

1 **Title Page** **11.6.2021**

2 **Research Article**

3

4 **Temporally selective modification of the tomato rhizosphere and root microbiome by a**
5 **dacitic tuff breccia (volcanic ash) containing minerals and trace elements**

6

7 Elijah C. Mehlferber^{1,*}, Kent F. McCue², Jon E. Ferrel^{3,4}, Britt Koskella¹, and Rajnish
8 Khanna^{4,5,*}

9 ¹ University of California Berkeley, Department of Integrative Biology, Berkeley, CA 94720,
10 USA

11 ² USDA, Agricultural Research Service, Western Regional Research Center, Crop Improvement
12 and Genetics Research Unit, 800 Buchanan Street, Albany, CA, 94710, USA

13 ³ Azomite Mineral Products, Inc., 645 N. Main Street, Nephi, UT 84648, USA

14 ⁴ i-Cultiver, Inc., 1810 Thicket Ln., Tracy, CA 95376, USA

15 ⁵ The Chopra Foundation, 13485 Veterans Way, Suite 105, Orlando, FL 32827, USA

16 *Corresponding Authors

17 Contact: R. Khanna, email: raj@i-cultiver.com, phone: +1 (707) 205-7084

18 E.C. Mehlferber: emehlferber@berkeley.edu, phone: +1 (706) 239-7063

19 ORCID ID: Elijah C. Mehlferber (<https://orcid.org/0000-0002-9958-3247>)

20 Kent F. McCue (<https://orcid.org/0000-0003-1914-4971>)

21 Jon E. Ferrel (<https://orcid.org/0000-0003-2067-1402>)

22 Britt Koskella (<https://orcid.org/0000-0003-1760-8496>)

23 Rajnish Khanna (<https://orcid.org/0000-0002-3469-7403>)

Keywords: Mineral nutrients, rhizosphere, root endophytes, volcanic ash, tomato microbiome

Funding: The authors declare that this work was funded and performed through i-Cultiver, Inc., which independently provides consultation services to soil amendment manufacturers; this includes AZOMITE® Mineral Products, Inc., which manufactures the Azomite product. This funding provided for materials, labor and research costs associated with this study. It did not influence the factual reporting of findings herein. E.M. was supported by a grant from the National Science Foundation grant number 1838299.

Conflicts of Interest: Rajnish Khanna is the founder of i-Cultiver, an independent company providing consultation and research assistance to food and agricultural industries. All aspects of this study were performed by independent researchers. The authors declare that they have no competing interests.

Author Contributions: E.M. conducted microbiome profiling and data analysis; R.K. designed the study and conducted the greenhouse trials; J.F. provided product specific details in study design. All work was performed in collaboration and with guidance from K.M., J.F., and B.K.; E.M. and R.K. drafted the manuscript supplemented with technical and editorial comments from K.M., J.F., and B.K.

Disclaimer: Mention of trade names or commercial products in this publication is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the U.S. Department of Agriculture. USDA is an equal opportunity provider and employer.

Abstract

Food crops are grown with fertilizers containing nitrogen, phosphorus, and potassium (macronutrients), along with magnesium, calcium, boron, and zinc (micronutrients) at different ratios during their cultivation. Soil and plant associated microbes have been implicated to promote plant growth, stress tolerance, and productivity. However, the high degree of variability across agricultural environments makes it difficult to assess the possible influences of nutrient fertilizers on these microbial communities. Uncovering the underlying mechanisms could lead us to achieving consistently improved food quality and productivity with minimal environmental impacts. For this purpose, we tested a commercially available fertilizer (surface-mined 38-million-year-old volcanic ash deposit AZOMITE®), applied as a supplement to the normal fertilizer program to tomato plants grown in the greenhouse. We examined its impact on the composition of below-ground microbial communities, focusing on those members we identified as “core taxa” that were enriched in the rhizosphere and root endosphere compared to bulk soil, and appeared above their predicted neutral distribution levels in control and treated samples. This analysis revealed that Azomite had little effect on soil or rhizosphere microbial composition overall, but it had a significant, temporally selective influence on the rhizosphere and root associated core taxa. Changes in the composition of the core taxa were correlated to associated functional pathway enrichment of carbohydrate metabolism over shorter chain carbon metabolism, suggesting a conversion of available microbial nutrient source within the roots. This finding exemplifies how the nutrient environment can specifically alter the functional capacity of root-associated bacterial taxa, with potential to improve crop productivity.

