminishes beyond early-mid phenology (GDD 605), shifting to host-specific interactions with environmental variables (Table 2.3).

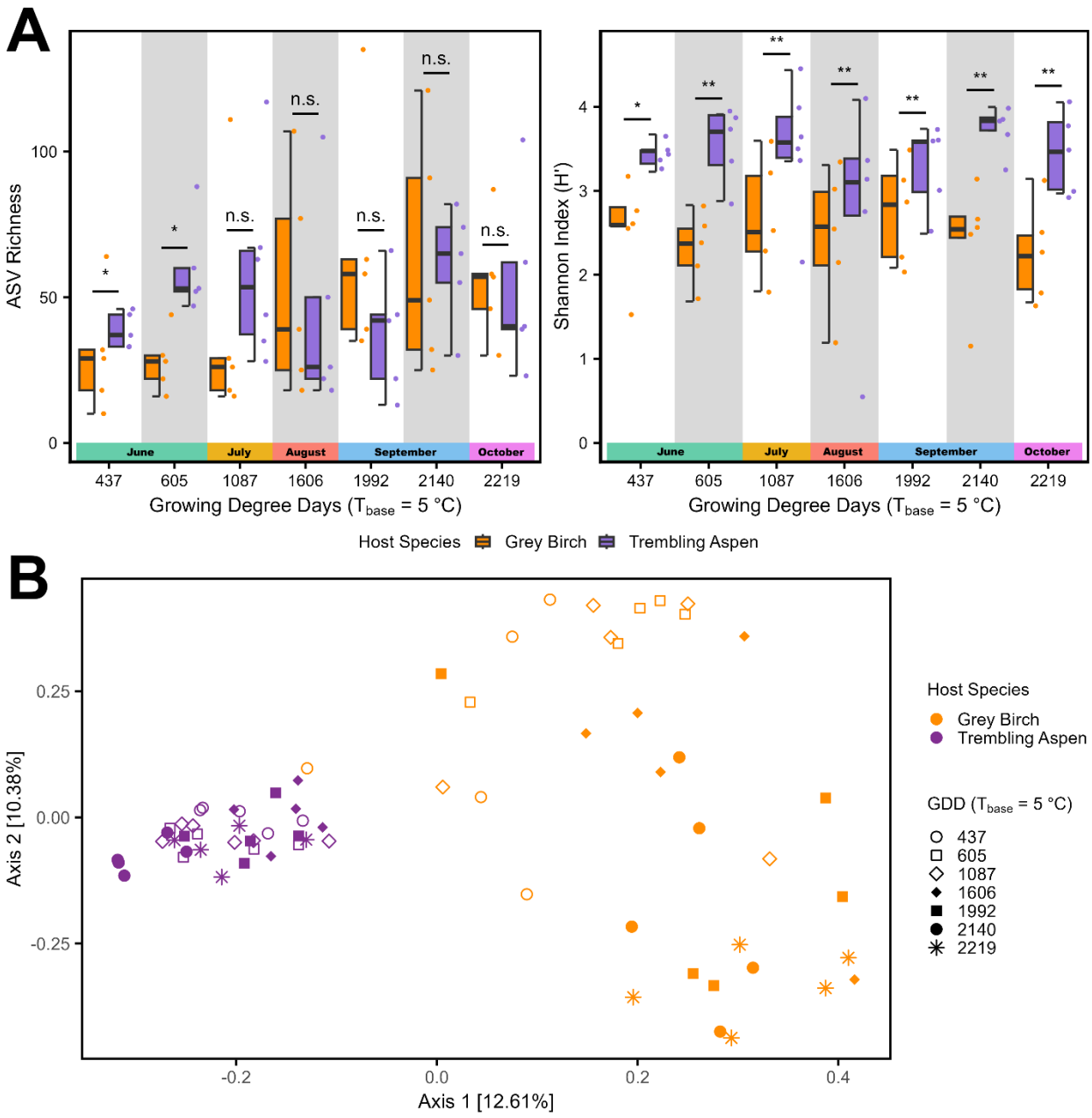

Figure 2.2. Leaf bacterial community diversity and composition patterns of two host tree species, grey birch (purple) and trembling aspen (orange), across a season phenological gradient of GDD accumulation (June–October 2018) using 16S rRNA gene amplicon sequencing showing **(A)** comparisons of amplicon sequence variant (ASV) richness (left) and Shannon diversity (right). Bold horizontal bars represent the median and the error bars indicate a measure of variability of the data at each GDD sampling value. Circular data points represent individual samples of birch and aspen leaves taken at each sampling point along the GDD continuum (total n = 71), which are horizontally jittered to avoid overlap. n.s. = non-significant host species differences (*P*-value ∗<0.05 and ∗∗<0.01); and **(B)** Principal Coordinate Analysis (PCoA) of leaf bacterial community beta diversity based on Bray-Curtis dissimilarities. Each data point denotes a host plant individual sampled at GDDs 437 (empty circle), 605 (empty square), 1087 (empty diamond), 1606 (filled diamond), 1992 (filled square), 2140 (filled circle), and 2219 (asterisk).

Table 2.2. Summary of the impact of host species identity (S), GDD accumulation at T_{base} = 5°C (GDD_5C), and their interaction (S x GDD_5C) on the leaf bacterial alpha diversities of grey birch and trembling aspen using linear mixed modeling (LMMs).[a]

	Host Species (S)			Growing Degree Days 5°C (GDD_5C)			Interaction (S x GDD_5C)		
	P	R^2_c	R^2_m	***P***	R^2_c	R^2_m	***P***	R^2_c	R^2_m
Interspecific[b]									
ASV R'	0.00855**	0.144	0.0133	0.000364***	0.192	0.0617	0.00531**	0.326	0.0994
H'	0.0413*	0.341	0.261	0.881	0.34	0.000551	0.978	0.262	0.159
Birch[c]									
ASV R'	—	—	—	0.000247***	0.513	0.25	—	—	—
H'	—	—	—	0.731	0.163	0.00297	—	—	—
Aspen[d]									
ASV R'	—	—	—	0.427	0.113	0.0164	—	—	—
H'	—	—	—	0.857	0.0374	0.000908	—	—	—

[a] Three separate LMMs were run for interspecific comparisons, intraspecific comparisons within each host species. Conditional-R^2 (R^2_c) and marginal-R^2 (R^2_m) values were calculated using r.squaredGLMM() in the *MuMIn* package (Bartoń 2023) by running separate models with the same random effect structure but only a single fixed effect included (*P*-value ∗<0.05, ∗∗<0.01 and ∗∗∗<0.001).
[b] Interspecific (between-species) results from LMMs for log-transformed ASV richness (ASV R') and square-root transformed Shannon diversity (H') comparing leaf microbiomes of grey birch and trembling aspen.
[c] Intraspecific (within-species) results from LMMs for ASV richness (ASV R') and Shannon diversity (H') in grey birch leaf microbiomes, which have both undergone reciprocal transformations.
[d] Intraspecific (within-species) results from LMMs for reciprocally-transformed ASV richness (ASV R') and square-root transformed Shannon diversity (H') in trembling aspen leaf microbiomes.

Intraspecific analyses further reinforced that the ASV richness of birch microbiomes significantly increased with GDD (P = 0.00025), explaining over 50% of variance when plant-level random effects were included (R^2_c = 0.513) and 25% of the variance through fixed effects (R^2_m = 0.25). However, richness did not differ significantly across individual GDD time points (Supplementary Table S2), suggesting a continuous overall trend rather than discrete shifts. Within aspen, neither richness nor Shannon diversity varied significantly with GDD. Moreover, no significant plant-level effects were observed within species across any GDD (Supplementary Tables S6–S7), indicating that environmental gradients, particularly temperature accumulation, exert more influence over alpha diversity patterns than individual plant identity. Collectively,

these results highlight that functionally similar hosts exhibit divergent alpha diversity responses over phenology.

Table 2.3. Summary of pairwise comparisons of host species-specific differences in leaf bacterial alpha diversity at each GDD sampling point (Tbase = 5°C) using the emmeans package in R to evaluate the effect of host species identity (S) as seasonal phenology progresses.[a]

GDD_5C	ASV Richness[b]				Shannon Diversity[c]			
	Host Species (S)				Host Species (S)			
	emmean	*SE*	*t-ratio*	*P*	emmean	*SE*	*t-ratio*	*P*
437	-0.6399	0.257	-2.489	0.0198*	-0.263	0.101	-2.602	0.0139*
605	-0.5553	0.238	-2.333	0.0305*	-0.263	0.0924	-2.851	0.0088**
1087	-0.3126	0.198	-1.578	0.146	-0.263	0.0732	-3.596	0.0046**
1606	-0.0513	0.191	-0.269	0.795	-0.263	0.0696	-3.782	0.0048**
1992	0.1431	0.212	0.675	0.512	-0.263	0.08	-3.288	0.0051**
2140	0.2176	0.225	0.967	0.348	-0.263	0.0863	-3.05	0.0065**
2219	0.2574	0.233	1.105	0.284	-0.263	0.09	-2.924	0.0078**

[a] Pairwise comparisons only show host species effects, independent of any interaction with GDD, since comparisons were isolated to each GDD sampling point, taking the original LMM structures into account. The table shows the estimated marginal means (emmean), standard error (*SE*), *t-ratio*, and *P-values* for each GDD sampling point (*P*-value $*<0.05$, $**<0.01$, and $***<0.001$).

[b] ASV richness (R') was log-transformed to align with interspecific LMM assumptions. While host species identity may significantly affect ASV R' at earlier GDDs, other seasonal factors may play a larger role in shaping interspecific variation in ASV richness beyond earlier-season, lower GDDs.

[c] Shannon diversity (H') was square-root transformed to align with interspecific LMM assumptions. H' is heavily impacted by host species identity at all points in the growing season, implying it is a strong predictor of interspecific variation in H'.

To compare seasonal phenological patterns of leaf bacterial beta diversity and community structure between birch and aspen across the GDD gradient, a Bray-Curtis dissimilarity matrix was generated. Initial analyses of homogeneity and multivariate dispersion helped determine the relative influence of between-community composition (variance among samples) and within-community composition (variance within replicates) on the overall structure of leaf bacterial communities (Moroenyane et al. 2021a). There was significant multivariate dispersion between host species (Supplementary Figs. S4–S5). Between birch and aspen, heterogeneous dispersion was significant ($F = 22.812$, $P = 0.001$) for host species identity, but little multivariate dispersion

was observed across GDDs (Supplementary Figs. S6–S7). Neither species exhibited significant heterogeneous dispersion across GDDs ($F = 0.242$, $P = 0.948$), and pairwise comparisons using Tukey HSD tests confirmed non-significant differences in community structure between GDDs. Thus, despite variations in data spread, central tendencies (means) remained similar.

Finally, the interaction between host species and GDDs was assessed, revealing increased multivariate dispersion compared to any individual variable alone (Supplementary Fig. S8). This interaction showed significant heterogeneity in dispersion ($F = 4.724$, $P = 0.001$). However, as this interaction compares all possible combinations of 'Species' and 'GDD_5C', including across dissimilar levels of GDDs, caution is warranted in interpreting these results. This interaction may not exclusively reflect variations within the same GDD levels, which was the primary focus of this analysis. Thus, for biological relevance, pairwise comparisons of dispersion using a Tukey HSD test were only assessed for species-GDD interactions occurring within shared GDDs, but not across differing GDDs. The Tukey HSD revealed relevant significant differences between birch leaf interactions with 605 GDDs and aspen leaf interactions with 605 GDDs (early phenology; $P = 0.023$), as well as between birch's interaction with 2219 GDDs and aspen's interaction with 2219 GDDs (senescence onset; $P = 0.0021$).

Principal Coordinate Analysis (PCoA) was performed using Bray-Curtis dissimilarity to visualize changes in leaf bacterial community structure between grey birch and trembling aspen across phenology (Fig. 2.2B). PERMANOVA found significant effects from host species identity ($F = 9.061$, $P = 0.001$), accumulated GDDs ($F = 3.384$, $P = 0.001$), and their interaction ($F = 3.022$, $P = 0.001$) on bacterial community variation (Table 2.4). Host species identity explained ~11% of the variation ($R^2 = 0.11$), GDDs ~4.1% ($R^2 = 0.041$), and the interaction ~3.67% ($R^2 =$

0.0367). The PCoA presents clear separation of bacterial communities based on host species identity, mostly along Axis 2, though there was no clear separation based on GDDs between species (Fig. 2.2B). A weak positive correlation was observed between Axis 1 and GDDs (Spearman's $\rho = 0.108$, $P = 0.368$), indicating no significant association between Axis 1 and GDDs. In contrast, Axis 2 showed a moderate negative correlation with GDDs ($\rho = -0.53$, $P = 2.25 \times 10^{-6}$), suggesting that increasing GDD values are significantly associated with lower Axis 2 scores. Therefore, the directionality in the PCoA from early-phenology (low GDDs) to late-phenology (high GDDs) is likely associated with Axis 2, which shows a statistically significant seasonal thermal gradient.

Table 2.4. Permutational analysis of variance (PERMANOVA) testing the impact of host species identity ('Species'), GDD accumulation at T_{base} = 5°C ('GDD_5C') as a proxy for host phenology, and their two-way interaction ('Species x GDD_5C') on differences in leaf beta diversity and bacterial community composition within and between grey birch and trembling aspen.

Source of Variation	*SS*	R^2	*F*	*P*
Species	3.3513	0.11	9.061	0.001***
GDD_5C	1.2516	0.041	3.384	0.001***
Species x GDD_5C	1.1178	0.0367	3.022	0.001***
Residuals	24.7794	0.812	—	—

[a] Asterisks indicate *P*-values ∗<0.05, ∗∗<0.01 and ∗∗∗<0.001.

Within each species, we tested whether bacterial community composition changed across GDDs. In grey birch, PERMANOVA showed that GDDs significantly shaped community composition ($F = 6.024$, P = 0.01, $R^2 = 0.149$), while trembling aspen showed a weaker but significant GDD effect ($F = 1.288$, P = 0.023, $R^2 = 0.037$). However, within-species PCoAs revealed limited visual separation across phenology, except for weak directional shifts along Axis 1 in both species (Spearman's $\rho = -0.715$ in birch; $\rho = -0.337$ in aspen). Analyses of multivariate dispersion (betadisper) indicated subtle shifts in variability, with late-season

dispersion changes in aspen ($F = 4.005$, $P = 0.004$) and marginal variation in birch ($F = 2.512$, $P = 0.048$), but no consistent or strongly significant dispersion patterns across most GDDs or Plant_IDs. Full dispersion and plant-level PERMANOVA results are presented in Supplementary Results (S3.1) and Supplementary Table S5.

In this study, both grey birch and trembling aspen exhibit significant associations between GDDs and Axis 1 when examined intraspecifically, indicating a clear relationship between community composition and GDDs within each species. However, when compared interspecifically, the relationship shifts, with GDDs associating significantly with Axis 2 instead. This phenomenon can be attributed to the interaction between species and GDDs, as highlighted by the significant 'Species:GDD_5C' term in the PERMANOVA analysis (Table 2.4).

3.2 Specific taxa were enriched in the leaf microbiomes of birch and aspen as GDDs accumulated across phenology—Across the seasonal GDD gradient, leaf bacterial communities of grey birch and trembling aspen were dominated by Proteobacteria but exhibited distinct taxonomic and temporal patterns (Fig. 2.3A; Supplementary Fig. S19). In birch, Proteobacteria steadily increased from ~52% relative abundance at 437 GDDs to a peak of ~87.5% at 2140 GDDs, coinciding with a marked decline in Actinobacteria from ~30% to ~3.5%. In contrast, aspen exhibited fluctuating Proteobacteria levels, peaking early and late in the season (~50% relative abundance) but dipping mid-season (~30% at 1606 GDDs), while Actinobacteria remained relatively stable (~25–35%).

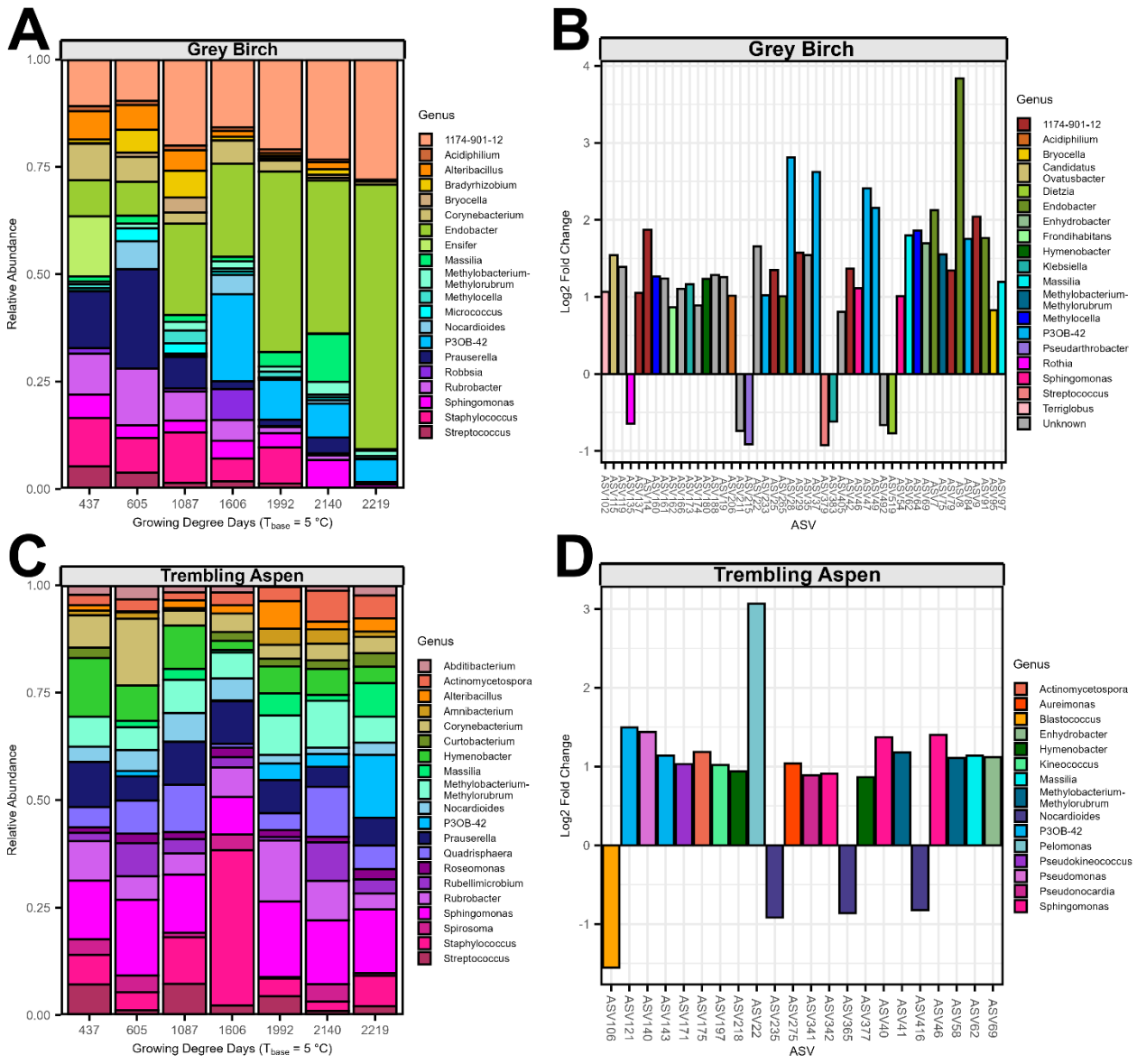

Figure 2.3. Taxonomic composition and differential abundance of leaf bacterial communities of grey birch and trembling aspen. **(A)** Genus-level taxonomic profiles of relative abundance for birch (top) and aspen (bottom) as GDDs (T_{base} = 5°C) accumulate over seasonal host phenology. For visual practicality, only the top 20 most abundant genera are shown, but the general pattern remains consistent, regardless. **(B)** Differential abundance analysis (*DESeq2*) showing significant changes ($p_{adj} < 0.05$) in the relative abundance of leaf bacterial ASVs (colour-coded) within birch (top) and aspen (bottom) in response to GDD accumulation (T_{base} = 5°C). The $\log_2$(fold–change) represents the rate of change in abundance for every 1-unit increase in GDD and can be interpreted as a regression slope on a log2 scale. A positive $\log_2$(fold–change) indicates that the ASV significantly increased in abundance as GDDs increased, while a negative $\log_2$(fold–change) demonstrates that there was a significant decline in the ASV's abundance as GDDs increased. Note that colours do not correlate to relatedness of taxa. The *P*-value is calculated using the Wald test, and the adjusted *P*-value (p_{adj}) is calculated using the Benjamini–Hochberg method. A full list of the significantly differentially abundant ASVs, including unidentified ASVs, and all summary statistics can be found in Supplementary Tables S9–S10.

Firmicutes followed host-specific trajectories: in birch, it declined from early peaks (~15%) to ~3.5% late-season, whereas in aspen, it peaked at ~35% mid-season (1606 GDDs) before tapering off. Additional phyla such as Myxococcota and Bacteroidota displayed distinct host and seasonal signatures. Myxococcota surged mid-season in birch (~15% at 1606 GDDs) but peaked later in aspen (~8.5% at 2219 GDDs). Bacteroidota, though minor overall, declined steadily in birch but remained higher and more variable in aspen (~5–27%).

At the genus level, birch microbiomes showed a clear directional shift toward dominance by *Endobacter* and *1174-901-12*, which rose from <10% to ~62.5% and ~28.5%, respectively, by senescence onset (2219 GDDs; Fig. 2.3A). This pattern was accompanied by successive replacements: early-season dominance by *Ensifer* (~13.5%) gave way to *Prauserella* (~22% at 605 GDDs), then *P3OB-42* (~20.5% at 1606 GDDs), and eventually *Massilia* (~11.5% at 2140 GDDs). These transitions suggest a seasonal succession of dominant taxa in birch. In contrast, aspen maintained a more stable community structure with moderate fluctuations across genera and fewer dominant shifts. Notable exceptions include a sharp mid-season spike in *Staphylococcus* (~37% at 1606 GDDs, primarily driven by a single plant) and a late-season increase in *Pelomonas* (~24% at 2219 GDDs).

Distinct genera were preferentially associated with each host. Birch harbored genera such as *1174-901-12*, *Bradyrhizobium*, *Endobacter*, *Methylocella*, and *Robbsia*—often absent or rare in aspen—while aspen was enriched in taxa like *Hymenobacter*, *Quadrisphaera*, and *Pelomonas*. Shared genera, including *Prauserella*, *Staphylococcus*, and *Rubrobacter*, displayed divergent trajectories across hosts. For example, *Prauserella* declined sharply in birch mid-season but persisted longer in aspen. *Methylobacterium-Methylorubrum* is a transient, low-abundance taxa in birch, but remains a persistent key genus in aspen. By the end of the season, birch

communities were strongly dominated by three genera—*Endobacter*, *1174-901-12*, and *P3OB-42*—suggesting a pronounced community simplification. Conversely, aspen retained a more even distribution of taxa, with no single genus maintaining long-term dominance. These contrasts underscore divergent community assembly trajectories: birch microbiomes trended toward reduced evenness, while aspen maintained higher taxonomic heterogeneity despite GDD accumulation.

Differential abundance analysis identified bacterial ASVs that significantly varied in abundance with increasing cumulative GDDs, indicating temperature-driven shifts in leaf microbiome composition (Fig. 2.3B; Supplementary Tables S6–S7). Analyses were conducted separately for birch and aspen using continuous GDD as a predictor. In birch, 47 ASVs were significantly differentially abundant across the thermal gradient (FDR < 0.05), showing both enrichment and depletion patterns indicative of dynamic microbial turnover; however, most ASVs were enriched at higher GDDs. Notably, ASVs within *Endobacter*, *1174-901-12*, *Massilia*, *P3OB-42*, and *Methylocella* exhibited strong positive log2 fold changes with GDD, particularly during late-season accumulation. Conversely, ASVs associated with genera such as *Pseudarthrobacter*, *Streptococcus*, *Rothia*, and *Dietzia* exhibited depletion patterns in their abundance with increasing GDD accumulation (Supplementary Fig. S6).

In contrast, aspen hosted fewer differentially abundant ASVs (22 total), where most ASVs were also enriched at increasing GDD values (Fig. 2.3B; Supplementary Table S7). ASVs of the *Pelomonas* genus displayed strong enrichment at higher cumulative GDDs; other genera, such as *Hymenobacter*, *Sphingomonas*, *Pseudomonas*, *P3OB-42*, and *Methylobacterium-Methylorubrum* also demonstrated positive enrichment in abundance as GDDs accumulated seasonally. Moreover, two major genera exhibited depletion trends with increasing GDD

accumulation: *Nocardioides* and *Blastococcus*. Some genera—like *P3OB-42*, *Enhydrobacter*, *Sphingomonas*, and *Massilia*—were shared between hosts but showed divergent responses. These patterns underscore differences in thermal microbiome trajectories between the two functionally similar hosts, with birch supporting more dynamic microbial succession along the GDD continuum. Nevertheless, ASVs of the leaf bacterial communities exhibited host-specific patterns of thermal enrichment. Notably, unclassified ASVs comprised a significant portion of differentially abundant microbes both when comparing host species, and when comparing across higher and lower GDDs, emphasizing potential deeper ecological significance. For results of temporal patterns in differential abundance between host species, see Supplementary Figures S21–S22 and Supplementary Tables S8–S9.

3.3 Leaf microbiomes exhibited host-specific thermal niche strategies dominated by specialists across a seasonal GDD gradient—To assess how bacterial thermal niche breadth varied across the growing season and between hosts, we calculated Levins' niche width index for each ASV using relative abundances scaled within each species × GDD sample. Most ASVs displayed narrow thermal persistence ranges, with 81.1% classified as thermal specialists (niche width ≤ 1.5) and only 8.5% as generalists (≥2.25), across all samples (Supplementary Fig. S23; Supplementary Table S10). When faceted by host species, results show that grey birch hosts slightly more thermal generalist ASVs (~10.3%) than aspen (~8%; $W = 376056$, $P = 0.3144$), whereas aspen hosts slightly more thermal specialists than birch (Fig. 2.4A; $W = 293830$, $P = 0.3455$); regardless, Wilcoxon rank sum tests determined that these differences were non-significant.

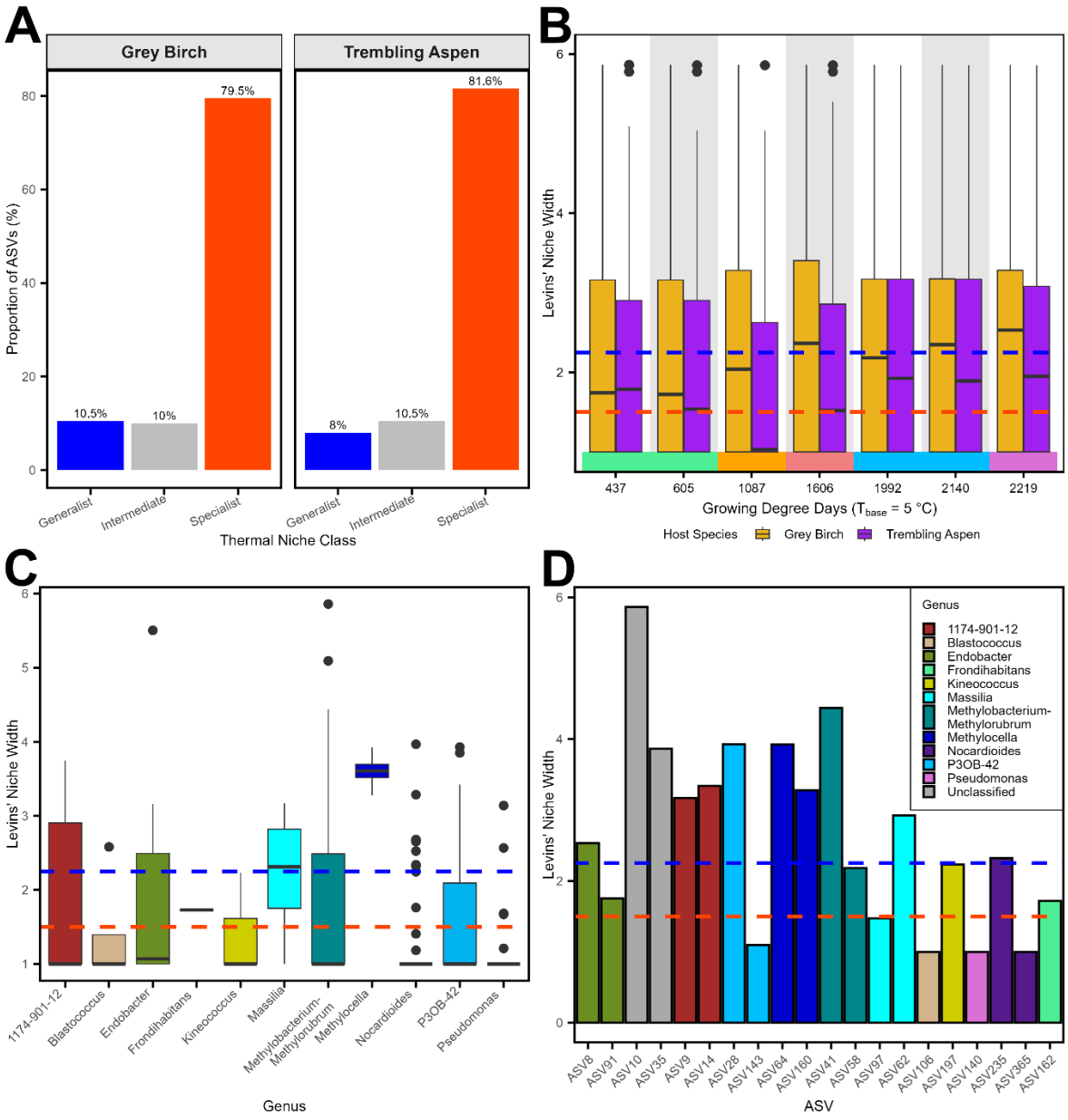

Figure 2.4. Thermal niche breadth of leaf-associated bacterial ASVs across seasonal heat accumulation and host species. Levins' niche width index was derived from relative abundances and used to quantify the breadth of thermal persistence for each ASV across a seasonal GDD (T_{base} = 5°C) gradient, a physiologically relevant measure of heat accumulation that tracks host phenological progression. ASVs with niche width ≤1.5 were classified as specialists, ≥2.25 as generalists, and those in between as intermediate. **(A)** Proportion of ASVs classified as thermal specialists, intermediates, or generalists, faceted by host species. **(B)** Seasonal trends in ASV niche width across GDD accumulation for each host species. Boxplots represent the distribution of ASV-level niche width values per GDD time point (median, IQR, whiskers), with outliers shown as points. Dashed red and blue lines indicate specialist and generalist thresholds, respectively. **(C)** Genus-level distributions of niche width among focal bacterial genera. Narrow boxes (e.g., *Frondihabitans*, *Nocardioides*, and *Pseudomonas*) reflect low genus-level diversity or consistent niche breadth. **(D)** Niche width of focal ASVs from key genera, illustrating intra-genus variability in thermal niche strategy and highlighting the ecological importance of unclassified ASVs. Bars represent individual ASVs; dashed lines mark classification thresholds as in prior panels, where red is the threshold for thermal specialists and blue is the threshold for thermal generalists. ASVs are colour-coded by genus.

When visualized over seasonal GDD accumulation, the distribution of niche widths per host revealed diverging dynamics: birch leaf communities trended toward broader generalist niche distributions mid- to late-phenology, whereas aspen communities remained more stable but maintained a higher proportion of thermal specialists (Fig. 2.4B). Several focal genera exhibited distinct GDD-directed ecological strategies, though within-genus variability in ASV-level niche breadths highlighted the limitations of genus-level generalizations (Fig. 2.4C–D). For example, ASVs of the *Methylocella* genus demonstrated strict thermal generalist strategies, both at the genus- and ASV-level. In contrast, at the genus-level, *Massilia* wavers above the threshold of a generalist and *Nocardioides* appears to be a strict thermal specialist (Fig. 2.4C) but both contain ASVs that can be either specialists or generalists (Fig. 2.4D). Again, these results warrant caution when generalizing genus-level observations to the ASV-level. As in differential abundance analysis, unclassified ASVs comprised a significant portion of both extremes, underscoring the ecological relevance of poorly characterized taxa. In summary, these findings implicate GDD accumulation gradients as more than a phenological index—they represent thermal and temporal microbial niche spaces in and on the leaf microhabitats of grey birch and trembling aspen. For detailed niche width results, see Supplementary Table S10.

4.0 DISCUSSION

This study demonstrates that growing degree days (GDDs; T_{base} = 5°C)—a physiologically grounded measure of cumulative temperature—serve not only as a proxy for plant phenology but also as a direct ecological axis that structures leaf-associated bacterial diversity, composition, and thermal niche strategies. Across a continuous seasonal gradient, leaf microbiomes of two functionally similar temperate tree species, grey birch (*B. populifolia*) and trembling aspen (*P. tremuloides*), exhibited divergent trajectories in alpha diversity, beta

diversity, taxonomic composition, and inferred ecological strategies. These findings support the emerging view that microbial community dynamics in the phyllosphere are shaped by both host traits and environmental conditions, particularly temperature accumulation as it relates to GDDs and phenology, and that these factors interact in species-specific ways to shape microbiome assembly dynamics over seasonal time.

4.1 GDD accumulation shapes species-specific patterns of alpha diversity—Alpha diversity patterns revealed decoupled responses between richness and Shannon diversity over phenology (Fig. 2.2A; Table 2.2). In birch, ASV richness increased significantly with GDD accumulation ($P = 0.0004$), while richness in aspen remained largely stable ($P = 0.427$). Notably, the host species × GDD interaction was significant ($P = 0.0053$), accounting for ~32.6% of fixed-effect variance in ASV richness, but post-hoc tests showed no significant interspecific differences at individual GDDs (Supplementary Table S1), suggesting this pattern reflects gradual divergence rather than sharp shifts. In contrast, Shannon diversity was consistently higher in aspen ($P = 0.0413$) and remained unaffected by GDDs in either species ($P = 0.857$), indicating host species as the primary driver of evenness.

These results imply that while GDD accumulation shapes bacterial ASV recruitment and presence, observed differences in evenness distributions were more strongly associated with host species identity. This supports prior work suggesting that host traits, rather than environmental factors like GDDs and temperature per se, regulate community evenness (Laforest-Lapointe et al. 2016a; Lajoie & Kembel 2021). Yet, the elevated responsiveness of ASV richness to GDDs suggests that thermal-time plays a foundational role in determining microbial presence, especially during mid-to-late phenology (1087–1992 GDDs)—a period of accelerated thermal accumulation and ecological change. Nonetheless, while GDD and host identity explained

758 significant variation in ASV richness and Shannon diversity, respectively, the high residual
759 variance (>70%) suggests that stochastic processes—such as ecological drift or unmeasured
760 microenvironmental factors—may contribute substantially to alpha diversity, even in a shared
761 environment. Regardless, these findings demonstrate that even functionally similar host species
762 can exhibit species-specific seasonal patterns in alpha diversity and responses to GDD
763 accumulation, despite their phylogenetic distance.

764 ***4.2 Community composition and turnover reflect host-specific thermal trajectories—***
765 Beta diversity patterns further underscore the distinct seasonal responses of birch and aspen to
766 thermal accumulation, despite similar leaf types (Fig. 2.2B). In birch, communities exhibited
767 significant turnover and multivariate dispersion mid-to-late season, with clear separation
768 between early and late GDD samples, suggesting microbiome restructuring events along the
769 GDD gradient (Supplementary Fig. S18A). In aspen, communities remained more
770 compositionally stable, though subtle directional changes were observed (Supplementary Fig.
771 S18B). These host-specific differences in microbial trajectories reflect the influence of both
772 deterministic filtering and potential functional redundancy among microbial taxa. Although host
773 species identity explained more variance in community composition than GDDs, the inclusion of
774 only two host species limits our ability to attribute this pattern to host-regulated control.

775 Together with the modest explanatory power of host identity in richness models (R^2 =
776 1.33%), and the greater contribution of GDDs and its interaction with host (R^2 = 6.17% and
777 9.94%, respectively), these results support the environmental filtering hypothesis (Weiher et al.
778 1998), where abiotic conditions—in this case, temperature accumulation—select for bacterial
779 taxa suited to prevailing thermal regimes. However, beta diversity models showed limited
780 explanatory power from fixed effects, with residuals exceeding 70% of total variance. This

underscores the potential role of stochastic processes—such as priority effects, drift, or fine-scale spatial heterogeneity—in shaping foliar community composition beyond host and thermal filtering alone. Regardless, that such turnover occurs between functionally similar hosts grown in a shared environment challenges prior findings that functional type predicts microbiome similarity (Grady et al. 2019) and instead aligns with work highlighting the primacy of phylogenetic distance and species-specific traits over broad ecological strategies and growth forms (Sangiorgio et al. 2024; Laforest-Lapointe et al. 2016b). Thus, these findings warrant caution when generalizing findings at the host functional type level to the species-level.

4.3 GDDs reveal distinct taxonomic and thermal enrichment patterns—Differential abundance analysis revealed taxa exhibiting strong enrichment or depletion across the thermal gradient, with pronounced species-specificity. Birch hosted a greater number of GDD-limited ASVs, many enriched during discrete thermal transitions (e.g., 1087–1606 GDDs), including genera such as *Methylocella*, *Endobacter*, *1174-901-12*, and *P3OB-42* (Fig. 2.3). In contrast, aspen microbiomes featured fewer differentially abundant ASVs but displayed consistent enrichment in specialist genera such as *Methylobacterium-Methylorubrum*, *Pelomonas*, *Quadrisphaera* and *Hymenobacter*. This taxon-level differentiation highlights the utility of GDDs in identifying thermal-time windows of microbiome reorganization and succession. Unclassified ASVs comprised a significant proportion of differentially enriched taxa and showed strong, consistent thermal-time signatures—especially in birch—underscoring their potential role in phenological microbiome restructuring and the ecological relevance of microbial "dark matter" (Bodor et al. 2020; Hedlund et al. 2014; Nobu et al. 2015; Zhang et al. 2023).

Among the most strongly enriched and thermally limited genus in grey birch was the newly assigned *Endobacter*, a genus of strictly aerobic, catalase-positive acetic acid bacteria

within Acetobacteraceae (Ramírez-Bahena et al. 2013). Interestingly, this family forms part of the early-branching acetous clade characterized by vestigial photosynthetic traits and incomplete oxidation metabolism (Raspor and Goranovič 2008). These traits suggest an epiphytic lifestyle well-adapted to oxidative phyllosphere environments. The catalase activity of *Endobacter* may be especially advantageous in birch, which is known to produce hydrogen peroxide (H_2O_2) as part of its leaf surface defenses; catalase-mediated detoxification would enable *Endobacter* to persist or even thrive under oxidative stress (Niu and Liao 2016; Oksanen et al. 2005; Pellinen et al. 2002).

Moreover, *Endobacter* species metabolize ethanol—a compound often emitted as a volatile organic compound (VOC) in birch foliage—into acetic acid (Hellén et al. 2021; Maja et al. 2014; Ramírez-Bahena et al. 2013; Rastogi et al. 2015). This metabolic niche likely confers a competitive advantage in birch canopies during periods of active VOC production, particularly in mid-to-late phenology. *Enodbacter*'s detection on the leaves of grey birch, particularly during late-season phenology and increased GDDs, may reflect adaptation to microaerobic, nutrient-fluctuating niches typical of maturing or senescing foliage. The strong, late-season enrichment of *Endobacter* observed in birch, but much less in aspen, aligns with these host-specific ecological traits and further highlights the role of temperature-driven phenological shifts in selecting for metabolically compatible microbiota. This positions *Endobacter* as a potential redox modulator or sugar-oxidizing commensal in the leaf phyllosphere-endosphere continuum, consistent with broader metacommunity responses to cumulative GDDs. This study encourages future work in elucidating the ecological roles of this potentially key bacterial genus.

4.4 Niche width patterns support ecological filtering and divergent strategies—Thermal niche breadths, calculated via Levins' index, revealed strong ecological filtering across the GDD

continuum: 81.1% of ASVs were classified as thermal specialists (niche width ≤1.5), with only 8.5% identified as generalists (≥2.25; Supplementary Fig. S23). Host-specific patterns were evident—birch hosted a slightly higher proportion of generalists (10.3%) than aspen (8.0%), while aspen maintained a higher proportion of specialists throughout the season (Fig. 2.4A–B). These patterns suggest that birch supports broader microbial turnover, potentially due to dynamic phenological shifts or weaker host-associated differences, whereas aspen maintains more compositionally stable and specialized communities. Notably, several genera contained both specialist and generalist ASVs (e.g., *Nocardioides*, *Massilia*), illustrating the limitations of genus-level inferences and reinforcing the need for ASV-level resolution in ecological studies (Fig. 2.4C–D). This is especially true since functional assessments of microbiomes can be confounded by strain-level variability and functional redundancy across bacterial taxa (Barnes et al. 2020).

When plotted across GDDs, birch showed a mid-to-late season increase in generalist ASVs, aligning with observed community restructuring and increased taxonomic dynamism. In contrast, aspen displayed narrower niche widths. These results align with classical niche theory (Chase and Leibold 2003), where community structure emerges from trait distributions along environmental gradients—in this case, thermally regulated phenological space. This study presents evidence for niche theory's extension into the microbial realm (Baquero et al. 2021)

Genera such as *Methylocella* exemplified consistent generalist strategies across hosts and GDDs, likely reflecting their facultative methanotrophic metabolism and broad thermal tolerance (Crombie and Murrell 2014; Dedysh et al. 2005; Dunfield and Dedysh 2014). In contrast, genera like *Nocardioides*, *Blastococcus*, and *Pseudarthrobacter* appeared as strict specialists at the genus level. Differential abundance of *Nocardioides* shows a preference for relatively lower

cumulative GDD conditions; as a mesophilic genus that includes psychrotolerant strains, its affinity for the earlier GDDs of June 2018—when temperatures were neither extreme—is ecologically consistent (Schiraldi and De Rose 2014). Nonetheless, genera such as *Massilia*, *Nocardioides*, and *P3OB-42* exemplify the intra-genus variation in thermal strategies revealed by ASV-level comparisons, underscoring the value of high-resolution ecological analysis.

Although we cannot make definitive claims about adaptive evolution, certain taxa such as *Methylocella*, *Nocardioides*, and *Pelomonas* showed GDD-specific enrichment patterns consistent with known thermal tolerances, suggesting potential physiological adaptation to seasonal temperature regimes. However, these interpretations remain cautious without functional or genomic validation. Instead, we emphasize that the observed patterns—bacterial turnover, niche partitioning, and host-specific responses to GDD accumulation—reflect ecological selection across a dynamic thermal-time gradient rather than adaptive shifts per se. This finding underscores that even closely related strains may exhibit divergent ecological strategies, and that niche theory applies at a microevolutionary scale in leaf bacterial communities.

4.5 Broader implications and future directions—Taken together, this study positions GDD accumulation not only as a model for plant phenological progression but as a predictive ecological filter shaping microbial assembly in the phyllosphere. By integrating alpha and beta diversity, DESeq2-derived enrichment, and thermal niche breadths, this study provides a multifaceted view of how seasonal temperature accumulation structures leaf bacterial communities across two functionally similar but phylogenetically distinct tree species. GDDs offer a biologically relevant and scalable index for understanding microbial phenology and may prove critical in forecasting microbial responses to ongoing climatic shifts. Future studies should extend this work by incorporating more diverse host species, interannual datasets, and trait-based

plant-microbe metrics (e.g., exudate profiles, cuticle chemistry). Metatranscriptomic or functional profiling approaches would also provide insight into the metabolic roles of differentially abundant and unclassified taxa. Additionally, experimental manipulation of GDD accumulation—via warming chambers or phenological decoupling—could disentangle the causal roles of temperature, host development, and microbial succession in shaping these complex and dynamic communities. Finally, the large proportion of residual variance observed in our models highlights the need to account for stochasticity and context-dependent variability when interpreting microbiome assembly, especially in natural forest systems.

Although our findings cannot directly test the extended phenotype concept—which requires demonstrating that externally expressed traits are shaped by host genotypes—they raise questions relevant to it. The extended phenotype framework describes traits influenced by an organism's genes but expressed outside its body, such as microbial communities modulated by host genetic or physiological factors (Dawkins 1982; Hawkes et al. 2021). In this study, we observed clear species-specific patterns in leaf microbiome structure and diversity that unfolded across phenological time, alongside consistent responses to GDD accumulation. These findings suggest that thermal filtering alone may not fully explain community dynamics; instead, host identity and phenology appear to also shape microbial trajectories through indirect mechanisms such as microhabitat structuring or developmental cues (Ginnan et al. 2022; Kembel and Mueller 2014; Laforest-Lapointe et al. 2016a,b).

If microbial communities track thermally regulated phenology and contribute to host function, they may act as ecologically relevant traits—and potential targets of selection—particularly as climate change disrupts plant–microbe synchrony (Ginnan et al. 2022; Meier et al. 2021; Piao et al. 2019; Xu et al. 2023). To evaluate whether leaf microbiomes truly constitute

extended host phenotypes, future work will require the integration of host plant genotype data, functional trait profiles, transcriptomics, and broader cross-species comparisons to disentangle the relative contributions of host regulation, environmentally contingent filtering, and stochasticity.

5.0 CONCLUSION

In summary, this study demonstrates that cumulative growing degree days (GDDs; T_{base} = 5 °C) act not only as a physiologically relevant proxy for plant phenology, but as a direct metric of the thermal ecological filtering that shapes leaf bacterial diversity and composition. Across a continuous seasonal gradient, GDDs more strongly explained ASV richness than host identity, while Shannon diversity reflected species-specific differences, being unimpacted by GDD accumulation. Host species identity explained a greater proportion of variance in community composition than GDDs, though both had significant effects. Given that this study included two host species, its findings should be interpreted cautiously and do not confirm host-regulated control. Birch (*B. populifolia*) leaf microbiomes underwent directional mid-to-late phenology restructuring, enriched in generalists and GDD-limited taxa like *Endobacter*, while aspen (*P. tremuloides*) communities remained compositionally stable and even with narrower thermal niches. Niche width analysis revealed ~81% of ASVs were thermal specialists, and unclassified taxa showed strong GDD-linked enrichment, underscoring the ecological role of microbial "dark matter". Collectively, the results position the leaf microbiome as a dynamic, environmentally responsive feature of the plant holobiont in functionally similar but phylogenetically distant hosts, jointly shaped by host identity and the cumulative thermal energy directing host phenology. Thus, GDDs offer a scalable tool for predicting leaf microbiome responses to phenological and climatic change—an increasingly urgent task in the face of global warming.

Chapter 3
General Conclusions

This study establishes growing degree days (GDDs; T_{base} = 5°C) as a biologically meaningful and mechanistically informative axis for interpreting microbiome dynamics in the leaf phyllosphere and endosphere. By sampling two functionally similar but phylogenetically distinct temperate tree species—grey birch (*B. populifolia*) and trembling aspen (*P. tremuloides*)—along a continuous seasonal gradient of cumulative heat energy, we show that GDDs structure leaf bacterial communities in a host-specific, ecologically directional manner. Specifically, GDDs more strongly predicted ASV richness than host identity alone, whereas Shannon diversity remained unimpacted and better explained by differences in host species identity, indicating a decoupling of microbial presence from evenness and revealing layered influences of environment and host. Across all comparisons, GDD accumulation significantly modulated community composition and beta diversity.

Thermal accumulation was also linked to microbial turnover events, GDD-limited taxonomic enrichments, and phenology-driven niche partitioning, particularly in birch, which exhibited directional restructuring of its microbiome in mid-to-late season. By senescence onset (2219 GDDs), however, interspecific differences diminished, potentially due to microhabitat homogenization, relaxed host filtering, or colonization by generalist, stress-tolerant taxa. Such findings emphasize the seasonal fluidity of host-microbe interactions and support the environmental filtering hypothesis under dynamic phenological conditions. These patterns were underpinned by a dominant prevalence of thermal specialists (~81%), but with host-specific variation: birch supported greater mid-season influxes of generalists, while aspen maintained

narrower niche widths and compositional stability. Such findings extend niche theory into the microbial domain and reinforce the importance of GDDs as both an indirect (via phenological interaction) and direct (via cumulative thermal filtering) force in microbial assembly.

Differential abundance analysis revealed that certain taxa—including *Endobacter*, *1174-901-12*, and *P3OB-42* in birch, and *Pelomonas*, *Nocardioides*, and *Hymenobacter* in aspen—were strongly limited by GDD accumulation. The late-season surge of *Endobacter*, an aerobic, catalase-positive acetic acid bacterium possibly adapted to hydrogen peroxide–rich birch phyllospheres, highlights how microbial metabolic traits may align with host-specific chemical environments and seasonally timed resource niches. The ecological responsiveness of unclassified ASVs, particularly in birch, underscores the relevance of microbial "dark matter" in phyllosphere ecology and emphasizes the limitations of genus-level resolution alone. They consistent appearance of understudied genera like *Endobacter* and unidentified ASVs in this study emphasize a need to improve culture-independent methods.

While this study offers novel insights, it is not without limitations. The focus on only two tree species—moderately related and ecologically similar—limits generalizability to more phylogenetically or functionally diverse systems; it also limits the ability to assess host species control. The absence of interannual data prevents robust conclusions about temporal stability or climate-linked interannual shifts. Additionally, constraints on sample size limited the ability to fully explore hierarchical variance structures, such as inter- versus intra-individual variation. High residual variance across models (>70%) further suggests that stochastic processes, such as ecological drift, likely interact with deterministic thermal filtering to shape community assembly.

Together, these findings support a view of the leaf bacterial microbiome as a dynamic, thermally responsive community shaped by both thermal environmental filtering and differences

in host species identity. While we cannot confirm that foliar microbiomes represent extended host phenotypes, the observed species-specific patterns across phenological time and thermal accumulation raise compelling questions for future study. As global temperatures rise and plant phenology shifts, understanding how thermal-time indices like GDDs shape microbiome dynamics will be critical for predicting microbiome resilience, turnover, and potential feedback to host function. By integrating high-resolution community analysis with a cumulative thermal framework, this study provides a scalable, ecologically grounded foundation for future research into the thermal ecology of plant–microbe interactions.

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APPENDIX

Table A1. Summary of the most common bacterial taxa found within the phyllosphere and endosphere of plant leaves. Major phyla are displayed with their most common associated member classes and genera. The Gram status of each is listed, along with a brief description of their most important functions in the phyllosphere and endosphere (Durand et al. 2018; Kembel et al. 2014; Redford et al. 2010).

Major Phyla	Common Member Classes	Common Member Genera	Examples of Function(s)	Gram Stain (+/-)
Pseudomonadota	Alphaproteobacteria	*Sphingomonas*	Highly associated with Poplar trees (*Populus* sp.). Produce growth hormones (e.g. sphingan) to promote plant growth (Asaf et al. 2020).	-
		Hyphomicrobium	Methanotrophic (i.e., carbon cycling); Methylobacterium is highly associated with Poplar (*Populus* sp.) trees (Chaudhry et al. 2021).	
		Methylibium		
		Methylobacterium		
		Methylocapsa		
		Methylocella		
		Methylocystis		
		Azospirillum	Diazotrophic (i.e., N_2 fixation).	
		Acetobacter		
	Betaproteobacteria	*Burkholderia*		
		Methylibium	Methanotrophic (i.e., carbon cycling)	
		Methylophilus		
	Gammaproteobacteria	*Pantoea*	Phytopathogens and necrotrophs, but many species promote plant growth, fix N_2, degrade toxins, and produce antibiotics (Chaudhry et al. 2021).	
		Erwinia	Common phytopathogens (cause bacterial fire blight and soft rot; can co-opt plant immune signals); pectolytic; leach and compete for iron from pant host tissues (Expert 1999).	

		Enterobacter	Many promote plant growth; bolster plant immunity via acetoin production in some hosts; role in sulfur metabolism and cycling (Andrés-Barrao et al. 2021; Khalifa et al. 2016). Some species are diazotrophic/N_2 fixing (Macedo-Raygoza et al. 2019). Some are phytopathogens.	
		Citrobacter	Plant-growth promoting bacteria; high heavy metal (HM) resistance helps host avoid HM toxicity (increasing concentrations of HMs reduces chlorophyll content). Has been shown reduce proline in leaves; Role in PO_4^{-3} sequestration (Ajmal et al. 2022).	
		Acinetobacter	Promotes plant growth (increase in biomass and chlorophyll content); solubilizes PO_4^{-3} (in solid or liquid media, e.g. leaf tissue). Some strains produce gibberellins (Kang et al. 2009); significant VOC production. Presence can completely alter leaf microbiome: e.g., presence is positively correlated with *Bacillus* sp. (Zheng et al. 2022).	
		Pseudomonas	Phytopathogens (*Pseudomonas syringae* is a common, economically destructive one); can produce lipopeptides that are lytic and inhibit growth (Preston 2004). Many strains promote plant growth by synthesizing phytohormones and suppressing many other pathogens. Distinct VOC profile (Passera et al. 2019). Syringafactin production adsorbs to	

			waxy leaf cuticle and increases rate of water diffusion across isolated cuticles and attracts water to hydrophobic surfaces exposed to high relative humidity; stomatal aperture regulation (Chaudhry et al. 2021).	
Actinomycetota	Actinomycetes	*Kineococcus*	Highly associated with Poplar trees (*Populus* sp.). Some strians contain carotenoid pigments that absorb light at wavelengths of 444, 471, and 501 nm (Phillips et al. 2002). Exhibits antibiotic resistance and produces many types of antibiotics: e.g., some strains produce chloramphenicol, which inhibits the uptake of salt ions by plant tissues, inhibiting growth (Mhatre et al. 2020).	+
		Curtobacterium	Economically significant phytopathogen. An agent of bacterial wilt and leaf spot (Osdaghi et al. 2020).	
Bacillota	Bacilli	*Bacillus*	Many functions in plant hosts; crucial role in plantimmunity, nutrient uptake, and N_2 fixation. Modulates gene expression profile of some plant leaves to promote plant growth; siderophores and exopolysaccharide production to adjust ionic balance and water content, and transport of toxic ions away. Regulates intracellular phytohormone metabolism. Promotes stress tolerance by modifying host stress-response genes, proteins, phytohormones, and metabolites	+

			(Rhadhakrishnan et al. 2017).	
Bacteroidota	Cytophagia	*Hymenobacter*	Plant growth-promoting bacteria that is highly associated with Poplar trees (*Populus* sp.). Can degrade fungal chitin. Phototrophic and isolated from high-UV environments, which is beneficial to phyllosphere (Stone and Jackson 2020).	-
	Sphingobacterii	*Sphingobacterium*	Sphingophospholipid production, which helps in plant immunity to regulate pathogens and mediate the delicate microbe-host balance (Zheng and Yao 2022). Order Sphingobacteriales represents approximately 21-22% of tree phyllosphere sequences (Redford et al. 2010).	
Deinococcota	Deinococcii	*Deinococcus*	Contains a pink-coloured carotenoid pigment called deinoxanthin (reflectance is a mixture of red and purple ends of the VIS spectrum). Extremophiles tolerant to high doses of UV and gamma radiation. Biosynthesis of cell-free metal nanoparticles to tolerate heavy metal stress (Chen et al. 2017).	+

S2.0 SUPPLEMENTAL MATERIALS AND METHODS

S2.2 DNA Extraction—This study uses a culture-independent sampling method, which is more representative of the true microbial community than culture-dependent methods (Bodor et al. 202; Hinsu et al. 2021; Hugerth and Andersson 2017; Redford et al. 2010).

To achieve complete lysis of plant cell walls and all microbial cells for representative sampling, two sterile 4.7 mm stainless steel beads were added to each PowerBead tube, and a vertical mixer mill was used to pulverize frozen samples at 25 Hz for five 1 min cycles. Once grinding was complete, each sample tube was incubated with lysis buffer in a heated shaker at 65℃ for 30 min at 800 rpm; additionally, samples were vortexed every 10 min. Rather than incubating the tubes at 2–8℃ for 5 min, the samples were incubated on ice for 7 min to yield optimal DNA purity. Isolated DNA was run on a 1% agarose gel and a Qubit 2.0 fluorometer assay was performed to quantify the DNA product for each sample.

S2.4 Sequence Quality Control, Filtering, and Taxonomic Assignment of ASVs— Quality of both forward and reverse reads was assessed with the 'plotQualityProfile()' function to ensure quality scores exceeded 30 and to determine the optimal truncation length for filtering. Using the 'filterAndTrim()' function, sequences were filtered and trimmed: forward reads were truncated to 240 bases, reverse reads to 230 bases, with a maximum of 0 ambiguous bases allowed, a maximum expected error (maxEE) of 2, a truncation quality threshold (truncQ) of 2, and PhiX sequences removed (rm.phix = TRUE). Paired reads were then merged with the 'mergePairs()' function, which only combines reads if they overlap by at least 12 bases and match exactly in the overlap region (Callahan et al. 2016). Notably, ASVs are exact sequences derived from high-throughput sequencing, providing a high resolution of microbial diversity without relying on

clustering thresholds like operational taxonomic units (OTUs). This approach improves accuracy and reproducibility by capturing fine genetic variations (Callahan et al. 2017; Callahan et al. 2019; Chiarello et al. 2022).

A total of 3046486 reads passed the quality filtering step, resulting in 1790 ASVs. Taxonomy was then assigned to these ASVs using the 'assignTaxonomy()' function, which employs the naive Bayesian classifier method (Callahan et al. 2016). This function requires a reference training set with known taxonomy and generates taxonomic assignments based on training FASTA files from the RDP, GreenGenes, and SILVA databases. Additionally, species-level classifications were obtained through exact matching of ASVs with reference strains, as this method is considered most accurate for 16S gene fragments with 100% identity (Callahan et al. 2016; Edgar 2018). The 'addSpecies()' function used species-assignment training FASTA files from the SILVA and RDP 16S databases for this purpose.

***S2.5 Statistical Analyses*—**All statistical analyses were conducted using R v.2024.09.0 (R Core Team, 2024).

***S2.5.1 Bacterial Alpha Diversity Patterns*— Statistical Model Construction and Diagnostics:** Preliminary analysis of the data included assessing homogeneity of slopes faceted by fixed effects and generating scatterplot matrices using the 'scatterplotMatrix()' function from the *car* package. Applying the 'lmer()' function from the *lme4* package, multiple linear mixed models (LMMs) were constructed to model ASV richness (ASV R′) and Shannon diversity (H′) within (intraspecific) and between (interspecific) host species to explore the impacts of host species identity, host phenology (GDDs), and their two-way interaction, with varying transformations on the response variable data and plant identity ('Plant_ID') set as the random effect (Bates et al. 2015; Faticov et al. 2021; Sweeny et al. 2023).

Subsequently, formal normality tests were conducted using the 'shapiro.test()' function in base R. Diagnostic statistics were generated using the 'check_model()' function from the *performance* package to assess homogeneity of variance, linearity, collinearity, influential observations, and normality of residuals for each LMM (Lüdecke et al. 2021). Model fits were compared using the 'anova()' function, and the best models were identified based on the lowest Akaike Information Criterion (AIC), the lowest Bayesian Information Criterion (BIC), the lowest deviance, and the highest log-likelihood.

Interspecific Model Selection (Alpha Diversity): For interspecific host comparisons of leaf bacterial alpha diversity, the best-fitting LMMs—which satisfied statistical diagnostic checks and normalized residuals—log-transformed ASV richness (log(ASV R′)) and square-root transformed Shannon diversity $\left(\sqrt{H'}\right)$. Both metrics were independently modeled as functions of the fixed effects of host tree species ('Species'), GDD accumulation ('GDD_5C'), and their two-way interaction ('Species:GDD_5C'), with 'Plant_ID' included as a random effect. A more complex model incorporating a nested random effect structure [(1 | Species / Plant_ID)] was considered but found to be unstable, producing convergence warnings and unreliable parameter estimates. This instability is likely due to the small sample size at the higher species-level, with only two species being compared, which limits the ability of the model to partition variability reliably. Often, studies suggest more than two grouping levels for reliable nesting—ideally, at least five (Aarts et al. 2014). Therefore, a simpler random effect structure [(1 | Plant_ID)] was used to ensure model stability and reliable inference, recognizing that this approach pools intraspecific data and does not explicitly account for potential differences between species in 'Plant_ID'-specific effects. While the simpler model provided reliable estimates, it does not explicitly partition intraspecific and interspecific variability. To address this for downstream

analyses of intraspecific variation, I fit separate models for each species to analyze intraspecific variation. However, comparisons of interspecific and intraspecific variation should be interpreted cautiously due to the absence of an explicit nested random effect structure and the limited sampling design. For ASV richness (ASV R′), the best fit interspecific LMM was as follows:

$$\log(ASV\ R') \sim Species + GDD\_5C + Species{:}\ GDD\_5C + (1 \mid Plant\_ID)$$

For Shannon diversity (H′), the best fit interspecific LMM was as follows:

$$\sqrt{H'} \sim Species + GDD\_5C + Species{:}\ GDD\_5C + (1 \mid Plant\_ID)$$

Intraspecific Model Selection (Alpha Diversity): To address this limitation, I also analyzed intraspecific (within-species) variation by fitting separate LMMs for each species, where 'Plant_ID' was modeled as a random effect. To satisfy diagnostic criteria and normalize residuals for sample data within-species, models selected for birch leaves involved reciprocal transformations of both bacterial ASV richness $\left(\frac{1}{\text{ASV R'}}\right)$ and Shannon diversity $\left(\frac{1}{\text{H'}}\right)$, both modeled as functions of the fixed effect 'GDD_5C' and the random effect 'Plant_ID'. For birch, the best fit intraspecific LMM for ASV richness (ASV R′) was as follows:

$$\frac{1}{ASV\ R'} \sim GDD\_5C + (1 \mid Plant\_ID)$$

For birch, the best fit intraspecific LMM for Shannon diversity (H′) was as follows:

$$\frac{1}{H'} \sim GDD\_5C + (1 \mid Plant\_ID)$$

Within aspen, ASV richness was reciprocally transformed $\left(\frac{1}{\text{ASV R'}}\right)$, while Shannon diversity was square-root transformed $\left(\sqrt{\text{H'}}\right)$, both also modeled as a function of the fixed effect

'GDD_5C' and the random effect 'Plant_ID'. Additionally, 'GDD_5C' was treated as a continuous numeric variable in the LMMs. For all intraspecific models within both tree species, 'Plant_ID' was modeled as a random effect to account for variability among individual plants while avoiding the overparameterization and instability that arose from including 'Plant_ID' as a fixed effect. This approach provided a more reliable model fit while still capturing individual-level variability. For aspen, the best fit intraspecific LMM for ASV richness (ASV R′) was as follows:

$$\frac{1}{ASV\ R'} \sim GDD\_5C + (1 \mid Plant\_ID)$$

For aspen, the best fit intraspecific LMM for Shannon diversity (H′) was as follows:

$$\sqrt{H'} \sim GDD\_5C + (1 \mid Plant\_ID)$$

Marginal and Conditional R^2 Calculation: For each statistically significant fixed effect, both marginal R^2 (R^2_m) and conditional R^2 (R^2_c) values were calculated separately using the 'r.squaredGLMM()' function from the *MuMIn* package, whilst retaining the same random effects (Faticov et al. 2021; Bartoń 2023). The R^2_m value quantifies the proportion of variance explained by the fixed effects alone, highlighting their contribution to the model. In contrast, the R^2_c value represents the total variance explained by both fixed and random effects, providing insight into the overall fit of the model (Nakagawa et al. 2017; Lüdecke et al. 2021).

Pairwise Comparisons of Host–Phenology Interaction Effects: To evaluate how leaf bacterial ASV richness and Shannon diversity vary in response to the interaction between their host species and accumulated GDDs ('Species:GDD_5C'), pairwise comparisons were conducted using the 'emmeans()' function from the *emmeans* package in R (Lenth 2024). The

‘emmeans()’ function calculates the estimated marginal means for each level of comparison using the fitted LMM, and then conducts t-tests on the differences (contrasts) between these means to assess the significance of pairwise comparisons. Its t-tests incorporated the regression slope for the continuous variable ‘GDD_5C’ and accounted for random effects (‘Plant_ID’), residual variance, and model-specific degrees of freedom, ensuring accurate p-values and confidence intervals (Lenth 2024). Note that only pairwise comparisons of interactions made within the same GDD were considered (e.g., comparing birch’s interaction with GDD 437 to aspen' interaction with GDD 437) for the sake of biological relevance. Overall, this permits investigation of how host species’ phenological change interacts with its physiology to impact leaf bacterial differences, and whether these species-specific differences are detectable.

Pairwise Comparisons of Host Species Effects Across Phenology: To isolate the ‘Species’ differences at each ‘GDD_5C’ value, independent of GDD but still taking the LMM structure into consideration, *emmeans* was used with the specification: “specs = pairwise ~ Species | GDD_5C” (Lenth 2024). The ‘emmeans()’ function calculates the estimated marginal means for each level of ‘Species’ at specified values of ‘GDD_5C’ using the fitted LMM, and it then conducts t-tests on the differences (contrasts) between these means to assess the significance of pairwise comparisons. This method permits accurate pairwise comparisons by avoiding the loss of nuance associated with subsetting the data by GDD, then comparing each species at each GDD, without the additional consideration of the random effect. This technique explores how the differential influence of host species identity on bacterial alpha diversity varies across temperature-driven phenological stages (GDDs).

Pairwise Comparisons of Growing Degree Day Effects Within Host Species: If the LMMs identified ‘GDD_5C’ as significantly impacting either alpha diversity metric within birch

or aspen (i.e., intraspecific comparisons), the *emmeans* package in R was used for pairwise comparisons of 'GDD_5C' to identify specific GDDs driving this variation and to pinpoint where bacterial alpha diversity differed most over host phenology (Lenth 2024). Since 'Plant_ID' was modeled as a random effect, direct pairwise comparisons of individual plants were not possible. Instead, I subset the data by GDD within each host species and compared differences in 'Plant_ID' effects within each subset.

To validate subsetting by GDD, I first assessed temporal autocorrelation using Kwiatkowski–Phillips–Schmidt–Shin (KPSS) tests for ASV richness and Shannon diversity using the 'ur.kpss()' function from the *urca* package (Moroenyane et al. 2021a; Pfaff 2008). Normality of alpha diversity data within each GDD subset was tested using 'shapiro.test()'. For normal data, ANOVAs assessed the effects of 'Plant_ID' on alpha diversity at each GDD with the 'aov()' function from the *stats* package, followed by residual normality checks. For non-normal data, non-parametric Kruskal-Wallis tests were conducted using the 'kruskal.test()' function from the *stats* package (Moroenyane et al. 2021a; R Core Team 2024). This approach identified GDDs and individual plants with significant impacts on bacterial alpha diversity, providing insights into thermo-temporal and individual variation within each host species.

***S2.5.4 Differential Abundance Analysis*—**To assess which ASVs (and their associated taxonomic assignments) were most differentially abundant between birch and trembling aspen as GDDs accumulate, and overall, differential abundance analysis was performed using the *DESeq2* package in conjunction with the *phyloseq* package (Faticov et al. 2021; Love et al. 2014; McMurdie and Holmes 2013). *DESeq2* takes count data and normalizes them. To account for multiple comparisons, *P*-values were adjusted using the Benjamini-Hochberg procedure (Faticov et al. 2021; Love et al. 2014). Differential abundance analysis was performed comparing the two

host tree species overall and then subsequently, the data were subset by GDD and differential abundance analysis at each GDD was assessed. *DESeq2* takes count data and normalizes them. To account for multiple comparisons, *P*-values were adjusted using the Benjamini-Hochberg procedure (Faticov et al. 2021; Love et al. 2014). Differential abundance analysis was performed comparing the two host tree species overall and then subsequently, the data were subset by GDD and differential abundance analysis at each GDD was assessed.

The purpose of conducting differential abundance analysis, in conjunction with visualizing relative abundance profiles over GDDs, is to statistically identify bacterial taxa that show significant changes in enrichment between birch and aspen across phenological progression overall, and at the specific GDDs sampled. This method allows for precise relative quantification of how specific taxa respond to the effects of host identity across cumulative GDDs, accounting for variability and noise in the data. Differential abundance analysis identifies taxa with significant patterns of variation, offering actionable insights into host-specific microbiome dynamics, phenological shifts, and the ecological or functional roles of bacterial ASVs. This approach complements taxonomic visualizations of relative abundance by highlighting rare, low-abundance, or unidentified ASVs that may disproportionately influence microbial dynamics but remain underrepresented in standard taxonomic profiles (Faticov et al. 2021; Love et al. 2014; McMurdie and Holmes 2013).

S3.0 SUPPLEMENTAL RESULTS

***S3.1 Alpha Diversity*—**In early-mid season comparisons, aspen had higher ASV richness than birch. However, this trend inverted mid-late season, with birch surpassing aspen, except near the end of the season (2140 GDDs). Shannon diversity differed significantly between the two tree

species (P = 0.0413), with consistently higher values observed in aspen compared to birch across phenology (Fig. 2.2). Despite the observed patterns, overlapping bar plots and large error bars suggest caution in visual interpretations. Therefore, the results of the LMMs were used to further assess the impact of host species identity and GDDs on alpha diversity more reliably (Table 2.2).

For ASV richness, which underwent logarithmic transformation when modelling, host species identity (P = 0.00855), GDDs (P = 0.000364), and their interaction (P = 0.00531) significantly influenced variation between host species' leaf bacterial microbiomes (Table 2.2). Host species identity explained ~1.33% of variance when considering only fixed effects (R^2_m = 0.0133) and ~14.4% when including random effects (R^2_c = 0.144). Specifically, the model revealed significant differences in ASV richness between the two species: aspen exhibited higher ASV richness compared to birch (estimate = 0.859), with back-transformed ASV richness estimates of approximately 48.7 for aspen and about 20.1 for birch at 'GDD_5C' = 0. GDDs alone explained ~6.17% of ASV richness variance (R^2_m = 0.0617); however, if random effects are included, GDDs describes ~19.2% of the variance in ASV richness (R^2_c = 0.192). Additionally, there was a positive association between GDDs and ASV richness for birch (estimate = 0.000463), indicating that each unit increase in GDD resulted in a multiplicative increase in ASV richness, though this increase was multi-phase and non-linear.

The interaction between species identity and GDDs explained ~9.94% (R^2_m = 0.0994) of the variation observed in ASV richness when considering only fixed effects (Table 2.2). When taking both fixed and random effects into account, the interaction between host tree species identity and accumulated GDDs explains ~32.6% of the variance in ASV richness (R^2_c = 0.326). Further, the interaction term (estimate = -0.000502) suggested that for aspen, the relationship was less positive, with a slight decrease in ASV richness as GDD increased (combined effect

estimate = -0.0000387). The interaction between host species-specific traits and temperature-dependent phenological shifts (i.e., accumulated GDDs) explains the most variation in leaf ASV richness and is more significant than either factor alone. This interaction drives differences in ASV richness among host species, with species identity moderating the effect of GDDs on microbial richness. However, caution is warranted in interpreting this result, as the interaction term includes all possible combinations of 'Species' and 'GDD_5C', spanning differing levels of GDDs. This broad comparison may not exclusively capture variations within the same GDD sampling points, which were the primary focus for biological relevance. Nonetheless, the findings emphasize significant species-specific responses to temperature accumulation ('GDD_5C') and its influence on microbial ASV richness within forest ecosystems.

As stated, while the LMM identifies significant 'Species:GDD_5C' interactions for ASV richness, it does not differentiate between biologically meaningful comparisons (e.g., interactions between host species at the same GDD) and less relevant ones (e.g., interactions across different GDDs). LMMs detect overall patterns but do not explicitly test interactions at specific GDD levels. Instead, they identify whether the relationship between the two variables, GDDs and ASV richness, differs between groups of host species overall. While this broad approach provides statistical evidence for an interaction, the interpretation requires careful contextualization, like narrowing comparisons to specific GDDs that reflect similar phenological stages. To refine interpretation, post-hoc pairwise comparisons were conducted using the *emmeans* package in R, comparing interactions within the same GDD values (e.g., the interaction of birch vs. aspen with GDD 437); comparisons across different GDD groupings were discarded for biological relevance (Supplementary Table S1). The significant interaction in the overall LMM indicates that ASV richness responds to phenological progression (GDDs) in a host-specific manner. However,

pairwise comparisons at individual GDDs revealed no significant differences between the two species, suggesting the interaction reflects cumulative trends across the phenological gradient rather than discrete shifts at specific GDDs.

Regarding Shannon diversity, which was square-root transformed during LMM analysis, only host species identity ($P = 0.0413$) significantly impacted bacterial diversity (Table 2.2). Host species identity alone explained ~26.1% of the variance in Shannon diversity when considering only fixed effects ($R^2_m = 0.261$), increasing to ~34.1% when random effects were included ($R^2_c = 0.341$). Specifically, aspen exhibited a higher Shannon diversity compared to the reference species birch (estimate = 0.264), with back-transformed estimates indicating an alpha diversity of approximately 2.56 for aspen relative to 2.49 for birch when 'GDD_5C' = 0. GDDs and their interaction with species identity had no significant effect on Shannon diversity, suggesting that the relationship between species identity and Shannon diversity remains independent of GDD accumulation (Table 2.2). Thus, species identity plays a crucial role in determining Shannon diversity, while the effects of accumulated GDDs may be minimal in this context. The model accounted for variability among different plants, with random effects associated with 'Plant_ID' contributing to the overall model fit. Overall, these findings underscore the importance of host species identity in shaping the leaf bacterial microbiome's Shannon diversity, independent of the effects of GDD.

Subsequently, the *emmeans* package was used to assess the points during host phenology where interspecific differences in ASV richness and Shannon diversity were most pronounced (Lenth 2024). By using "specs = pairwise ~ Species | GDD_5C", *emmeans*—whilst respecting the structure of the LMM—calculated pairwise comparisons between 'Species' alone at each level of 'GDD_5C' to investigate species-specific differences in alpha diversity independent of

their interaction with GDDs to see where 'Species' exert their greatest influence on alpha diversity during the growing season (Table 2.3). Regarding ASV richness, significant interspecific differences were observed at GDD 437 (t = -2.489, P = 0.0198) and GDD 605 (t = -2.333, P = 0.0305). Similarly, Shannon diversity was analyzed across GDD intervals, revealing significant species-specific impacts at all GDD values (all $P < 0.05$; Table 2.3). This pattern highlights strong species-specific differences in evenness throughout the growing season. Notably, Shannon diversity, which accounts for both richness and evenness, showed a more persistent impact of host species across the entire season compared to ASV richness.

Within birch, there was no overall change in Shannon diversity over the GDD gradient, though bacterial ASV richness increased with GDD accumulation (Fig. 2.2; Supplementary Fig. S3). Conversely, aspen exhibited no change in both ASV richness and Shannon diversity as GDDs accumulated (Fig. 2.2; Supplementary Fig. S3). When examining variation from one GDD to the next, birch demonstrated non-linear relationships in both ASV richness and Shannon diversity, though the trajectory of these cycles differed between the two metrics (Fig. 2.2). In aspen, oscillating non-linear relationships were observed, with increases in diversity during early-mid season, followed by mid-late season declines, and a final increase near the season's end, with reductions in diversity at maximal GDDs (Fig. 2.2).

Intraspecific (within-species) statistical analyses of GDD influence on bacterial diversity in birch revealed that GDDs had a significant impact on the inverse of ASV richness (P = 0.000247), explaining ~25% of variance in the fixed model (R^2_m = 0.25) and ~51.3% (R^2_c = 0.513) when random effects were included (Table 2.2). The negative coefficient for GDD (estimate = -1.47×10^{-5}) indicates that as GDD increases, the value of $\frac{1}{\text{ASV R'}}$ decreases. Thus, a

decrease in $\frac{1}{\text{ASV R'}}$ means that ASV richness itself is increasing with increasing GDD, indicating that higher temperatures positively affect biodiversity by enhancing ASV richness. The estimated intercept indicates a baseline species richness of approximately 19.1 individuals at zero GDD within birch. The model accounted for variability among different plants, with random effects associated with 'Plant_ID' contributing to the overall model fit. These findings underscore the importance of temperature in shaping the species richness of leaf bacterial communities in birch, while also demonstrating that host plant identity has a minimal effect on variability in species richness among individuals. However, GDDs did not significantly affect Shannon diversity (P = 0.731) in birch. In contrast, GDD accumulation exhibited no significant effect in aspen on either ASV richness (P = 0.427) or Shannon diversity (P = 0.857), suggesting that other variables not considered in this study and stochastic processes likely drive diversity within aspen (Table 2.2).

Within birch, only ASV richness was significantly impacted by GDDs; therefore, pairwise comparisons of GDDs were conducted using the *emmeans* package in R to investigate whether specific GDDs were driving variation in ASV richness with birch, or if the impact of GDDs is more global or consistent across the season (Supplementary Table S2). Results of this test indicate that no combination of pairwise comparisons between GDDs were significantly different. In other words, within birch, ASV richness is not significantly different between any given set of GDDs. This suggests that while GDDs have a significant overarching, consistent effect on ASV richness within birch across the season, the differences in richness between individual time points are not substantial enough to be statistically significant. Pairwise comparisons between GDDs within aspen were not conducted since neither alpha diversity metric was significantly impacted by GDDs.

Finally, further testing with ANOVA and Kruskal-Wallis methods on GDD-subset data assessed intraspecific variation of individuals in both species ('Plant_ID') at each GDD (Supplementary Tables S6–S7). However, since 'GDD_5C' is treated as a continuous variable, KPSS tests were performed to assess the appropriateness of GDDs being subset and categorized in this manner. All KPSS tests for temporal autocorrelation indicate that—both interspecifically and intraspecifically—ASV richness and Shannon diversity were not temporally autocorrelated. The tests were unable to reject the null hypothesis that the datasets were stationary ($P > 0.05$). Therefore, this data is not temporally linked, and it is appropriate to subset the data by GDD value to determine 'Plant_ID' differences within each host species.

For birch, individual plant attributes ('Plant_ID') did not significantly affect either ASV richness or Shannon diversity at any GDD sampling point (i.e., plant individuals did not differ significantly in their alpha diversity at any given GDD), indicating that GDDs are a more critical driver of bacterial diversity (Supplementary Table S3). Similarly, aspen showed no significant effect of 'Plant_ID' on bacterial diversity at any given GDD sampling point (Supplementary Table S4). However, since GDDs have no significant impact on alpha diversity within aspen, it reinforces the notion that environmental and host factors not investigated here may be driving alpha diversity dynamics within aspen.

***S3.2 Community Composition and Structure*—**When subset by GDD, the greatest differences between the host tree species in bacterial community structure occurred at 605 (early-mid phenology), 1606 (mid-late phenology), 2140, and 2219 GDDs, representing key stages of seasonal phenology—the latter two of which represent late phenology and near senescence (Supplementary Fig. S17). Thus, variation in leaf bacterial community structure between birch

and aspen is driven primarily by host species, with the most pronounced differences occurring early-mid, mid-late, and late phenology. To assess beta-diversity patterns and the structure of bacterial communities within birch, a Bray-Curtis dissimilarity matrix was applied. Similarly, the Bray-Curtis dissimilarity matrix was used to assess community structure within aspen, starting with homogeneity and multivariate dispersion analyses to gauge the impact of these variances on the structure of leaf bacterial communities. Analyses of homogeneity and multivariate dispersion assessed the relative impact of between- and within-community compositions (Moroenyane et al. 2021).

In birch, increased multivariate dispersion occurred at GDDs that aligned with early-mid and late phenological stages (Supplementary Figs. S9–S10). Leaf bacterial communities of birch leaves exhibited marginally significant heterogeneous dispersion across GDDs ($F = 2.512$, $P = 0.048$). However, Tukey's HSD post-hoc tests revealed that while some specific comparisons, such as between 437 and 2219 GDDs, approached significance ($P = 0.0549$), most comparisons showed no statistically significant differences in dispersion (all $P > 0.05$). This suggests that while certain GDD thresholds may influence community variability, the differences are not consistently strong across all groups. Despite variations in data spread, central tendencies (means) remained similar. Analysis revealed only one plant (Plant_ID: 8553879) with a deviation in multivariate dispersion, suggesting it is potentially driving most within-species differences. However, across all birch trees, there was no significant multivariate dispersion (Supplementary Figs. S11–S12). The leaf bacterial communities did not show significant heterogenous dispersion ($F = 0.848$, $P = 0.51$), with a Tukey HSD test confirming non-significant differences in means between groups.

In trembling aspen, multivariate dispersion was limited across GDDs, except during late phenological stages (Supplementary Figs. S13–S14). Here, leaf bacterial communities demonstrated significant heterogeneous dispersion ($F = 4.005$, $P = 0.004$). Post-hoc Tukey HSD tests identified the point at which the season reaches 2140 GDDs as a potential driver of these differences, demonstrating significant dispersion compared to other GDD sampling points: 437 ($P = 0.0367$), 605 ($P = 0.0173$), 1087 ($P = 0.00768$), 1606 ($P = 0.00342$), 1992 ($P = 0.0278$), and 2219 ($P = 0.0231$). This indicates that the conditions at 2140 GDDs promote greater homogeneity in bacterial community structure, particularly distinguishing late-season stages from mid-late and early-season stages, while no significant differences were found between early and mid-season stages (Supplementary Fig. S11). Regarding individual plants, only one tree (Plant_ID: 8987955) showed slight deviation in multivariate dispersion (Supplementary Figs. S15–S16), but overall, there was no significant multivariate dispersion across all aspen plants ($F = 0.582$; $P = 0.678$), with a Tukey HSD test further confirming non-significant differences between groups.

To visualize and investigate bacterial community structure changes across GDDs within each species, Principal Coordinate Analysis (PCoA) using Bray-Curtis dissimilarity was performed for each host, exclusively (Supplementary Fig. S18). Within birch, PERMANOVA (Supplementary Table S5) revealed that GDDs significantly impacted leaf bacterial community shifts throughout host phenology ($F = 6.024$, $P = 0.01$), explaining ~14.9% of the variation ($R^2 = 0.149$). 'Plant_ID' did not significantly influence community variation ($F = 1.159$, $P = 0.231$), nor did the interaction between 'Plant_ID' and GDDs ($F = 1.159$, $P = 0.231$; Supplementary Fig. S18A; Supplementary Table S5). In aspen, PERMANOVA showed GDDs significantly impacted community variation across host phenology ($F = 1.288$, $P = 0.023$), though the effect was modest

(R^2 = 0.037). In contrast, 'Plant_ID' (F = 0.91; P = 0.952) and its interaction with GDDs (F = 0.963; P = 0.735) did not significantly affect leaf bacterial community structure (Supplementary Fig. S18B; Supplementary Table S5).

Despite the significant impact of GDDs, the PCoA did not clearly separate bacterial communities across GDDs within either species (Supplementary Fig. S18). When grouped by generalized phenological periods (early-mid, mid-late, late-senescence), there is no clear separation, except for in birch where early-mid phenology and late phenology-senescence demonstrate clear separation (Supplementary Fig. S18A). Both groupings share overlap with mid-phenology, supporting the idea of mid-season restructuring. However, it is important to note that generalized phenological periods are unbalanced in their groupings. Within birch, a significant negative correlation was observed between Axis 1 and GDDs (Spearman's ρ = -0.715, $P = 1.344 \times 10^{-6}$), indicating that increasing GDD values correspond to lower Axis 1 scores and demonstrating directionality within birch leaf microbiomes. Axis 2 showed a weak, non-significant correlation with GDDs (ρ = 0.272, P = 0.115), suggesting this axis is not strongly associated with the seasonal variation captured in the ordination. Therefore, the directionality in the PCoA, from early-mid phenology (low GDDs) to late phenology and early senescence (high GDDs), is likely driven by Axis 1, reflecting a significant seasonal phenological gradient along this axis.

Despite no clear separation in the PCoA for aspen, a significant negative correlation was observed between Axis 1 and GDDs (Spearman's ρ = -0.337, P = 0.044; Supplementary Fig. S18B). In contrast, Axis 2 showed no significant correlation with GDDs (Spearman's ρ = -0.17, P = 0.32). This indicates that increasing GDD values are associated with lower Axis 1 values,

suggesting a potential seasonal directional relationship. Therefore, the observed negative correlation along Axis 1 indicates a significant seasonal phenological trend in response to GDDs within the aspen dataset. The low R^2 and high residual R^2 further implies that a combination of unexamined environmental variables and stochasticity likely shape leaf microbiome structure.

***S3.3 Differential Abundance Analysis*—**Across the entire growing season, differential abundance analysis revealed a notable contrast in the number of differentially abundant ASVs between birch and aspen, measured as $\log_2$ fold change ($\log_2$FC). Overall, birch had only three ASVs that were significantly more abundant compared to aspen, whereas aspen exhibited a total of 14 ASVs that were significantly more abundant relative to birch (Supplementary Fig. S20; Supplementary Table S8). In birch, the ASVs with the highest positive $\log_2$FC (indicating greater relative abundance compared to aspen) were ASV10 (unidentified Proteobacteria), ASV39 (*Endobacter* sp.), and ASV186 (*PMMR1* sp.), in descending order. Conversely, aspen exhibited over four times as many ASVs with a negative $\log_2$FC (indicating greater relative abundance compared to birch), including ASV86 (*Erwiniaceae*), ASV106 (*Blastococcus* sp.), ASV44 (*Methylobacterium-Methylorubrum* sp.), ASV33 (*Quadrisphaera* sp.), ASV81 (*Hymenobacter* sp.), and ASV36 (*Rubellimicrobium* sp.).