Importance

Various types of soil fertilizers are used routinely to increase crop yields globally. The effects of these treatments are assessed mainly by the benefits they provide in increased crop productivity. There exists a gap in our understanding of how soil fertilizers act on the plant-associated microbial communities. The underlying mechanisms of nutrient uptake are widely complex and thus difficult to evaluate fully, but have critical influences on both soil and plant health. Here we present a systematic approach to analyze the effects of a fertilizer on core microbial communities in soil and plants, leading to predictable outcomes that can be empirically tested and used to develop simple and affordable field tests. The methods described here can be used for any fertilizer and crop system. Continued effort in advancing our understanding of how fertilizers affect plant and microbe relations is needed to advance scientific understanding and help growers make better-informed decisions.

Introduction

The below-ground components of the plant support a diverse set of microbes that can interact intimately with their host. These bacteria are broadly split into two compartments, those surrounding the root surface (the rhizosphere) and those living inside the root (the endosphere). External inputs can cause changes in plant microbiome communities, which in turn may boost plant growth by controlling hormonal signaling, competing with pathogens, and increasing bioavailability of nutrients (1–5). In particular, bacteria and fungi act to depolymerize and mineralize organic forms of N, P, and S, allowing for more efficient uptake by the plant (6–8). Plants also benefit from symbiotic relationships with mycorrhiza and nodulating bacteria, which help the plant to more efficiently acquire nutrients (9, 10). One of the primary factors that shapes

below-ground, plant-associated microbial community composition is the production of plant root exudates (11, 12). It is believed that these exudates are often targeted to attract beneficial bacteria which provide a fitness benefit for the plant (13). Such specifically recruited bacteria can provide benefits to the plant through disease suppression (14), increased nutrient acquisition (15), and/or improved resilience to abiotic stress (16). Furthermore, these bacteria can in turn modify the exudates that the plant is releasing, further altering the community and conditions of their local environment (17).

Understanding the factors that influence interactions between plants and below-ground microbial communities is critical to predicting the composition and function of the microbial community, especially in the context of agricultural practices of soil and plant amendments. These functions can be altered directly, through modifying the environment in which the bacteria are developing, as well as indirectly by modifying the interactions between the plant and its associated microbes. For example, studies have shown that microbial communities inhabiting agricultural soils can be impacted by nitrogen and phosphorus fertilizers (18, 19). Long-term use of N fertilizer reduced soil bacterial diversity, decreased soil pH and reduced microbial P solubilization and mineralization capacity, whereas long-term use of P application increased microbial P immobilization (20, 21). N and P inputs have also been linked to specific changes in microbiome composition, with increased abundance of copiotrophic microorganisms such as Proteobacteria compared to oligotrophic Acidobacteria (22–24).

The nutrient environment can also change a plant's ability to control the composition and function of its associated communities. It has been shown in *Arabidopsis thaliana* that the

phosphate stress response is linked to transcriptional regulators in the defense response, leading to a tradeoff between phosphate starvation response and defense signaling, ultimately causing the development of an altered root associated community (25). Specific inputs and practices introduced by the grower may thus lead to unintended consequences. In a controlled environment study, it was found that the addition of fertilizer abolished the ability of pre-inoculated tomato leaf-associated microbiota to protect against the pathogen *Pseudomonas syringae* (26). Studies thus far have focused primarily on the role of major nutrients (N, P, K) in altering microbial community composition and dynamics, but relatively little work has been done to understand the effect of micronutrient amendments on the plant microbiome. Fortification of soil micronutrients is increasing in popularity, as it can increase yield, fruit nutritional quality and resilience to biotic and abiotic stress (27–30). In addition to B, Fe, Mn, Cu, Zn and Mo, three other elements, selenium (Se), silicon (Si) and sodium (Na), have been shown to improve plant productivity and provide other benefits (31, 32). It is therefore important to include these rarer micronutrients in our understanding of how soil amendments impact the composition and function of planta associated microbial communities.

In this work, we sought to better understand the role of micronutrient amendments in shaping below-ground microbial community composition. To do this, we used a popular commercially available amendment, Azomite, which is a surface-mined volcanic ash deposit a Dacite by chemical composition. Previous but unpublished work has suggested that this amendment increases the total number of fruits produced, as well as the weight per fruit. Given that this amendment impacts the productivity of the plant, we were interested in determining if, and to what extent, it might alter the associated microbial community. By looking at microbial

community composition across bulk soil, rhizosphere and root endosphere, we established that the amendment has a relatively small impact on community composition as a whole, but it has an impact on which bacteria seem to be the most closely associated with the plant. We present a novel approach to identify core microbes within a given microbial community being shaped by the combined effects of external and internal selective pressures. Using this new method, we identified specific taxa that show significant differences in abundance in response to Azomite treatment and suggest potential functional relevance for these changes in their abundance.