When the data were subset by GDD sampling points, differential abundance analysis identified one ASV (ASV10) with a positive $\log_2$FC, indicating significantly greater relative abundance in birch compared to aspen at GDD 437 (Supplementary Fig. S22; Supplementary Table S9). At 605 GDDs, 15 ASVs were identified as differentially abundant, with 4 showing positive $\log_2$FC (birch enriched) and 11 showing negative $\log_2$FC (aspen enriched). At 1087 GDDs (mid-phenology), the number of differentially abundant ASVs increased to 18, with 10

enriched in birch and 8 in aspen. By 1606 accumulated GDDs, the total decreased to 10 differentially abundant ASVs, with 1 enriched in aspen and 9 in birch. As phenology progressed to late-season (1992 GDDs), the number rose to 29, with 25 ASVs enriched in birch and 4 in aspen. The number of differentially abundant ASVs peaked at 2140 GDDs, with 45 identified—25 enriched in birch and 20 in aspen. At 2219 accumulated GDDs (senescence onset), the total decreased to 32, with 20 ASVs enriched in birch and 12 in aspen.

At each GDD along host phenology, birch consistently exhibited a higher number of ASVs with significant differential abundance compared to aspen. From the beginning of phenological sampling (437 GDDs), the number of differentially abundant ASVs increased steadily until 1087 GDDs. This was followed by a decrease at 1606 GDDs, before rising again into late-season (1992 and 2140 GDDs) and tapering slightly by 2219 GDDs. Both hosts share this similar trend, with peaks in $\log_2$FC occurring earlier and late in the growing season (Supplementary Fig. S22; Supplementary Table S9). Notably, ASV10, identified only to the phylum Proteobacteria in the SILVA database, was consistently more abundant in birch than aspen across all GDDs, highlighting its potential ecological and functional relevance to birch.

Across the phenological gradient, several ASVs were consistently enriched in birch compared to aspen, with notable shifts in the composition of these ASVs across GDDs (Supplementary Figs. S21-S22; Supplementary Tables S11-S12). At 437 GDDs, only ASV10 (unidentified Proteobacteria) was enriched in birch. By 605 GDDs, ASV19 (unidentified Proteobacteria) emerged as the second most enriched ASV in birch. By 1087 GDDs, ASV10 and ASV19 were joined by ASV35 (unidentified beyond Bacteria), ASV8 (*Endobacter* sp.), ASV42 (*1174-901-12* sp.), and ASV95 (*Bryocella* sp.). At GDD 1606, ASV9 (*1174-901-12* sp.) and

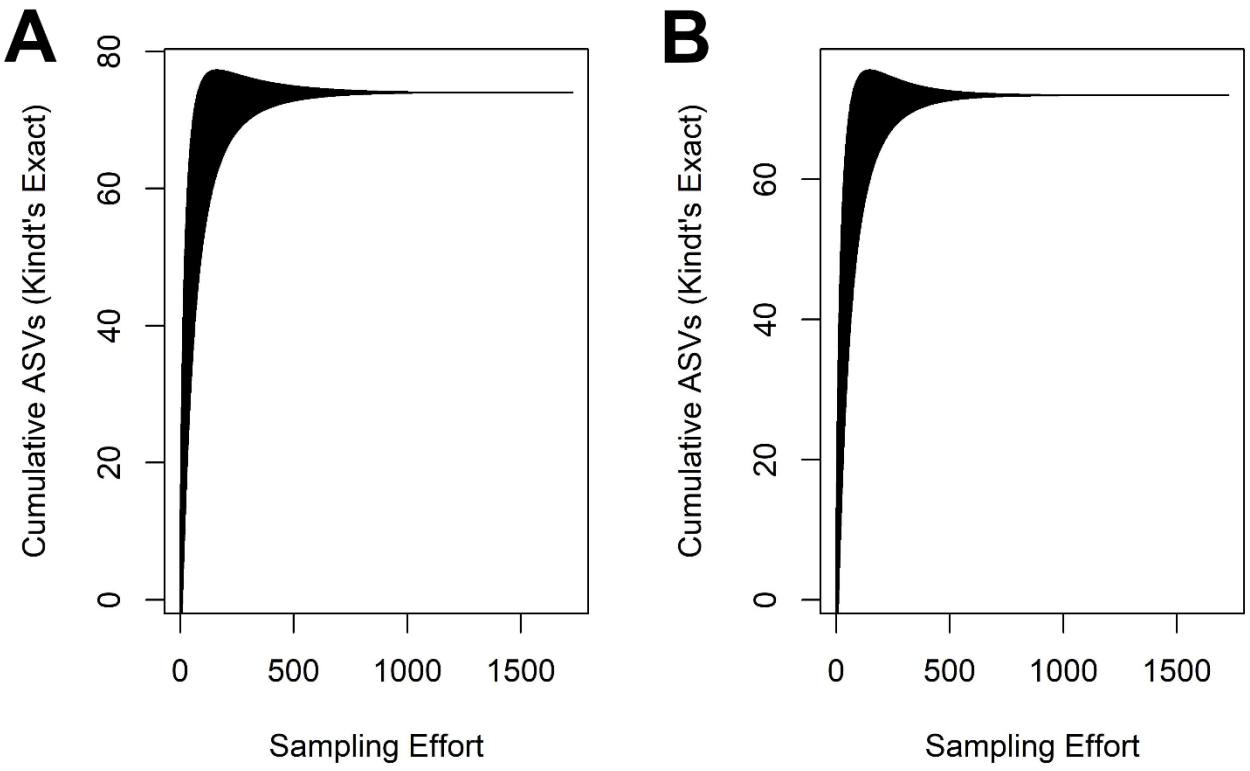
ASV49 (*P3OB-42* sp.) became prominent. By 1992 GDDs, 16 additional ASVs exhibited significant enrichment in birch, with ASV10 remaining the most enriched. New ASVs, such as ASV7 (*Endobacter* sp.), ASV14 (*1174-901-12* sp.), and ASV97 (*Massilia* sp.), appeared at this stage. At GDD 2140, ASV7 (*Endobacter* sp.) overtook ASV10 as the most enriched ASV, followed by ASV9, ASV19, ASV29, ASV25, ASV14, ASV8, and ASV35. By GDD 2219, ASV7 and ASV8 (both *Endobacter* sp.) surpassed ASV10, while ASV109 (*Massilia* sp.) and ASV37 (Myxococcota) also emerged among the most enriched ASVs.

In contrast, aspen had fewer differentially abundant ASVs across phenology, overall (Supplementary Fig. S22; Supplementary Table S9). At the start (437 GDDs), no ASVs were differentially abundant relative to birch, but by 605 GDDs, 11 ASVs were differentially abundant, including ASV33 (*Quadrisphaera* sp.), ASV59 (unidentified Bacteria), ASV54 (*Sphingomonas* sp.), and ASV32 (*Sphingomonas* sp.), in descending order of abundance. By 1087 GDDs, the number of differentially abundant ASVs decreased slightly, with ASV33 remaining the most prominent. Other significant ASVs at this time included ASV106 (*Blastococcus* sp.), ASV81 (*Hymenobacter* sp.), ASV60 (*Sphingomonas* sp.), and ASV93 (*Corynebacterium* sp.). At 1606 GDDs, the number decreased further, with only ASV44 (*Methylobacterium-Methylorubrum* sp.) being significantly enriched—a pattern also observed at 605, 1087, and 2140 GDDs. By 1992 GDDs, the number of differentially abundant ASVs slightly increased, with ASV172 (*Massilia timonae*) showing the most significant enrichment, followed by ASV59, ASV33, and ASV414 (*Amnibacterium* sp.). At 2140 GDDs, there was a more substantial increase in differentially abundant ASVs. ASV36 (*Rubellimicrobium* sp.) exhibited the greatest change, followed by ASV45 (*Actinomycetospora iriomotensis*), ASV33, and ASV44. Other notable ASVs at this stage included ASV41 (*Methylobacterium-*

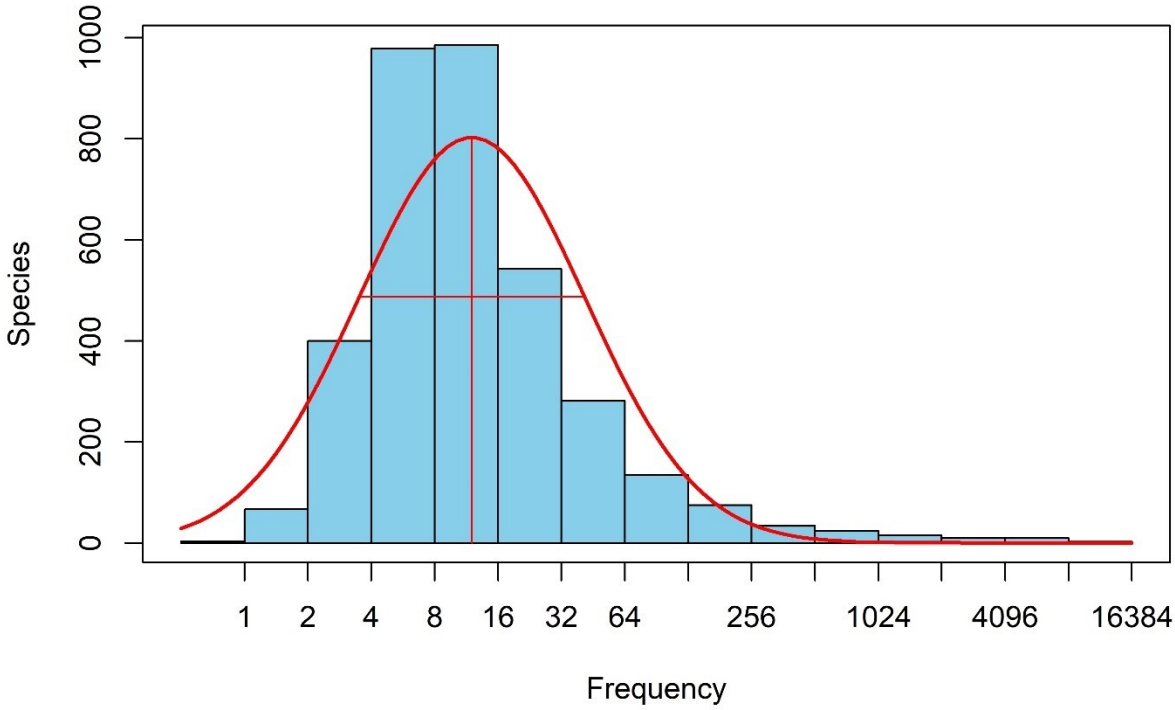
Methylorubrum sp.), ASV80 (*Amnibacterium* sp.), and ASV59 (unidentified Bacteria). By 2219 GDDs, ASV45 remained the most abundant, followed by ASV59 and ASV33, among others.

Overall, differentially abundant ASVs in birch were primarily dominated by Proteobacteria, Acidobacteriota, and Myxococcota (Supplementary Figs. S21–S22; Supplementary Tables S11–S12). Key genera in birch included *Endobacter* sp., *1174-901-12* sp., *Bryocella* sp., *P3OB-42* sp., and *Massilia* sp. Notably, ASV10, which was the most consistently differentially abundant ASV across birch's seasonal phenology, could only be identified to the phylum level. In contrast, aspen exhibited differential enrichment of ASVs from Actinobacteriota and Bacteroidota, though it shared some Proteobacteria ASVs with birch. Key genera in aspen included *Quadrisphaera*, *Sphingomonas*, *Blastococcus*, *Hymenobacter*, *Methylobacterium-Methylorubrum*, *Corynebacterium*, and *Rubellimicrobium*, with *Massilia timonae* and *Actinomycetospora iriomotensis* identified as significant at the species level.

SUPPLEMENTAL FIGURES AND TABLES

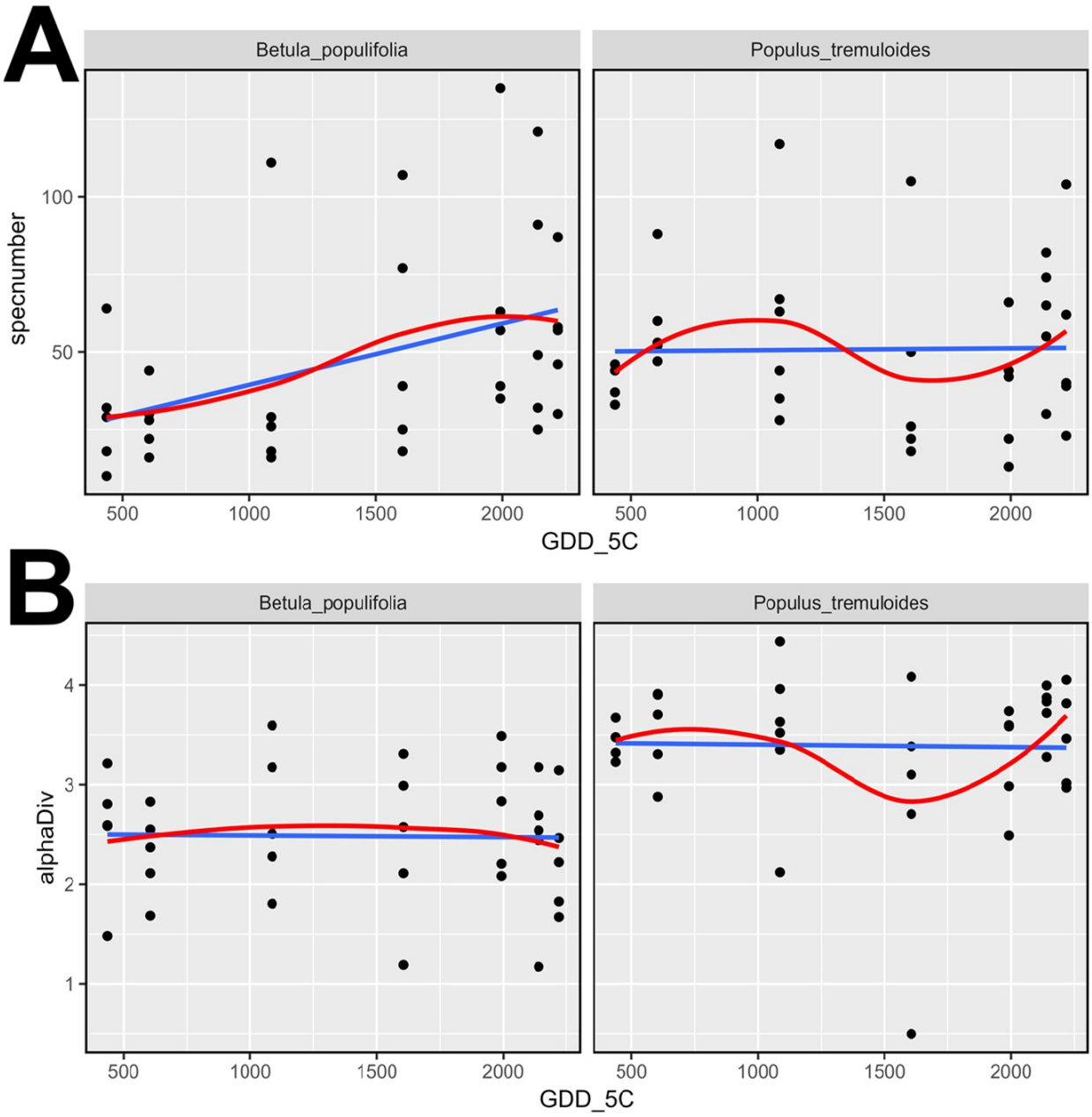


Supplementary Figure S1. Leaf bacterial ASV accumulation curve indicating the cumulative number of recovered ASVs (Kindt's exact method) as a function of sampling effort with 95% confidence interval for **(A)** all samples and **(B)** the positive control.



1754

1755 **Supplementary Figure S2.** Preston log-normal curve indicating the total number of leaf
1756 bacterial ASVs recovered (area under the curve) and the proportion of rare ASVs recovered.
1757 Sequencing recovered both abundant and rare ASVs, as indicated by the peak and truncation
1758 points at both ends of the curve.



1759

1760 **Supplementary Figure S3.** Untransformed relationship between accumulated growing degree
1761 days at a base temperature of 5°C (GDD_5C) and the **(A)** ASV richness and **(B)** Shannon
1762 diversity index (H′) across two host tree species, grey birch (left panels) and trembling aspen
1763 (right panels). The scatter plots show individual sample data points, while the blue lines
1764 represent linear regression fits. The red lines depict additional smoothing for trend visualization.

Supplementary Table S1. Summary of pairwise comparisons using the *emmeans* package in R to assess the interaction between host species identity and GDDs at a base temperature of 5°C ('Species:GDD_5C') on leaf ASV richness comparing each GDD sampling point in the growing season between grey birch (*Betula*) and trembling aspen (*Populus*).[a]

	ASV Richness[b]			
Species x GDD_5C	**emmean**	***SE***	***t-ratio***	***P***
Betula.437-*Populus*.437	-0.63991	0.257	-2.489	0.451
Betula.605-*Populus*.605	-0.55532	0.238	-2.333	0.552
Betula.1087-*Populus*.1087	-0.31261	0.198	-1.578	0.917
Betula.1606-*Populus*.1606	-0.05127	0.191	-0.269	1
Betula.1992-*Populus*.1992	0.1431	0.212	0.675	1
Betula.2140-*Populus*.2140	0.21763	0.225	0.967	0.999
Betula.2219-*Populus*.2219	0.25741	0.233	1.105	0.996

[a] Table shows the test statistics and associated estimated marginal means (emmean), standard error (*SE*), the *t-ratio*, and *P*-values for each comparison. Results indicate that while the interaction between host species identity and GDDs is significant in the overall model, pairwise comparisons of the species interaction at individual GDD points show no significant differences (*P*-value ∗<0.05, ∗∗<0.01 and ∗∗∗<0.001).

[b] ASV richness was log-transformed to meet model assumptions.

Supplementary Table S2. Summary of pairwise comparisons using the *emmeans* package in R to evaluate the differential effects of GDDs at a base temperature of 5°C ('GDD_5C') on leaf bacterial ASV richness within grey birch. Analyses were conducted between each sampling point combination of 'GDD_5C', accounting for the LMM structure.[a]

Grey Birch				
ASV Richness[b]				
GDD_5C	**emmean**	***SE***	***t-ratio***	***P***
437-605	6.85E-03	0.00972	0.705	0.991
437-1087	6.78E-03	0.00972	0.697	0.992
437-1606	1.84E-02	0.00972	1.89	0.505
437-1992	2.79E-02	0.00972	2.869	0.102
437-2140	2.43E-02	0.00972	2.5	0.203
437-2219	2.66E-02	0.00972	2.735	0.132
605-1087	-7.23E-05	0.00972	-0.007	1
605-1606	1.15E-02	0.00972	1.186	0.893
605-1992	2.10E-02	0.00972	2.164	0.35
605-2140	1.75E-02	0.00972	1.796	0.563
605-2219	1.97E-02	0.00972	2.03	0.423
1087-1606	1.16E-02	0.00972	1.193	0.89
1087-1992	2.11E-02	0.00972	2.172	0.346
1087-2140	1.75E-02	0.00972	1.803	0.559
1087-2219	1.98E-02	0.00972	2.037	0.419
1606-1992	9.52E-03	0.00972	0.979	0.954
1606-2140	5.93E-03	0.00972	0.61	0.996
1606-2219	8.21E-03	0.00972	0.844	0.977
1992-2140	-3.58E-03	0.00972	-0.368	0.999
1992-2219	-1.31E-03	0.00972	-0.134	1
2140-2219	2.28E-03	0.00972	0.234	1

[a] The table shows the estimated marginal means (emmean), standard error (*SE*), *t-ratio*, and *P-values* for each GDD sampling point. Results highlight that while 'GDD_5C' exerts a significant overall impact on (1/ASV R') within *B. populifolia*, the changes in richness between specific 'GDD_5C' values are not large enough to reach statistical significance. (*P*-value $*<0.05$, $**<0.01$, and $***<0.001$).

[b] ASV richness underwent a reciprocal transformations to meet model assumptions.

Supplementary Table S3. Summary of statistical tests (ANOVA and Kruskal-Wallis) evaluating the impact of overall individual host plant characteristics ('Plant_ID') on leaf ASV richness and Shannon diversity at different points in the growing season for grey birch.[a]

GDD_5C	ASV Richness[b]			Shannon Diversity[c]		
	Plant_ID			Plant_ID		
	χ^2	*F-value*	*P*	χ^2	*F-value*	*P*
437	—	0.034	0.866	4	—	0.406
605	—	0.32	0.611	—	6.09	0.0902
1087	4	—	0.406	—	2.274	0.229
1606	—	1.848	0.267	—	0.511	0.526
1992	—	0.198	0.686	—	3.369	0.164
2140	—	0.063	0.819	—	0.047	0.842
2219	—	0.001	0.979	—	0.001	0.981

[a] The analyses were performed on data subset by accumulated GDDs at a base temperature of 5°C ('GDD_5C'). The table shows the test statistics and associated χ^2-, *F*-, and *P*-values for each phenological stage. Results indicate that 'Plant_ID' did not significantly affect ASV richness nor Shannon diversity at any point in the season in both host species (*P*-value $*<0.05$, $**<0.01$ and $***<0.001$).

[b] ASV richness underwent a reciprocal transformation to meet model assumptions.

[c] Shannon diversity underwent a reciprocal transformation to meet model assumptions.

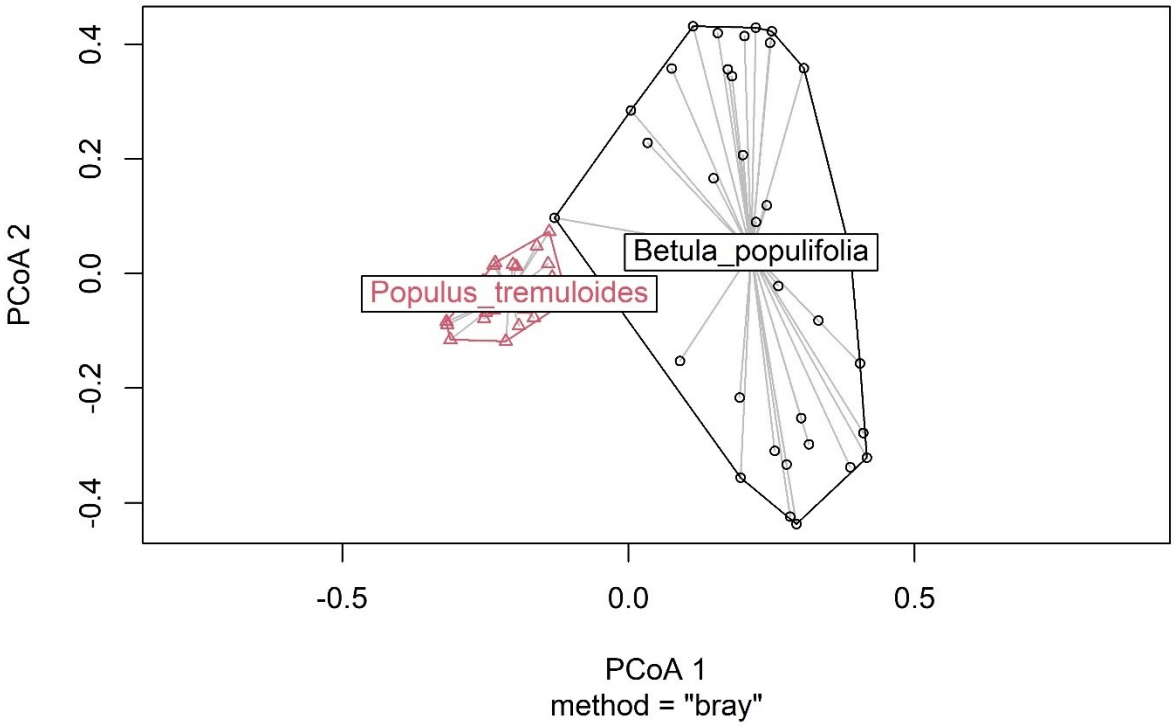
Supplementary Table S4. Summary of statistical tests (ANOVA and Kruskal-Wallis) evaluating the impact of overall individual host plant characteristics ('Plant_ID') on the inverse of foliar ASV richness and Shannon diversity at different points in the growing season for trembling aspen.

GDD_5C	ASV Richness[b]			Shannon Diversity[c]		
	Plant_ID			Plant_ID		
	χ^2	*F-value*	*P*	χ^2	*F-value*	*P*
437	—	0.963	0.399	—	0.058	0.825
605	—	0.241	0.657	—	0.134	0.739
1087	—	0.049	0.836	—	1.402	0.302
1606	4	—	0.406	—	0.213	0.676
1992	—	0.045	0.846	—	0.345	0.598
2140	—	1.492	0.309	—	1.083	0.374
2219	—	0.07	0.809	—	0.617	0.489

[a] The analyses were performed on data subset by accumulated growing degree days at a base temperature of 5°C ('GDD_5C'). The table shows the test statistics and associated χ^2-, *F-,* and *P*-values for each phenological stage. Results indicate that 'Plant_ID' did not significantly affect ASV richness nor Shannon diversity at any point in the season in both host species (*P*-value $*<0.05$, $**<0.01$ and $***<0.001$).

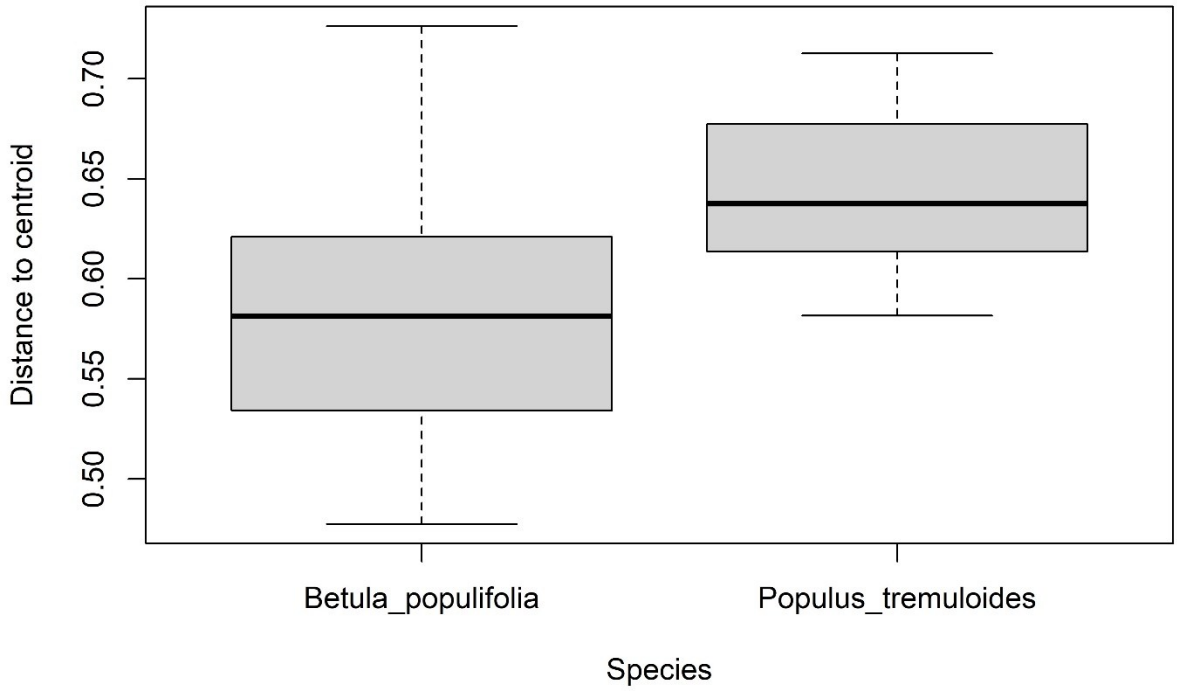
[b] ASV richness underwent a reciprocal transformation to meet model assumptions.

[c] Shannon diversity was square-root transformed to meet model assumptions.

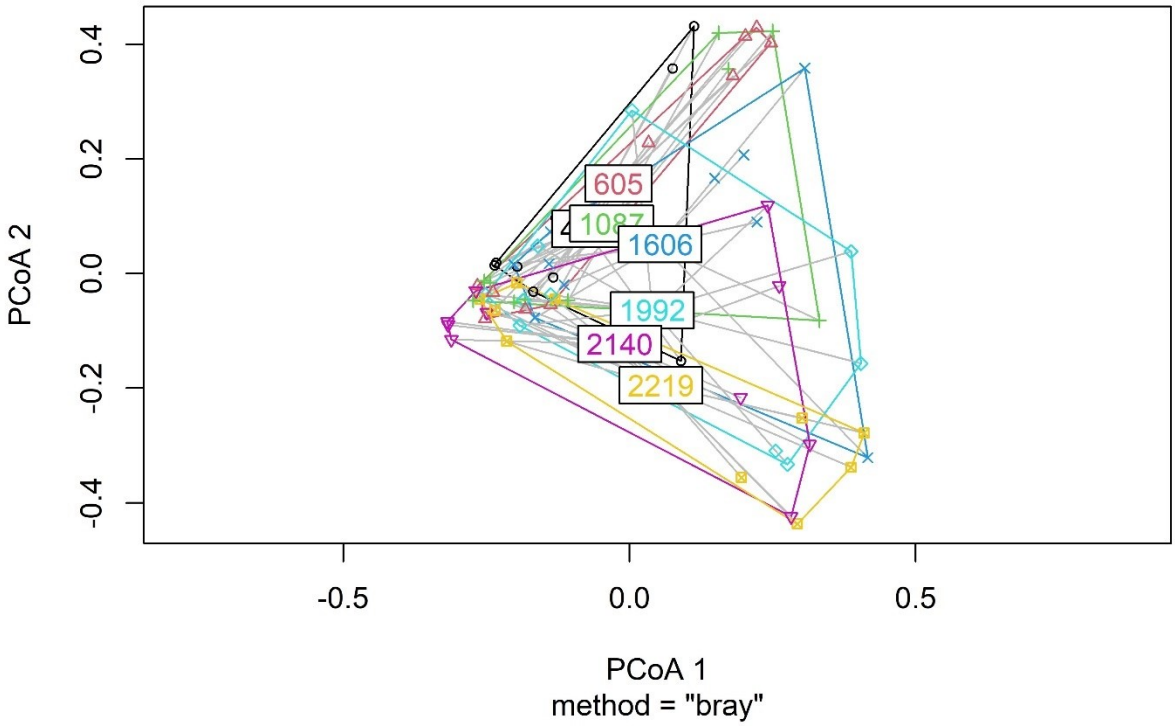


1806

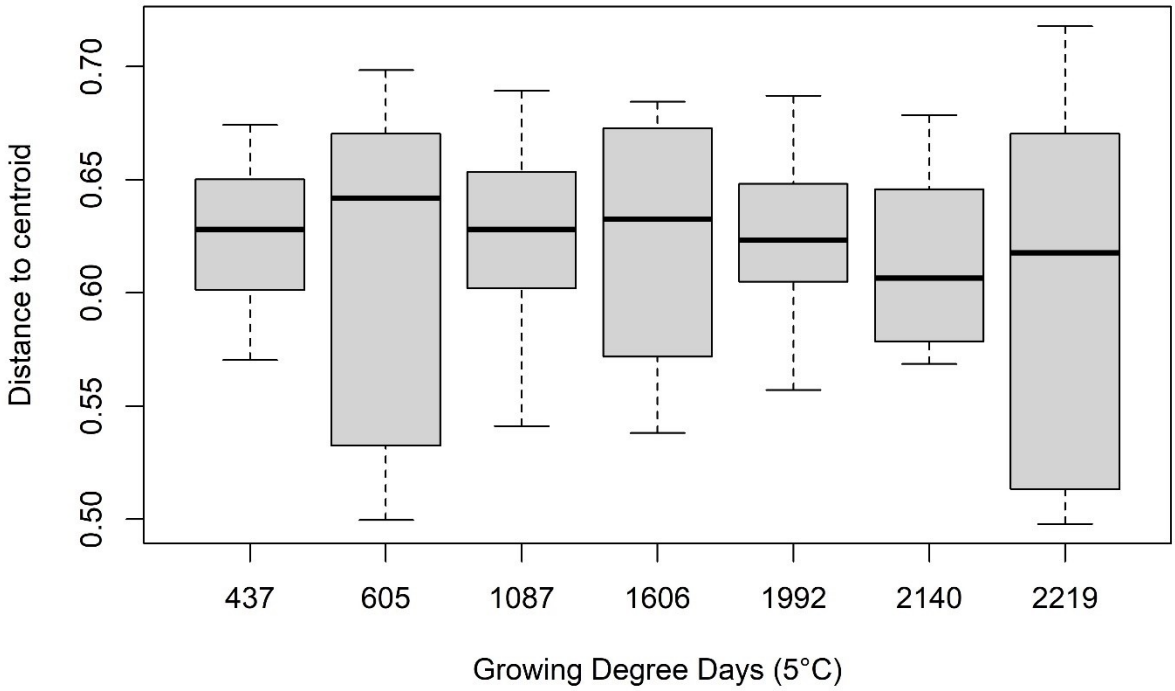
1807 **Supplementary Figure S4.** Principal Coordinate Analysis (PCoA) showing multivariate
1808 dispersion of leaf bacterial communities comparing interspecific differences between grey birch
1809 and trembling aspen, represented by the host 'Species' variable. This figure is based on the Bray-
1810 Curtis dissimilarity between the two host tree species' leaf bacterial communities, denoted by
1811 'Species'.



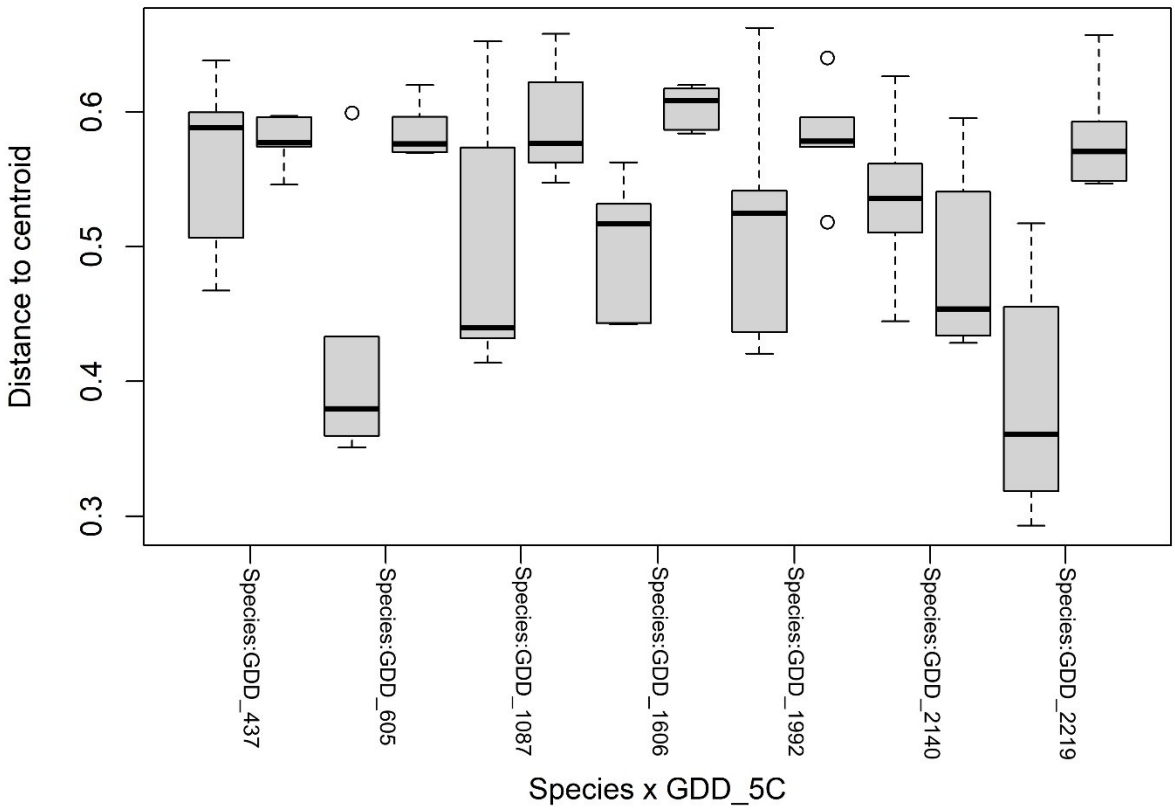
Supplementary Figure S5. Homogeneity of multivariate dispersion (distance to centroid) of leaf bacterial communities comparing interspecific differences between grey birch and trembling aspen represented by the host 'Species' variable. This figure is based on the Bray-Curtis dissimilarity between the two host tree species' leaf bacterial communities, denoted by 'Species'.



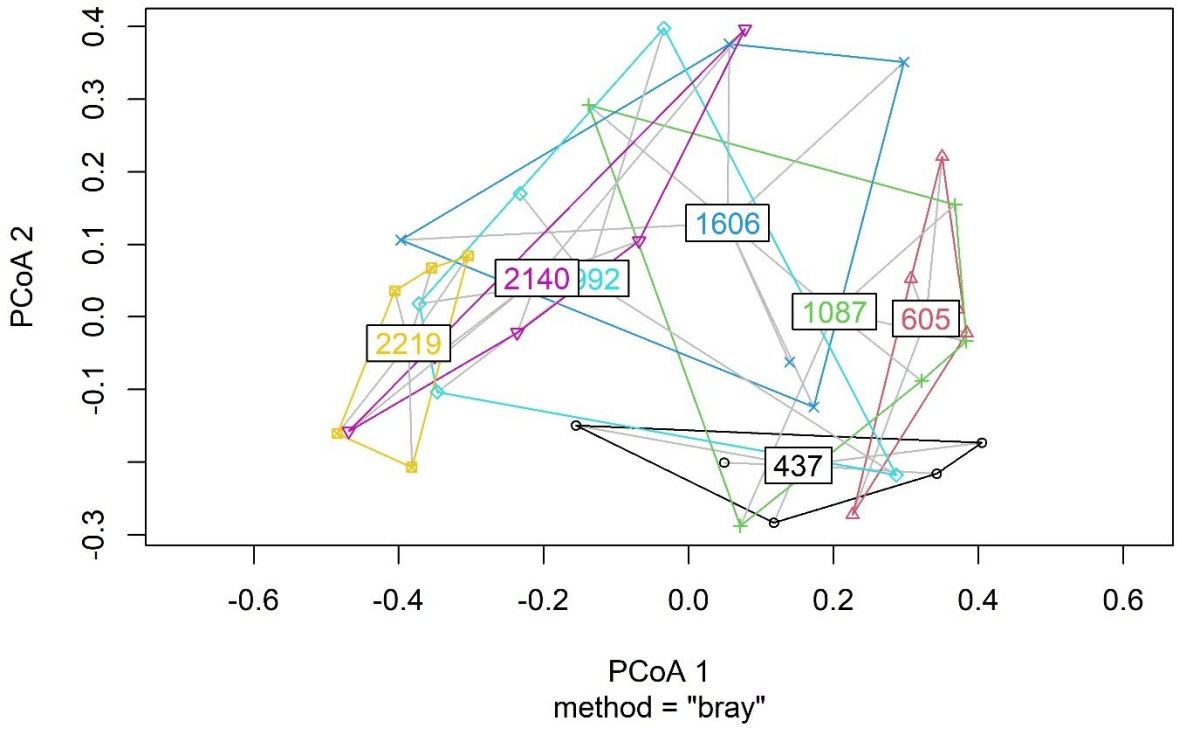
Supplementary Figure S6. Principal Coordinate Analysis (PCoA) showing multivariate dispersion of leaf bacterial communities comparing interspecific differences between grey birch and trembling aspen throughout seasonal phenology, considering only the variable of accumulated growing degree days at a base temperature of 5°C ('GDD_5C'). This figure is based on the Bray-Curtis dissimilarity between the two host tree species' leaf bacterial communities regarding 'GDD_5C'.



Supplementary Figure S7. Homogeneity of multivariate dispersion (distance to centroid) of leaf bacterial communities comparing interspecific differences between grey birch and trembling aspen throughout seasonal phenology, considering only the variable of accumulated growing degree days at a base temperature of 5°C ('GDD_5C'). This figure is based on the Bray-Curtis dissimilarity between the two host tree species' leaf bacterial communities regarding 'GDD_5C'.



Supplementary Figure S8. Homogeneity of multivariate dispersion (distance to centroid) of leaf bacterial communities comparing interspecific differences between the interaction of grey birch with GDDs and the interaction of trembling aspen with GDDs, throughout seasonal phenology, considering the interaction variable ('Species:GDD_5C'). This figure is based on the Bray-Curtis dissimilarity between the two host tree species' leaf bacterial communities regarding 'GDD_5C'. Comparisons of interest are those between host species at shared GDD points.