Results

The purpose of this study was to determine whether a broadly used micronutrient soil supplement influences plant-associated microbial communities. We chose an amendment called Azomite (AZOMITE® Mineral Products, Inc.), which has been used in plant and animal agriculture for decades. Azomite is commonly used by animal feed manufacturers to increase feed mill pellet production efficiency (33). It is also widely used in commercial crop production and is available at local garden stores as a general soil fertilizer. Treatment with Azomite was reported to reduce drought stress in greenhouse grown tomatoes (34). Because of these considerations, we selected Azomite for this study to examine its impact on belowground microbiomes (soil, rhizosphere, and root endosphere) of greenhouse grown tomatoes.

To substantiate previous reports that Azomite increases fruit production, we grew an indeterminate (var. moneymaker) cultivar of greenhouse tomatoes in independent pots under controlled conditions for 22 weeks (as described in Methods). As a supplement to the conventional nutrient program, we applied two different grades of Azomite in treated pots-

Granular, a coarser grade was mixed with soil, and Ultrafine, a finer grade was applied later to the soil surface as described. Total number of tomatoes produced were counted per plant weekly, starting from the appearance of the first tomato until the end of the trial. We found that treatment with Azomite significantly increased the total number of tomatoes produced per plant as shown in Supplemental Figure 1 (SM Fig. 1). These data are consistent with reported increases in tomato yield on Azomite treated plants and are representative of other ongoing studies (E. Mehlferber et al., unpublished data). The observed increase in tomato production provided sufficient reason to examine potential changes in soil and plant microbiomes in response to Azomite application.

Microbial Diversity

We examined microbial diversity in the three compartments (bulk soil, rhizosphere, and root endosphere) at two timepoints (week 8 and 18) in control and Azomite treated plants. Application of Azomite to the soil had minimal impact on microbial community diversity metrics. We found that community beta-diversity was most impacted by the compartment, explaining 20% of variation ($p = 0.001$), followed by sampling time, explaining 16% of variation ($p = 0.001$), and with finally treatment explaining only 5% of the variation ($p = 0.001$; Fig. 1). Furthermore, there were significant interactions between compartment and date ($p = 0.001$), and treatment and date ($p = 0.002$), but not between compartment and treatment ($p = 0.112$). This implies that bacterial communities changed in composition relatively independently over time in the soil, rhizosphere, and root endosphere, and while there was a significant effect of treatment, the amount of variation it explained was small. It should be noted that the amounts of Azomite applied to the bulk soil were relatively small (see Methods). At 8 weeks Alpha

diversity was significantly lower in the roots when compared to the soil ($p < 0.001$), and at 18 weeks it was significantly lower than both the soil ($p < 0.001$) and the rhizosphere ($p < 0.001$) (Fig. 2), suggesting that the root endosphere became more and more selective, or less divergent in bacterial community structure, over time. Both, Compartment ($p < .001$) and Sampling Time ($p < .001$) were identified as significant, but there was no significant impact of Azomite treatment on Alpha Diversity.

Differential abundance

Overall, as would be expected, time had a greater influence on differential abundance than treatment. Across all compartments there were more differentially abundant taxa between weeks 8 and 18 samples than there were between Azomite and control (SM Fig. 2 and SM Table 1). Across time, the roots had the greatest number of differentially abundant taxa, followed by soil and rhizosphere (SM Fig. 2 and SM Table). Comparing between Azomite and control plants, the rhizosphere had the greatest number of differentially abundant taxa, followed by the roots, and finally the soil (SM Fig. 2 and SM Table). In summary, Azomite had relatively lower influence on differential abundance of bacteria in the three compartments than time, and over the ten-week period examined, roots exhibited the greatest change.