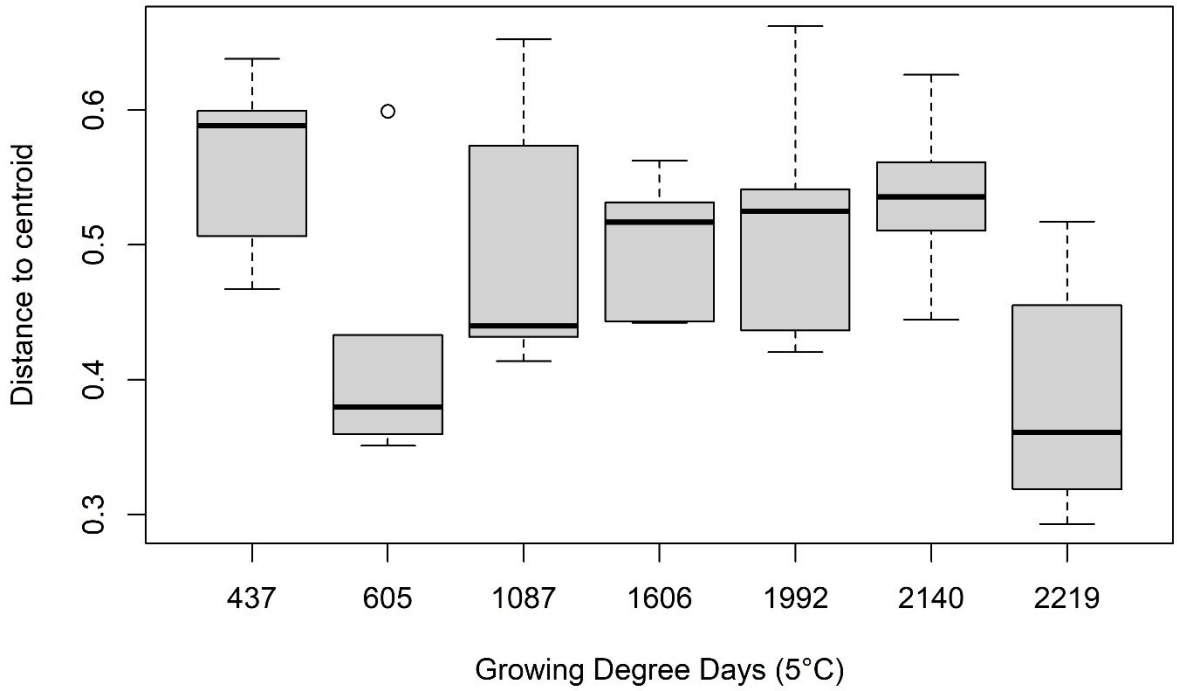


1837

1838 **Supplementary Figure S9.** Principal Coordinate Analysis (PCoA) showing multivariate

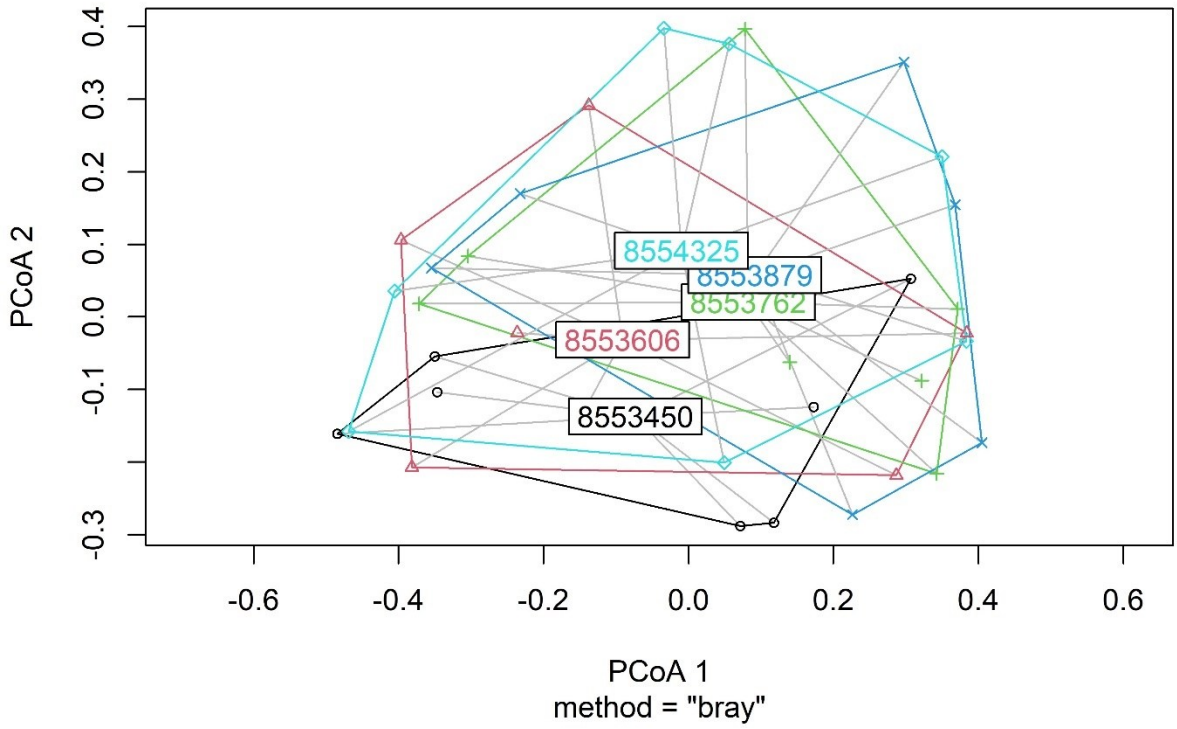
1839 dispersion of leaf bacterial communities within grey birch based on the Bray-Curtis dissimilarity

1840 across growing degree days at a base temperature of 5°C ('GDD_5C').



1841

1842 **Supplementary Figure S10.** Homogeneity of multivariate dispersion (distance to centroid) of
1843 leaf bacterial communities within grey birch based on the Bray-Curtis dissimilarity across
1844 growing degree days at a base temperature of 5°C ('GDD_5C').

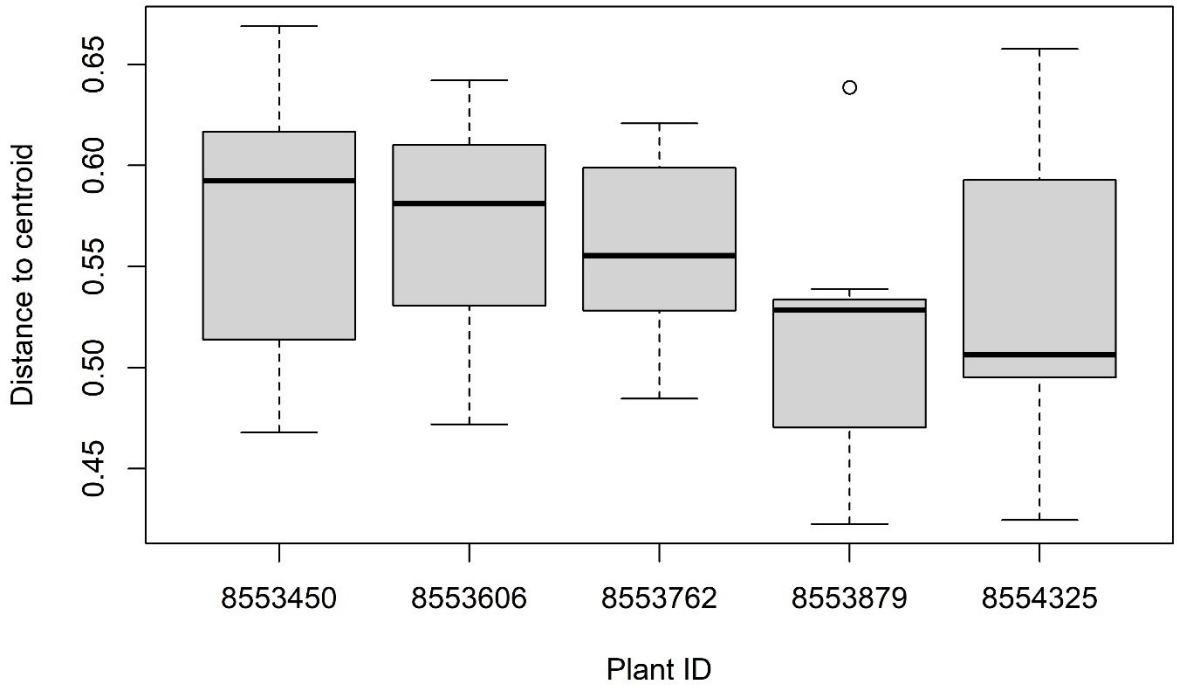


1845

1846 **Supplementary Figure S11.** Principal Coordinate Analysis (PCoA) showing multivariate

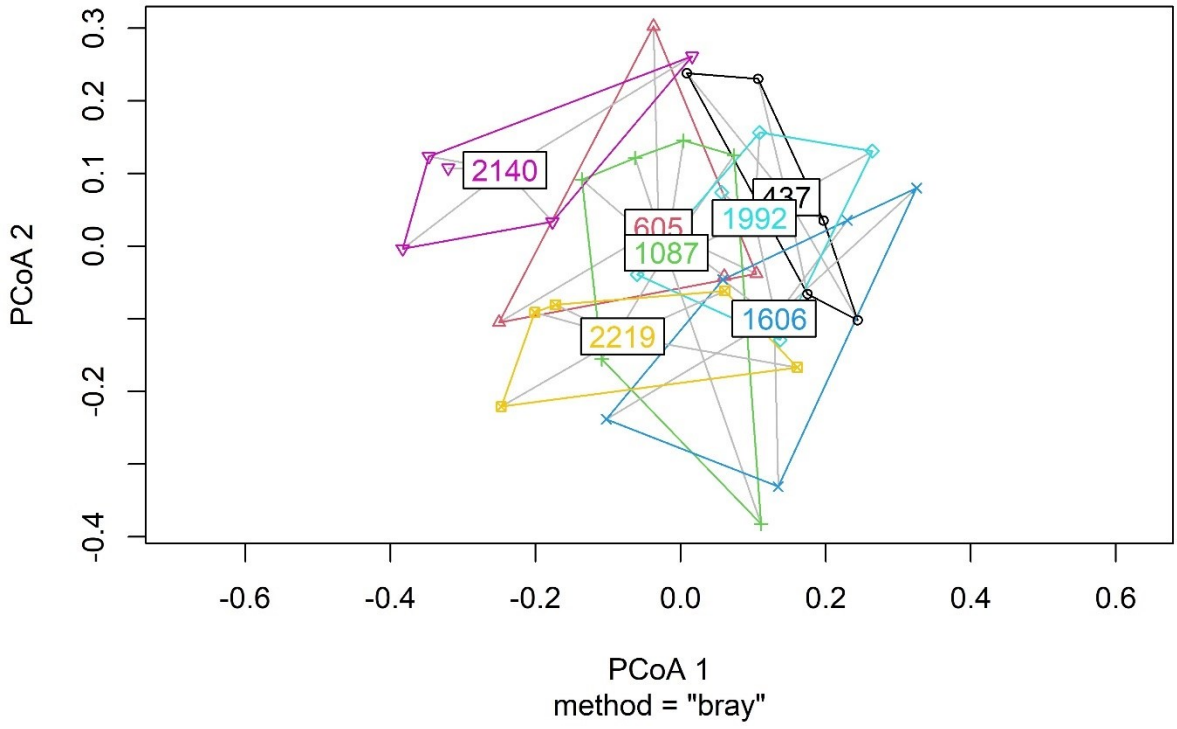
1847 dispersion of leaf bacterial communities within grey birch based on the Bray-Curtis dissimilarity

1848 across individual plant identifiers, or Plant ID ('Plant_ID').



1849

1850 **Supplementary Figure S12.** Homogeneity of multivariate dispersion (distance to centroid) of
1851 leaf bacterial communities within grey birch based on the Bray-Curtis dissimilarity across
1852 individual plant identifiers, or Plant ID ('Plant_ID').

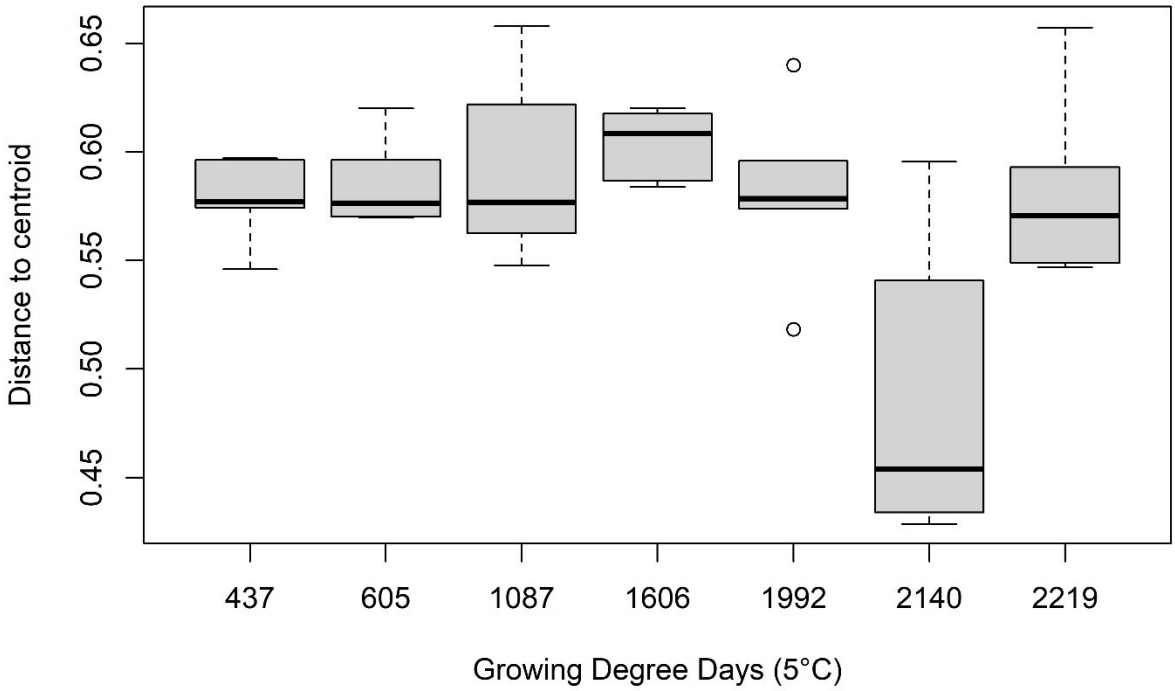


1853

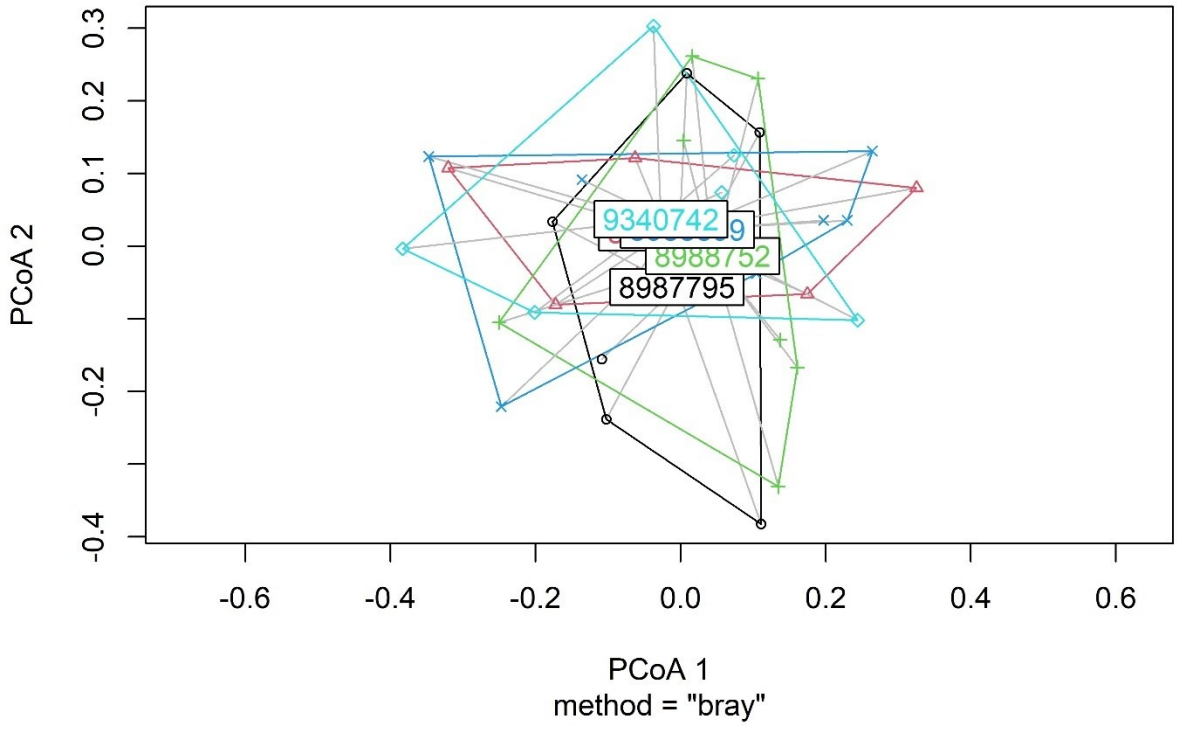
1854 **Supplementary Figure S13.** Principal Coordinate Analysis (PCoA) showing multivariate

1855 dispersion of leaf bacterial communities within trembling aspen based on the Bray-Curtis

1856 dissimilarity across growing degree days at a base temperature of 5°C ('GDD_5C').



Supplementary Figure S14. Homogeneity of multivariate dispersion (distance to centroid) of leaf bacterial communities within trembling aspen based on the Bray-Curtis dissimilarity across growing degree days at a base temperature of 5°C ('GDD_5C').

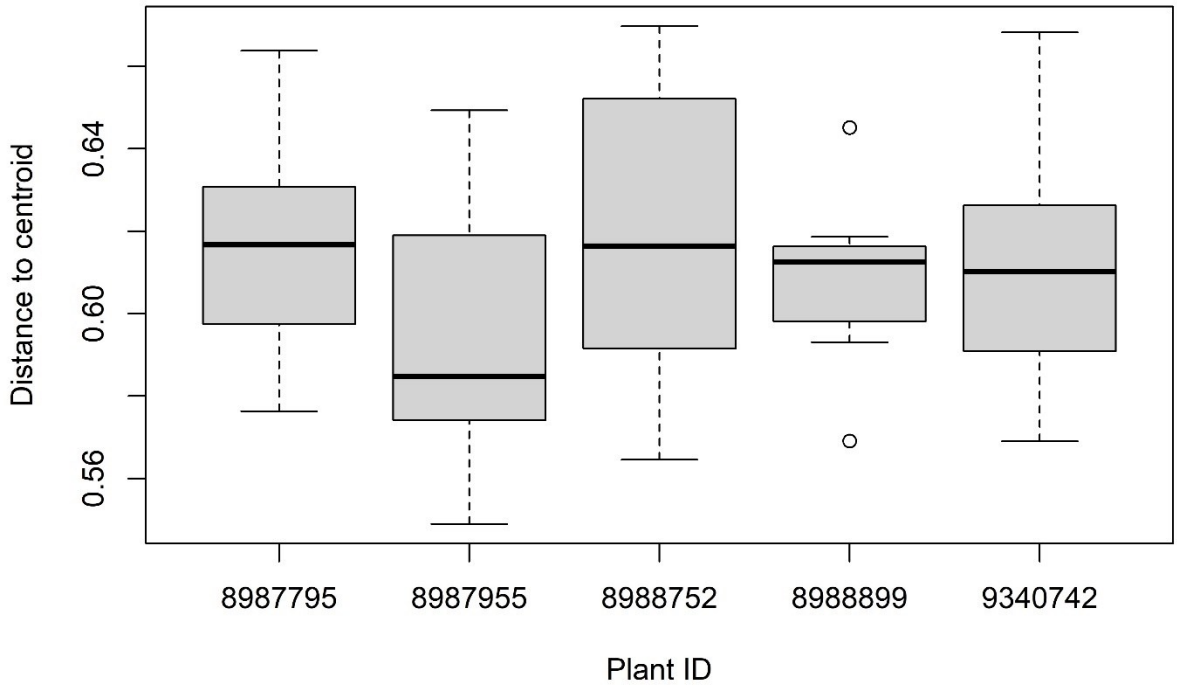


1861

1862 **Supplementary Figure S15.** Principal Coordinate Analysis (PCoA) showing multivariate

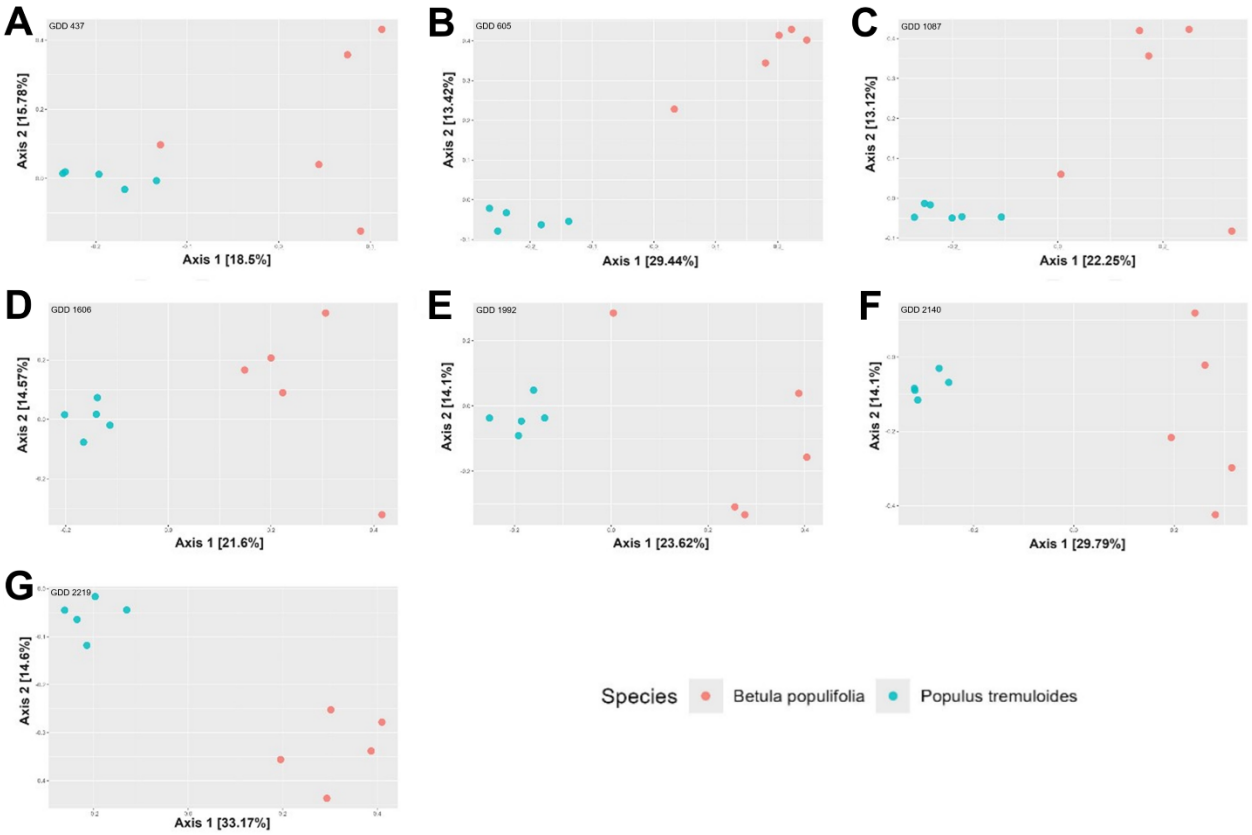
1863 dispersion of leaf bacterial communities within trembling aspen based on the Bray-Curtis

1864 dissimilarity across individual plant identifiers, or Plant ID ('Plant_ID').

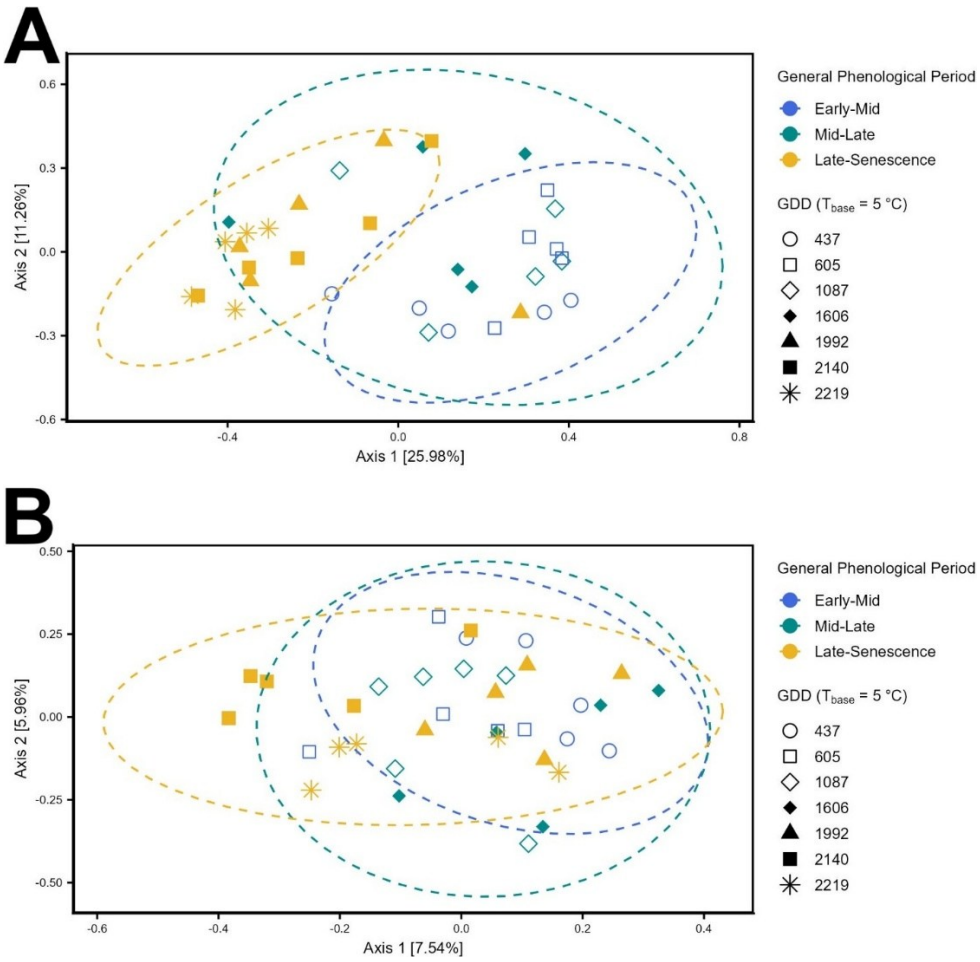


1865

1866 **Supplementary Figure S16.** Homogeneity of multivariate dispersion (distance to centroid) of
1867 leaf bacterial communities within trembling aspen based on the Bray-Curtis dissimilarity across
1868 individual plant identifiers, or Plant ID ('Plant_ID').



Supplementary Figure S17. Principal Coordinate Analysis (PCoA) comparing leaf bacterial communities of grey birch (pink) and trembling aspen (turquoise) based on Bray-Curtis dissimilarity as host seasonal phenological change progresses, represented by accumulated growing degree days at a base temperature of 5°C (GDDs). Data has been subset by GDD to pinpoint the greatest differences between host species' bacterial community composition. Each data point denotes a plant individual sampled at GDDs **(A)** 437, **(B)** 605, **(C)** 1087, **(D)** 1606, **(E)** 1992, **(F)** 2140, and **(G)** 2219. The more proximal samples are to one another, the more similar their community composition is. In contrast, samples that are further from one another are more dissimilar and distinct in their foliar bacterial community composition.

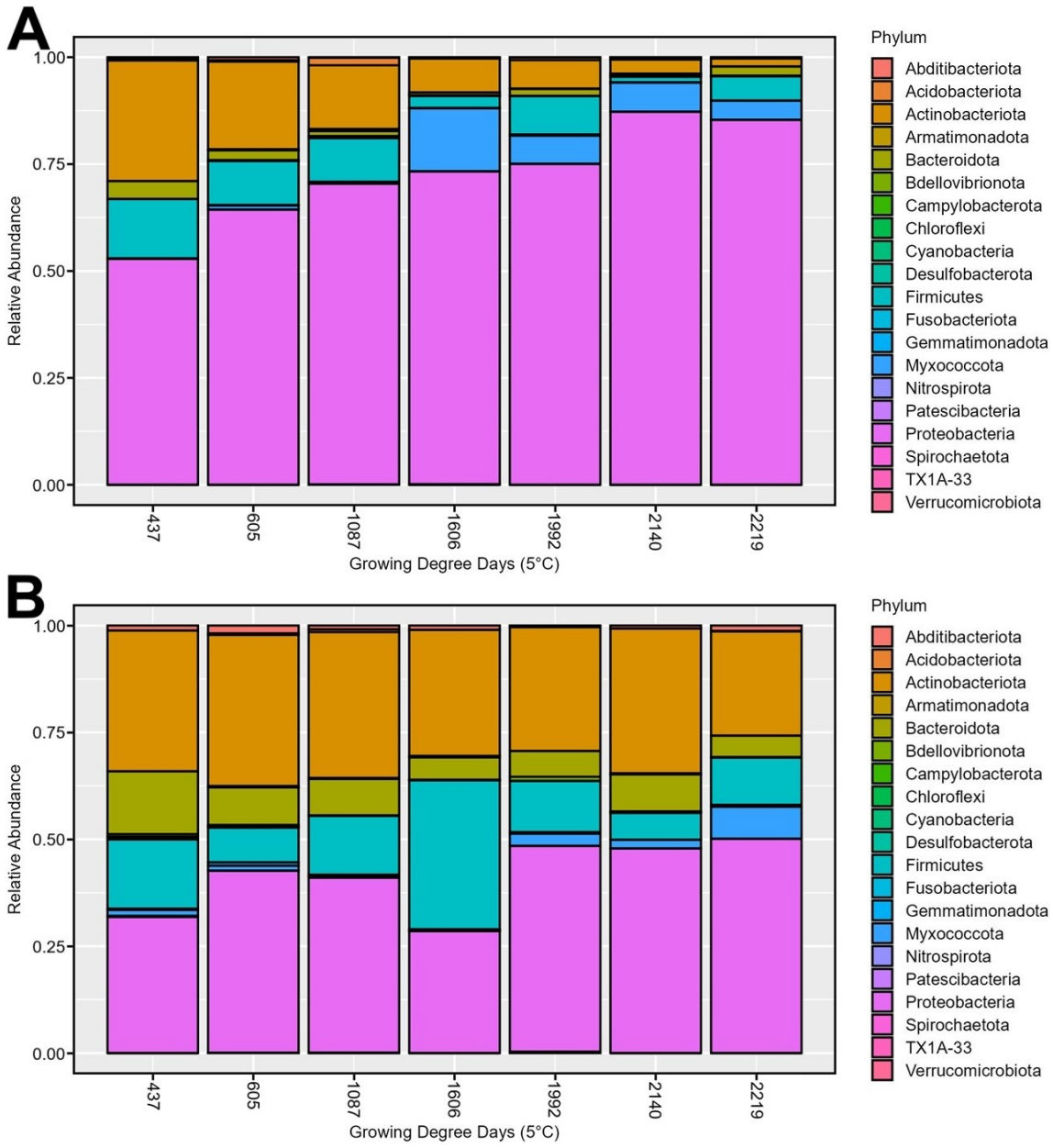


Supplementary Figure S18. Principal Coordinate Analysis (PCoA) of leaf bacterial communities within a population of **(A)** grey birch and **(B)** trembling aspen individuals based on Bray-Curtis dissimilarity along host seasonal phenology, represented by accumulated GDDs (T_{base} = 5°C) and grouped by general phenology. Each data point denotes a plant individual sampled at GDDs 437 (open circle), 605 (open square), 1087 (open diamond), 1606 (filled diamond), 1992 (filled triangle), 2140 (filled square), and 2219 (asterisk). Early-mid phenology (blue) encompasses 437 and 605 GDDs; mid-late phenology (green) denotes 1087 and 1606 GDDs; and late phenology to senescence onset (goldenrod) corresponds to 1992, 2140, and 2219 GDDs. Samples that are more distal from one another are more dissimilar and distinct in their foliar bacterial community composition than those proximal.

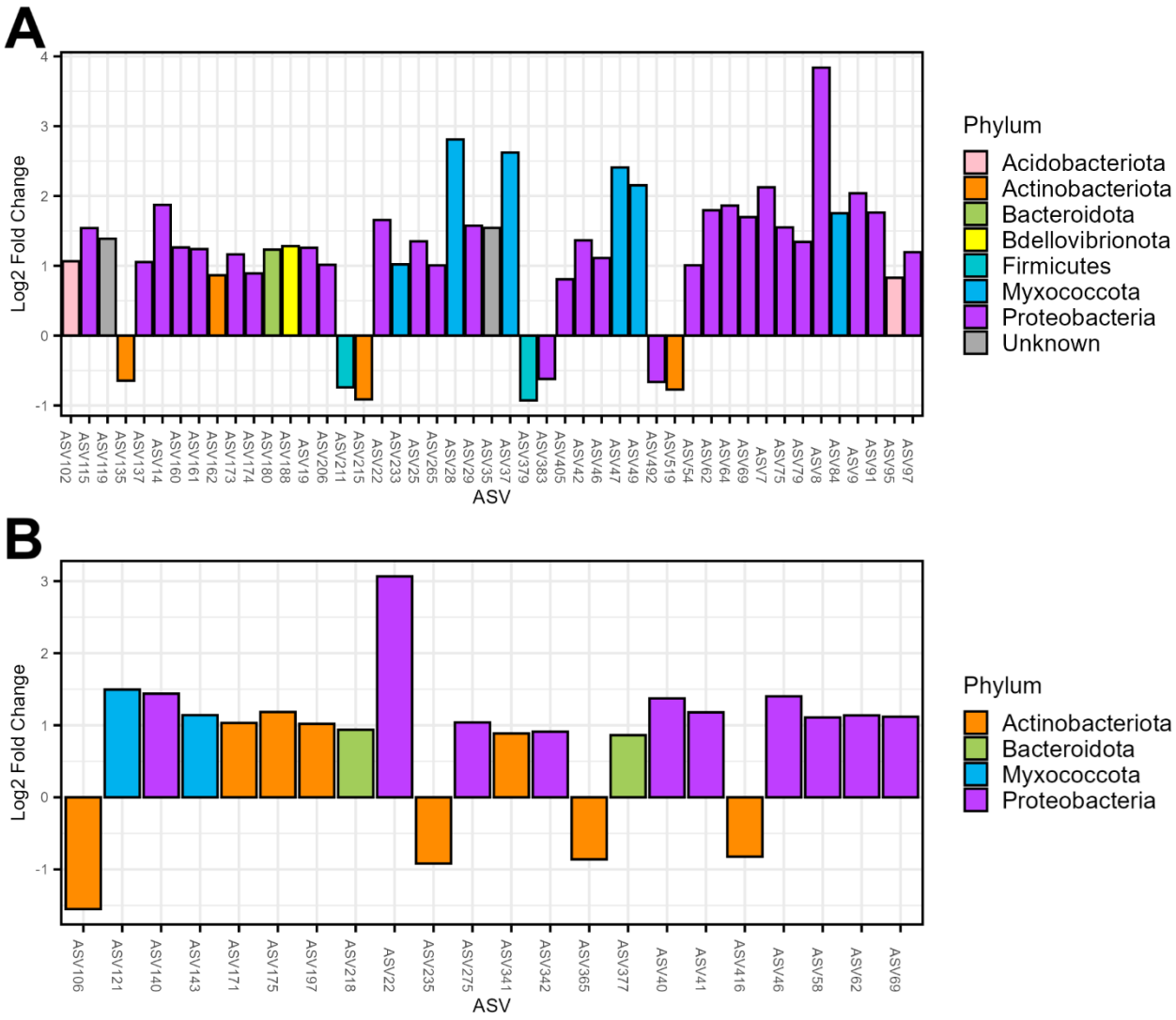
Supplementary Table S5. Permutational analysis of variance (PERMANOVA) for grey birch (top) and trembling aspen (bottom) testing the impact of GDDs at a base temperature of 5°C ('GDD_5C') as a proxy for host phenology, individual plant identification ('Plant_ID'), and their interaction on leaf bacterial beta diversity and community structure.[a]

	Source of Variation	*SS*	R^2	*F*	*P*
Grey Birch	GDD_5C	1.8135	0.149	6.024	0.001***
	Plant_ID	1.3958	0.115	1.159	0.231
	GDD_5C x Plant_ID	1.3958	0.115	1.159	0.231
	Residuals	7.526	0.62	—	—
Trembling Aspen	GDD_5C	0.5559	0.037	1.288	0.023*
	Plant_ID	1.5715	0.105	0.91	0.952
	GDD_5C x Plant_ID	1.664	0.111	0.963	0.735
	Residuals	11.2264	0.748	—	—

[a] *P*-value $*<0.05$, $**<0.01$ and $***<0.001$

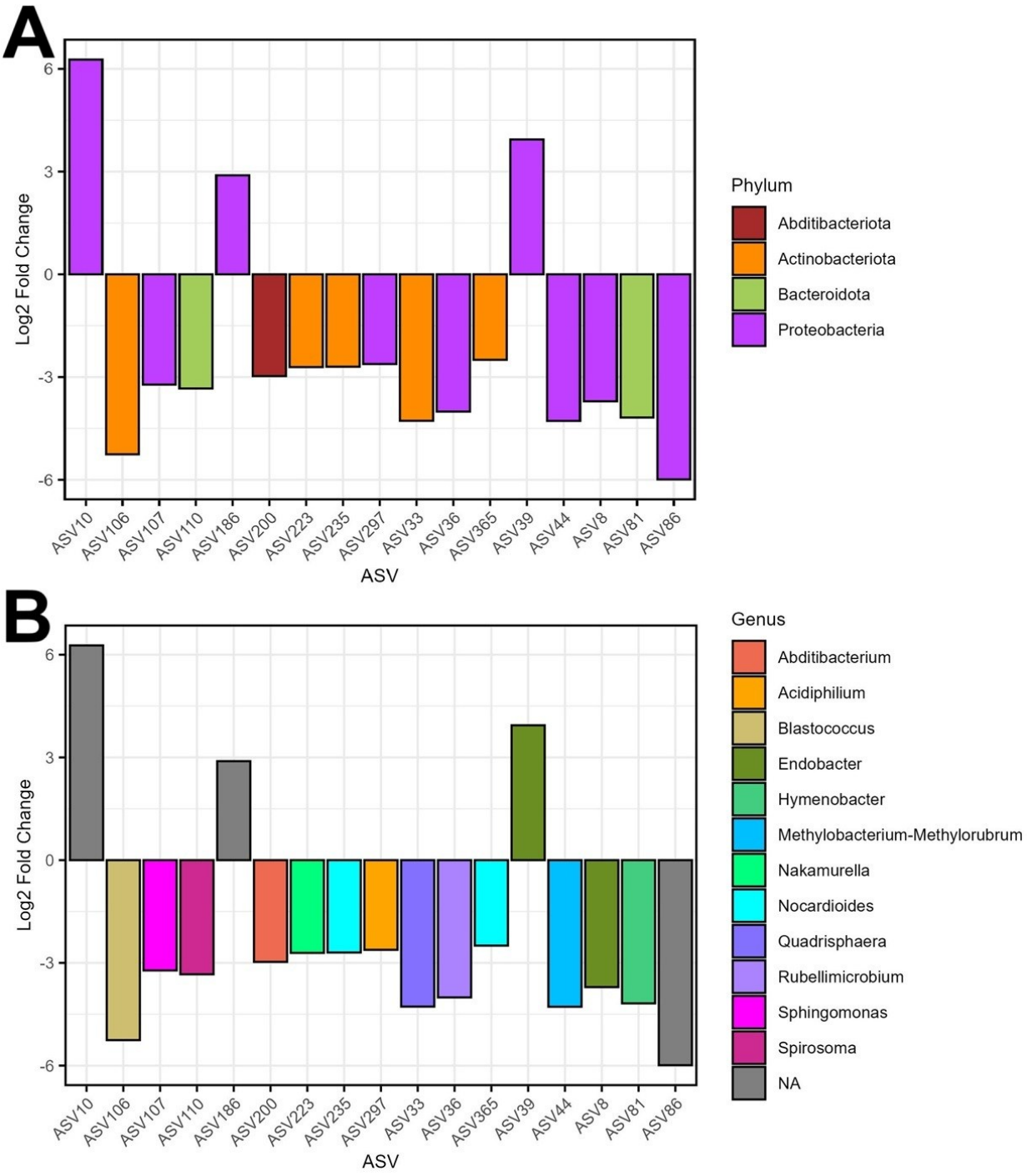


Supplementary Figure S19. Phylum–level comparison of taxonomic profiles showing the interspecific and intraspecific patterns of change in the relative abundances of leaf bacterial communities of **(A)** grey birch and **(B)** trembling aspen throughout seasonal host phenological change (measured as GDDs at a base temperature of 5°C). Note that the relatedness of colour shades does not reflect the relatedness of bacterial phylogenetic relationships.



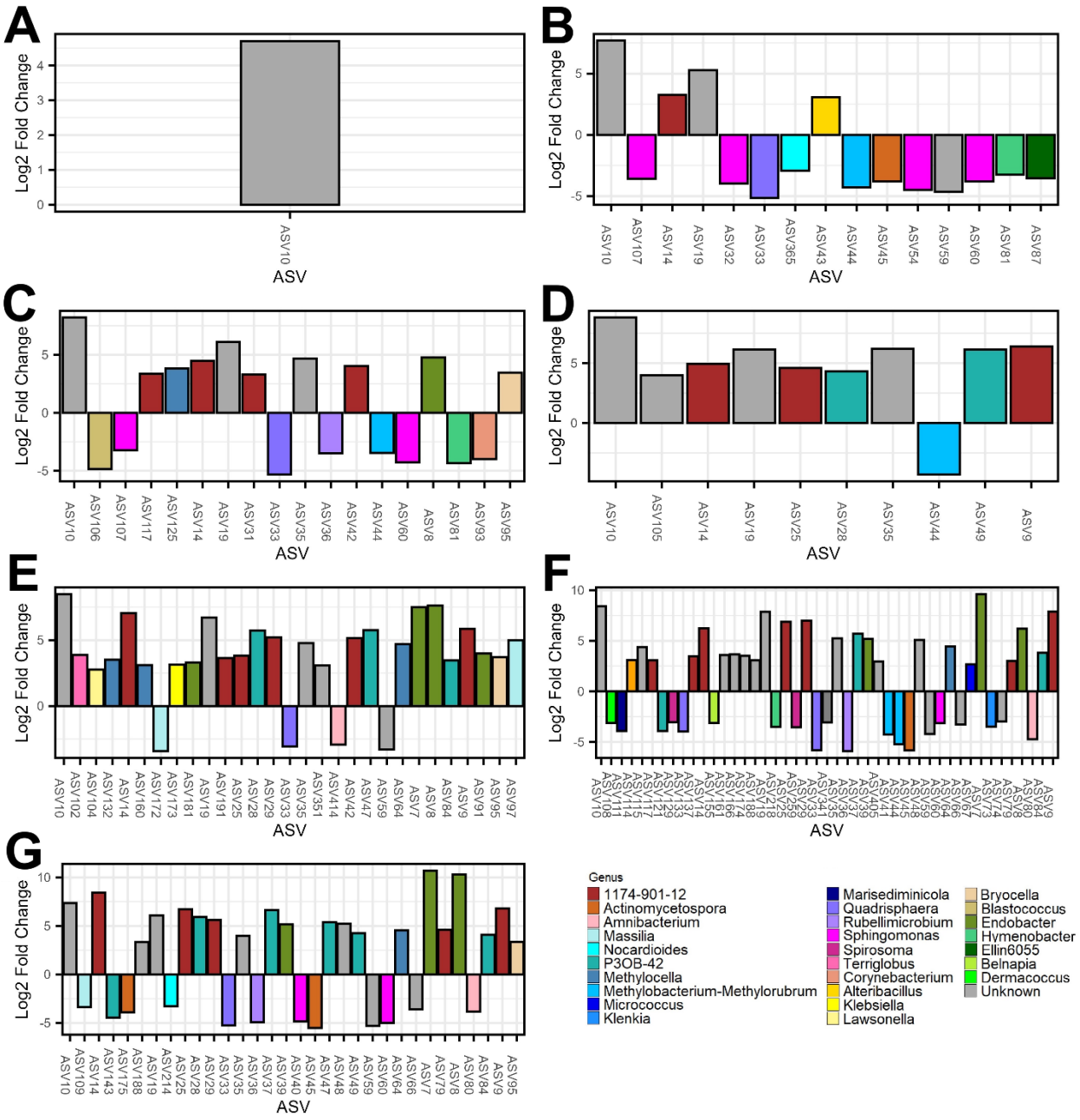
Supplementary Figure S20. Differential abundance analysis (*DESeq2*) at the phylum-level showing significant changes ($p_{adj} < 0.05$) in the relative abundance of leaf bacterial ASVs (colour-coded) within **(A)** birch and **(B)** aspen in response to GDD accumulation ($T_{base} = 5°C$). The log_2(fold–change) represents the rate of change in abundance for every 1-unit increase in GDD and can be interpreted as a regression slope on a log2 scale. A positive log_2(fold–change) indicates that the ASV significantly increased in abundance as GDDs increased, while a negative log_2(fold–change) demonstrates that there was a significant decline in the ASV's abundance as GDDs increased. Note that colours do not correlate to relatedness of taxa. The *P*-value is

calculated using the Wald test, and the adjusted *P*-value (p_{adj}) is calculated using the Benjamini–Hochberg method. A full list of the significantly differentially abundant ASVs, including unidentified ASVs, and all summary statistics can be found in Supplementary Tables S9–S10.



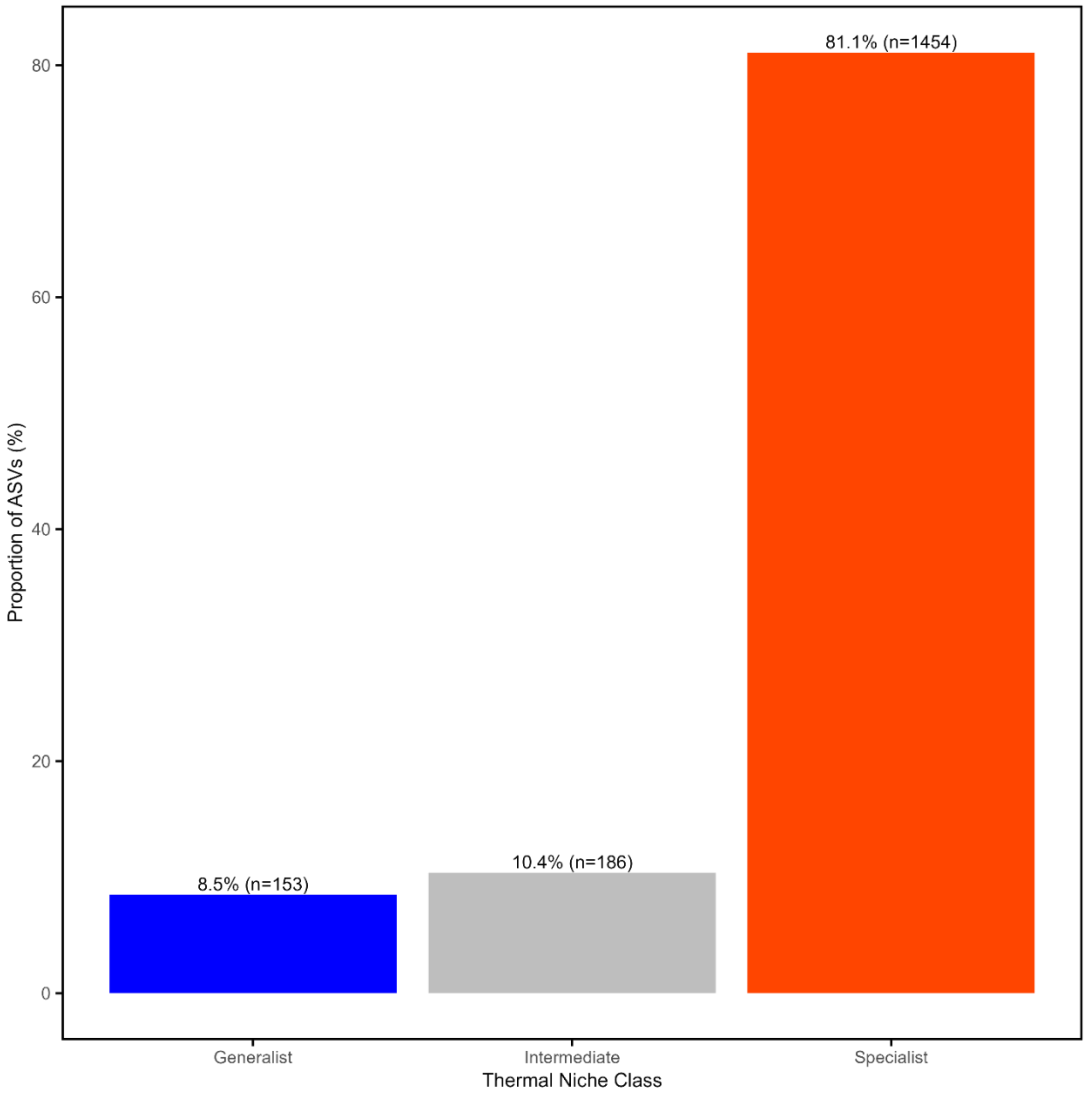
Supplementary Figure S21. Differential abundance analysis (*DESeq2*) showing significant changes (padj < 0.05) in the relative abundance of leaf bacterial ASVs within and between grey birch and trembling aspen across the entirety of host phenology at **(A)** the phylum-level and **(B)** the genus-level. A positive $\log_2$(fold–change) indicates that ASVs were significantly more

differentially abundant in birch, while a negative log_2(fold–change) demonstrates that ASVs were significantly more differentially abundant in aspen. Note that colours do not correlate to relatedness of taxa. A full list of the significantly differentially abundant ASVS, including unidentified ASVs, and all summary statistics can be found in *Supplementary Table S8* of the Supplementary Information section.

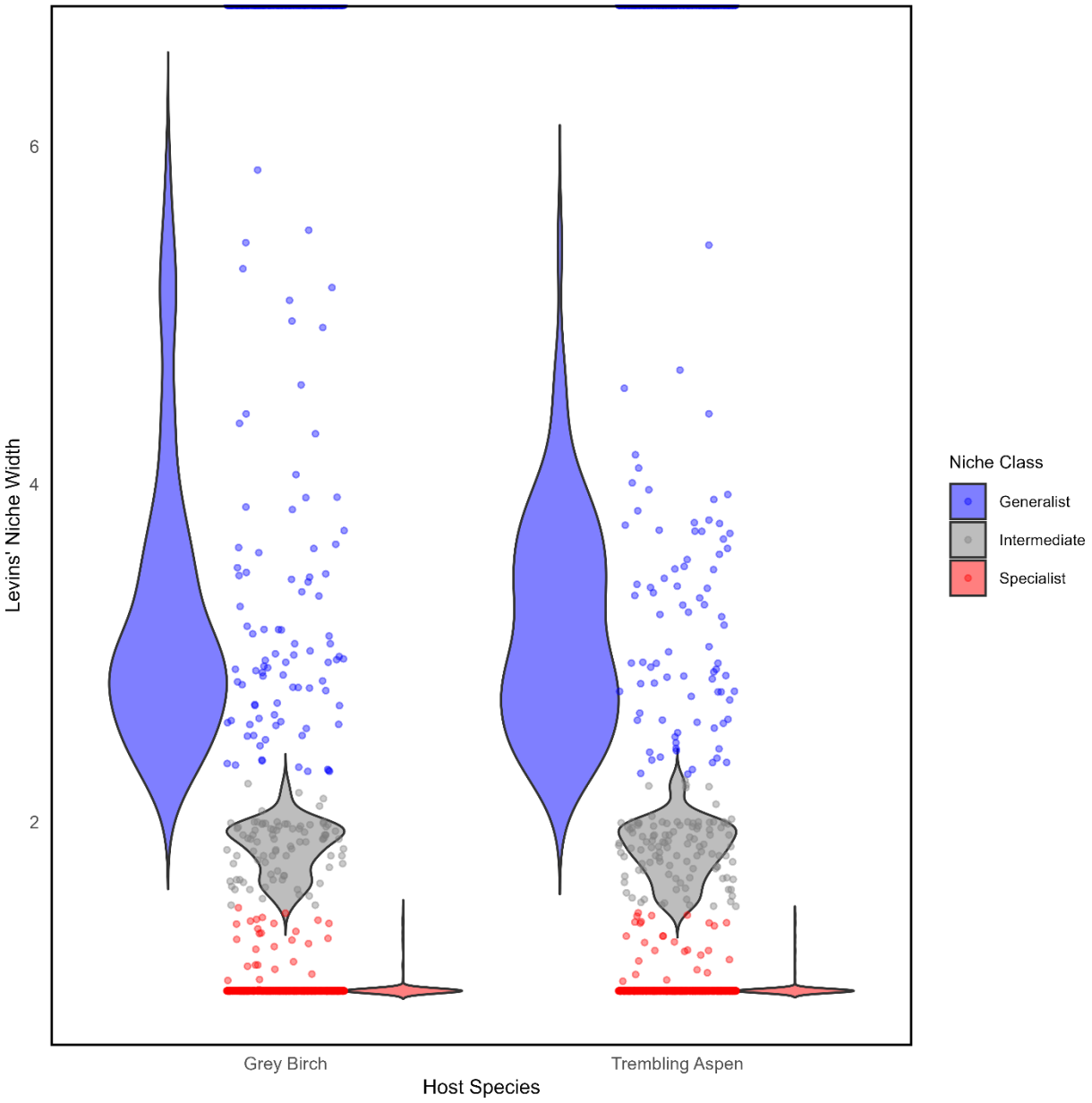


Supplementary Figure S22. Differential abundance analysis (*DESeq2*) showing significant changes (padj < 0.05) in the relative abundance of leaf bacterial ASVs (genus-level colour-coded) within and between grey birch and trembling aspen GDDs (T_{base} = 5°C) are accumulated at a base temperature of 5°C at GDD sampling points **(A)** 437, **(B)** 605, **(C)** 1087, **(D)** 1606, **(E)** 1992, **(F)** 2140, and **(G)** 2219. GDDs are a thermo–temporal measure of host plant seasonal phenological change. A positive log_2(fold–change) indicates that ASVs were significantly more

differentially abundant in birch, while a negative log_2(fold–change) demonstrates that ASVs were significantly more differentially abundant in aspen. A full list of the significantly differentially abundant ASVS, including unidentified ASVs, and all summary statistics can be found in *Supplementary Table S9* of the Supplementary Information section.



Supplementary Figure S23. Thermal niche breadth of leaf-associated bacterial ASVs across seasonal heat accumulation and host species. Levins' niche width index was derived from relative abundances and used to quantify the breadth of thermal persistence for each ASV across a seasonal GDD (T_{base} = 5°C) gradient, a physiologically relevant measure of heat accumulation that tracks host phenological progression. ASVs with niche width ≤1.5 were classified as specialists, ≥2.25 as generalists, and those in between as intermediate. This figure shows the proportion of ASVs across all samples, regardless of host species, classified as thermal specialists, intermediates, or generalists.



Supplementary Figure S24. Distribution of ASV-level thermal niche breadths across host species. Violin plots show the distribution and density of Levins' niche width values for bacterial ASVs associated with grey birch and trembling aspen, calculated using relative abundance across continuous growing degree day (GDD_5°C) values. Horizontal dashed lines represent fixed classification thresholds for thermal specialists (≤1.5, red) and generalists (≥2.25, blue), with

intermediate values falling in between. Distributions are based on ASVs present in at least two GDD timepoints.

Supplementary Table S6. List of differentially abundant ASVs within grey birch leaf samples across a GDD (T_{base} = 5°C) gradient as determined by differential abundance analysis (*DESeq2*).[a]

ASV	Phylum	Class	Order	Family	Genus	Species	Base Mean	Log2 Fold Change	lfcSE	*P*-value	Adjusted *P*-value
ASV7	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Endobacter	NA	502.7	2.1242	0.415	3.06E-07	9.13E-06
ASV8	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Endobacter	NA	333.2	3.8387	0.355	2.63E-27	7.08E-25
ASV9	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	272	2.0397	0.413	7.96E-07	1.95E-05
ASV14	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	267.8	1.8734	0.312	9.13E-08	3.51E-06
ASV19	Proteobacteria	NA	NA	NA	NA	NA	22.11	1.2589	0.3	2.52E-03	1.94E-02
ASV22	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	NA	NA	1	1.6566	0.258	2.88E-05	4.56E-04
ASV25	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	153.2	1.3497	0.351	9.69E-04	9.31E-03
ASV28	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	NA	1	2.8095	0.258	1.48E-12	1.99E-10
ASV29	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	1.086	1.5749	0.25	6.15E-05	8.84E-04
ASV35	NA	NA	NA	NA	NA	NA	92.89	1.5433	0.513	2.26E-05	3.80E-04
ASV37	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	NA	1	2.6218	0.258	1.14E-10	1.02E-08
ASV42	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	93	1.3655	0.417	2.05E-04	2.30E-03
ASV46	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	NA	1	1.1118	0.258	4.31E-03	3.05E-02
ASV47	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	NA	22	2.4086	0.239	8.14E-09	5.47E-07
ASV49	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	NA	9.171	2.1533	0.396	4.91E-07	1.32E-05
ASV54	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	NA	16.83	1.0076	0.224	6.47E-03	4.14E-02
ASV62	Proteobacteria	Gammaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	NA	44.14	1.796	0.493	1.24E-07	4.16E-06
ASV64	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylocella	NA	48.74	1.8622	0.409	5.11E-08	2.60E-06
ASV69	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Enhydrobacter	aerosaccus	1.057	1.6977	0.253	7.80E-06	1.75E-04
ASV75	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylobacterium-Methylorubrum	NA	39.17	1.5502	0.397	1.04E-05	1.92E-04
ASV79	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	38.06	1.3426	0.393	9.66E-05	1.30E-03
ASV84	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	NA	37.57	1.7524	0.448	5.80E-08	2.60E-06
ASV91	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Endobacter	NA	31.37	1.7629	0.467	8.77E-06	1.81E-04
ASV95	Acidobacteriota	Acidobacteriae	Acidobacteriales	Acidobacteriaceae (Subgroup 1)	Bryocella	NA	24.26	0.8287	0.468	7.96E-03	4.64E-02
ASV97	Proteobacteria	Gammaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	NA	1	1.1951	0.258	1.52E-03	1.28E-02
ASV102	Acidobacteriota	Acidobacteriae	Acidobacteriales	Acidobacteriaceae (Subgroup 1)	Terriglobus	NA	1	1.0656	0.258	2.88E-03	2.15E-02
ASV115	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria Incertae Sedis	Unknown Family	Candidatus Ovatusbacter	NA	26.06	1.5397	0.364	1.07E-05	1.92E-04
ASV119	NA	NA	NA	NA	NA	NA	1.343	1.389	0.229	1.64E-04	1.94E-03
ASV135	Actinobacteriota	Actinobacteria	Micrococcales	Micrococcaceae	Rothia	mucilaginosa	25	-0.646	0.407	5.10E-03	3.52E-02
ASV137	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	24.83	1.0531	0.481	1.06E-03	9.85E-03
ASV160	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylocella	NA	23.69	1.2631	0.397	1.66E-04	1.94E-03
ASV161	Proteobacteria	Gammaproteobacteria	NA	NA	NA	NA	4.714	1.2397	0.351	6.25E-05	8.84E-04

ASV162	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Frondihabitans	NA	4.971	0.864	0.356	7.24E-03	4.43E-02
ASV173	Proteobacteria	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	NA	NA	20.69	1.1626	0.368	1.18E-03	1.02E-02
ASV174	Proteobacteria	Alphaproteobacteria	Rickettsiales	AB1	NA	NA	7.971	0.8904	0.306	6.39E-03	4.14E-02
ASV180	Bacteroidota	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	NA	2.857	1.2322	0.343	2.54E-04	2.73E-03
ASV188	Bdellovibrionota	Oligoflexia	0319-6G20	NA	NA	NA	1.514	1.2828	0.245	1.27E-04	1.63E-03
ASV206	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Acidiphilium	NA	11.71	1.0149	0.389	2.08E-03	1.65E-02
ASV211	Firmicutes	Bacilli	Bacillales	Marinococcaceae	NA	NA	19	-0.74	0.418	6.06E-03	4.07E-02
ASV215	Actinobacteriota	Actinobacteria	Micrococcales	Micrococcaceae	Pseudarthrobacter	NA	18.17	-0.914	0.393	1.65E-03	1.34E-02
ASV233	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	NA	17.91	1.02	0.428	7.76E-04	8.02E-03
ASV265	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Endobacter	NA	16.43	1.0065	0.459	1.12E-03	1.00E-02
ASV379	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus	NA	1	-0.927	0.258	9.63E-04	9.31E-03
ASV383	Proteobacteria	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	NA	11.37	-0.621	0.421	7.47E-03	4.47E-02
ASV405	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	NA	NA	15.86	0.8065	0.46	7.09E-03	4.43E-02
ASV492	Proteobacteria	Gammaproteobacteria	CCD24	NA	NA	NA	5.857	-0.664	0.37	8.10E-03	4.64E-02
ASV519	Actinobacteriota	Actinobacteria	Corynebacteriales	Dietziaceae	Dietzia	NA	12.77	-0.772	0.433	3.34E-03	2.43E-02

[a] Base mean is the mean of normalized counts of all samples, log2 fold change refers to the effect size estimate (where positive values mean the ASV significantly increase with GDD accumulation and negative values mean the ASV significantly declines in abundance as GDDs accumulate), lfcSE is the standard error of the log2 fold change, the *P*-value is calculated using the Wald test, and the adjusted *P*-value (padj) is calculated using the Benjamini–Hochberg method. Shown are ASVs that changed significantly (padj < 0.05) in relative abundance among accumulated GDD sampling points.

Supplementary Table S7. List of differentially abundant ASVs within trembling aspen leaf samples across a GDD (T_{base} = 5°C) gradient as determined by differential abundance analysis (*DESeq2*).[a]

ASV	Phylum	Class	Order	Family	Genus	Species	Base Mean	Log2 Fold Change	lfcSE	*P*-value	Adjusted *P*-value
ASV22	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	NA	NA	3.023	3.0657	0.324	3.65E-15	1.19E-12
ASV40	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	NA	2.762	1.3723	0.292	7.93E-04	2.36E-02
ASV41	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylobacterium-Methylorubrum	NA	4.302	1.1795	0.334	1.59E-03	3.24E-02
ASV46	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	NA	1.193	1.4018	0.237	1.17E-04	7.65E-03
ASV58	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylobacterium-Methylorubrum	NA	114.7	1.1076	0.408	5.53E-04	1.85E-02
ASV62	Proteobacteria	Gammaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	NA	1.047	1.1368	0.258	3.85E-04	1.85E-02
ASV69	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Enhydrobacter	aerosaccus	1.717	1.1185	0.257	5.65E-04	1.85E-02
ASV106	Actinobacteriota	Actinobacteria	Frankiales	Geodermatophilaceae	Blastococcus	NA	1.047	-1.551	0.258	7.00E-05	7.63E-03
ASV121	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	NA	1.047	1.4946	0.258	1.33E-05	2.18E-03
ASV140	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	NA	22.59	1.438	0.435	1.03E-04	7.65E-03
ASV143	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	NA	1.047	1.1399	0.258	1.24E-03	3.19E-02
ASV171	Actinobacteriota	Actinobacteria	Kineosporiales	Kineosporiaceae	Pseudokineococcus	lusitanus	1.193	1.0319	0.24	1.31E-03	3.19E-02
ASV175	Actinobacteriota	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Actinomycetospora	NA	1.047	1.1833	0.258	5.37E-04	1.85E-02
ASV197	Actinobacteriota	Actinobacteria	Kineosporiales	Kineosporiaceae	Kineococcus	NA	37.65	1.02	0.225	5.17E-04	1.85E-02
ASV218	Bacteroidota	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	NA	48.22	0.9378	0.39	2.41E-03	4.31E-02
ASV235	Actinobacteriota	Actinobacteria	Propionibacteriales	Nocardioidaceae	Nocardioides	NA	29.14	-0.918	0.221	2.07E-03	3.99E-02
ASV275	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Aureimonas	NA	8.472	1.0389	0.405	1.38E-03	3.19E-02
ASV341	Actinobacteriota	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Pseudonocardia	NA	1.425	0.8867	0.26	2.52E-03	4.31E-02
ASV342	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	NA	1.309	0.9108	0.228	2.83E-03	4.31E-02
ASV365	Actinobacteriota	Actinobacteria	Propionibacteriales	Nocardioidaceae	Nocardioides	alpinus	1.396	-0.86	0.231	1.46E-03	3.19E-02
ASV377	Bacteroidota	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	NA	2.173	0.8629	0.307	2.90E-03	4.31E-02
ASV416	Actinobacteriota	Actinobacteria	Propionibacteriales	Nocardioidaceae	Nocardioides	NA	1.047	-0.824	0.258	2.66E-03	4.31E-02

[a] Base mean is the mean of normalized counts of all samples, log2 fold change refers to the effect size estimate (where positive values mean the ASV significantly increase with GDD accumulation and negative values mean the ASV significantly declines in abundance as GDDs accumulate), lfcSE is the standard error of the log2 fold change, the *P*-value is calculated using the Wald test, and the adjusted *P*-value (padj) is calculated using the Benjamini–Hochberg method. Shown are ASVs that changed significantly (padj < 0.05) in relative abundance among accumulated GDD sampling points.

Supplementary Table S8. List of total differentially abundant taxa between grey birch and trembling aspen across host phenology as determined by differential abundance analysis (*DESeq2*).[a]

ASV	Phylum	Class	Order	Family	Genus	Species	Base Mean	Log2 Fold Change	lfcSE	P-value	Adjusted P-value
ASV8	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Endobacter	NA	171.2687	-3.70784	1.085316	0.000635	0.025385
ASV10	Proteobacteria	NA	NA	NA	NA	NA	137.118	6.270755	0.974832	1.25398866067e-10	4.0127637e-08
ASV33	Actinobacteriota	Actinobacteria	Kineosporiales	Kineosporiaceae	Quadrisphaera	NA	14.84484	-4.2775	1.040408	3.93327896473e-05	0.003147
ASV36	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	NA	13.34271	-4.00882	1.1506	0.000494	0.022573
ASV39	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Endobacter	NA	12.90497	3.938015	1.197973	0.001012	0.029434
ASV44	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylobacterium-Methylorubrum	NA	10.89408	-4.28117	1.138312	0.000169	0.009027
ASV81	Bacteroidota	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	NA	4.399651	-4.18257	1.048903	6.67545952102e-05	0.004272
ASV86	Proteobacteria	Gammaproteobacteria	Enterobacterales	Erwiniaceae	NA	NA	4.155869	-5.98926	1.152333	2.01979954147e-07	3.2316793e-05
ASV106	Actinobacteriota	Actinobacteria	Frankiales	Geodermatophilaceae	Blastococcus	NA	3.435446	-5.25636	1.110372	2.20278631775e-06	0.000235
ASV107	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	NA	3.394058	-3.22048	1.008219	0.001402	0.034512
ASV110	Bacteroidota	Bacteroidia	Cytophagales	Spirosomaceae	Spirosoma	NA	3.350635	-3.33335	0.992034	0.000779	0.027701
ASV186	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	PMMR1	NA	2.258111	2.891122	0.928947	0.001857	0.035712
ASV200	Abditibacteriota	Abditibacteria	Abditibacteriales	Abditibacteriaceae	Abditibacterium	NA	2.112661	-2.97113	0.898428	0.000943	0.029434
ASV223	Actinobacteriota	Actinobacteria	Frankiales	Nakamurellaceae	Nakamurella	NA	2.01064	-2.70895	0.868453	0.001813	0.035712
ASV235	Actinobacteriota	Actinobacteria	Propionibacteriales	Nocardioidaceae	Nocardioides	NA	1.980932	-2.6976	0.868549	0.001897	0.035712
ASV297	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Acidiphilium	NA	1.734082	-2.61921	0.81449	0.001301	0.034512
ASV365	Actinobacteriota	Actinobacteria	Propionibacteriales	Nocardioidaceae	Nocardioides	alpinus	1.51536	-2.49622	0.795004	0.00169	0.035712

[a] Base mean is the mean of normalized counts of all samples, log2fold change refers to the effect size estimate (where positive values mean the ASV is differentially abundant in birch and negative values mean the ASV is differentially abundant in aspen), lfcSE is the standard error of the log2 fold change, the *P*-value is calculated using the Wald test, and the adjusted *P*-value (padj) is calculated

using the Benjamini–Hochberg method. Shown are ASVs that changed significantly (padj < 0.05) in relative abundance among accumulated GDD sampling points.

Supplementary Table S9. List of differentially abundant taxa between grey birch and trembling aspen as growing degree days (GDDs) are accumulated at a base temperature of 5°C at GDD sampling points (a) 437, (b) 605, (c) 1087, (d) 1606, (e) 1992, (f) 2140, and (g) 2219 as determined by differential abundance analysis (*DESeq2*).[a]

ASV	Phylum	Class	Order	Family	Genus	Species	Base Mean	Log2 Fold Change	lfcSE	P-value	Adjusted P-value
(a) GDD_437											
ASV10	Proteobacteria	NA	NA	NA	NA	NA	27	4.700431039	1.106807847	2.17E-05	0.037183063
(b) GDD_605											
ASV10	Proteobacteria	NA	NA	NA	NA	NA	102.7	7.675246219	7.675246219	1.26E-23	9.35E-22
ASV14	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	5.3	3.263029044	1.104431163	0.003131879	0.023946342
ASV19	Proteobacteria	NA	NA	NA	NA	NA	19.7	5.263024351	1.186902855	9.24E-06	0.000227903
ASV32	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	NA	8.3	-3.96346694	1.346111181	0.003235992	0.023946342
ASV33	Actinobacteriota	Actinobacteria	Kineosporiales	Kineosporiaceae	Quadrisphaera	NA	18.2	-5.14567163	1.063969378	1.32E-06	4.89E-05
ASV43	Firmicutes	Bacilli	Bacillales	Marinococcaceae	Alteribacillus	NA	4.7	3.07038395	1.136781764	0.006914297	0.039358304
ASV44	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylobacterium-Methylorubrum	NA	10.2	-4.27797855	1.203968212	0.000380529	0.005631822
ASV45	Actinobacteriota	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Actinomycetospora	iriomotensis	7.5	-3.80734999	1.138078739	0.000821584	0.010132871
ASV54	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	NA	11.8	-4.49824413	1.227719895	0.000248403	0.004595453
ASV59	NA	NA	NA	NA	NA	NA	13	-4.64384693	1.412023807	0.001006198	0.010636949
ASV60	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	NA	7.5	-3.80734864	1.284544646	0.003037003	0.023946342
ASV81	Bacteroidota	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	NA	5.3	-3.26302946	1.231972655	0.008082075	0.042719541
ASV87	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Ellin6055	NA	6.3	-3.53604727	1.261383621	0.005058128	0.031191789
ASV107	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	NA	6.5	-3.58495676	1.265923995	0.004627385	0.031129681
ASV365	Actinobacteriota	Actinobacteria	Propionibacteriales	Nocardioidaceae	Nocardioides	alpinus	4.3	-2.92599574	1.122054859	0.009114965	0.044967161
(c) GDD_1087											
ASV8	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Endobacter	NA	12.90909	4.765525036	1.198503968	7.00E-05	0.001347827
ASV10	Proteobacteria	NA	NA	NA	NA	NA	135.8182	8.217218848	1.028010923	1.31E-15	1.01E-13
ASV14	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	10.63636	4.472476352	1.330505224	0.000775239	0.007461679
ASV19	Proteobacteria	NA	NA	NA	NA	NA	31.63636	6.095910617	1.259258845	1.29E-06	4.98E-05
ASV31	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	5	3.29277514	1.187771856	0.005567392	0.026053463

ASV33	Actinobacteriota	Actinobacteria	Kineosporiales	Kineosporiaceae	Quadrisphaera	NA	22.27273	-5.32192086	1.170177557	5.42E-06	0.000139032
ASV35	NA	NA	NA	NA	NA	NA	12.09091	4.666746506	1.23589863	0.00015937	0.002454305
ASV36	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	NA	6.545455	-3.48112117	1.260549526	0.005752063	0.026053463
ASV42	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	8	4.035614497	1.274540534	0.001543761	0.011886963
ASV44	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylobacterium-Methylorubrum	NA	6.454545	-3.45942687	1.176886439	0.003287701	0.021096079
ASV60	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	NA	10.90909	-4.26052111	1.229747474	0.00053112	0.005931704
ASV81	Bacteroidota	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	NA	11.45455	-4.33389394	1.252402634	0.000539246	0.005931704
ASV93	Actinobacteriota	Actinobacteria	Corynebacteriales	Corynebacteriaceae	Corynebacterium	NA	9.090909	-3.98488540	1.390983543	0.004172767	0.023195384
ASV95	Acidobacteriota	Acidobacteriae	Acidobacteriales	Acidobacteriaceae (Subgroup 1)	Bryocella	NA	5.545455	3.459424488	1.208984374	0.004217343	0.023195384
ASV106	Actinobacteriota	Actinobacteria	Frankiales	Geodermatophilaceae	Blastococcus	NA	16	-4.8328795	1.47591305	0.001058486	0.009055934
ASV107	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	NA	5.545455	-3.22238775	1.204010701	0.007442266	0.031836358
ASV117	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	5.181818	3.350490231	1.210520022	0.005643423	0.026053463
ASV125	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylocella	NA	6.909091	3.807346243	1.260468549	0.002522909	0.017660366
(d) GDD_1606											
ASV9	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	42.4	6.388859844	1.437691527	8.84E-06	0.000159067
ASV10	Proteobacteria	NA	NA	NA	NA	NA	227	8.823348757	1.238943648	1.07E-12	7.68E-11
ASV14	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	22.2	4.940828596	1.149434266	1.72E-05	0.000247634
ASV19	Proteobacteria	NA	NA	NA	NA	NA	71.3	6.135438503	1.243866514	8.12E-07	1.95E-05
ASV25	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	12.6	4.59692239	1.407998407	0.001095169	0.009856521
ASV28	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	NA	35.9	4.330377253	1.315845823	0.000998512	0.009856521
ASV35	NA	NA	NA	NA	NA	NA	37.1	6.193760229	1.173125099	1.29E-07	4.66E-06
ASV44	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylobacterium-Methylorubrum	NA	10.4	-4.30742016	1.393673691	0.001996887	0.014377587
ASV49	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	NA	35.6	6.133378832	1.532770245	6.29E-05	0.000755309
ASV105	NA	NA	NA	NA	NA	NA	8.5	3.999991059	1.272888713	0.001675395	0.013403157
(e) GDD_1992											
ASV7	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Endobacter	NA	306.4	7.485688943	1.364915204	4.15E-08	1.05E-06
ASV8	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Endobacter	NA	196.8	7.613216633	1.334032315	1.15E-08	4.37E-07
ASV9	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	206.3	5.856533266	1.598912719	0.000249452	0.00157986
ASV10	Proteobacteria	NA	NA	NA	NA	NA	180.4	8.491029067	1.374771545	6.56E-10	4.99E-08
ASV14	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	199.3	7.042912351	1.465173923	1.53E-06	2.91E-05

ASV19	Proteobacteria	NA	NA	NA	NA	NA	53.2	6.719711315	1.448000869	3.47E-06	5.28E-05
ASV25	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	27.1	3.813055748	1.406620245	0.00671226	0.025077988
ASV28	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	NA	26.9	5.722447965	1.496693406	0.000131627	0.001278823
ASV29	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	18.8	5.193758277	1.365634567	0.000142849	0.001278823
ASV33	Actinobacteriota	Actinobacteria	Kineosporiales	Kineosporiaceae	Quadrisphaera	NA	4.7	-3.07038527	1.150674496	0.007622816	0.026333365
ASV35	NA	NA	NA	NA	NA	NA	14.2	4.776093018	1.294399719	0.000224419	0.00155053
ASV42	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	18.3	5.153792508	1.339477395	0.000119274	0.001278823
ASV47	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	NA	27.5	5.754868761	1.518957284	0.00015144	0.001278823
ASV59	NA	NA	NA	NA	NA	NA	5.4	-3.29277659	1.253256665	0.008604617	0.027563185
ASV64	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylocella	NA	13.6	4.711484115	1.294652219	0.000273498	0.001598911
ASV84	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	NA	6	3.459423976	1.271075008	0.006495648	0.025077988
ASV91	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Endobacter	NA	8.4	3.981842919	1.326590713	0.002685992	0.013609028
ASV95	Acidobacteriota	Acidobacteriae	Acidobacteriales	Acidobacteriaceae (Subgroup 1)	Bryocella	NA	7	3.70043271	1.179739468	0.001708886	0.009276808
ASV97	Proteobacteria	Gammaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	NA	16.5	4.999987671	1.333498118	0.000177168	0.001346478
ASV102	Acidobacteriota	Acidobacteriae	Acidobacteriales	Acidobacteriaceae (Subgroup 1)	Terriglobus	NA	7.8	3.867886743	1.346518959	0.004072275	0.019343307
ASV104	Actinobacteriota	Actinobacteria	Corynebacteriales	Corynebacteriaceae	Lawsonella	clevelandensis	3.9	2.765530219	1.099921682	0.011926981	0.033572243
ASV132	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylocella	NA	6.2	3.510954606	1.230914695	0.004340227	0.019403369
ASV160	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylocella	NA	4.8	3.104330183	1.230352143	0.01163176	0.033572243
ASV172	Proteobacteria	Gammaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	timonae	5.9	-3.43295386	1.271362617	0.006929444	0.025077988
ASV173	Proteobacteria	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	NA	9.8	3.137495199	1.294244617	0.015342565	0.041644105
ASV181	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Endobacter	NA	5.4	3.29277441	1.269055679	0.009468314	0.028783675
ASV191	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	6.7	3.632259709	1.299569003	0.005190412	0.021915073
ASV351	Proteobacteria	Gammaproteobacteria	Enterobacterales	NA	NA	NA	4.7	3.070383582	1.170356494	0.008704164	0.027563185
ASV414	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Amnibacterium	NA	4.3	-2.9259951	1.215686473	0.016090049	0.042167024
(f) GDD_2140											
ASV7	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Endobacter	NA	392.2	9.61358684	1.19163255	7.17E-16	1.03E-13
ASV8	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Endobacter	NA	186.1	6.198475795	1.337456851	3.58E-06	4.68E-05
ASV9	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	281.5	7.867772108	1.336519153	3.94E-09	1.89E-07
ASV10	Proteobacteria	NA	NA	NA	NA	NA	172.1	8.422885001	1.334184738	2.73E-10	1.97E-08
ASV14	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	121	6.221572596	1.215688867	3.09E-07	8.91E-06
ASV19	Proteobacteria	NA	NA	NA	NA	NA	115.9	7.850466656	1.708787758	4.34E-06	5.21E-05

ASV25	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	59.1	6.872807919	1.46937483	2.91E-06	4.18E-05
ASV29	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	64.3	6.995464698	1.423600457	8.93E-07	2.14E-05
ASV33	Actinobacteriota	Actinobacteria	Kineosporiales	Kineosporiaceae	Quadrisphaera	NA	28.6	-5.81249145	1.079338229	7.23E-08	2.60E-06
ASV35	NA	NA	NA	NA	NA	NA	19.3	5.232648199	1.317193279	7.11E-05	0.00068256
ASV36	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	NA	30.6	-5.91168241	1.245337087	2.06E-06	3.30E-05
ASV37	Myxococcota	NA	NA	NA	NA	NA	26.3	5.689284715	1.353167653	2.62E-05	0.000289942
ASV39	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Endobacter	NA	18.5	5.169909179	1.474876983	0.000456066	0.003648532
ASV41	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylobacterium-Methylorubrum	NA	10.1	-4.26302772	1.252897414	0.000667637	0.004578084
ASV44	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylobacterium-Methylorubrum	NA	19.2	-5.22496009	1.097740057	1.94E-06	3.30E-05
ASV45	Actinobacteriota	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Actinomycetospora	iriomotensis	29	-5.83288152	1.207676508	1.37E-06	2.81E-05
ASV48	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	NA	NA	17.4	5.078939496	1.299795183	9.33E-05	0.000839332
ASV59	NA	NA	NA	NA	NA	NA	9.7	-4.2016282	1.161064339	0.000296003	0.002507321
ASV60	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	NA	4.9	-3.13749871	1.238482705	0.011298106	0.040673182
ASV64	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylocella	NA	11.4	4.446246261	1.275558642	0.000490806	0.003719792
ASV66	Firmicutes	Bacilli	Bacillales	Bacillaceae	NA	NA	8.5	-3.26678314	1.090616689	0.002741264	0.014097931
ASV67	Actinobacteriota	Actinobacteria	Micrococcales	Micrococcaceae	Micrococcus	NA	3.7	2.678067935	1.051318496	0.010854694	0.040078871
ASV73	Actinobacteriota	Actinobacteria	Frankiales	Geodermatophilaceae	Klenkia	NA	12.1	-3.47248431	1.094502392	0.001510491	0.008736434
ASV74	Firmicutes	Bacilli	Bacillales	Marinococcaceae	NA	NA	4.4	-2.96346973	1.217738161	0.014950111	0.047840355
ASV79	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	4.5	2.999993777	1.226653401	0.014458185	0.047317695
ASV80	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Amnibacterium	NA	13.7	-4.72245948	1.180120064	6.29E-05	0.000646921
ASV84	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	NA	7.5	3.807347119	1.222794897	0.001847928	0.010234676
ASV108	Actinobacteriota	Actinobacteria	Micrococcales	Dermacoccaceae	Dermacoccus	nishinomiyaensis	4.8	-3.10433196	1.230742874	0.011658236	0.040946
ASV111	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Marisediminicola	NA	8	-3.90688479	1.218639943	0.001346227	0.008428553
ASV114	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Acidiphilium	NA	4.8	3.104330952	1.165072866	0.007710399	0.031722784
ASV115	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria Incertae Sedis	Unknown Family	Candidatus Ovatusbacter	NA	11	4.392306971	1.310930741	0.000806584	0.005279456
ASV117	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	4.7	3.070383695	1.164118458	0.008351513	0.0325813
ASV121	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	NA	8	-3.90688375	1.324513962	0.003181099	0.015269275
ASV129	Bacteroidota	Bacteroidia	Cytophagales	Spirosomaceae	Spirosoma	NA	4.6	-3.0356199	1.151293383	0.008371584	0.0325813
ASV133	Actinobacteriota	Actinobacteria	Kineosporiales	Kineosporiaceae	Quadrisphaera	NA	8.3	-3.96346886	1.152838354	0.000586008	0.004219256
ASV137	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	6	3.45942492	1.190417232	0.003660103	0.017001767

ASV155	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Belnapia	NA	4.8	-3.10433192	1.235441261	0.011980054	0.041074472
ASV161	Proteobacteria	Gammaproteobacteria	NA	NA	NA	NA	6.5	3.584956314	1.130380056	0.001516742	0.008736434
ASV166	Proteobacteria	Alphaproteobacteria	Rickettsiales	NA	NA	NA	6.8	3.655344643	1.199286702	0.002304219	0.012289166
ASV174	Proteobacteria	Alphaproteobacteria	Rickettsiales	AB1	NA	NA	6.2	3.510953603	1.306063822	0.007183953	0.031348161
ASV188	Bdellovibrionota	Oligoflexia	0319-6G20	NA	NA	NA	4.7	3.070382897	1.232411923	0.012725478	0.042615554
ASV218	Bacteroidota	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	NA	6.2	-3.51095696	1.188099463	0.003125641	0.015269275
ASV259	Bacteroidota	Bacteroidia	Cytophagales	Spirosomaceae	Spirosoma	NA	6.3	-3.53604707	1.283696124	0.005876704	0.02644517
ASV341	Actinobacteriota	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Pseudonocardia	NA	4.7	-3.07038527	1.151063378	0.007643296	0.031722784
ASV405	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	NA	NA	4.4	2.963468761	1.155276511	0.010312832	0.039080207
(g) GDD_2219											
ASV7	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Endobacter	NA	817.3	10.67382273	1.076134031	3.45E-23	2.76E-21
ASV8	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Endobacter	NA	631.2	10.30079566	1.037466248	3.12E-23	2.76E-21
ASV9	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	394.6	6.804021674	1.224673669	2.76E-08	1.11E-06
ASV10	Proteobacteria	NA	NA	NA	NA	NA	82.7	7.361047507	1.362841915	6.62E-08	2.12E-06
ASV14	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	171.8	8.420366945	1.130535769	9.47E-14	5.05E-12
ASV19	Proteobacteria	NA	NA	NA	NA	NA	33.7	6.053094702	1.409277236	1.75E-05	0.000310319
ASV25	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	53.3	6.722443974	1.524634699	1.04E-05	0.000207491
ASV28	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	NA	30.4	5.902059023	1.33618928	1.00E-05	0.000207491
ASV29	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	24.8	5.602869697	1.373506963	4.52E-05	0.000602433
ASV33	Actinobacteriota	Actinobacteria	Kineosporiales	Kineosporiaceae	Quadrisphaera	NA	19.6	-5.25549118	1.348390443	9.71E-05	0.001110278
ASV35	NA	NA	NA	NA	NA	NA	8.4	3.981843273	1.304004022	0.0022615	0.014449167
ASV36	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	NA	15.7	-4.9259907	1.330493628	0.000213588	0.002010239
ASV37	Myxococcota	NA	NA	NA	NA	NA	49.7	6.620566552	1.46195289	5.94E-06	0.000158352
ASV39	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Endobacter	NA	18.5	5.169914032	1.244752065	3.28E-05	0.000476533
ASV40	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	NA	23.4	-4.82016914	1.487134994	0.001190088	0.008655184
ASV45	Actinobacteriota	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Actinomycetospora	iriomotensis	23.3	-5.51095140	1.382965343	6.75E-05	0.000830943
ASV47	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	NA	21.4	5.385414411	1.4811417	0.000276917	0.00246148
ASV48	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	NA	NA	19.3	5.232646645	1.390337541	0.000167498	0.001674981
ASV49	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	NA	10	4.247917493	1.308894643	0.001172761	0.008655184
ASV59	NA	NA	NA	NA	NA	NA	20	-5.28539395	1.250603332	2.38E-05	0.000380146
ASV60	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	NA	16.3	-4.98184238	1.436331294	0.000523471	0.004187769
ASV64	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylocella	NA	12.2	4.548425964	1.302283918	0.000478247	0.004027346

ASV66	Firmicutes	Bacilli	Bacillales	Bacillaceae	NA	NA	6.5	-3.58495648	1.296009912	0.005672262	0.031295237
ASV79	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	1174-901-12	NA	12.6	4.596925937	1.211831919	0.000148617	0.001585247
ASV80	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Amnibacterium	NA	7.7	-3.84799075	1.264840776	0.00234799	0.014449167
ASV84	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	NA	9	4.087453754	1.269943956	0.001288138	0.008960957
ASV95	Acidobacteriota	Acidobacteriae	Acidobacteriales	Acidobacteriaceae (Subgroup 1)	Bryocella	NA	5.6	3.35049058	1.204869023	0.005422641	0.030986519
ASV109	Proteobacteria	Gammaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	NA	5.7	-3.37850603	1.286852406	0.008654649	0.044669157
ASV143	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	NA	11.4	-4.44624759	1.394413165	0.001429558	0.009530389
ASV175	Actinobacteriota	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Actinomycetospora	NA	7.9	-3.88751837	1.332840581	0.003537369	0.020962188
ASV188	Bdellovibrionota	Oligoflexia	0319-6G20	NA	NA	NA	5.5	3.321920815	1.260606763	0.008409364	0.044669157
ASV214	Actinobacteriota	Actinobacteria	Propionibacteriales	Nocardioidaceae	Nocardioides	NA	5.3	-3.26302928	1.254956009	0.009319267	0.046596334

[a] Base mean is the mean of normalized counts of all samples, log2fold change refers to the effect size estimate (where positive values mean the ASV is differentially abundant in birch and negative values mean the ASV is differentially abundant in aspen), lfcSE is the standard error of the log2 fold change, the *P*-value is calculated using the Wald test, and the adjusted *P*-value (padj) is calculated using the Benjamini–Hochberg method. Shown are ASVs that changed significantly (padj < 0.05) in relative abundance among accumulated GDD sampling points.