Abundance occupancy relationships

We used the Sloan Neutral Community Model (see Methods) to assess whether the relative abundance of taxa correlated with their relative percent occurrence across compartments. Based upon the neutral hypothesis, this model assumes that no other pressures are at work. Broadly, the abundance occupancy neutral model provided a good fit across the different samples, with a

mean R^2 value of 0.6899 for the Soil, 0.7345 for the rhizosphere, and 0.7036 for the roots (SM Fig. 3). It is important to note that the model generally assumes free dispersal between samples, which may not be possible in this experiment due to each plant being separated into a pot in a greenhouse setting. The pots were proximally placed in a randomized order on benches in an enclosed greenhouse room. There was some variation in the fit of the neutral model across compartments, treatments, and timepoints. In the control plants, the early season samples (except for the rhizosphere) had a worse fit to the model (lower R^2 values) than the later samples (SM Fig. 3). The opposite pattern was observed in Azomite treated plants where the early season (week 8, before fruiting) samples showed a better fit to the neutral model (indicated by higher R^2 values across all compartments) than the later season (week 18, during fruiting) samples (SM Fig. 3). This implies that their composition was more heavily influenced by stochastic forces earlier in the experiment with an increasing contribution of environmental/plant associated factors in the later samples. This raised the possibility that the product, Azomite (Granular and Ultrafine) may itself have introduced taxa in the treated bulk metacommunity after treatment, and possibly subsequently to rhizosphere and root endosphere, over time.

Azomite fertilizer associated taxa

To examine possible taxa harbored by the Azomite fertilizer, we collected Azomite samples (as described) and analyzed the Granular and Ultrafine products that were used in the study. We identified 337 taxa in Azomite Granular (SM Table 2) and 248 taxa in Azomite Ultrafine (SM Table 3), there were a total of 435 unique taxa across both Azomite samples. We then compared these taxa to the bulk soil of control plants, to determine which taxa were common to soil environments and which were likely introduced by the addition of the Azomite. SM Fig 4. shows

the mean relative abundance of these taxa across the compartments and treatments. There was no significant difference in the relative abundance between Azomite treated and control samples of any compartment indicating that the contributions that Azomite makes to shaping the microbiome are not due to the direct introduction of bacteria. Each plant was initiated with the same potting soil mixture (with or without Azomite), was exposed to the same fertilizer, pesticide program, and watering regime, so that it can be assumed that overall, the same bacteria were available to colonize each compartment in treated and control plants, and under a neutral model this colonization would proceed randomly based on their initial abundance.

Temporal evolution of core taxa

Using the combination of differential abundance and abundance occupancy curves, as suggested in Shade and Stopnisek 2019 (35) we were able to identify a conservative set of “core” microbes in the rhizosphere and root endosphere, as well as across treatment and time. This scheme is illustrated in Fig. 3. First, we used DESeq2 (36) to identify microbes that were significantly enriched in root endosphere and rhizosphere when compared to the surrounding bulk soil (Fig. 3a). These bacteria may be preferentially recruited by the plant from the bulk soil metacommunity, or these bacteria may preferentially occupy the compartment under the given conditions. These potentially enriched bacteria were then cross-referenced with the list of bacteria identified as being overrepresented in the occupancy abundance curve (Fig. 3b), thereby identifying the bacteria as likely being important to the plant due to their relatively higher occupancy occurrence, than the bacteria expected based upon their relative abundance (Fig. 3c). We saw a stark difference between the rhizosphere and the root endosphere, with only 24 unique bacteria identified as “core” in the rhizosphere (across all treatments and timepoints) compared

with 66 unique bacteria identified in the root endosphere as core taxa (Fig. 4). In the rhizosphere, these bacteria were primarily unique to their time point and treatment (Fig. 4a). Remarkably, 23 of the 24 rhizosphere core bacteria were identified in week 18 samples, with 10 unique to control and 10 unique to Azomite treated (Fig 4a). Notably, only 1 unique taxon was identified in control 8 weeks, and no taxa were identified as being core to the Azomite week 8 timepoint (Fig 4a). These results suggest that the core rhizosphere community was being shaped during development between the tested timepoints of weeks 8 and 18 and that the rhizosphere was relatively less stable, more dynamic, in core community structure compared to the root endosphere during early plant growth (Fig. 4).

There were appreciably more core taxa (66) identified in the root endosphere. The total number of core taxa in Azomite treated roots were 71% (15 vs. 21) of the control roots in week 8, and the number of core taxa in Azomite treated roots increased to 90% (26 vs. 29) in week 18 (Fig. 4b). Some of the core microbes were common between the sets, but the majority were unique to the time and treatment. The control roots had 10 unique taxa each in both sampling times, whereas the Azomite roots had 8 unique taxa in week 8 and 17 unique in week 18 (Fig. 4b). There were 6 taxa unique to control samples at both timepoints, while none were unique to Azomite across timepoints (Fig. 4b). Only 1/36 (2.8%) core taxon was common to all week 8 samples, and 7 (12.7%) core taxa were common to all week 18 samples, regardless of treatment (Fig. 4b). These data contrast the total taxa composition of the microbial communities, in which 45% of taxa were common to all treatments and time points in soil (168/370) and rhizosphere (170/370), and 39% (158/404) were common in all root samples (SM Fig. 5). Collectively, these data show that the taxa identified as core by the method described above, displayed relatively greater change over

time than the total community composition, and particularly demonstrate that the Azomite week 18 root endosphere had the greatest shift in core taxa makeup.

Predicted functions in the Rhizosphere and Root Endosphere across treatments

We identified potential functional differences between the core microbiota across both time and condition by looking at the differentially abundant predicted genes from PICRUSt 2. Glyoxylate ($C_2H_2O_3$) and dicarboxylate metabolism was the most frequently identified function associated with the control core communities, across compartments and over time; with it representing 19% of functions identified as differentially abundant in the control root at 8 weeks and then increasing to 32% in the control root at 18 weeks (Fig. 5). Similarly, glyoxylate and dicarboxylate metabolism comprised 36% of functions in the control rhizosphere core, and Methane (CH_4) metabolism was also identified as a relatively common function associated with the control core communities at 18 weeks, representing 21% of functions in the rhizosphere and 12% of functions in the root endosphere. Meanwhile, glycolysis and gluconeogenesis were the most common function in the Azomite treated core communities for the rhizosphere at 18 weeks, representing 19% of differentially abundant functions, and the roots at 8 weeks, representing 33% of differentially abundant functions (Fig. 5). The roots of plants treated with Azomite also shared a large fraction of differentially abundant genes associated with the Citrate cycle across both 8 and 18 weeks (Fig. 5). There seemed to be an increase in the number of differentially abundant predicted gene functions across the Azomite treated root samples from 8 weeks to 18 weeks, with 8 identified at 8 weeks compared to 19 identified at 18 weeks (Fig. 5). These data suggested a possible shift in the type of substrates available to root endophytes in Azomite treated roots.

Discussion

Overall, these data indicate that the addition of the Azomite micronutrient supplement, shown to increase tomato yield (SM Fig. 1), plays a subtle but important role in influencing the composition of the plant-associated microbial community. At the whole community level, we observed a small but significant impact on community composition measured through beta diversity, with no significant change in alpha diversity (regardless of compartment). This indicates that the community composition is shifting over time, while retaining a similar level of richness, which is important given the noted contribution of species diversity in maintaining a healthy and disease resistant community (37–40). The minimal impact of Azomite application on soil microbiota is not surprising since the amount of Azomite applied was relatively small (5% wt/wt of Granular mixed in potted soil, and 1g per plant of Ultrafine applied three times, every other week, to the base of the plant). These low amounts may not have been sufficient to cause any major shifts in the soil, but these treatments were enough to increase tomato production (SM Fig. 1) and influence the root endosome composition over time with a greater change observed at the later time point (week 18). This also suggested that Azomite was not itself introducing new microbial taxa to the soil, as further exemplified by the fact that there were no significant differences in the relative abundance of taxa that may have been unique to the Azomite fertilizer across any treatment or compartment (SM Fig 4).

Using DESeq2 we identified dozens of bacteria that are differentially abundant between the control and Azomite conditions across all treatments and timepoints. When comparing the Azomite and control plants we found a greater number of differentially abundant taxa in the

rhizosphere and roots than in the bulk soil, indicating that the effect of micronutrient may be partially due to the altered interactions between the host plant and its associated microbiota. This could be due to shifts in plant available nutrients resulting in altered exudate profiles, a shift in immune signaling, and/or the result of the plant recruiting a different community to maximize its available environmental resources to support its developmental stage specific growth and physiological processes.

We found minor differences in the R^2 values associated with the abundance occupancy curves for each compartment and time point, with all values falling within the range (0.6 to 0.8), associated with neutral assembly. Therefore, we can conclude that most bacterial communities found in each treatment and time point are likely to be shaped primarily by stochastic – rather than deterministic - forces. Despite this, some taxa in each treatment broke the assumptions of neutrality, providing further evidence that a portion of the community is being specifically recruited by the plant, either because of, or aided by, the current growing conditions.