Supplementary Table S10. ASV-level thermal niche width, classification, and taxonomic annotation. This table reports Levins' niche width index for each bacterial ASV, calculated from scaled relative abundance across continuous GDD (Tbase = 5°C) values.[a]

ASV	Niche Width	GDD Peak	Relative Abundance	Levin's Niche Class	Genus
ASV7	3.159	2219	2.488E-02	Generalist	Endobacter
ASV8	2.532	2219	2.155E-02	Generalist	Endobacter
ASV9	3.171	2219	1.816E-02	Generalist	1174-901-12
ASV10	5.866	2140	9.561E-03	Generalist	NA
ASV12	2.545	1606	1.646E-02	Generalist	Staphylococcus
ASV14	3.341	1992	1.377E-02	Generalist	1174-901-12
ASV16	1.000	1992	2.257E-05	Specialist	Escherichia-Shigella
ASV17	2.192	2140	1.538E-02	Intermediate	Massilia
ASV19	4.418	2140	7.409E-03	Generalist	NA
ASV22	1.660	2219	7.823E-04	Intermediate	NA
ASV24	2.794	2140	5.642E-03	Generalist	Sphingomonas
ASV25	3.748	2219	4.009E-03	Generalist	1174-901-12
ASV27	1.424	1087	6.770E-05	Specialist	Enterococcus
ASV28	3.929	2140	2.543E-03	Generalist	P3OB-42
ASV29	3.283	2140	4.258E-03	Generalist	1174-901-12
ASV30	1.000	437	8.004E-03	Specialist	Ensifer
ASV31	1.410	2219	7.387E-03	Specialist	1174-901-12
ASV32	3.404	2140	2.731E-03	Generalist	Sphingomonas
ASV33	4.494	605	9.553E-04	Generalist	Quadrisphaera
ASV34	1.000	1992	4.513E-05	Specialist	Pseudomonas
ASV35	3.865	1606	1.625E-03	Generalist	NA
ASV36	3.802	605	2.076E-03	Generalist	Rubellimicrobium
ASV37	2.138	2219	1.963E-03	Intermediate	P3OB-42
ASV38	1.000	2219	6.747E-03	Specialist	Enterococcus
ASV39	5.504	2140	1.309E-03	Generalist	Endobacter
ASV40	3.974	1606	1.557E-03	Generalist	Sphingomonas
ASV41	4.442	1606	1.647E-03	Generalist	Methylobacterium-Methylorubrum

ASV42	3.435	2219	1.249E-03	Generalist	1174-901-12
ASV43	1.000	1087	1.279E-04	Specialist	Alteribacillus
ASV44	5.860	2140	5.943E-04	Generalist	Methylobacterium-Methylorubrum
ASV45	3.611	2219	8.500E-04	Generalist	Actinomycetospora
ASV46	3.520	1992	1.414E-03	Generalist	Sphingomonas
ASV47	2.957	1992	1.805E-03	Generalist	P3OB-42
ASV48	4.337	2219	1.294E-03	Generalist	NA
ASV49	2.554	1606	1.685E-03	Generalist	P3OB-42
ASV50	1.007	2219	4.348E-03	Specialist	Tepidimonas
ASV52	3.171	1992	1.301E-03	Generalist	Massilia
ASV53	1.000	2219	4.205E-03	Specialist	Cloacibacterium
ASV54	4.741	1606	8.425E-04	Generalist	Sphingomonas
ASV55	2.135	2140	1.896E-03	Intermediate	Methylobacterium-Methylorubrum
ASV58	2.182	2140	1.700E-03	Intermediate	Methylobacterium-Methylorubrum
ASV59	3.389	605	6.695E-04	Generalist	NA
ASV60	4.681	2219	6.018E-04	Generalist	Sphingomonas
ASV61	5.038	1606	3.611E-04	Generalist	Bradyrhizobium
ASV62	2.926	1992	1.091E-03	Generalist	Massilia
ASV63	1.000	2219	3.295E-03	Specialist	Anoxybacillus
ASV64	3.923	1992	5.491E-04	Generalist	Methylocella
ASV65	2.963	1606	1.339E-03	Generalist	Curtobacterium
ASV66	1.998	2219	1.204E-04	Intermediate	NA
ASV67	4.345	1992	3.235E-04	Generalist	Micrococcus
ASV68	3.281	1606	1.181E-03	Generalist	Robbsia
ASV69	1.643	1992	1.324E-03	Intermediate	Enhydrobacter
ASV70	3.266	1606	8.876E-04	Generalist	Sphingomonas
ASV71	1.068	2219	2.919E-03	Specialist	P3OB-42
ASV72	1.145	2140	2.625E-03	Specialist	Sphingomonas
ASV73	3.814	605	7.597E-04	Generalist	Klenkia
ASV75	3.488	2219	5.190E-04	Generalist	Methylobacterium-Methylorubrum
ASV76	1.177	2219	2.106E-03	Specialist	P3OB-42
ASV77	1.000	1992	1.956E-03	Specialist	Hymenobacter
ASV78	1.107	1606	1.820E-03	Specialist	Rhizobacter

ASV79	2.905	1992	6.845E-04	Generalist	1174-901-12
ASV80	2.876	2140	4.212E-04	Generalist	Amnibacterium
ASV81	2.862	1087	4.889E-04	Generalist	Hymenobacter
ASV83	2.835	2219	8.199E-04	Generalist	1174-901-12
ASV84	3.421	2219	3.686E-04	Generalist	P3OB-42
ASV85	1.101	605	1.339E-03	Specialist	Erwinia
ASV86	1.000	1087	1.512E-03	Specialist	NA
ASV87	3.620	2219	6.544E-04	Generalist	Ellin6055
ASV88	2.978	1992	8.124E-04	Generalist	Neorhizobium
ASV89	1.000	1087	1.414E-03	Specialist	Pseudomonas
ASV90	1.000	1992	1.647E-03	Specialist	Spirosoma
ASV91	1.753	2219	1.076E-03	Intermediate	Endobacter
ASV92	4.297	437	3.912E-04	Generalist	Streptococcus
ASV93	2.954	1087	5.341E-04	Generalist	Corynebacterium
ASV94	1.803	1087	9.403E-04	Intermediate	Paracoccus
ASV95	4.057	1992	2.783E-04	Generalist	Bryocella
ASV96	1.000	1606	1.331E-03	Specialist	Spirosoma
ASV97	1.471	1992	6.620E-04	Specialist	Massilia
ASV98	3.758	1992	4.513E-04	Generalist	NA
ASV99	1.509	1606	1.038E-03	Intermediate	Roseomonas
ASV100	4.135	2219	3.310E-04	Generalist	Corynebacterium
ASV101	1.062	2219	1.459E-03	Specialist	Methylobacterium-Methylorubrum
ASV102	3.055	2140	5.040E-04	Generalist	Terriglobus
ASV103	3.747	1087	4.438E-04	Generalist	Streptococcus
ASV104	2.836	1606	4.288E-04	Generalist	Lawsonella
ASV105	3.055	1606	3.535E-04	Generalist	NA
ASV106	1.000	1087	1.000E-03	Specialist	Blastococcus
ASV107	3.715	2219	2.633E-04	Generalist	Sphingomonas
ASV108	5.403	1087	3.460E-04	Generalist	Dermacoccus
ASV109	2.033	1087	8.801E-04	Intermediate	Massilia
ASV110	2.785	605	6.695E-04	Generalist	Spirosoma
ASV111	3.581	2219	2.257E-04	Generalist	Marisediminicola
ASV112	1.271	1087	1.053E-03	Specialist	Streptococcus

ASV113	1.000	2219	1.256E-03	Specialist	NA
ASV114	3.174	2219	2.181E-04	Generalist	Acidiphilium
ASV115	2.346	2140	4.739E-04	Generalist	Candidatus Ovatusbacter
ASV116	1.999	1087	4.664E-04	Intermediate	Oxalicibacterium
ASV117	3.044	1087	2.633E-04	Generalist	1174-901-12
ASV118	3.407	605	5.566E-04	Generalist	Roseomonas
ASV119	2.184	2219	6.168E-04	Intermediate	NA
ASV120	2.633	2140	4.212E-04	Generalist	Aureimonas
ASV121	2.774	2140	4.664E-04	Generalist	P3OB-42
ASV122	2.018	2140	7.447E-04	Intermediate	Sphingomonas
ASV123	1.000	2219	1.106E-03	Specialist	Paramesorhizobium
ASV124	1.028	2219	1.083E-03	Specialist	Corynebacterium
ASV125	3.595	1087	3.535E-04	Generalist	Methylocella
ASV126	1.000	605	1.128E-03	Specialist	Corynebacterium
ASV128	3.633	1087	3.235E-04	Generalist	Skermanella
ASV129	3.284	605	4.664E-04	Generalist	Spirosoma
ASV130	1.068	1087	8.801E-04	Specialist	Endobacter
ASV131	1.000	2219	1.031E-03	Specialist	NA
ASV132	3.619	2140	2.332E-04	Generalist	Methylocella
ASV133	2.603	2140	2.031E-04	Generalist	Quadrisphaera
ASV134	5.778	1087	1.204E-04	Generalist	Corynebacterium
ASV135	1.732	1087	6.695E-04	Intermediate	Rothia
ASV137	2.885	2219	2.482E-04	Generalist	1174-901-12
ASV138	1.413	2140	5.566E-04	Specialist	Roseomonas
ASV139	1.972	1992	4.212E-04	Intermediate	Aureimonas
ASV140	1.000	2219	6.695E-04	Specialist	Pseudomonas
ASV141	1.870	1606	9.027E-05	Intermediate	Dermacoccus
ASV142	1.000	1087	7.372E-04	Specialist	Shewanella
ASV143	1.097	2219	5.491E-04	Specialist	P3OB-42
ASV144	2.644	1606	4.363E-04	Generalist	Methylobacterium-Methylorubrum
ASV145	1.000	2219	8.726E-04	Specialist	Thermoanaerobacterium
ASV147	2.759	2140	2.858E-04	Generalist	Brevundimonas
ASV149	1.856	1992	4.664E-04	Intermediate	NA

ASV150	1.305	437	5.566E-04	Specialist	Endobacter
ASV151	1.000	1087	6.695E-04	Specialist	Algoriella
ASV152	3.048	605	2.031E-04	Generalist	Marmoricola
ASV153	1.402	2219	6.093E-04	Specialist	NA
ASV154	4.388	2219	1.881E-04	Generalist	Sphingomonas
ASV155	3.554	2140	1.956E-04	Generalist	Belnapia
ASV156	2.239	2219	4.062E-04	Intermediate	Staphylococcus
ASV157	1.000	1992	7.823E-04	Specialist	Aureimonas
ASV158	1.000	2219	8.726E-04	Specialist	1174-901-12
ASV159	1.290	1606	6.093E-04	Specialist	Neorhizobium
ASV160	3.276	2219	2.031E-04	Generalist	Methylocella
ASV161	2.577	2219	1.279E-04	Generalist	NA
ASV162	1.716	1992	2.633E-04	Intermediate	Frondihabitans
ASV163	1.185	1087	5.642E-04	Specialist	Nocardioides
ASV164	2.571	1087	3.385E-04	Generalist	Endobacter
ASV165	2.832	1087	2.633E-04	Generalist	Rathayibacter
ASV167	1.174	1606	6.018E-04	Specialist	Roseomonas
ASV168	1.000	1087	6.920E-04	Specialist	NA
ASV169	1.076	1606	2.934E-04	Specialist	Brachybacterium
ASV170	3.757	2219	1.730E-04	Generalist	Quadrisphaera
ASV171	2.387	2219	2.257E-04	Generalist	Pseudokineococcus
ASV172	2.347	1992	2.257E-04	Generalist	Massilia
ASV173	1.000	1992	4.363E-04	Specialist	NA
ASV174	2.600	2140	2.633E-04	Generalist	NA
ASV175	1.608	2219	3.009E-04	Intermediate	Actinomycetospora
ASV176	2.142	605	9.779E-05	Intermediate	Lipingzhangella
ASV178	3.709	605	2.106E-04	Generalist	NA
ASV179	3.068	1087	2.783E-04	Generalist	Methylobacterium-Methylorubrum
ASV180	3.227	2140	2.482E-04	Generalist	Hymenobacter
ASV181	2.451	1087	2.106E-04	Generalist	Endobacter
ASV182	1.000	1606	5.717E-04	Specialist	Tumebacillus
ASV183	1.134	1087	7.823E-04	Specialist	Cellulomonas
ASV184	2.487	1992	3.686E-04	Generalist	Methylobacterium-Methylorubrum

ASV185	1.000	605	7.297E-04	Specialist	Corynebacterium
ASV186	4.167	437	2.031E-04	Generalist	PMMR1
ASV187	3.484	2140	1.580E-04	Generalist	Sphingomonas
ASV188	1.962	2140	2.332E-04	Intermediate	NA
ASV189	2.675	2140	2.708E-04	Generalist	Polaromonas
ASV190	2.529	2219	3.084E-04	Generalist	Sphingomonas
ASV191	1.681	1992	3.159E-04	Intermediate	1174-901-12
ASV192	1.093	2219	5.867E-04	Specialist	NA
ASV193	1.520	1606	4.288E-04	Intermediate	NA
ASV194	2.268	1087	2.106E-04	Generalist	Amnibacterium
ASV195	1.000	2219	6.243E-04	Specialist	NA
ASV197	2.229	2140	1.279E-04	Intermediate	Kineococcus
ASV198	5.092	1087	1.504E-04	Generalist	Methylobacterium-Methylorubrum
ASV199	1.000	1606	5.115E-04	Specialist	NA
ASV200	2.556	605	3.235E-04	Generalist	Abditibacterium
ASV201	1.000	1606	5.190E-04	Specialist	Rubellimicrobium
ASV202	1.795	1606	3.611E-04	Intermediate	Rubellimicrobium
ASV203	2.584	1606	2.858E-04	Generalist	Sphingomonas
ASV204	3.003	1606	2.558E-04	Generalist	NA
ASV205	2.680	1087	2.482E-04	Generalist	Nocardioides
ASV206	2.613	1992	2.858E-04	Generalist	Acidiphilium
ASV207	1.064	1087	4.664E-04	Specialist	Flavisolibacter
ASV208	1.877	2219	3.611E-04	Intermediate	P3OB-42
ASV209	1.840	1087	3.460E-04	Intermediate	NA
ASV210	1.140	2219	5.341E-04	Specialist	Chungangia
ASV211	3.124	1087	1.881E-04	Generalist	NA
ASV212	1.524	2219	4.137E-04	Intermediate	Kineosporia
ASV213	1.253	605	5.266E-04	Specialist	NA
ASV214	2.245	2219	1.956E-04	Intermediate	Nocardioides
ASV215	2.346	1087	1.354E-04	Generalist	Pseudarthrobacter
ASV216	1.000	1087	6.695E-04	Specialist	Acinetobacter
ASV217	1.000	2219	4.513E-04	Specialist	Sphingobium
ASV218	1.679	2140	1.279E-04	Intermediate	Hymenobacter

ASV219	2.857	1606	1.655E-04	Generalist	NA
ASV220	1.000	1606	4.814E-04	Specialist	Kineococcus
ASV221	1.000	1087	4.438E-04	Specialist	NA
ASV222	3.720	1992	1.354E-04	Generalist	Modestobacter
ASV223	3.498	437	1.053E-04	Generalist	Nakamurella
ASV224	1.000	1606	4.739E-04	Specialist	NA
ASV225	2.433	1087	2.558E-04	Generalist	Sphingomonas
ASV226	3.127	437	1.354E-04	Generalist	Massilia
ASV227	2.311	1992	3.084E-04	Generalist	Massilia
ASV228	1.658	2140	3.009E-04	Intermediate	Noviherbaspirillum
ASV229	1.000	2219	5.416E-04	Specialist	Pseudoxanthomonas
ASV230	1.000	1087	4.438E-04	Specialist	Myroides
ASV231	1.888	1087	2.332E-04	Intermediate	Marmoricola
ASV232	2.384	1992	2.558E-04	Generalist	Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium
ASV233	3.850	1992	1.053E-04	Generalist	P3OB-42
ASV234	1.000	1992	5.266E-04	Specialist	NA
ASV235	2.323	1087	2.407E-04	Generalist	Nocardioides
ASV236	1.000	1087	4.363E-04	Specialist	Myroides
ASV237	2.619	2140	1.204E-04	Generalist	Novosphingobium
ASV238	2.896	1087	2.407E-04	Generalist	Terriglobus
ASV239	2.904	1606	2.257E-04	Generalist	Nakamurella
ASV241	1.407	1087	3.535E-04	Specialist	Nocardioides
ASV242	2.017	2219	3.084E-04	Intermediate	Sphingomonas
ASV243	1.683	1992	3.009E-04	Intermediate	Pseudomonas
ASV244	4.676	1087	1.128E-04	Generalist	Aurantimonas
ASV245	3.357	2219	1.655E-04	Generalist	Hymenobacter
ASV246	1.000	1992	4.814E-04	Specialist	Sphingomonas
ASV247	1.000	1992	4.814E-04	Specialist	1174-901-12
ASV248	1.856	1087	3.611E-04	Intermediate	Acidiphilium
ASV249	3.161	605	2.332E-04	Generalist	Abditibacterium
ASV250	3.675	1992	1.354E-04	Generalist	NA
ASV251	1.234	605	4.438E-04	Specialist	Corynebacterium

ASV252	1.000	2140	3.310E-04	Specialist	Methylobacterium-Methylorubrum
ASV253	1.000	1087	3.836E-04	Specialist	Planomicrobium
ASV254	1.787	2219	1.805E-04	Intermediate	Haemophilus
ASV255	1.614	2140	2.633E-04	Intermediate	Roseomonas
ASV256	1.140	2219	4.288E-04	Specialist	Chungangia
ASV258	1.000	1087	3.987E-04	Specialist	Endobacter
ASV259	1.125	2140	2.858E-04	Specialist	Spirosoma
ASV260	2.818	1992	1.354E-04	Generalist	Actinomyces
ASV261	1.000	437	3.460E-04	Specialist	NA
ASV262	1.000	1087	3.686E-04	Specialist	Frateuria
ASV263	1.085	1087	3.535E-04	Specialist	Amaricoccus
ASV264	2.678	1606	1.730E-04	Generalist	Nocardioides
ASV265	2.551	2219	1.580E-04	Generalist	Endobacter
ASV266	3.228	2140	2.106E-04	Generalist	Ellin6055
ASV267	1.000	1606	3.310E-04	Specialist	NA
ASV268	1.825	2219	1.655E-04	Intermediate	Hymenobacter
ASV269	1.933	2219	2.708E-04	Intermediate	Curtobacterium
ASV270	1.000	2140	3.084E-04	Specialist	Methylobacterium-Methylorubrum
ASV271	1.401	1087	2.031E-04	Specialist	Streptococcus
ASV272	3.644	1992	1.429E-04	Generalist	Granulicella
ASV273	1.735	2219	2.934E-04	Intermediate	Kineosporia
ASV274	1.000	1606	3.836E-04	Specialist	Spirosoma
ASV275	1.000	2219	2.708E-04	Specialist	Aureimonas
ASV276	1.000	2140	4.589E-04	Specialist	Subgroup 10
ASV277	2.196	1087	1.881E-04	Intermediate	Kocuria
ASV278	1.910	2219	2.106E-04	Intermediate	Methylobacterium-Methylorubrum
ASV279	1.000	2140	1.956E-04	Specialist	Sphingomonas
ASV280	1.000	1087	3.460E-04	Specialist	Mycobacterium
ASV281	1.000	1087	3.460E-04	Specialist	Sphingomonas
ASV282	1.981	1087	1.204E-04	Intermediate	Kocuria
ASV283	1.000	1087	3.385E-04	Specialist	Amaricoccus
ASV284	1.000	1087	3.385E-04	Specialist	Ornithinicoccus
ASV285	1.000	1087	3.385E-04	Specialist	NA

ASV286	3.215	2219	1.429E-04	Generalist	Corynebacterium
ASV287	1.000	1606	3.611E-04	Specialist	NA
ASV288	1.843	1606	1.956E-04	Intermediate	Paracoccus
ASV289	1.000	2140	2.858E-04	Specialist	Novosphingobium
ASV290	1.000	1087	3.310E-04	Specialist	Agromyces
ASV291	2.599	2140	1.204E-04	Generalist	Ramlibacter
ASV292	2.436	2140	1.580E-04	Generalist	Roseomonas
ASV293	1.000	1087	3.235E-04	Specialist	Bosea
ASV294	1.000	1087	3.235E-04	Specialist	Rothia
ASV295	3.139	1992	1.580E-04	Generalist	Pseudomonas
ASV296	1.000	1087	3.235E-04	Specialist	Pseudomonas
ASV297	2.413	437	1.053E-04	Generalist	Acidiphilium
ASV298	1.000	1606	3.235E-04	Specialist	NA
ASV299	2.840	1606	1.580E-04	Generalist	Actinomycetospora
ASV301	1.210	605	3.535E-04	Specialist	Pseudomonas
ASV302	1.000	1087	3.159E-04	Specialist	NA
ASV303	1.333	1087	2.633E-04	Specialist	Mycobacterium
ASV304	4.299	2219	1.053E-04	Generalist	Finegoldia
ASV305	1.434	1606	2.633E-04	Specialist	NA
ASV306	1.000	2140	2.934E-04	Specialist	Sphingomonas
ASV307	1.241	605	3.686E-04	Specialist	Rubrivirga
ASV308	1.000	1087	3.084E-04	Specialist	Hirschia
ASV309	1.446	1087	2.558E-04	Specialist	Gaiella
ASV310	2.566	1992	9.779E-05	Generalist	Pseudomonas
ASV311	2.367	2219	1.580E-04	Generalist	NA
ASV312	3.007	2219	1.128E-04	Generalist	Fibrella
ASV313	1.000	2219	3.686E-04	Specialist	Fonticella
ASV314	2.704	2140	1.279E-04	Generalist	Bryocella
ASV315	4.174	2219	5.266E-05	Generalist	Abditibacterium
ASV316	1.161	1087	2.783E-04	Specialist	NA
ASV317	2.000	1992	2.106E-04	Intermediate	Roseomonas
ASV318	1.986	1087	1.279E-04	Intermediate	Galbitalea
ASV319	1.000	437	2.783E-04	Specialist	Rhizorhapis

ASV320	1.984	1992	1.805E-04	Intermediate	Novosphingobium
ASV321	2.640	1087	1.429E-04	Generalist	Novosphingobium
ASV322	4.483	2219	9.779E-05	Generalist	NA
ASV323	1.682	1992	2.482E-04	Intermediate	Hymenobacter
ASV324	1.000	1087	4.363E-04	Specialist	NA
ASV325	1.000	1087	2.858E-04	Specialist	NA
ASV326	1.000	1087	4.288E-04	Specialist	Acinetobacter
ASV327	4.927	2140	5.266E-05	Generalist	NA
ASV328	1.000	1087	2.783E-04	Specialist	Sphingomonas
ASV329	1.000	1087	2.783E-04	Specialist	Chryseobacterium
ASV330	1.000	1087	2.783E-04	Specialist	Rubellimicrobium
ASV331	1.000	1087	2.407E-04	Specialist	Caenimonas
ASV332	2.870	1992	1.204E-04	Generalist	Novosphingobium
ASV333	2.299	1606	8.274E-05	Generalist	Roseomonas
ASV334	3.415	1087	1.279E-04	Generalist	Sphingomonas
ASV335	2.996	1606	9.779E-05	Generalist	NA
ASV336	2.822	605	1.429E-04	Generalist	Hymenobacter
ASV337	1.968	437	1.655E-04	Intermediate	Duganella
ASV338	1.742	1992	1.128E-04	Intermediate	Xylophilus
ASV339	2.455	2140	1.128E-04	Generalist	Kineococcus
ASV340	1.000	1087	2.708E-04	Specialist	Thermomonas
ASV341	1.239	2140	9.779E-05	Specialist	Pseudonocardia
ASV342	2.034	2219	1.805E-04	Intermediate	Sphingomonas
ASV343	1.994	1606	9.027E-05	Intermediate	Marmoricola
ASV344	3.013	2219	1.805E-04	Generalist	1174-901-12
ASV345	1.324	1087	2.708E-04	Specialist	Streptococcus
ASV346	1.000	2219	2.633E-04	Specialist	Brevundimonas
ASV347	3.967	1087	7.522E-05	Generalist	Nocardioides
ASV348	1.000	1087	2.633E-04	Specialist	NA
ASV349	1.410	1087	2.106E-04	Specialist	Aeromicrobium
ASV350	1.000	1606	2.858E-04	Specialist	Segetibacter
ASV351	1.146	1992	2.106E-04	Specialist	NA
ASV352	2.913	1606	1.279E-04	Generalist	Sphingomonas

ASV353	1.978	1087	1.580E-04	Intermediate	NA
ASV354	1.508	1992	2.482E-04	Intermediate	1174-901-12
ASV355	1.956	2219	1.730E-04	Intermediate	Abditibacterium
ASV356	1.000	1087	3.987E-04	Specialist	Oryzihumus
ASV357	1.486	437	2.031E-04	Specialist	Dyadobacter
ASV358	1.000	1087	2.633E-04	Specialist	Iamia
ASV359	1.000	1087	2.633E-04	Specialist	Demequina
ASV360	1.239	2219	2.482E-04	Specialist	Hymenobacter
ASV361	1.000	2140	2.181E-04	Specialist	Methylobacterium-Methylorubrum
ASV362	1.000	1087	2.558E-04	Specialist	NA
ASV363	1.443	1606	2.257E-04	Specialist	Hymenobacter
ASV364	1.000	2219	3.084E-04	Specialist	Georgenia
ASV365	1.000	605	1.053E-04	Specialist	Nocardioides
ASV366	1.000	1087	2.482E-04	Specialist	Xylophilus
ASV367	1.000	1087	2.482E-04	Specialist	Psychrobacter
ASV368	1.000	1087	2.482E-04	Specialist	Mycobacterium
ASV369	2.246	1087	1.204E-04	Intermediate	Flavobacterium
ASV371	2.625	1087	1.580E-04	Generalist	Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium
ASV372	1.955	1606	1.429E-04	Intermediate	P3OB-42
ASV373	2.830	605	1.128E-04	Generalist	NA
ASV374	1.385	1606	2.257E-04	Specialist	Brevundimonas
ASV375	2.059	1087	1.805E-04	Intermediate	Pseudonocardia
ASV376	1.819	2140	1.429E-04	Intermediate	Acinetobacter
ASV377	2.351	2219	1.204E-04	Generalist	Hymenobacter
ASV378	1.153	437	2.934E-04	Specialist	Conyzicola
ASV379	1.280	437	1.881E-04	Specialist	Streptococcus
ASV380	1.000	1087	3.686E-04	Specialist	NA
ASV381	1.000	1087	2.407E-04	Specialist	Sphingomonas
ASV382	1.000	1087	2.407E-04	Specialist	NA
ASV383	2.905	1087	1.053E-04	Generalist	Klebsiella
ASV384	1.000	1992	2.558E-04	Specialist	Polaromonas
ASV385	2.541	437	7.522E-05	Generalist	Actinomycetospora

ASV386	2.138	2219	1.655E-04	Intermediate	Chryseobacterium
ASV387	1.000	2219	3.235E-04	Specialist	1174-901-12
ASV388	1.000	1992	2.858E-04	Specialist	1174-901-12
ASV389	2.445	1992	1.429E-04	Generalist	Corynebacterium
ASV390	2.170	437	1.805E-04	Intermediate	Kytococcus
ASV391	1.000	2219	2.934E-04	Specialist	Moheibacter
ASV392	1.000	2219	2.332E-04	Specialist	Sphingomonas
ASV393	2.626	1606	9.779E-05	Generalist	Amaricoccus
ASV394	2.941	1606	9.027E-05	Generalist	MN 122.2a
ASV395	2.524	1606	1.279E-04	Generalist	Nocardioides
ASV396	2.219	2140	9.779E-05	Intermediate	Huanghella
ASV397	2.716	2219	1.204E-04	Generalist	Massilia
ASV398	1.000	2219	2.858E-04	Specialist	Prevotella_7
ASV399	1.000	1087	3.460E-04	Specialist	Marmoricola
ASV400	1.000	437	2.106E-04	Specialist	NA
ASV401	1.000	1087	2.257E-04	Specialist	Oryzihumus
ASV402	1.000	1087	2.257E-04	Specialist	Novosphingobium
ASV403	1.000	1087	2.257E-04	Specialist	Actinoallomurus
ASV404	1.581	1087	1.053E-04	Intermediate	Hymenobacter
ASV405	1.000	2140	1.053E-04	Specialist	NA
ASV406	1.600	1992	2.031E-04	Intermediate	Corynebacterium
ASV407	4.588	2140	8.274E-05	Generalist	NA
ASV408	1.000	1087	2.181E-04	Specialist	Pedococcus-Phycicoccus
ASV409	1.000	1087	1.730E-04	Specialist	Nocardioides
ASV410	1.942	2219	1.279E-04	Intermediate	Altererythrobacter
ASV411	1.618	1992	1.956E-04	Intermediate	NA
ASV412	1.000	1606	1.504E-04	Specialist	Corynebacterium
ASV413	1.000	1606	2.332E-04	Specialist	Rhizobacter
ASV414	1.000	1992	2.558E-04	Specialist	Amnibacterium
ASV415	1.000	1087	2.332E-04	Specialist	NA
ASV416	2.340	605	1.504E-04	Generalist	Nocardioides
ASV417	2.786	2219	1.053E-04	Generalist	Acinetobacter
ASV418	1.890	605	8.274E-05	Intermediate	Azohydromonas

ASV419	1.000	1087	3.310E-04	Specialist	Blautia
ASV420	1.000	1087	2.106E-04	Specialist	NA
ASV421	1.000	1087	2.106E-04	Specialist	Subtercola
ASV422	1.000	1087	2.106E-04	Specialist	NA
ASV423	1.000	1087	2.106E-04	Specialist	Haliea
ASV424	2.576	605	8.274E-05	Generalist	NA
ASV425	1.000	2140	2.708E-04	Specialist	NA
ASV426	1.000	2140	2.257E-04	Specialist	NA
ASV427	1.454	2219	1.881E-04	Specialist	Kocuria
ASV428	1.000	2219	2.558E-04	Specialist	Clostridium sensu stricto 10
ASV429	1.000	2219	2.558E-04	Specialist	Geobacillus
ASV430	1.000	2140	2.106E-04	Specialist	NA
ASV431	1.000	437	1.956E-04	Specialist	Sphingomonas
ASV432	1.000	1087	2.106E-04	Specialist	Corynebacterium
ASV433	1.000	1087	2.106E-04	Specialist	NA
ASV434	1.000	1087	2.106E-04	Specialist	Hymenobacter
ASV435	2.362	2140	1.204E-04	Generalist	Sphingomonas
ASV436	1.748	2140	8.274E-05	Intermediate	NA
ASV437	1.000	1087	2.558E-04	Specialist	Sphingomonas
ASV438	1.923	1087	1.580E-04	Intermediate	Caulobacter
ASV439	1.780	1087	1.881E-04	Intermediate	Corynebacterium
ASV440	1.220	2219	2.031E-04	Specialist	Gaiella
ASV441	1.000	1087	3.084E-04	Specialist	Granulicella
ASV442	1.000	1087	3.084E-04	Specialist	Pseudomonas
ASV443	1.508	2219	9.027E-05	Intermediate	MN 122.2a
ASV444	1.492	437	1.429E-04	Specialist	Acidiphilium
ASV445	1.000	1087	2.031E-04	Specialist	Chryseobacterium
ASV446	2.504	1606	1.053E-04	Generalist	Hymenobacter
ASV447	2.796	437	7.522E-05	Generalist	Robbsia
ASV448	3.240	1992	8.274E-05	Generalist	Neisseria
ASV449	2.445	1087	6.770E-05	Generalist	Spirosoma
ASV450	1.000	1606	2.106E-04	Specialist	Rubellimicrobium
ASV451	1.845	1606	1.504E-04	Intermediate	Spirosoma

ASV452	1.293	2140	9.027E-05	Specialist	Cryobacterium
ASV453	1.000	1992	1.881E-04	Specialist	Methylobacterium-Methylorubrum
ASV454	1.000	2140	1.730E-04	Specialist	Ensifer
ASV455	1.000	2219	1.956E-04	Specialist	Sphingomonas
ASV456	2.594	1606	1.053E-04	Generalist	1174-901-12
ASV457	1.415	1087	9.027E-05	Specialist	Kineosporia
ASV458	1.000	1087	2.181E-04	Specialist	Paracoccus
ASV459	1.874	2219	1.279E-04	Intermediate	NA
ASV460	1.000	2140	2.332E-04	Specialist	Methylobacterium-Methylorubrum
ASV461	1.220	1992	2.031E-04	Specialist	Mucilaginibacter
ASV462	1.000	1992	2.332E-04	Specialist	NA
ASV463	1.600	1992	1.128E-04	Intermediate	Endobacter
ASV464	1.624	2219	1.128E-04	Intermediate	Sphingomonas
ASV465	1.000	2219	1.881E-04	Specialist	Rubellimicrobium
ASV466	2.904	1992	8.274E-05	Generalist	Polaromonas
ASV467	1.000	1087	1.881E-04	Specialist	Rubellimicrobium
ASV468	1.000	1087	1.881E-04	Specialist	Myroides
ASV469	1.715	1606	1.429E-04	Intermediate	Hymenobacter
ASV470	2.580	1606	6.018E-05	Generalist	Blastococcus
ASV471	2.300	2219	1.204E-04	Generalist	NA
ASV472	1.000	1606	1.956E-04	Specialist	Psychroglaciecola
ASV473	1.990	1606	1.128E-04	Intermediate	Modestobacter
ASV474	2.455	1606	9.027E-05	Generalist	Mucilaginibacter
ASV475	2.753	1606	8.274E-05	Generalist	Corynebacterium
ASV476	1.972	2140	1.053E-04	Intermediate	Subdoligranulum
ASV477	1.923	2219	7.522E-05	Intermediate	Pseudonocardia
ASV478	1.000	2219	2.257E-04	Specialist	Chelatococcus
ASV479	3.286	1606	7.522E-05	Generalist	Nocardioides
ASV480	2.195	1087	9.779E-05	Intermediate	Abditibacterium
ASV481	1.508	437	8.274E-05	Intermediate	Alloprevotella
ASV482	1.000	1087	1.805E-04	Specialist	Adhaeribacter
ASV483	1.000	1992	1.580E-04	Specialist	Sphingomonas
ASV484	1.986	1992	9.779E-05	Intermediate	NA

ASV485	1.000	2140	1.655E-04	Specialist	NA
ASV486	1.855	2140	9.027E-05	Intermediate	NA
ASV487	1.000	1087	1.730E-04	Specialist	Corynebacterium
ASV488	1.000	1087	1.730E-04	Specialist	Sphingomonas
ASV489	1.000	1087	1.730E-04	Specialist	Amaricoccus
ASV490	1.293	1087	1.504E-04	Specialist	Acinetobacter
ASV491	2.840	437	8.274E-05	Generalist	Rothia
ASV492	1.338	605	1.204E-04	Specialist	NA
ASV493	1.000	1087	1.805E-04	Specialist	Endobacter
ASV494	1.000	1992	2.031E-04	Specialist	Chryseobacterium
ASV495	1.000	1992	1.956E-04	Specialist	P3OB-42
ASV496	1.000	605	2.332E-04	Specialist	Hymenobacter
ASV497	1.000	605	2.332E-04	Specialist	Variovorax
ASV498	1.000	1087	2.633E-04	Specialist	NA
ASV499	1.658	437	6.770E-05	Intermediate	Brevundimonas
ASV500	2.793	2219	9.027E-05	Generalist	Acidiphilium
ASV501	1.000	1606	1.730E-04	Specialist	Sphingomonas
ASV502	1.000	1606	1.730E-04	Specialist	NA
ASV503	1.690	605	1.504E-04	Intermediate	Piscinibacter
ASV504	1.000	2140	2.106E-04	Specialist	Amantichitinum
ASV505	1.988	2219	1.053E-04	Intermediate	Hymenobacter
ASV506	1.280	437	1.580E-04	Specialist	Clostridium sensu stricto 13
ASV507	1.000	2219	2.031E-04	Specialist	Levilactobacillus
ASV508	1.000	2219	2.031E-04	Specialist	Tepidimonas
ASV509	1.000	605	2.257E-04	Specialist	Sphingomonas
ASV510	1.000	605	2.257E-04	Specialist	Amnibacterium
ASV511	1.000	1087	1.580E-04	Specialist	Streptomyces
ASV512	1.000	1087	1.580E-04	Specialist	Solirubrobacter
ASV513	1.742	437	9.027E-05	Intermediate	Hymenobacter
ASV514	1.855	605	6.018E-05	Intermediate	Bacillus
ASV515	1.000	1087	1.655E-04	Specialist	Prauserella
ASV516	1.800	2140	5.266E-05	Intermediate	Abditibacterium
ASV517	1.403	1606	1.429E-04	Specialist	Rubellimicrobium

ASV518	1.862	1606	1.053E-04	Intermediate	Kineosporia
ASV519	1.827	437	1.279E-04	Intermediate	Dietzia
ASV520	2.989	2219	6.018E-05	Generalist	Methylobacterium-Methylorubrum
ASV521	1.734	2219	1.204E-04	Intermediate	Paenibacillus
ASV522	1.000	2219	1.730E-04	Specialist	NA
ASV523	1.000	2219	1.730E-04	Specialist	Methylobacterium-Methylorubrum
ASV524	1.000	2219	1.730E-04	Specialist	Hansschlegelia
ASV525	1.665	1087	1.580E-04	Intermediate	Phenylobacterium
ASV526	1.000	2219	1.580E-04	Specialist	Brevundimonas
ASV527	1.208	1606	1.429E-04	Specialist	Acidipropionibacterium
ASV528	1.766	1992	6.018E-05	Intermediate	Sphingomonas
ASV529	1.000	1087	1.504E-04	Specialist	Pseudomonas
ASV530	1.742	2140	1.354E-04	Intermediate	Frondihabitans
ASV531	1.960	1087	9.027E-05	Intermediate	Clostridium sensu stricto 1
ASV532	1.000	1606	1.655E-04	Specialist	Sphingomonas
ASV533	1.000	2140	1.504E-04	Specialist	P3OB-42
ASV534	1.000	2140	1.881E-04	Specialist	PMMR1
ASV535	1.000	1992	1.730E-04	Specialist	NA
ASV536	1.000	2219	9.779E-05	Specialist	Falsirhodobacter
ASV537	1.000	2140	1.279E-04	Specialist	Pedobacter
ASV538	1.980	2140	8.274E-05	Intermediate	Skermanella
ASV539	1.000	1087	2.332E-04	Specialist	NA
ASV540	1.000	1087	1.504E-04	Specialist	Hymenobacter
ASV541	1.000	1087	1.504E-04	Specialist	NA
ASV542	1.954	437	1.128E-04	Intermediate	Corynebacterium
ASV543	1.000	1087	1.504E-04	Specialist	Alteribacillus
ASV544	1.000	605	1.429E-04	Specialist	Noviherbaspirillum
ASV545	1.835	1606	9.779E-05	Intermediate	Rubellimicrobium
ASV546	1.835	1606	9.779E-05	Intermediate	Aerosphaera
ASV547	1.324	2219	1.354E-04	Specialist	Rubellimicrobium
ASV548	1.000	1606	1.580E-04	Specialist	Spirosoma
ASV549	1.000	1606	1.580E-04	Specialist	Devosia
ASV550	1.923	1992	1.128E-04	Intermediate	Devosia

ASV551	2.689	1992	7.522E-05	Generalist	Blautia
ASV552	1.967	1992	9.779E-05	Intermediate	Hymenobacter
ASV553	1.000	1992	1.730E-04	Specialist	NA
ASV554	1.541	2219	1.279E-04	Intermediate	Bifidobacterium
ASV555	1.000	2219	9.027E-05	Specialist	Bacteroides
ASV556	1.000	2219	1.580E-04	Specialist	Granulicella
ASV557	1.000	1087	1.655E-04	Specialist	Rothia
ASV558	1.000	2219	1.429E-04	Specialist	Devosia
ASV559	1.000	1087	2.181E-04	Specialist	Nocardioides
ASV560	1.000	1087	1.429E-04	Specialist	Acinetobacter
ASV561	1.000	1087	1.429E-04	Specialist	NA
ASV562	1.000	1087	1.429E-04	Specialist	Stenotrophomonas
ASV563	2.656	2140	6.018E-05	Generalist	Actinomyces
ASV564	2.418	1087	6.770E-05	Generalist	NA
ASV566	1.000	1606	1.504E-04	Specialist	Flavisolibacter
ASV567	1.342	2219	1.279E-04	Specialist	Williamsia
ASV568	2.384	1087	9.027E-05	Generalist	Pseudonocardia
ASV569	1.000	1087	1.580E-04	Specialist	Sphingomonas
ASV570	1.870	1087	9.027E-05	Intermediate	Hymenobacter
ASV571	1.761	2140	5.266E-05	Intermediate	Nocardioides
ASV572	1.569	1087	1.204E-04	Intermediate	Jatrophihabitans
ASV573	1.000	1087	9.779E-05	Specialist	Hymenobacter
ASV574	1.000	2140	1.429E-04	Specialist	Hymenobacter
ASV575	1.000	2140	1.504E-04	Specialist	NA
ASV576	1.000	2140	1.504E-04	Specialist	Quadrisphaera
ASV577	1.976	1992	7.522E-05	Intermediate	Acidiphilium
ASV578	1.000	1992	1.655E-04	Specialist	Endobacter
ASV579	1.000	1992	1.204E-04	Specialist	Bryocella
ASV580	1.724	2140	1.053E-04	Intermediate	Acinetobacter
ASV581	1.000	2219	1.730E-04	Specialist	NA
ASV582	1.000	2219	1.504E-04	Specialist	Rubellimicrobium
ASV583	1.000	2219	1.504E-04	Specialist	Pseudomonas
ASV584	1.000	605	1.881E-04	Specialist	NA