These potentially important bacteria were identified using a novel method of combining abundance occupancy measures and differential abundance, as suggested by Shade and Stopnisek, 2019 (35). To our knowledge this is the first time that this method has been applied to identify the composition of the core microbiome of plant roots. This core microbial community was found to shift between time points and treatment, with most of the bacteria identified as core being unique (specifically being identified uniquely as core, they may still be present in other conditions) to their condition or timepoint. Given that this method was applied independently to replicate samples across different treatments, it provides further evidence that while most

bacteria are not impacted by micronutrient addition, the bacteria that may be most important to the plant shift depending on the changes in its nutrient and metabolic needs over the developmental stages from early growth to maturity. This suggests, and is supported by other recent evidence, that the plant associated microbial community is important to the survival and function of the plant and will shift to allow the plant to adapt to changing conditions.

Interestingly, fewer bacteria (24/370, 6%) were identified as being core in the rhizosphere compared to (66/404, 18%) in the root endosphere, with the Azomite week 8 condition having no taxa identified as core. This could, in part, be attributed to the conservative nature of this test, which requires bacterial abundance and distribution to reach significance across two independent statistical tests. However, it also suggests that the plant is exerting greater control over the composition of its endospheric microbial community, a common observation as reviewed in Kandel et. al 2017 (41). In the presence of the micronutrient, the plant may directly recruit these bacteria, or these bacteria may favorably occupy the altered compartment, or the micronutrient may cause changes in plant exudate compositions, which in turn may exert and influence these closely associated microbiotas, or, more likely, is some combination of the above.

The data presented here provides only a snapshot of the dynamic nature of the microbiomes that support plant growth and development. We applied a new method to identify core microbes, which are expected to be specific to the controlled conditions and the tomato variety used. The microbial communities may differ greatly between controlled and field conditions, as well as for different varieties of tomatoes and other crops. The study, however, indicates that there is a subtle but potentially significant impact of nutrient amendments such as Azomite on the bacteria

that form the endosphere community. Furthermore, we identified several bacterial taxa that could be defined as being “core” members of the plant associated community in each treatment and determined that the predicted functional profiles of these core taxa shift between control and Azomite conditions.

We present a working model (Fig. 6) to propose that induced changes in the plant’s production of endosomal substrates and possibly exudates in the presence of Azomite, causes the observed shift in root core taxa. The predicted functional shift in the root core at 18 weeks, with glyoxylate and dicarboxylate, and methane metabolism (cumulatively 44% of core functions) in control roots to citrate cycle and glycolysis / gluconeogenesis (cumulatively 33% of core functions) in Azomite roots (Fig. 5), suggests that the substrates available to core taxa in roots may have changed in response to Azomite treatments (Fig. 6); possibly, from substrates involved in carbohydrate biosynthesis to carbohydrate metabolism. Further studies are being performed to determine if these predicted core functional changes underly a real shift in plant exudates, and the potential causes for such biochemical transitions.

The identified core bacteria warrant further investigation to conclusively determine the role that they play in the broader community. Due to the combination of two independent statistical analyses, this method is quite conservative in its predictions, and therefore it can be applied for preliminary identification of candidate, important bacterial taxa to be studied more closely for their roles in plant performance in different environments and in response to soil inputs. In this study, the method revealed that Azomite, which is a commercially available product and is applied widely in agricultural production of a variety of specialty crops, has a precise effect on

the root endosphere community without any major changes in the microbial diversity. Further studies on the functional relevance of the microbes recruited into the plant in response to Azomite alone and in combination with other treatments and in other environments will provide us a better understanding of how plants, such as tomatoes, utilize available nutrients and other inputs to optimize their growth and development. It is anticipated that studies such as these will lead to the development of new approaches combining nutrient inputs with microbial amendments to improve agricultural outputs in both quantity and nutrient density of harvested specialty crops, like tomatoes. These combinatorial approaches are well poised to transform the specialty crop production with potential economic benefits to growers and consumers.

In summary, the plant associated microbial community shifts in response to the addition of a micronutrient supplement with these changes primarily impacting the bacteria that may be most closely associated with the plant. Further work should be done to evaluate the consequences of this shift and whether this is driven by a shift in the microbial population or the plants associations with those bacteria. This method can be used widely to identify changes in core microbial compositions in response to various treatments or environmental stimuli, and to develop testable functional models.

Materials and Methods

Plant generation and Azomite application

Seeds of tomato (*Solanum lycopersicum*) variety moneymaker were surface sterilized by gently shaking in a solution of sodium hypochlorite and Tween 20 for 20 minutes, followed by two rinses with filter sterilized H₂O. Seeds were placed into soil pots and germinated in the

greenhouse. When the seedlings were 3-4 inches tall, they were transplanted into larger pots, where they were grown for a total duration of 22 weeks with blocked placement on benches in a single greenhouse room. Plants were grown in the greenhouse under controlled conditions with supplemented lights to maintain long days and fans to control high temperature fluctuations. Liquid nutrient supplementation program consisting of Peters Professional 20/20/20 water soluble fertilizer was applied (1:64 ppm) once per week, as well as a disease suppression program consisting of Floramite and Decathlon at a rate of ¼ tsp per gallon of water, mixed/agitated, was applied through a controlled sprayer at the rate of 1-2 gal per 100 plants. Sunshine mix #1 (Sun Gro®) containing 5% wt/wt chicken manure (EB Stone & Son, Inc.) was used either with or without 5% wt/wt Azomite Granular (AZOMITE® Mineral Products, Inc.) for sowing and transplanting. After transplanting, the treated plants were supplemented with Azomite Ultrafine (AZOMITE® Mineral Products, Inc.) by adding 1g per plant to the soil surface at the base of the plant at 7, 9 and 12 weeks after sowing. 16 plants each, either with or without Azomite fertilizer were grown and maintained through maturity. Number of red tomatoes produced per plant per week were quantified from week 9 until termination week 22.

Sample collection

Soil, rhizosphere and root samples (as indicated) were collected from 6 control and 6 treated plants for microbiome profiling at two different time points: once at the onset of fruiting at week 8 and another one later during fruiting at week 18. Duplicate samples of Azomite Granular and Ultrafine fertilizer formulations were collected from their original packaging to determine whether any microbial taxa in treated soil could be linked to the Azomite product itself as the

source. All samples were collected as described in (Deng et al., 2019) on ice and kept frozen for DNA extraction.

DNA extractions, 16s rRNA amplification and sequencing

DNA was extracted using the Qiagen DNeasy Powersoil Kit. The V3-V4 region of 16S ribosomal gene was amplified using a dual-indexed 16s rRNA Illumina iTags primer (341 F (5'-CCTACGGGNNBGCASCAG-3') and 785 R (5'-GACTACNVGGGTATCTAATCC-3') as described in (Deng et al., 2019). Samples were sequenced by the QB3 Vincent J. Coates Genomics Sequencing Laboratory facility at the University of California, Berkeley using Illumina Miseq. 300 bp pair-end with v3 chemistry.

Data analysis

Sequence files were demultiplexed and the adapters were removed by the sequencing facility. Raw reads were analyzed through the Dada2 pipeline in R using the default suggestions from their [pipeline tutorial version 1.16](#) (42). Once ASVs were produced in Dada2 we used Decontam to identify and remove contaminate sequences (42). Data were then imported into Phyloseq (43) for the remaining analysis. ASVs were merged at the genus level using the taxglom function in Phyloseq. Using Bray-Curtis dissimilarity measures we performed an ADONIS test (nonparametric multivariate analysis of variance) on all samples together to determine the relative contribution of treatment (control vs. Azomite-treated), compartment (soil, rhizosphere, root endosphere), and sampling time (8 or 18 weeks) on the composition of the microbiota. Alpha diversity was calculated using Shannon's diversity index, which accounts for the richness (number of species) and evenness (distribution of species abundances within a sample) of each

sample. We used an ANOVA to determine the impact of the various conditions on alpha diversity and then, after splitting by time point, a Tukey Post Hoc test to determine the differences between each compartment at each time point.

We used DESeq2 package to identify taxa that show a significant difference in abundance across different conditions. DESeq2 package was originally developed with the primary goal of identifying statistically significant variation in RNA seq data using a negative binomial distribution. However, to avoid the issues inherent in sample normalization McMurdie and Holmes, 2014 proposed its use in microbiome data analysis.