ASV585	1.000	1087	1.354E-04	Specialist	Kocuria
ASV586	1.835	1992	6.018E-05	Intermediate	Acidiphilium
ASV587	1.000	437	1.504E-04	Specialist	Abiotrophia
ASV588	1.000	1606	1.204E-04	Specialist	Flavobacterium
ASV589	1.000	1606	1.429E-04	Specialist	Gaiella
ASV590	1.000	605	9.779E-05	Specialist	Psychroglaciecola
ASV591	1.000	1992	1.279E-04	Specialist	NA
ASV593	1.000	1992	1.580E-04	Specialist	Spirosoma
ASV594	1.000	1992	1.580E-04	Specialist	Abditibacterium
ASV595	1.342	437	8.274E-05	Specialist	Anaerococcus
ASV596	1.000	2219	1.655E-04	Specialist	Timonella
ASV597	1.000	2219	1.429E-04	Specialist	Sphingomonas
ASV598	1.000	2219	1.429E-04	Specialist	Qipengyuania
ASV599	1.000	2219	1.429E-04	Specialist	Abditibacterium
ASV600	1.976	2140	7.522E-05	Intermediate	Hymenobacter
ASV601	1.000	2219	1.429E-04	Specialist	Sphingomonas
ASV602	1.000	2219	1.279E-04	Specialist	Defluviicoccus
ASV603	1.000	605	9.027E-05	Specialist	Hymenobacter
ASV604	1.642	2140	8.274E-05	Intermediate	Nakamurella
ASV605	1.000	1087	1.279E-04	Specialist	Sphingomonas
ASV606	1.000	1087	1.279E-04	Specialist	Solirubrobacter
ASV607	1.976	1087	7.522E-05	Intermediate	NA
ASV608	1.000	1606	1.128E-04	Specialist	MND1
ASV609	1.670	1992	9.779E-05	Intermediate	Pseudomonas
ASV610	1.000	1606	1.354E-04	Specialist	Craurococcus-Caldovatus
ASV611	1.690	605	1.128E-04	Intermediate	Haliangium
ASV612	1.000	2140	1.580E-04	Specialist	Bryobacter
ASV613	1.633	2219	1.053E-04	Intermediate	Mogibacterium
ASV614	1.000	2140	7.522E-05	Specialist	Spirosoma
ASV615	1.000	1606	1.279E-04	Specialist	NA
ASV616	1.000	1992	1.504E-04	Specialist	Acidiphilium
ASV617	1.000	2219	1.354E-04	Specialist	Nocardioides
ASV618	1.000	2140	1.053E-04	Specialist	NA

ASV619	1.000	2219	1.354E-04	Specialist	NA
ASV620	1.600	2140	9.027E-05	Intermediate	Aureimonas
ASV621	1.000	1087	1.204E-04	Specialist	NA
ASV622	1.800	1606	5.266E-05	Intermediate	Neisseria
ASV623	1.800	1992	9.027E-05	Intermediate	NA
ASV624	2.651	1606	6.018E-05	Generalist	Nocardioides
ASV625	1.000	1606	1.279E-04	Specialist	Hymenobacter
ASV626	1.835	1087	5.266E-05	Intermediate	NA
ASV627	1.000	1087	1.279E-04	Specialist	Kineosporia
ASV628	1.923	437	9.027E-05	Intermediate	Methylobacterium-Methylorubrum
ASV629	1.000	2140	1.504E-04	Specialist	NA
ASV630	1.000	1606	1.504E-04	Specialist	NA
ASV631	1.000	2219	1.279E-04	Specialist	Roseomonas
ASV632	1.000	605	1.580E-04	Specialist	Arthrobacter
ASV633	1.000	1087	1.128E-04	Specialist	Lysobacter
ASV634	1.000	1087	1.128E-04	Specialist	Acidiphilium
ASV635	1.000	1087	1.128E-04	Specialist	Shewanella
ASV637	1.800	2140	7.522E-05	Intermediate	Novosphingobium
ASV639	1.000	1087	1.128E-04	Specialist	Kribbella
ASV640	1.000	1606	9.779E-05	Specialist	Quadrisphaera
ASV641	1.923	2140	6.770E-05	Intermediate	Methylobacterium-Methylorubrum
ASV642	1.600	1606	9.027E-05	Intermediate	Streptococcus
ASV643	1.000	1992	1.730E-04	Specialist	Corynebacterium
ASV644	1.000	1087	1.204E-04	Specialist	Pajaroellobacter
ASV645	1.000	1087	1.204E-04	Specialist	Huanghella
ASV646	2.945	1087	5.266E-05	Generalist	Rubrivirga
ASV647	1.000	2140	1.429E-04	Specialist	Massilia
ASV648	1.841	1087	8.274E-05	Intermediate	Paenarthrobacter
ASV649	1.301	2140	5.266E-05	Specialist	Fibrella
ASV650	1.923	1992	6.770E-05	Intermediate	NA
ASV651	1.000	1992	1.354E-04	Specialist	1174-901-12
ASV652	1.000	1992	1.354E-04	Specialist	Spirosoma
ASV653	1.000	2140	1.053E-04	Specialist	Hymenobacter

ASV654	1.000	2219	1.354E-04	Specialist	NA
ASV655	1.000	2219	1.354E-04	Specialist	Ethanoligenens
ASV656	1.000	2219	1.354E-04	Specialist	Tepidiphilus
ASV657	1.000	2219	1.204E-04	Specialist	NA
ASV658	1.000	2219	1.204E-04	Specialist	Staphylococcus
ASV659	1.000	2219	1.204E-04	Specialist	Capnocytophaga
ASV660	1.000	605	1.429E-04	Specialist	Leucobacter
ASV661	1.000	2140	9.779E-05	Specialist	Sphingomonas
ASV662	1.000	2140	9.779E-05	Specialist	NA
ASV663	1.000	1087	1.053E-04	Specialist	Iamia
ASV664	1.000	1992	1.128E-04	Specialist	Sphingomonas
ASV665	1.753	437	8.274E-05	Intermediate	Aggregatibacter
ASV666	1.000	1606	9.779E-05	Specialist	Nocardioides
ASV667	1.849	1606	6.770E-05	Intermediate	Microvirga
ASV668	1.841	605	8.274E-05	Intermediate	Acidiphilium
ASV669	1.000	2219	6.770E-05	Specialist	NA
ASV670	1.000	1606	1.128E-04	Specialist	NA
ASV671	1.000	2219	1.429E-04	Specialist	Endobacter
ASV672	1.000	1087	1.128E-04	Specialist	P3OB-42
ASV673	1.000	1087	1.128E-04	Specialist	NA
ASV674	1.000	1992	6.018E-05	Specialist	Nocardioides
ASV675	1.000	1606	1.053E-04	Specialist	NA
ASV676	1.000	1992	1.279E-04	Specialist	Conexibacter
ASV677	1.000	2219	1.204E-04	Specialist	Chryseobacterium
ASV678	1.000	2219	1.204E-04	Specialist	Limosilactobacillus
ASV679	1.000	2140	9.027E-05	Specialist	Endobacter
ASV680	1.000	605	1.279E-04	Specialist	NA
ASV681	1.000	2219	1.053E-04	Specialist	Hymenobacter
ASV682	1.000	2219	1.053E-04	Specialist	Mycobacterium
ASV683	1.000	1606	9.027E-05	Specialist	Caedibacter
ASV684	1.562	605	9.779E-05	Intermediate	Leucobacter
ASV685	1.000	605	9.779E-05	Specialist	NA
ASV686	1.000	437	1.279E-04	Specialist	Hymenobacter

ASV687	1.000	1087	1.053E-04	Specialist	Anaerococcus
ASV688	1.969	605	6.770E-05	Intermediate	NA
ASV690	1.991	2219	6.018E-05	Intermediate	NA
ASV691	1.000	1606	1.053E-04	Specialist	Domibacillus
ASV692	1.000	1606	1.053E-04	Specialist	NA
ASV693	1.000	1087	1.128E-04	Specialist	Corynebacterium
ASV694	1.923	437	6.770E-05	Intermediate	Hymenobacter
ASV695	1.899	1087	6.018E-05	Intermediate	Prevotella_7
ASV696	1.923	1992	6.770E-05	Intermediate	Hymenobacter
ASV697	1.882	605	7.522E-05	Intermediate	Porphyromonas
ASV698	1.000	1087	1.279E-04	Specialist	Aurantisolimonas
ASV699	2.000	1087	6.018E-05	Intermediate	NA
ASV700	1.993	605	6.018E-05	Intermediate	NA
ASV701	1.800	437	9.027E-05	Intermediate	Abditibacterium
ASV702	1.000	2140	1.204E-04	Specialist	Blastococcus
ASV703	1.000	1992	1.204E-04	Specialist	Methylopila
ASV704	1.000	1992	1.204E-04	Specialist	Chryseobacterium
ASV705	1.000	437	1.128E-04	Specialist	NA
ASV706	1.000	437	1.279E-04	Specialist	Aurantimonas
ASV707	1.000	2219	1.128E-04	Specialist	Sphingomonas
ASV708	1.000	605	1.354E-04	Specialist	Marmoricola
ASV709	1.000	2140	1.053E-04	Specialist	Brachybacterium
ASV710	1.000	2140	9.779E-05	Specialist	P3OB-42
ASV711	1.000	2140	8.274E-05	Specialist	Microvirga
ASV712	1.000	2140	8.274E-05	Specialist	NA
ASV713	1.000	2219	1.128E-04	Specialist	Hymenobacter
ASV714	1.000	2140	8.274E-05	Specialist	Mucilaginibacter
ASV715	1.000	2140	8.274E-05	Specialist	Sphingomonas
ASV716	1.000	1087	1.504E-04	Specialist	Nocardioides
ASV717	1.550	1087	7.522E-05	Intermediate	Dyadobacter
ASV718	1.000	1087	9.027E-05	Specialist	Candidatus Alysiosphaera
ASV719	2.528	437	6.018E-05	Generalist	NA
ASV720	1.000	2219	1.128E-04	Specialist	Bacillus

ASV721	1.000	2219	1.128E-04	Specialist	Nocardioides
ASV722	1.000	1606	8.274E-05	Specialist	Sphingobium
ASV723	1.800	605	7.522E-05	Intermediate	Lactobacillus
ASV724	1.988	1992	5.266E-05	Intermediate	Halomonas
ASV725	1.000	1606	9.779E-05	Specialist	Psychroglaciecola
ASV726	1.000	1606	9.779E-05	Specialist	Rhizorhapis
ASV727	1.000	605	9.779E-05	Specialist	Craurococcus-Caldovatus
ASV728	1.000	1087	1.053E-04	Specialist	Altererythrobacter
ASV729	1.000	1087	7.522E-05	Specialist	Roseomonas
ASV730	1.000	1992	1.429E-04	Specialist	Catenuloplanes
ASV731	1.000	2140	1.204E-04	Specialist	P3OB-42
ASV732	1.000	437	6.770E-05	Specialist	Hymenobacter
ASV733	1.849	2140	6.770E-05	Intermediate	Pajaroellobacter
ASV734	1.753	605	8.274E-05	Intermediate	Ellin6055
ASV735	1.000	2140	1.128E-04	Specialist	NA
ASV736	1.000	2140	1.128E-04	Specialist	Butyricicoccus
ASV737	1.969	605	6.770E-05	Intermediate	Abditibacterium
ASV738	1.508	1992	8.274E-05	Intermediate	Blastococcus
ASV739	1.000	2140	9.027E-05	Specialist	Spirillospora
ASV740	1.000	2140	9.027E-05	Specialist	Aureimonas
ASV741	1.562	1992	9.779E-05	Intermediate	NA
ASV742	1.000	2219	1.053E-04	Specialist	Ruminococcus
ASV743	1.000	2140	9.779E-05	Specialist	Hymenobacter
ASV744	1.000	2140	8.274E-05	Specialist	Cnuella
ASV745	1.000	2140	4.513E-05	Specialist	Herbiconiux
ASV746	1.000	2219	9.779E-05	Specialist	Marisediminicola
ASV747	1.000	605	1.204E-04	Specialist	Leucobacter
ASV748	1.000	2140	8.274E-05	Specialist	NA
ASV749	1.000	2140	8.274E-05	Specialist	NA
ASV750	1.000	1087	1.429E-04	Specialist	Pseudoclavibacter
ASV751	1.000	1087	8.274E-05	Specialist	Ornithinimicrobium
ASV752	1.800	1087	6.018E-05	Intermediate	Agathobacter
ASV753	1.000	437	8.274E-05	Specialist	Sphingomonas

ASV754	1.988	437	5.266E-05	Intermediate	NA
ASV755	1.000	605	8.274E-05	Specialist	Cedecea
ASV756	1.000	1992	9.027E-05	Specialist	NA
ASV758	1.000	1087	7.522E-05	Specialist	1174-901-12
ASV759	1.984	2140	4.513E-05	Intermediate	Paucibacter
ASV760	1.000	1606	7.522E-05	Specialist	Sphingomonas
ASV761	1.000	1606	7.522E-05	Specialist	Aureimonas
ASV762	1.000	1606	7.522E-05	Specialist	Adhaeribacter
ASV763	1.000	605	8.274E-05	Specialist	Paracoccus
ASV764	1.000	605	9.779E-05	Specialist	NA
ASV765	1.000	1606	9.027E-05	Specialist	NA
ASV766	1.000	1606	9.027E-05	Specialist	Dyella
ASV767	1.000	1606	9.027E-05	Specialist	NA
ASV768	1.000	1606	9.027E-05	Specialist	Sphingomonas
ASV769	1.899	1606	6.018E-05	Intermediate	NA
ASV771	1.000	1087	9.779E-05	Specialist	NA
ASV772	1.000	2219	1.204E-04	Specialist	Larkinella
ASV773	1.642	1992	8.274E-05	Intermediate	Granulicella
ASV774	1.000	2140	7.522E-05	Specialist	Haemophilus
ASV775	1.000	1087	9.027E-05	Specialist	Acidiphilium
ASV776	1.000	1087	9.027E-05	Specialist	1174-901-12
ASV777	1.000	1087	9.027E-05	Specialist	NA
ASV778	1.000	1087	1.053E-04	Specialist	Granulicella
ASV779	1.324	605	9.027E-05	Specialist	Ferruginibacter
ASV780	1.000	1992	9.779E-05	Specialist	NA
ASV781	1.000	1992	9.779E-05	Specialist	Pseudolabrys
ASV782	1.000	2140	1.053E-04	Specialist	Bacteroides
ASV783	1.000	2140	1.053E-04	Specialist	Mycobacterium
ASV784	1.000	2140	1.053E-04	Specialist	Rhizobacter
ASV785	1.000	1992	9.779E-05	Specialist	Acidiphilium
ASV786	1.000	2140	8.274E-05	Specialist	NA
ASV787	1.000	2140	8.274E-05	Specialist	Defluviicoccus
ASV788	1.000	2140	8.274E-05	Specialist	Spirosoma

ASV789	1.000	2219	9.779E-05	Specialist	Brevibacterium
ASV790	1.000	2219	9.779E-05	Specialist	P3OB-42
ASV791	1.000	2219	1.053E-04	Specialist	NA
ASV792	1.000	605	1.128E-04	Specialist	Abditibacterium
ASV793	1.000	605	1.128E-04	Specialist	Hymenobacter
ASV794	1.000	605	1.128E-04	Specialist	NA
ASV795	1.000	2140	9.027E-05	Specialist	Corynebacterium
ASV796	1.000	2140	7.522E-05	Specialist	NA
ASV797	1.000	2140	7.522E-05	Specialist	NA
ASV798	1.000	605	1.053E-04	Specialist	NA
ASV799	1.000	2219	9.027E-05	Specialist	Quadrisphaera
ASV800	1.000	2219	8.274E-05	Specialist	Spirosoma
ASV801	1.000	2219	8.274E-05	Specialist	NA
ASV802	1.000	437	7.522E-05	Specialist	Aurantisolimonas
ASV803	1.000	437	7.522E-05	Specialist	NA
ASV804	1.000	605	7.522E-05	Specialist	Methylobacterium-Methylorubrum
ASV805	1.000	1992	8.274E-05	Specialist	Bdellovibrio
ASV806	2.000	1992	4.513E-05	Intermediate	Abditibacterium
ASV808	2.778	1087	3.009E-05	Generalist	Lactococcus
ASV809	1.000	1606	7.522E-05	Specialist	Nocardioides
ASV810	1.000	1606	7.522E-05	Specialist	NA
ASV811	1.000	605	9.027E-05	Specialist	Nordella
ASV812	1.000	605	9.027E-05	Specialist	NA
ASV813	1.000	2219	6.770E-05	Specialist	P3OB-42
ASV814	1.000	1606	8.274E-05	Specialist	Solirubrobacter
ASV815	1.000	1606	8.274E-05	Specialist	Actinomycetospora
ASV816	1.000	1606	8.274E-05	Specialist	Psychroglaciecola
ASV817	1.000	605	6.770E-05	Specialist	Gemmatimonas
ASV818	1.000	1087	9.027E-05	Specialist	Solirubrobacter
ASV819	1.000	2219	1.053E-04	Specialist	NA
ASV820	1.000	1992	1.204E-04	Specialist	Conexibacter
ASV821	1.000	1087	8.274E-05	Specialist	Dermacoccus
ASV822	1.000	1087	8.274E-05	Specialist	NA

ASV823	1.000	1087	9.779E-05	Specialist	Ellin6055
ASV824	1.550	1087	7.522E-05	Intermediate	Abditibacterium
ASV825	1.000	2140	1.053E-04	Specialist	Prauserella
ASV826	1.899	2140	6.018E-05	Intermediate	Streptococcus
ASV827	1.000	1992	8.274E-05	Specialist	Sphingomonas
ASV828	2.000	1992	4.513E-05	Intermediate	Sphingobacterium
ASV829	1.000	2140	8.274E-05	Specialist	Sphingoaurantiacus
ASV830	1.000	2140	8.274E-05	Specialist	Rhabdobacter
ASV831	1.000	2140	8.274E-05	Specialist	Actinoplanes
ASV832	1.000	2140	8.274E-05	Specialist	Hymenobacter
ASV833	1.000	2140	9.779E-05	Specialist	Marmoricola
ASV834	1.000	1992	9.779E-05	Specialist	1174-901-12
ASV835	1.000	1992	9.779E-05	Specialist	NA
ASV836	1.000	437	9.027E-05	Specialist	Marisediminicola
ASV837	1.000	437	1.053E-04	Specialist	PMMR1
ASV838	1.000	2219	9.027E-05	Specialist	Nocardioides
ASV839	1.000	2219	9.779E-05	Specialist	Caldibacillus
ASV840	1.000	2219	9.779E-05	Specialist	Proteiniphilum
ASV841	1.000	2219	9.027E-05	Specialist	Aliidongia
ASV842	1.000	2219	9.027E-05	Specialist	Hymenobacter
ASV843	1.000	605	1.053E-04	Specialist	Cellulomonas
ASV844	1.000	2140	6.770E-05	Specialist	NA
ASV845	1.000	2140	6.770E-05	Specialist	NA
ASV846	1.000	605	9.779E-05	Specialist	Sphingobium
ASV847	1.000	2219	8.274E-05	Specialist	Clostridium sensu stricto 1
ASV848	1.000	2219	7.522E-05	Specialist	Hymenobacter
ASV849	1.000	1087	6.770E-05	Specialist	NA
ASV850	1.000	1992	7.522E-05	Specialist	NA
ASV851	2.000	1992	2.257E-05	Intermediate	Caulobacter
ASV852	1.000	437	6.770E-05	Specialist	Sphingomonas
ASV853	1.724	1606	5.266E-05	Intermediate	Ferruginibacter
ASV854	2.632	437	3.761E-05	Generalist	Gemella
ASV855	1.000	2219	9.027E-05	Specialist	Hymenobacter

ASV856	1.000	1606	6.770E-05	Specialist	Rhizobacter
ASV857	1.000	1606	6.770E-05	Specialist	Methylobacterium-Methylorubrum
ASV858	1.000	1606	6.770E-05	Specialist	Acinetobacter
ASV859	1.000	1606	3.761E-05	Specialist	Sediminibacterium
ASV860	1.000	1606	3.009E-05	Specialist	Pseudomonas
ASV861	1.000	1606	7.522E-05	Specialist	Sphingomonas
ASV862	1.000	1606	7.522E-05	Specialist	NA
ASV863	1.000	1606	7.522E-05	Specialist	Nitrospira
ASV864	1.000	1992	1.128E-04	Specialist	NA
ASV865	1.000	1087	7.522E-05	Specialist	Amaricoccus
ASV866	1.000	1087	7.522E-05	Specialist	Melittangium
ASV867	1.000	1087	7.522E-05	Specialist	Sphingomonas
ASV868	1.000	605	9.027E-05	Specialist	Pseudonocardia
ASV870	1.000	1087	9.027E-05	Specialist	Sphingomonas
ASV871	1.000	1087	9.027E-05	Specialist	Clavibacter
ASV872	1.000	1087	9.027E-05	Specialist	Hymenobacter
ASV873	1.000	2140	9.027E-05	Specialist	NA
ASV874	2.000	2140	3.761E-05	Intermediate	Dyadobacter
ASV875	1.000	2140	7.522E-05	Specialist	NA
ASV876	1.000	2140	7.522E-05	Specialist	Sphingomonas
ASV877	1.000	2140	7.522E-05	Specialist	Craurococcus-Caldovatus
ASV878	1.000	2140	7.522E-05	Specialist	NA
ASV879	1.000	2140	7.522E-05	Specialist	NA
ASV880	1.000	1992	8.274E-05	Specialist	Hymenobacter
ASV881	1.000	1992	6.770E-05	Specialist	Solirubrobacter
ASV882	1.000	2140	9.027E-05	Specialist	[Eubacterium] siraeum group
ASV883	1.000	2140	9.027E-05	Specialist	Rhizorhapis
ASV884	1.000	2140	9.027E-05	Specialist	NA
ASV885	1.000	1992	9.027E-05	Specialist	Nocardioides
ASV886	1.000	1992	9.027E-05	Specialist	Sphingomonas
ASV887	1.000	1992	9.027E-05	Specialist	NA
ASV888	1.923	1992	4.513E-05	Intermediate	Brevibacillus
ASV889	1.000	1992	8.274E-05	Specialist	NA

ASV890	1.923	2219	4.513E-05	Intermediate	Melittangium
ASV891	1.000	1606	8.274E-05	Specialist	P3OB-42
ASV892	1.000	1606	8.274E-05	Specialist	Nocardioides
ASV894	1.000	437	9.779E-05	Specialist	Spirosoma
ASV895	1.000	2219	9.027E-05	Specialist	Schlegelella
ASV896	1.000	2219	8.274E-05	Specialist	Rubellimicrobium
ASV898	1.000	2219	8.274E-05	Specialist	Coprococcus
ASV899	1.000	2140	6.770E-05	Specialist	NA
ASV900	1.000	2140	6.018E-05	Specialist	Roseomonas
ASV901	1.000	2140	6.018E-05	Specialist	Muricoccus
ASV902	1.000	2140	6.018E-05	Specialist	Sphingomonas
ASV903	1.000	2219	7.522E-05	Specialist	Sphingomonas
ASV904	1.000	2219	8.274E-05	Specialist	Amnibacterium
ASV905	1.000	2219	8.274E-05	Specialist	Caedibacter
ASV906	1.000	2219	7.522E-05	Specialist	Stenotrophomonas
ASV907	1.000	2219	7.522E-05	Specialist	Fibrella
ASV908	1.000	437	8.274E-05	Specialist	1174-901-12
ASV909	1.000	1087	1.128E-04	Specialist	NA
ASV910	1.000	437	4.513E-05	Specialist	Arcticibacter
ASV911	1.000	1087	6.770E-05	Specialist	Pseudomonas
ASV912	1.000	1087	5.266E-05	Specialist	Staphylococcus
ASV913	1.000	437	8.274E-05	Specialist	NA
ASV914	1.000	1606	6.018E-05	Specialist	NA
ASV915	1.000	1606	6.018E-05	Specialist	NA
ASV916	1.000	1606	6.018E-05	Specialist	Methylobacterium-Methylorubrum
ASV917	1.000	1606	6.018E-05	Specialist	Rubellimicrobium
ASV918	1.000	1606	6.018E-05	Specialist	NA
ASV919	1.976	1606	3.761E-05	Intermediate	Rothia
ASV920	1.000	605	7.522E-05	Specialist	Microvirga
ASV921	1.000	1606	6.770E-05	Specialist	Sphingomonas
ASV922	1.000	1606	6.770E-05	Specialist	OM27 clade
ASV923	1.000	1606	6.770E-05	Specialist	Acidothermus
ASV924	1.000	1606	6.770E-05	Specialist	Thermoactinomyces

ASV925	1.000	1606	6.770E-05	Specialist	NA
ASV926	1.000	605	6.770E-05	Specialist	Sphingomonas
ASV927	1.000	1087	7.522E-05	Specialist	Defluviicoccus
ASV928	1.000	2219	9.027E-05	Specialist	Actinomycetospora
ASV929	1.000	1992	1.053E-04	Specialist	NA
ASV930	1.000	1087	6.770E-05	Specialist	1174-901-12
ASV931	1.000	1087	8.274E-05	Specialist	Spirosoma
ASV932	1.000	1087	8.274E-05	Specialist	Hymenobacter
ASV933	1.000	1087	8.274E-05	Specialist	NA
ASV934	2.000	1992	3.761E-05	Intermediate	Collinsella
ASV935	1.000	2140	6.770E-05	Specialist	NA
ASV936	1.000	2140	6.770E-05	Specialist	Hymenobacter
ASV937	1.000	2140	6.770E-05	Specialist	Iamia
ASV938	1.000	2140	6.770E-05	Specialist	Pajaroellobacter
ASV939	1.000	1992	7.522E-05	Specialist	Hyphomicrobium
ASV940	1.000	1992	6.018E-05	Specialist	Citricoccus
ASV941	1.000	2140	8.274E-05	Specialist	Sphingomonas
ASV942	1.000	1606	8.274E-05	Specialist	NA
ASV943	1.000	1992	8.274E-05	Specialist	Micromonospora
ASV944	1.000	437	7.522E-05	Specialist	Prevotella_9
ASV945	1.000	437	5.266E-05	Specialist	NA
ASV946	1.000	2140	6.018E-05	Specialist	Sphingomonas
ASV947	1.000	2140	6.018E-05	Specialist	Methylobacterium-Methylorubrum
ASV948	1.000	1606	7.522E-05	Specialist	Terriglobus
ASV949	1.000	437	9.027E-05	Specialist	Neomicrococcus
ASV950	1.000	2219	8.274E-05	Specialist	Actinomycetospora
ASV951	1.000	2219	8.274E-05	Specialist	Prevotella_7
ASV952	1.000	2219	7.522E-05	Specialist	Acidibacter
ASV953	1.000	437	8.274E-05	Specialist	NA
ASV954	1.000	605	9.027E-05	Specialist	Ferruginibacter
ASV955	1.000	605	9.027E-05	Specialist	Sphingoaurantiacus
ASV956	1.000	605	9.027E-05	Specialist	Bryobacter
ASV957	1.000	2140	7.522E-05	Specialist	NA

ASV958	1.000	2140	6.018E-05	Specialist	Novosphingobium
ASV960	1.000	1087	7.522E-05	Specialist	Ellin6055
ASV961	1.000	1087	7.522E-05	Specialist	NA
ASV962	1.000	605	8.274E-05	Specialist	Oligoflexus
ASV963	1.000	605	8.274E-05	Specialist	Nocardioides
ASV964	1.000	605	8.274E-05	Specialist	Solirubrobacter
ASV965	1.000	605	8.274E-05	Specialist	Sphingomonas
ASV966	1.000	2219	6.770E-05	Specialist	Abditibacterium
ASV967	1.000	2219	6.770E-05	Specialist	NA
ASV968	1.000	2219	6.770E-05	Specialist	Streptomyces
ASV969	1.000	605	8.274E-05	Specialist	Vagococcus
ASV970	1.000	605	8.274E-05	Specialist	NA
ASV971	1.000	437	7.522E-05	Specialist	Qipengyuania
ASV972	1.000	2140	6.018E-05	Specialist	Nocardioides
ASV973	1.000	1087	6.018E-05	Specialist	Clostridium sensu stricto 1
ASV974	2.000	1087	3.009E-05	Intermediate	Peptoniphilus
ASV976	1.000	1992	6.018E-05	Specialist	NA
ASV977	1.000	1992	6.018E-05	Specialist	NA
ASV978	1.000	437	5.266E-05	Specialist	Rhodoferax
ASV979	1.000	437	5.266E-05	Specialist	Cellulomonas
ASV980	1.000	437	5.266E-05	Specialist	Hymenobacter
ASV981	1.000	605	6.018E-05	Specialist	Pajaroellobacter
ASV982	1.976	1087	3.761E-05	Intermediate	NA
ASV983	1.000	1992	6.018E-05	Specialist	Acinetobacter
ASV984	1.000	1992	6.018E-05	Specialist	Amnibacterium
ASV985	1.528	2140	5.266E-05	Intermediate	Spirosoma
ASV986	1.000	437	6.770E-05	Specialist	Capnocytophaga
ASV987	1.000	437	4.513E-05	Specialist	Gardnerella
ASV988	1.000	1087	6.018E-05	Specialist	Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium
ASV989	1.000	2219	7.522E-05	Specialist	NA
ASV990	1.000	1606	5.266E-05	Specialist	Granulicatella
ASV991	1.000	1606	5.266E-05	Specialist	Devosia

ASV992	1.000	1606	5.266E-05	Specialist	Brevundimonas
ASV993	1.000	605	6.770E-05	Specialist	NA
ASV994	1.000	605	6.770E-05	Specialist	Abditibacterium
ASV995	1.000	1606	6.018E-05	Specialist	Gaiella
ASV996	1.800	2219	3.009E-05	Intermediate	NA
ASV997	1.000	1606	6.018E-05	Specialist	NA
ASV998	1.000	1606	6.018E-05	Specialist	Rhodovarius
ASV999	1.000	605	6.018E-05	Specialist	Gaiella
ASV1000	1.000	2140	5.266E-05	Specialist	Amaricoccus
ASV1001	1.000	1087	6.018E-05	Specialist	Sphingomonas
ASV1002	1.000	1087	6.018E-05	Specialist	Nakamurella
ASV1003	1.000	1087	6.018E-05	Specialist	NA
ASV1004	1.000	1087	6.018E-05	Specialist	Huanghella
ASV1005	1.000	1087	6.018E-05	Specialist	Sphingomonas
ASV1006	1.000	1087	6.018E-05	Specialist	NA
ASV1007	1.000	1087	6.018E-05	Specialist	Limnobacter
ASV1008	1.000	2219	6.770E-05	Specialist	Ligilactobacillus
ASV1009	1.000	2140	7.522E-05	Specialist	NA
ASV1010	1.000	2140	7.522E-05	Specialist	NA
ASV1011	1.000	1992	6.770E-05	Specialist	Pseudomonas
ASV1012	1.000	2140	6.770E-05	Specialist	NA
ASV1013	1.000	2140	6.770E-05	Specialist	Blautia
ASV1014	1.000	2140	6.770E-05	Specialist	Sphingomonas
ASV1015	1.000	1992	6.770E-05	Specialist	Hymenobacter
ASV1016	1.000	1992	6.770E-05	Specialist	P3OB-42
ASV1017	1.000	1992	5.266E-05	Specialist	Streptosporangium
ASV1018	1.000	1606	7.522E-05	Specialist	Spirosoma
ASV1019	1.000	1606	7.522E-05	Specialist	NA
ASV1020	1.000	1992	7.522E-05	Specialist	Pseudonocardia
ASV1021	1.000	1992	7.522E-05	Specialist	Pedobacter
ASV1022	1.000	1606	5.266E-05	Specialist	Cellulosimicrobium
ASV1023	1.000	2140	5.266E-05	Specialist	NA
ASV1024	1.000	1606	6.770E-05	Specialist	Hymenobacter

ASV1025	1.000	1606	6.770E-05	Specialist	Solirubrobacter
ASV1026	1.000	1606	6.770E-05	Specialist	Monoglobus
ASV1027	1.000	437	7.522E-05	Specialist	Marmoricola
ASV1028	1.000	437	7.522E-05	Specialist	NA
ASV1029	1.000	2219	6.770E-05	Specialist	Flavisolibacter
ASV1030	1.000	2219	6.770E-05	Specialist	Carnobacterium
ASV1031	1.000	2219	6.770E-05	Specialist	Ruminococcus
ASV1032	1.000	2219	6.770E-05	Specialist	Aureimonas
ASV1033	1.724	605	5.266E-05	Intermediate	Corynebacterium
ASV1034	1.000	605	8.274E-05	Specialist	NA
ASV1035	1.000	605	8.274E-05	Specialist	NA
ASV1036	1.000	605	8.274E-05	Specialist	Abditibacterium
ASV1037	1.000	605	8.274E-05	Specialist	NA
ASV1038	1.000	2140	5.266E-05	Specialist	Edaphobaculum
ASV1039	1.000	2140	5.266E-05	Specialist	NA
ASV1040	1.000	2140	5.266E-05	Specialist	NA
ASV1041	1.000	2140	5.266E-05	Specialist	Paenibacillus
ASV1042	1.000	1087	6.770E-05	Specialist	Methylorosula
ASV1043	1.000	1087	6.770E-05	Specialist	Parviterribacter
ASV1044	1.000	1087	6.770E-05	Specialist	Acidibacter
ASV1045	1.000	1087	6.770E-05	Specialist	Polymorphobacter
ASV1046	1.000	605	7.522E-05	Specialist	NA
ASV1048	1.000	2219	6.770E-05	Specialist	Sphingoaurantiacus
ASV1049	1.882	2219	3.761E-05	Intermediate	Frederiksenia
ASV1050	1.000	1606	5.266E-05	Specialist	Nocardioides
ASV1051	1.000	1606	5.266E-05	Specialist	Abditibacterium
ASV1052	1.000	605	7.522E-05	Specialist	Bacillus
ASV1053	1.000	1992	4.513E-05	Specialist	NA
ASV1054	1.000	1992	4.513E-05	Specialist	Pseudomonas
ASV1055	1.000	2140	5.266E-05	Specialist	NA
ASV1056	1.000	1087	9.027E-05	Specialist	Acidibacter
ASV1057	1.000	437	5.266E-05	Specialist	Acidiphilium
ASV1058	1.000	437	5.266E-05	Specialist	NA

ASV1059	1.000	605	5.266E-05	Specialist	Amaricoccus
ASV1060	1.000	605	5.266E-05	Specialist	P3OB-42
ASV1061	1.000	605	5.266E-05	Specialist	Sphingomonas
ASV1062	1.882	1087	3.761E-05	Intermediate	Agathobacter
ASV1063	1.000	1087	5.266E-05	Specialist	NA
ASV1064	1.000	437	6.018E-05	Specialist	Prevotella
ASV1065	1.000	437	6.018E-05	Specialist	Corynebacterium
ASV1066	1.000	437	6.018E-05	Specialist	Corynebacterium
ASV1067	1.000	2219	6.770E-05	Specialist	NA
ASV1068	2.000	2219	3.009E-05	Intermediate	Dolosigranulum
ASV1069	1.000	1606	4.513E-05	Specialist	Jatrophihabitans
ASV1070	1.000	1606	4.513E-05	Specialist	NA
ASV1071	1.000	1606	4.513E-05	Specialist	Chitinophaga
ASV1072	1.000	605	6.018E-05	Specialist	Flavobacterium
ASV1073	1.000	605	6.018E-05	Specialist	NA
ASV1074	1.000	1606	5.266E-05	Specialist	Gemmatimonas
ASV1075	1.000	1606	5.266E-05	Specialist	Ohtaekwangia
ASV1076	1.000	1606	6.018E-05	Specialist	Spirosoma
ASV1077	1.976	2219	3.761E-05	Intermediate	NA
ASV1078	1.000	1087	6.018E-05	Specialist	Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium
ASV1079	1.000	1087	6.018E-05	Specialist	Kineosporia
ASV1080	1.000	1087	6.018E-05	Specialist	NA
ASV1081	1.000	1087	6.018E-05	Specialist	NA
ASV1082	1.000	1087	6.018E-05	Specialist	Acidiphilium
ASV1083	1.000	1087	6.018E-05	Specialist	NA
ASV1085	1.000	605	6.770E-05	Specialist	Qipengyuania
ASV1086	1.000	605	6.770E-05	Specialist	Romboutsia
ASV1087	1.000	1087	6.770E-05	Specialist	NA
ASV1088	1.000	2140	6.770E-05	Specialist	NA
ASV1089	1.000	2140	6.770E-05	Specialist	Gemmatimonas
ASV1090	1.000	1992	6.018E-05	Specialist	Fusobacterium
ASV1091	1.000	2140	6.018E-05	Specialist	Sphingobium

ASV1092	1.000	2140	6.018E-05	Specialist	Saccharibacillus
ASV1093	1.000	2140	6.018E-05	Specialist	NA
ASV1094	1.000	1992	4.513E-05	Specialist	Hymenobacter
ASV1095	1.000	1992	4.513E-05	Specialist	Phenylobacterium
ASV1096	1.000	2140	6.770E-05	Specialist	NA
ASV1097	1.000	1606	6.770E-05	Specialist	Jatrophihabitans
ASV1098	1.000	1606	6.770E-05	Specialist	Nocardioides
ASV1099	1.000	1992	6.018E-05	Specialist	NA
ASV1100	1.000	1992	6.018E-05	Specialist	Hymenobacter
ASV1101	1.000	1992	6.018E-05	Specialist	Bdellovibrio
ASV1102	1.000	1606	4.513E-05	Specialist	NA
ASV1103	1.000	1606	4.513E-05	Specialist	NA
ASV1104	1.000	1992	6.018E-05	Specialist	alphaI cluster
ASV1105	1.000	1992	6.018E-05	Specialist	NA
ASV1106	1.000	437	6.018E-05	Specialist	Rheinheimera
ASV1107	1.000	2140	5.266E-05	Specialist	Hymenobacter
ASV1108	1.000	1606	6.018E-05	Specialist	Pseudoxanthomonas
ASV1109	1.000	1606	6.018E-05	Specialist	Chryseobacterium
ASV1110	1.000	437	6.770E-05	Specialist	Dyadobacter
ASV1111	1.000	437	6.770E-05	Specialist	Paracoccus
ASV1112	1.000	2219	6.018E-05	Specialist	Flavobacterium
ASV1113	1.000	2219	6.018E-05	Specialist	Flavobacterium
ASV1114	1.000	2219	6.018E-05	Specialist	Rubrobacter
ASV1115	1.000	437	6.018E-05	Specialist	Fusicatenibacter
ASV1116	1.000	605	6.770E-05	Specialist	Buchnera
ASV1117	1.000	605	6.770E-05	Specialist	Ellin6055
ASV1118	1.000	605	6.770E-05	Specialist	Arenimonas
ASV1119	1.000	605	6.770E-05	Specialist	Solirubrobacter
ASV1120	1.000	2140	6.018E-05	Specialist	Prevotella
ASV1121	1.000	2140	5.266E-05	Specialist	Roseburia
ASV1122	1.000	2140	4.513E-05	Specialist	Endobacter
ASV1123	1.000	2140	4.513E-05	Specialist	Haliangium
ASV1124	1.000	2140	4.513E-05	Specialist	Qipengyuania

ASV1126	1.000	1087	6.018E-05	Specialist	Actinomycetospora
ASV1127	1.000	1087	6.018E-05	Specialist	Hymenobacter
ASV1128	1.000	605	6.770E-05	Specialist	NA
ASV1129	1.000	605	6.770E-05	Specialist	Bryobacter
ASV1130	1.000	605	6.770E-05	Specialist	Sphingomonas
ASV1131	1.000	605	6.770E-05	Specialist	Rubellimicrobium
ASV1132	1.000	605	6.770E-05	Specialist	Sphingomonas
ASV1133	1.000	605	6.770E-05	Specialist	Hymenobacter
ASV1134	1.000	2219	5.266E-05	Specialist	Ferruginibacter
ASV1135	1.000	1606	4.513E-05	Specialist	NA
ASV1136	1.000	1992	4.513E-05	Specialist	Pseudomonas
ASV1137	1.000	437	6.018E-05	Specialist	Arenimonas
ASV1138	1.000	2140	4.513E-05	Specialist	NA
ASV1139	1.000	1087	4.513E-05	Specialist	NA
ASV1140	1.000	437	4.513E-05	Specialist	Aurantimonas
ASV1141	1.000	437	4.513E-05	Specialist	Acidiphilium
ASV1142	1.000	437	4.513E-05	Specialist	Paenisporosarcina
ASV1143	1.800	437	3.009E-05	Intermediate	Sphingomonas
ASV1144	2.000	437	2.257E-05	Intermediate	Anaerococcus
ASV1145	1.000	1087	5.266E-05	Specialist	Nocardioides
ASV1146	1.000	1992	5.266E-05	Specialist	Bdellovibrio
ASV1147	1.000	437	5.266E-05	Specialist	Porphyromonas
ASV1148	1.000	437	5.266E-05	Specialist	[Eubacterium] brachy group
ASV1149	1.000	437	6.018E-05	Specialist	NA
ASV1150	1.000	437	6.018E-05	Specialist	Hymenobacter
ASV1151	2.000	437	2.257E-05	Intermediate	Nannocystis
ASV1152	1.000	2219	6.018E-05	Specialist	Flavobacterium
ASV1153	1.000	1606	4.513E-05	Specialist	Nocardioides
ASV1154	1.000	1606	4.513E-05	Specialist	NA
ASV1155	1.000	605	6.018E-05	Specialist	Skermanella
ASV1156	1.000	605	5.266E-05	Specialist	Spirosoma
ASV1157	1.000	605	5.266E-05	Specialist	Sphingomonas
ASV1158	1.000	1606	4.513E-05	Specialist	NA

ASV1159	1.000	1606	4.513E-05	Specialist	Stomatobaculum
ASV1160	1.000	1606	4.513E-05	Specialist	Nakamurella
ASV1161	1.000	2219	6.018E-05	Specialist	NA
ASV1162	1.000	1606	5.266E-05	Specialist	Romboutsia
ASV1163	1.000	1606	5.266E-05	Specialist	NA
ASV1164	1.000	1606	5.266E-05	Specialist	Aurantisolimonas
ASV1165	1.000	605	5.266E-05	Specialist	Chryseobacterium
ASV1166	1.000	2219	6.018E-05	Specialist	Rubellimicrobium
ASV1167	1.000	1087	5.266E-05	Specialist	NA
ASV1168	1.000	1087	5.266E-05	Specialist	Roseomonas
ASV1169	1.000	1087	5.266E-05	Specialist	NA
ASV1170	1.000	605	5.266E-05	Specialist	Lactobacillus
ASV1171	1.000	605	5.266E-05	Specialist	Luteibacter
ASV1172	1.000	1087	6.018E-05	Specialist	Hymenobacter
ASV1173	1.000	1087	6.018E-05	Specialist	Kineosporia
ASV1174	1.000	1087	6.018E-05	Specialist	Ramlibacter
ASV1175	1.000	2140	6.018E-05	Specialist	NA
ASV1176	1.000	2140	6.018E-05	Specialist	NA
ASV1177	1.000	1992	5.266E-05	Specialist	Peptoniphilus
ASV1178	1.000	437	5.266E-05	Specialist	Acidiphilium
ASV1179	1.000	437	5.266E-05	Specialist	Chryseobacterium
ASV1180	1.000	2140	3.761E-05	Specialist	Spirosoma
ASV1181	1.000	1992	5.266E-05	Specialist	NA
ASV1182	1.000	1992	3.761E-05	Specialist	Hymenobacter
ASV1183	1.000	1992	3.761E-05	Specialist	Pedosphaera
ASV1184	1.000	1606	4.513E-05	Specialist	Nocardioides
ASV1186	1.000	1606	4.513E-05	Specialist	NA
ASV1187	1.000	2140	6.018E-05	Specialist	Nocardioides
ASV1188	1.000	2140	6.018E-05	Specialist	Sphingomonas
ASV1189	1.000	2140	6.018E-05	Specialist	Parabacteroides
ASV1190	1.000	1606	6.018E-05	Specialist	Solirubrobacter
ASV1191	1.000	1992	5.266E-05	Specialist	Marmoricola
ASV1192	1.000	1992	5.266E-05	Specialist	Sphingomonas

ASV1193	1.000	1606	4.513E-05	Specialist	Nocardioides
ASV1194	1.000	1992	5.266E-05	Specialist	P3OB-42
ASV1195	1.000	1992	5.266E-05	Specialist	Terriglobus
ASV1196	1.000	2140	4.513E-05	Specialist	Hyphomicrobium
ASV1197	1.000	1606	5.266E-05	Specialist	Nocardioides
ASV1198	1.000	437	6.018E-05	Specialist	NA
ASV1199	1.000	2219	6.018E-05	Specialist	Lactobacillus
ASV1201	1.000	605	6.018E-05	Specialist	NA
ASV1202	1.000	605	6.018E-05	Specialist	NA
ASV1203	1.000	605	6.018E-05	Specialist	Marmoricola
ASV1204	1.000	605	6.018E-05	Specialist	Gulbenkiania
ASV1205	1.000	2140	3.761E-05	Specialist	Edaphobaculum
ASV1206	1.000	2140	3.761E-05	Specialist	NA
ASV1207	1.000	2140	3.761E-05	Specialist	NA
ASV1208	1.000	2140	3.761E-05	Specialist	Alloprevotella
ASV1209	1.000	1087	5.266E-05	Specialist	Mesorhizobium
ASV1210	1.000	1087	5.266E-05	Specialist	Sphingomonas
ASV1211	1.000	1087	5.266E-05	Specialist	NA
ASV1212	1.000	1087	5.266E-05	Specialist	NA
ASV1213	1.000	1087	5.266E-05	Specialist	Actinomyces
ASV1214	1.000	605	6.018E-05	Specialist	Rathayibacter
ASV1215	1.000	2219	5.266E-05	Specialist	Pedobacter
ASV1216	1.000	2219	5.266E-05	Specialist	NA
ASV1217	1.000	1606	3.761E-05	Specialist	Sphingomonas
ASV1218	1.000	605	6.018E-05	Specialist	Paenibacillus
ASV1219	1.000	605	6.018E-05	Specialist	Aureimonas
ASV1220	1.000	605	6.018E-05	Specialist	Leuconostoc
ASV1221	1.000	605	6.018E-05	Specialist	NA
ASV1222	1.000	2140	3.761E-05	Specialist	Lachnoanaerobaculum
ASV1223	1.000	2140	3.761E-05	Specialist	NA
ASV1224	1.000	2140	3.761E-05	Specialist	Amaricoccus
ASV1225	1.000	2140	3.761E-05	Specialist	Hymenobacter
ASV1226	1.000	1087	3.761E-05	Specialist	Glutamicibacter

ASV1227	1.000	1992	3.761E-05	Specialist	Flavobacterium
ASV1228	1.000	437	3.761E-05	Specialist	1174-901-12
ASV1229	1.000	605	3.761E-05	Specialist	NA
ASV1230	1.000	605	3.761E-05	Specialist	NA
ASV1231	1.000	605	3.761E-05	Specialist	Rubellimicrobium
ASV1232	1.000	605	3.761E-05	Specialist	Streptococcus
ASV1233	1.000	1087	4.513E-05	Specialist	Pseudomonas
ASV1234	1.000	1087	4.513E-05	Specialist	Pseudoclavibacter
ASV1235	1.000	1087	3.761E-05	Specialist	Iamia
ASV1236	1.000	1087	3.761E-05	Specialist	NA
ASV1238	1.000	1992	4.513E-05	Specialist	NA
ASV1239	1.000	1087	3.009E-05	Specialist	NA
ASV1240	1.000	437	4.513E-05	Specialist	Prevotella
ASV1241	1.000	437	4.513E-05	Specialist	Alloprevotella
ASV1242	1.000	437	5.266E-05	Specialist	Endobacter
ASV1243	1.000	437	5.266E-05	Specialist	Nocardioides
ASV1244	1.000	1087	3.761E-05	Specialist	Devosia
ASV1245	1.000	2219	5.266E-05	Specialist	Anaerococcus
ASV1246	1.000	2219	5.266E-05	Specialist	Methylobacterium-Methylorubrum
ASV1247	1.000	2219	5.266E-05	Specialist	Kineococcus
ASV1248	1.000	1606	3.761E-05	Specialist	Xanthomonas
ASV1249	1.000	1606	3.761E-05	Specialist	Frigoribacterium
ASV1250	1.000	1606	3.761E-05	Specialist	Solirubrobacter
ASV1251	1.000	1606	3.761E-05	Specialist	Herpetosiphon
ASV1252	1.000	1606	3.761E-05	Specialist	Nocardioides
ASV1253	1.000	605	3.761E-05	Specialist	Quadrisphaera
ASV1254	1.000	605	3.761E-05	Specialist	Steroidobacter
ASV1255	1.000	605	3.761E-05	Specialist	Novosphingobium
ASV1256	1.000	605	3.761E-05	Specialist	NA
ASV1257	1.000	605	5.266E-05	Specialist	Nocardioides
ASV1258	1.000	605	4.513E-05	Specialist	Nocardioides
ASV1259	1.000	605	4.513E-05	Specialist	NA
ASV1260	1.000	605	4.513E-05	Specialist	NA

ASV1261	1.000	605	4.513E-05	Specialist	NA
ASV1262	1.000	605	4.513E-05	Specialist	NA
ASV1263	1.000	1606	3.761E-05	Specialist	Marmoricola
ASV1264	1.000	1606	3.761E-05	Specialist	Rhodopseudomonas
ASV1265	1.000	2219	5.266E-05	Specialist	NA
ASV1267	1.000	1606	3.761E-05	Specialist	Lachnospiraceae NK4A136 group
ASV1268	1.000	605	4.513E-05	Specialist	NA
ASV1269	1.000	1087	4.513E-05	Specialist	Pseudonocardia
ASV1270	1.000	1087	4.513E-05	Specialist	Flavobacterium
ASV1271	1.000	2140	3.761E-05	Specialist	Oryzihumus
ASV1272	1.000	2140	3.761E-05	Specialist	Conexibacter
ASV1273	1.000	2140	3.761E-05	Specialist	NA
ASV1274	1.000	1992	6.018E-05	Specialist	Phaselicystis
ASV1275	1.000	1992	6.018E-05	Specialist	Bdellovibrio
ASV1276	1.000	1087	4.513E-05	Specialist	NA
ASV1277	1.000	1087	4.513E-05	Specialist	Granulicella
ASV1278	1.000	605	4.513E-05	Specialist	Nocardioides
ASV1279	1.000	605	4.513E-05	Specialist	NA
ASV1280	1.000	605	4.513E-05	Specialist	Spirosoma
ASV1281	1.000	605	4.513E-05	Specialist	Haliangium
ASV1282	1.000	2219	4.513E-05	Specialist	Nocardioides
ASV1283	1.000	2140	5.266E-05	Specialist	Sphingomonas
ASV1284	1.000	1992	4.513E-05	Specialist	Corynebacterium
ASV1285	1.000	1992	4.513E-05	Specialist	NA
ASV1286	1.000	437	4.513E-05	Specialist	NA
ASV1287	1.000	437	4.513E-05	Specialist	NA
ASV1288	1.000	2140	4.513E-05	Specialist	Sphingomonas
ASV1289	1.000	1992	4.513E-05	Specialist	Nocardioides
ASV1290	1.000	1992	4.513E-05	Specialist	Sphingomonas
ASV1291	1.000	1992	3.761E-05	Specialist	Hymenobacter
ASV1292	1.000	1992	3.761E-05	Specialist	NA
ASV1293	1.000	1992	3.761E-05	Specialist	NA
ASV1294	1.000	1992	3.761E-05	Specialist	NA

ASV1295	1.000	1992	3.761E-05	Specialist	Roseomonas
ASV1296	1.000	1992	3.761E-05	Specialist	Bdellovibrio
ASV1298	1.000	1606	3.761E-05	Specialist	Abditibacterium
ASV1299	1.000	1606	3.761E-05	Specialist	NA
ASV1300	1.000	2140	5.266E-05	Specialist	Hymenobacter
ASV1301	1.000	1606	5.266E-05	Specialist	Piscinibacter
ASV1302	1.000	1992	4.513E-05	Specialist	NA
ASV1303	1.000	1992	4.513E-05	Specialist	NA
ASV1304	1.000	1606	3.761E-05	Specialist	Solirubrobacter
ASV1305	1.000	1992	4.513E-05	Specialist	Granulicella
ASV1306	1.000	1992	4.513E-05	Specialist	NA
ASV1307	1.000	437	4.513E-05	Specialist	Alcanivorax
ASV1308	1.000	2140	3.761E-05	Specialist	MN 122.2a
ASV1309	1.000	2140	3.761E-05	Specialist	Jeotgalicoccus
ASV1310	1.000	2140	3.761E-05	Specialist	Spirosoma
ASV1311	1.000	1606	4.513E-05	Specialist	Nocardioides
ASV1312	1.000	1606	4.513E-05	Specialist	NA
ASV1313	1.000	1606	4.513E-05	Specialist	Bdellovibrio
ASV1314	1.000	1606	4.513E-05	Specialist	Haemophilus
ASV1315	1.000	437	5.266E-05	Specialist	Hymenobacter
ASV1316	1.000	1992	6.018E-05	Specialist	NA
ASV1317	1.000	437	5.266E-05	Specialist	Methylobacterium-Methylorubrum
ASV1318	1.000	437	5.266E-05	Specialist	Spirosoma
ASV1319	1.000	437	5.266E-05	Specialist	Salinimicrobium
ASV1320	1.000	2219	4.513E-05	Specialist	Bacteroides
ASV1321	1.000	2219	4.513E-05	Specialist	NA
ASV1322	1.000	2219	4.513E-05	Specialist	NA
ASV1323	1.000	2219	4.513E-05	Specialist	Rubellimicrobium
ASV1324	1.000	605	5.266E-05	Specialist	Sphingomonas
ASV1325	1.000	605	5.266E-05	Specialist	Pedobacter
ASV1326	1.000	605	5.266E-05	Specialist	Pedomicrobium
ASV1327	1.000	2140	4.513E-05	Specialist	Flavobacterium
ASV1328	1.000	2140	3.761E-05	Specialist	Hyphomicrobium

ASV1329	1.000	2140	3.761E-05	Specialist	Pedobacter
ASV1330	1.000	1087	3.761E-05	Specialist	Sphingomonas
ASV1333	1.000	1087	4.513E-05	Specialist	Nakamurella
ASV1334	1.000	1087	4.513E-05	Specialist	Devosia
ASV1335	1.000	605	5.266E-05	Specialist	Gaiella
ASV1336	1.000	1606	3.761E-05	Specialist	Marmoricola
ASV1337	1.000	605	5.266E-05	Specialist	Sphingomonas
ASV1338	1.000	605	5.266E-05	Specialist	NA
ASV1339	1.000	1992	3.009E-05	Specialist	Endobacter
ASV1340	1.000	2140	3.761E-05	Specialist	Psychroglaciecola
ASV1342	1.000	1087	3.009E-05	Specialist	Chthonobacter
ASV1343	1.000	1992	3.009E-05	Specialist	Fibrella
ASV1344	1.000	437	3.009E-05	Specialist	Sphingomonas
ASV1345	1.000	605	3.009E-05	Specialist	Longimicrobium
ASV1346	1.000	605	3.009E-05	Specialist	Rubellimicrobium
ASV1347	1.000	605	3.009E-05	Specialist	Sphingomonas
ASV1348	1.000	605	3.009E-05	Specialist	NA
ASV1349	1.000	1087	3.761E-05	Specialist	Dorea
ASV1350	1.923	1087	2.257E-05	Intermediate	Bacteroides
ASV1351	1.000	1992	3.761E-05	Specialist	1174-901-12
ASV1352	1.000	1992	3.761E-05	Specialist	Roseomonas
ASV1353	1.000	1087	3.009E-05	Specialist	Thiobacillus
ASV1354	1.000	1087	3.009E-05	Specialist	NA
ASV1355	1.000	1087	3.009E-05	Specialist	Brevibacterium
ASV1356	1.000	437	3.761E-05	Specialist	Lautropia
ASV1357	1.000	437	3.761E-05	Specialist	Sphingomonas
ASV1358	1.000	2219	3.761E-05	Specialist	NA
ASV1359	1.000	1606	3.009E-05	Specialist	Nocardioides
ASV1360	1.000	1606	3.009E-05	Specialist	Sphingomonas
ASV1361	1.000	1606	3.009E-05	Specialist	Roseomonas
ASV1362	1.000	605	3.009E-05	Specialist	NA
ASV1363	1.000	605	3.761E-05	Specialist	NA
ASV1364	1.000	605	3.761E-05	Specialist	Cellulomonas

ASV1365	1.000	605	3.761E-05	Specialist	Actinoallomurus
ASV1366	1.000	605	3.761E-05	Specialist	Iamia
ASV1367	1.000	1606	3.009E-05	Specialist	NA
ASV1368	1.000	1606	3.009E-05	Specialist	Corynebacterium
ASV1369	1.000	1606	3.009E-05	Specialist	Psychroglaciecola
ASV1370	1.000	2219	4.513E-05	Specialist	NA
ASV1371	1.000	605	3.761E-05	Specialist	Marmoricola
ASV1372	1.000	605	3.761E-05	Specialist	Hymenobacter
ASV1373	1.000	605	3.761E-05	Specialist	Psychroglaciecola
ASV1374	1.000	605	3.761E-05	Specialist	Rubellimicrobium
ASV1375	1.000	605	3.761E-05	Specialist	Segetibacter
ASV1376	1.000	605	3.761E-05	Specialist	Iamia
ASV1377	1.000	2219	4.513E-05	Specialist	Novosphingobium
ASV1379	1.000	2219	4.513E-05	Specialist	Acinetobacter
ASV1381	1.000	1087	3.761E-05	Specialist	NA
ASV1382	1.000	1087	3.761E-05	Specialist	Pajaroellobacter
ASV1383	1.000	605	3.761E-05	Specialist	Bryocella
ASV1384	1.000	605	3.761E-05	Specialist	Bdellovibrio
ASV1385	1.000	2219	3.761E-05	Specialist	UCG-002
ASV1386	1.000	2219	3.761E-05	Specialist	Sphingomonas
ASV1387	1.000	1087	4.513E-05	Specialist	Mucilaginibacter
ASV1388	1.000	2140	4.513E-05	Specialist	NA
ASV1389	1.000	2140	4.513E-05	Specialist	Novosphingobium
ASV1390	1.000	2140	4.513E-05	Specialist	Candidatus Trichorickettsia
ASV1391	1.000	2140	4.513E-05	Specialist	Knoellia
ASV1392	1.000	2140	4.513E-05	Specialist	Hydrogenophaga
ASV1393	1.000	2140	4.513E-05	Specialist	Lacibacter
ASV1394	1.000	2140	4.513E-05	Specialist	NA
ASV1395	1.000	2140	4.513E-05	Specialist	NA
ASV1396	1.000	1992	3.761E-05	Specialist	Azospirillum
ASV1397	1.000	1992	3.761E-05	Specialist	NA
ASV1398	1.000	1992	3.761E-05	Specialist	Pajaroellobacter
ASV1399	1.000	1992	3.009E-05	Specialist	Hymenobacter

ASV1401	1.000	1606	3.761E-05	Specialist	Jatrophihabitans
ASV1402	1.000	1606	3.761E-05	Specialist	UCG-002
ASV1403	1.000	1606	3.761E-05	Specialist	Ellin6067
ASV1405	1.000	437	4.513E-05	Specialist	Altererythrobacter
ASV1406	1.000	2140	3.761E-05	Specialist	NA
ASV1407	1.000	2140	3.761E-05	Specialist	Hyphomicrobium
ASV1408	1.000	1606	3.761E-05	Specialist	Tardiphaga
ASV1409	1.000	1992	3.761E-05	Specialist	Williamsia
ASV1410	1.000	1992	3.761E-05	Specialist	NA
ASV1411	1.000	1992	3.761E-05	Specialist	NA
ASV1412	1.000	1992	3.761E-05	Specialist	Solirubrobacter
ASV1413	1.000	1992	3.761E-05	Specialist	1174-901-12
ASV1414	1.000	1992	3.761E-05	Specialist	Paracoccus
ASV1415	1.000	437	3.761E-05	Specialist	Anaerococcus
ASV1416	1.000	2140	3.009E-05	Specialist	Actibacter
ASV1417	1.000	2140	3.761E-05	Specialist	Bryocella
ASV1418	1.000	1606	3.761E-05	Specialist	NA
ASV1419	1.000	1606	3.761E-05	Specialist	Hymenobacter
ASV1420	1.000	1606	3.761E-05	Specialist	NA
ASV1421	1.000	1606	3.761E-05	Specialist	Marmoricola
ASV1422	1.000	1992	5.266E-05	Specialist	Prevotella
ASV1423	1.000	1992	5.266E-05	Specialist	Spirosoma
ASV1424	1.000	1992	5.266E-05	Specialist	NA
ASV1425	1.000	1992	5.266E-05	Specialist	P3OB-42
ASV1426	1.000	437	4.513E-05	Specialist	Spirosoma
ASV1427	1.000	437	4.513E-05	Specialist	Pseudomonas
ASV1428	1.000	2219	3.761E-05	Specialist	Starkeya
ASV1429	1.000	2219	3.761E-05	Specialist	NA
ASV1430	1.000	2219	3.761E-05	Specialist	Paenibacillus
ASV1431	1.000	2219	3.761E-05	Specialist	NA
ASV1432	1.000	2219	3.761E-05	Specialist	Wolinella
ASV1433	1.000	437	3.761E-05	Specialist	Asticcacaulis
ASV1434	1.000	437	3.761E-05	Specialist	Pseudomonas

ASV1435	1.000	437	3.761E-05	Specialist	NA
ASV1436	1.000	437	3.761E-05	Specialist	Ellin6055
ASV1437	1.000	1606	3.009E-05	Specialist	NA
ASV1438	1.000	605	4.513E-05	Specialist	Hymenobacter
ASV1439	1.000	605	4.513E-05	Specialist	NA
ASV1440	1.000	605	4.513E-05	Specialist	Flavobacterium
ASV1441	1.000	605	4.513E-05	Specialist	NA
ASV1442	1.000	605	4.513E-05	Specialist	YC-ZSS-LKJ147
ASV1443	1.000	2140	3.009E-05	Specialist	Aeromicrobium
ASV1444	1.000	2140	3.009E-05	Specialist	NA
ASV1445	1.000	2140	3.009E-05	Specialist	Chryseobacterium
ASV1446	1.000	2140	3.009E-05	Specialist	PMMR1
ASV1449	1.000	1087	3.761E-05	Specialist	NA
ASV1450	1.000	1087	3.761E-05	Specialist	Streptomyces
ASV1451	1.000	1087	3.761E-05	Specialist	NA
ASV1452	1.000	1087	3.761E-05	Specialist	Ferruginibacter
ASV1453	1.000	1087	3.761E-05	Specialist	CL500-29 marine group
ASV1454	1.000	605	3.761E-05	Specialist	Spirosoma
ASV1455	1.000	605	3.761E-05	Specialist	NA
ASV1456	1.000	605	3.761E-05	Specialist	Segetibacter
ASV1457	1.000	605	3.761E-05	Specialist	Acidiphilium
ASV1458	1.000	2219	3.761E-05	Specialist	Motilibacter
ASV1459	1.000	1606	3.009E-05	Specialist	Rubrobacter
ASV1460	1.000	605	4.513E-05	Specialist	Oryzihumus
ASV1461	1.000	605	4.513E-05	Specialist	Nakamurella
ASV1462	1.000	605	4.513E-05	Specialist	NA
ASV1463	1.000	605	4.513E-05	Specialist	Microvirga
ASV1464	1.000	605	4.513E-05	Specialist	Hymenobacter
ASV1465	1.000	605	4.513E-05	Specialist	Kineosporia
ASV1466	1.000	1992	3.009E-05	Specialist	Hymenobacter
ASV1467	1.000	2140	3.009E-05	Specialist	NA
ASV1468	1.000	2140	3.009E-05	Specialist	NA
ASV1469	1.000	2140	3.009E-05	Specialist	Hymenobacter

ASV1470	1.000	1087	5.266E-05	Specialist	Serratia
ASV1471	1.000	1087	2.257E-05	Specialist	Jatrophihabitans
ASV1472	1.000	1992	2.257E-05	Specialist	Prevotella_7
ASV1473	1.000	1992	2.257E-05	Specialist	NA
ASV1474	1.000	437	2.257E-05	Specialist	Nocardioides
ASV1475	1.000	437	2.257E-05	Specialist	Flavobacterium
ASV1476	1.000	437	2.257E-05	Specialist	Micrococcus
ASV1477	1.000	437	2.257E-05	Specialist	Pedobacter
ASV1478	1.000	437	2.257E-05	Specialist	1174-901-12
ASV1479	1.000	605	2.257E-05	Specialist	Alteribacillus
ASV1480	1.000	1087	3.009E-05	Specialist	YC-ZSS-LKJ147
ASV1481	1.000	1087	3.009E-05	Specialist	Ilumatobacter
ASV1482	1.000	1087	3.009E-05	Specialist	NA
ASV1483	1.000	1087	3.009E-05	Specialist	Ornithinibacter
ASV1484	1.000	1087	3.009E-05	Specialist	Staphylococcus
ASV1485	1.000	1992	3.009E-05	Specialist	NA
ASV1486	1.000	1992	3.009E-05	Specialist	Polymorphobacter
ASV1487	1.000	437	3.009E-05	Specialist	Blastococcus
ASV1488	1.000	437	3.009E-05	Specialist	Alloprevotella
ASV1489	1.000	437	3.009E-05	Specialist	NA
ASV1490	1.000	437	3.009E-05	Specialist	NA
ASV1491	1.000	437	3.009E-05	Specialist	Bergeyella
ASV1492	1.000	437	3.761E-05	Specialist	Piscinibacter
ASV1493	1.000	437	3.761E-05	Specialist	Flavisolibacter
ASV1494	1.000	437	3.761E-05	Specialist	Sphingomonas
ASV1495	1.000	2219	3.009E-05	Specialist	Modestobacter
ASV1496	1.000	1606	2.257E-05	Specialist	Rhodococcus
ASV1497	1.000	1606	2.257E-05	Specialist	Streptacidiphilus
ASV1498	1.000	605	2.257E-05	Specialist	Nocardioides
ASV1499	1.000	605	2.257E-05	Specialist	Phytohabitans
ASV1500	1.000	605	3.761E-05	Specialist	Abditibacterium
ASV1501	1.000	1606	3.009E-05	Specialist	Nocardioides
ASV1502	1.000	1606	3.009E-05	Specialist	Lactobacillus

ASV1503	1.000	2219	3.761E-05	Specialist	Granulicatella
ASV1504	1.000	2219	3.761E-05	Specialist	NA
ASV1505	1.000	2219	3.761E-05	Specialist	NA
ASV1506	1.000	1606	3.009E-05	Specialist	Craurococcus-Caldovatus
ASV1507	1.000	605	3.009E-05	Specialist	Spirosoma
ASV1508	1.000	605	3.009E-05	Specialist	Croceicoccus
ASV1509	1.000	605	3.009E-05	Specialist	NA
ASV1510	1.000	605	3.009E-05	Specialist	Rubellimicrobium
ASV1511	1.000	1087	3.009E-05	Specialist	Glutamicibacter
ASV1512	1.000	2140	2.257E-05	Specialist	Aeromicrobium
ASV1513	1.000	2140	2.257E-05	Specialist	Hymenobacter
ASV1514	1.000	1087	3.009E-05	Specialist	Spirosoma
ASV1515	1.000	1087	3.009E-05	Specialist	Klenkia
ASV1516	1.000	605	3.009E-05	Specialist	Hymenobacter
ASV1517	1.000	2219	3.009E-05	Specialist	NA
ASV1518	1.000	1087	3.009E-05	Specialist	NA
ASV1519	1.000	1087	3.009E-05	Specialist	Jatrophihabitans
ASV1520	1.000	1087	3.009E-05	Specialist	Jeotgalicoccus
ASV1521	1.000	2140	3.761E-05	Specialist	YC-ZSS-LKJ147
ASV1522	1.000	2140	3.761E-05	Specialist	Devosia
ASV1523	1.000	2140	3.761E-05	Specialist	Rhodovarius
ASV1524	1.000	2140	3.761E-05	Specialist	NA
ASV1525	1.000	2140	3.761E-05	Specialist	Mycobacterium
ASV1526	1.000	1992	3.009E-05	Specialist	NA
ASV1527	1.000	1992	3.009E-05	Specialist	Subdoligranulum
ASV1528	1.000	1992	3.009E-05	Specialist	Weissella
ASV1529	1.000	1992	3.009E-05	Specialist	Endobacter
ASV1530	1.000	437	3.009E-05	Specialist	Phaselicystis
ASV1531	1.000	2140	3.009E-05	Specialist	Rubellimicrobium
ASV1532	1.000	2140	3.009E-05	Specialist	NA
ASV1533	1.000	2140	3.009E-05	Specialist	Legionella
ASV1534	1.000	1992	3.009E-05	Specialist	Sphingomonas
ASV1535	1.000	1992	2.257E-05	Specialist	Edaphobaculum

ASV1536	1.000	1992	2.257E-05	Specialist	NA
ASV1537	1.000	1992	2.257E-05	Specialist	Nocardioides
ASV1538	1.000	2140	3.009E-05	Specialist	Rothia
ASV1539	1.000	2140	3.009E-05	Specialist	Ferruginibacter
ASV1540	1.000	1992	3.009E-05	Specialist	Byssovorax
ASV1541	1.000	1992	3.009E-05	Specialist	Neisseria
ASV1542	1.000	437	3.009E-05	Specialist	NA
ASV1543	1.000	437	3.009E-05	Specialist	NA
ASV1544	1.000	437	3.009E-05	Specialist	NA
ASV1545	1.000	2140	3.009E-05	Specialist	Geodermatophilus
ASV1546	1.000	1606	3.009E-05	Specialist	NA
ASV1547	1.000	437	3.761E-05	Specialist	NA
ASV1548	1.000	437	3.761E-05	Specialist	Marmoricola
ASV1549	1.000	437	3.761E-05	Specialist	NA
ASV1550	1.000	437	3.761E-05	Specialist	Hymenobacter
ASV1551	1.000	2219	3.009E-05	Specialist	Paenibacillus
ASV1552	1.000	2219	3.009E-05	Specialist	NA
ASV1553	1.000	2219	3.009E-05	Specialist	NA
ASV1554	1.000	2219	3.009E-05	Specialist	NA
ASV1555	1.000	2219	3.009E-05	Specialist	NA
ASV1556	1.000	2219	3.009E-05	Specialist	Flavobacterium
ASV1557	1.000	2219	3.009E-05	Specialist	Clostridium sensu stricto 1
ASV1559	1.000	437	3.009E-05	Specialist	NA
ASV1560	1.000	437	3.009E-05	Specialist	Psychroglaciecola
ASV1561	1.000	437	3.009E-05	Specialist	Hymenobacter
ASV1562	1.000	437	3.009E-05	Specialist	Hymenobacter
ASV1563	1.000	437	3.009E-05	Specialist	Paracoccus
ASV1564	1.000	1606	2.257E-05	Specialist	Spirochaeta 2
ASV1565	1.000	605	3.761E-05	Specialist	Pseudomonas
ASV1566	1.000	605	3.761E-05	Specialist	Conexibacter
ASV1567	1.000	605	3.761E-05	Specialist	Solirubrobacter
ASV1568	1.000	2140	3.009E-05	Specialist	Caulobacter
ASV1569	1.000	2140	3.009E-05	Specialist	Puia

ASV1570	1.000	2140	2.257E-05	Specialist	Streptococcus
ASV1571	1.000	2140	2.257E-05	Specialist	Exiguobacterium
ASV1572	1.000	2140	2.257E-05	Specialist	Telluria
ASV1573	1.000	1087	3.009E-05	Specialist	NA
ASV1574	1.000	1087	3.009E-05	Specialist	Sphingomonas
ASV1575	1.000	1087	3.009E-05	Specialist	Incertae Sedis
ASV1577	1.000	1087	3.009E-05	Specialist	Novosphingobium
ASV1578	1.000	1087	3.009E-05	Specialist	NA
ASV1579	1.000	1087	3.009E-05	Specialist	Gemmatimonas
ASV1580	1.000	1087	3.009E-05	Specialist	Paracoccus
ASV1581	1.000	1087	3.009E-05	Specialist	NA
ASV1582	1.000	1087	3.009E-05	Specialist	Arenimonas
ASV1583	1.000	1087	3.009E-05	Specialist	Gaiella
ASV1584	1.000	605	3.009E-05	Specialist	Prosthecomicrobium
ASV1585	1.000	605	3.009E-05	Specialist	Fibrella
ASV1586	1.000	2219	3.009E-05	Specialist	Sphingomonas
ASV1587	1.000	2219	3.009E-05	Specialist	Lachnospiraceae FCS020 group
ASV1588	1.000	2219	3.009E-05	Specialist	Corynebacterium
ASV1589	1.000	2219	2.257E-05	Specialist	Dyadobacter
ASV1590	1.000	1606	2.257E-05	Specialist	Hymenobacter
ASV1591	1.000	605	3.761E-05	Specialist	Alcaligenes
ASV1592	1.000	605	3.761E-05	Specialist	Psychroglaciecola
ASV1594	1.000	1992	2.257E-05	Specialist	Nocardioides
ASV1595	1.000	1992	2.257E-05	Specialist	Stenotrophomonas
ASV1596	1.000	1992	2.257E-05	Specialist	Dyadobacter
ASV1597	1.000	437	3.009E-05	Specialist	NA
ASV1598	1.000	437	3.009E-05	Specialist	Aurantisolimonas
ASV1599	1.000	2140	2.257E-05	Specialist	NA
ASV1600	1.000	2140	2.257E-05	Specialist	NA
ASV1601	1.000	1087	3.761E-05	Specialist	Flavisolibacter
ASV1603	1.000	1992	2.257E-05	Specialist	Nocardioides
ASV1604	1.000	437	1.504E-05	Specialist	Actinoplanes
ASV1605	1.000	605	2.257E-05	Specialist	Iamia

ASV1606	1.000	605	2.257E-05	Specialist	Sphingomonas
ASV1608	1.000	605	2.257E-05	Specialist	NA
ASV1609	1.000	605	2.257E-05	Specialist	Ancylobacter
ASV1610	1.000	605	2.257E-05	Specialist	Legionella
ASV1611	1.000	1087	2.257E-05	Specialist	Sphingomonas
ASV1612	1.000	1087	2.257E-05	Specialist	Cutibacterium
ASV1613	1.000	1087	2.257E-05	Specialist	IMCC26207
ASV1614	1.000	1992	2.257E-05	Specialist	Phytohabitans
ASV1615	1.000	1992	2.257E-05	Specialist	NA
ASV1616	1.000	1992	2.257E-05	Specialist	NA
ASV1617	1.000	1992	2.257E-05	Specialist	Nocardioides
ASV1618	1.000	437	2.257E-05	Specialist	Shuttleworthia
ASV1619	1.000	437	2.257E-05	Specialist	Prevotella
ASV1620	1.000	437	2.257E-05	Specialist	Abditibacterium
ASV1621	1.000	437	2.257E-05	Specialist	Leucobacter
ASV1622	1.000	437	2.257E-05	Specialist	Rhodovarius
ASV1623	1.000	1606	1.504E-05	Specialist	Sphingomonas
ASV1624	1.000	1606	1.504E-05	Specialist	NA
ASV1625	1.000	1606	1.504E-05	Specialist	Bosea
ASV1626	1.000	605	2.257E-05	Specialist	Microvirga
ASV1627	1.000	605	2.257E-05	Specialist	NA
ASV1628	1.000	605	2.257E-05	Specialist	NA
ASV1629	1.000	605	2.257E-05	Specialist	Pseudokineococcus
ASV1630	1.000	605	2.257E-05	Specialist	Flavobacterium
ASV1631	1.000	605	2.257E-05	Specialist	Limibaculum
ASV1632	1.000	605	2.257E-05	Specialist	NA
ASV1634	1.000	1606	2.257E-05	Specialist	Massilia
ASV1635	1.000	2219	2.257E-05	Specialist	Sphingomonas
ASV1636	1.000	2219	2.257E-05	Specialist	NA
ASV1637	1.000	1606	2.257E-05	Specialist	Anaerococcus
ASV1638	1.000	1606	2.257E-05	Specialist	Wolbachia
ASV1639	1.000	1606	2.257E-05	Specialist	NA
ASV1640	1.000	1606	2.257E-05	Specialist	Actinomyces

ASV1641	1.000	1606	2.257E-05	Specialist	NA
ASV1643	1.000	2219	3.009E-05	Specialist	Sphingomonas
ASV1644	1.000	2140	1.504E-05	Specialist	Methylobacterium-Methylorubrum
ASV1645	1.000	1087	2.257E-05	Specialist	Motilibacter
ASV1646	1.000	1087	2.257E-05	Specialist	NA
ASV1647	1.000	605	2.257E-05	Specialist	Acidiphilium
ASV1648	1.000	2219	2.257E-05	Specialist	[Eubacterium] ruminantium group
ASV1649	1.000	2219	2.257E-05	Specialist	Kocuria
ASV1650	1.000	2219	2.257E-05	Specialist	Pseudomonas
ASV1651	1.000	2219	2.257E-05	Specialist	Blautia
ASV1652	1.000	1087	2.257E-05	Specialist	Microvirga
ASV1653	1.000	2140	2.257E-05	Specialist	NA
ASV1654	1.000	2140	2.257E-05	Specialist	Caedibacter
ASV1655	1.000	1992	2.257E-05	Specialist	Myxococcus
ASV1656	1.000	1992	2.257E-05	Specialist	Capnocytophaga
ASV1657	1.000	1992	2.257E-05	Specialist	Paenibacillus
ASV1658	1.000	437	2.257E-05	Specialist	Flavobacterium
ASV1659	1.000	437	2.257E-05	Specialist	Thermoactinomyces
ASV1660	1.000	2140	2.257E-05	Specialist	Dactylosporangium
ASV1661	1.000	2140	2.257E-05	Specialist	Psychroglaciecola
ASV1662	1.000	2140	2.257E-05	Specialist	NA
ASV1663	1.000	1992	2.257E-05	Specialist	Actinoplanes
ASV1664	1.000	1992	2.257E-05	Specialist	Brachybacterium
ASV1665	1.000	1992	2.257E-05	Specialist	Devosia
ASV1666	1.000	1992	2.257E-05	Specialist	NA
ASV1667	1.000	1606	2.257E-05	Specialist	Turicella
ASV1668	1.000	1606	2.257E-05	Specialist	NA
ASV1669	1.000	1606	2.257E-05	Specialist	Leptotrichia
ASV1670	1.000	1606	2.257E-05	Specialist	Nocardioides
ASV1671	1.000	2140	2.257E-05	Specialist	Hymenobacter
ASV1672	1.000	1606	2.257E-05	Specialist	PMMR1
ASV1673	1.000	1606	2.257E-05	Specialist	Legionella
ASV1674	1.000	1992	2.257E-05	Specialist	Terrimonas

ASV1675	1.000	1606	1.504E-05	Specialist	Acidiphilium
ASV1676	1.000	1606	1.504E-05	Specialist	Nocardioides
ASV1677	1.000	1992	2.257E-05	Specialist	Sphingomonas
ASV1678	1.000	1992	2.257E-05	Specialist	NA
ASV1679	1.000	1992	2.257E-05	Specialist	NA
ASV1680	1.000	1992	2.257E-05	Specialist	NA
ASV1681	1.000	437	2.257E-05	Specialist	1174-901-12
ASV1682	1.000	437	2.257E-05	Specialist	NA
ASV1683	1.000	437	2.257E-05	Specialist	Streptomyces
ASV1684	1.000	2140	1.504E-05	Specialist	NA
ASV1685	1.000	2140	2.257E-05	Specialist	NA
ASV1686	1.000	1606	2.257E-05	Specialist	Pedomicrobium
ASV1687	1.000	1606	2.257E-05	Specialist	NA
ASV1688	1.000	1606	2.257E-05	Specialist	Nakamurella
ASV1689	1.000	1606	2.257E-05	Specialist	NA
ASV1690	1.000	1992	3.009E-05	Specialist	Corynebacterium
ASV1691	1.000	437	2.257E-05	Specialist	Roseisolibacter
ASV1692	1.000	437	2.257E-05	Specialist	Altererythrobacter
ASV1693	1.000	437	2.257E-05	Specialist	Dyadobacter
ASV1694	1.000	437	2.257E-05	Specialist	Nocardioides
ASV1695	1.000	2219	2.257E-05	Specialist	Roseburia
ASV1696	1.000	2219	2.257E-05	Specialist	Roseomonas
ASV1697	1.000	2219	2.257E-05	Specialist	Thiofaba
ASV1698	1.000	2219	2.257E-05	Specialist	NA
ASV1699	1.000	437	2.257E-05	Specialist	Campylobacter
ASV1700	1.000	437	2.257E-05	Specialist	Devosia
ASV1701	1.000	1606	1.504E-05	Specialist	NA
ASV1702	1.000	1606	1.504E-05	Specialist	NA
ASV1703	1.000	1606	1.504E-05	Specialist	Staphylococcus
ASV1704	1.000	1606	1.504E-05	Specialist	NA
ASV1705	1.000	605	3.009E-05	Specialist	NA
ASV1706	1.000	2140	2.257E-05	Specialist	Friedmanniella
ASV1707	1.000	2140	2.257E-05	Specialist	NA

ASV1708	1.000	2140	2.257E-05	Specialist	Clostridium sensu stricto 1
ASV1709	1.000	2140	2.257E-05	Specialist	P3OB-42
ASV1710	1.000	2140	1.504E-05	Specialist	Ilumatobacter
ASV1716	1.000	1087	2.257E-05	Specialist	Sphingomonas
ASV1717	1.000	605	2.257E-05	Specialist	NA
ASV1718	1.000	605	2.257E-05	Specialist	Hymenobacter
ASV1719	1.000	605	2.257E-05	Specialist	Pseudonocardia
ASV1720	1.000	605	2.257E-05	Specialist	Cytophaga
ASV1721	1.000	1992	1.504E-05	Specialist	NA
ASV1723	1.000	2140	1.504E-05	Specialist	Dermabacter
ASV1724	1.000	2140	1.504E-05	Specialist	YC-ZSS-LKJ90
ASV1725	1.000	2140	1.504E-05	Specialist	Flavobacterium
ASV1726	1.000	1087	1.504E-05	Specialist	NA
ASV1727	1.000	605	1.504E-05	Specialist	Pseudomonas
ASV1728	1.000	605	1.504E-05	Specialist	Ferruginibacter
ASV1729	1.000	605	1.504E-05	Specialist	Candidatus Alysiosphaera
ASV1730	1.000	1087	7.522E-06	Specialist	Bifidobacterium
ASV1731	1.000	437	1.504E-05	Specialist	Prevotella_7
ASV1732	1.000	1606	1.504E-05	Specialist	Haloechinothrix
ASV1733	1.000	605	1.504E-05	Specialist	NA
ASV1734	1.000	605	1.504E-05	Specialist	CL500-29 marine group
ASV1735	1.000	605	1.504E-05	Specialist	Rubellimicrobium
ASV1736	1.000	2219	1.504E-05	Specialist	NA
ASV1737	1.000	1606	1.504E-05	Specialist	NA
ASV1738	1.000	1606	1.504E-05	Specialist	Patulibacter
ASV1739	1.000	605	1.504E-05	Specialist	Anaerococcus
ASV1740	1.000	2219	1.504E-05	Specialist	NA
ASV1741	1.000	2219	1.504E-05	Specialist	NA
ASV1742	1.000	1087	1.504E-05	Specialist	NA
ASV1743	1.000	605	1.504E-05	Specialist	Cellvibrio
ASV1744	1.000	2140	1.504E-05	Specialist	NA
ASV1745	1.000	2140	1.504E-05	Specialist	Segetibacter
ASV1746	1.000	437	1.504E-05	Specialist	NA

ASV1747	1.000	2140	1.504E-05	Specialist	Abditibacterium
ASV1748	1.000	2140	1.504E-05	Specialist	NA
ASV1749	1.000	1992	1.504E-05	Specialist	NA
ASV1750	1.000	1992	1.504E-05	Specialist	Methylobacterium-Methylorubrum
ASV1751	1.000	437	2.257E-05	Specialist	Euzebya
ASV1752	1.000	1606	1.504E-05	Specialist	NA
ASV1754	1.000	1992	1.504E-05	Specialist	Enhydrobacter
ASV1755	1.000	1606	1.504E-05	Specialist	Streptomyces
ASV1756	1.000	1606	1.504E-05	Specialist	NA
ASV1759	1.000	1992	1.504E-05	Specialist	Caedibacter
ASV1760	1.000	1606	1.504E-05	Specialist	Sellimonas
ASV1764	1.000	437	1.504E-05	Specialist	Hyphomicrobium
ASV1766	1.000	2219	1.504E-05	Specialist	Ruminiclostridium
ASV1767	1.000	2219	1.504E-05	Specialist	Desulfovibrio
ASV1768	1.000	2219	1.504E-05	Specialist	Aliidongia
ASV1769	1.000	437	1.504E-05	Specialist	Micromonospora
ASV1770	1.000	1606	1.504E-05	Specialist	NA
ASV1771	1.000	1606	1.504E-05	Specialist	NA
ASV1772	1.000	1606	1.504E-05	Specialist	Lachnoclostridium
ASV1773	1.000	2140	1.504E-05	Specialist	Melittangium
ASV1775	1.000	2140	1.504E-05	Specialist	NA
ASV1776	1.000	2140	1.504E-05	Specialist	Phenylobacterium
ASV1778	1.000	1087	1.504E-05	Specialist	NA
ASV1781	1.000	1087	1.504E-05	Specialist	Sandaracinus
ASV1782	1.000	605	1.504E-05	Specialist	CL500-29 marine group
ASV1783	1.000	2219	1.504E-05	Specialist	NA
ASV1785	1.000	2219	1.504E-05	Specialist	Friedmanniella
ASV1786	1.000	605	1.504E-05	Specialist	NA
ASV1787	1.000	1992	7.522E-06	Specialist	Conexibacter
ASV1788	1.000	1992	7.522E-06	Specialist	Methylobacterium-Methylorubrum
ASV1789	1.000	1992	7.522E-06	Specialist	NA
ASV1790	1.000	2140	1.504E-05	Specialist	NA

[a] ASVs were retained only if they exhibited non-zero abundance in at least two distinct GDD values. ASVs were classified as thermal specialists (niche width ≤ 1.5), generalists (≥2.25), or intermediates (between thresholds). The table includes each ASV's niche width, peak GDD (the GDD at which its relative abundance was highest), relative abundance at that peak, niche classification, and assigned bacterial genus.