Abundance occupancy curve

To understand the forces that shape a microbial community it can be useful to assume a neutral hypothesis (that no forces are at work) and then evaluate how well this hypothesis matches the data. This can be done by utilizing the Sloan Neutral Community Model developed by Sloan and Curtis (44, 45) and applied to plant associated microbial communities by Shade and Stopnisek (35). This method fits the neutral model to the abundance-occupancy distribution under the assumption that bacteria that are more abundant (have a higher mean relative abundance) will have a correspondingly higher occupancy (percent occurrence across samples), given unlimited dispersal and equal fitness. The goodness of fit for this model can be used to determine the extent to which stochastic or deterministic forces are influencing the community composition, the former in cases where the model fits well, the latter when it fits poorly. The model can also be used to identify significant outliers, bacteria whose occupancy is likely to be influenced by some factors in the given environment. Bacteria that are significantly above the curve have a higher

occupancy than expected given their abundance, and therefore are more likely to be selected for by the plant environment or may be exceptionally good dispersers. Meanwhile, bacteria that fall significantly below the curve are likely to have been selected against by the plant environment or have poor dispersal capabilities. These methods allow for the identification of broad trends in terms of community composition, as well as identifying specific taxa that may warrant further investigation.

Identifying core taxa in the Rhizosphere and Root Endosphere

There are many different approaches for defining the core microbiome, but generally these approaches aim to identify which bacteria are consistently associated with the host, either broadly or under certain conditions. These bacteria are often seen as being important to the host, and so provide a way to understand the microbiome at a more manageable level of complexity.

One method for identifying the core microbiome is to use an abundance occupancy curve to select the bacteria that are appearing at higher occupancy than would be expected given their abundance, as these bacteria could be selected for by the plant or by the present conditions. In their 2019 paper Shade and Stopnisek propose that these bacteria should be compared against bulk soil samples to determine if they are being selected for out of this meta-community reserve. Bacteria that are at higher-than-expected occupancy and appear at consistently higher relative abundance in the compartments associated with the plant are more likely to be relevant to the plant under the given conditions, as potentially beneficial microbes. It is important to note, however, that not all bacteria selected may represent beneficial species, but the bacteria selected by this process will include species that play mutually beneficial roles and are either host-

selected or seek the present condition. Combining this method with DESeq2 provides a more conservative selection criteria for potential core membership. DESeq2 was used to identify the bacteria that are consistently at higher relative abundance in the rhizosphere and root endosphere when compared to the surrounding bulk soil. These bacteria were then compared to those identified as having significantly non-neutral (deterministic) occupancy. Bacteria that met both criteria were defined as the core microbiome (Core Taxa) for that condition. This scheme was used to determine the Core Taxa independently for each sample (N=6) under each condition, as illustrated in (Fig. 3 a, b, and c). Core Taxa for each condition represent the bacteria that were present in abundance higher than randomly expected, and thereby form the core community in the host under that condition, implying that these species are likely to have been selected by the host, or they prefer the host environment under the tested condition.

Functional analysis

To better understand the compositional shifts in the predicted Core Taxa across each condition we used PICRUST2 (Phylogenetic Investigation of Communities by Reconstruction of Unobserved States) set at default parameters to predict the gene family content of each core microbiome (46, 47). After the gene content was predicted by PICRUST2, we used DESeq2 to determine which sets of predicted genes were differentially abundant between the Azomite treated and control core microbiota across the relevant timepoints and compartments. We then cross referenced the identified genes against the KEGG (Kyoto Encyclopedia of Genes and Genomes) BRITE database to determine predicted functions (48–50).

Acknowledgements

The authors thank Priyanka Mehta for assistance with sample collection and DNA extraction for sequencing, Norma Morella for help with preparing the samples for microbiome sequencing, Lia Marie Poasa and her team at the Plant Gene Expression Center greenhouse, Albany, California for help with plant care and maintenance, Gerard R. Lazo and Roberto A. Bogomolni for constructive comments on bioinformatics and research presented in this manuscript.

References

1. Mendes R, Garbeva P, Raaijmakers JM. 2013. The rhizosphere microbiome: significance of plant beneficial, plant pathogenic, and human pathogenic microorganisms. *FEMS Microbiol Rev* 37:634–663.
2. Van Der Heijden MGA, Bardgett RD, Van Straalen NM. 2008. The unseen majority: soil microbes as drivers of plant diversity and productivity in terrestrial ecosystems. *Ecology Letters* 11:296–310.
3. Verbon EH, Liberman LM. 2016. Beneficial Microbes Affect Endogenous Mechanisms Controlling Root Development. *Trends in Plant Science* 21:218–229.
4. Chaudhari D, Rangappa K, Das A, Layek J, Basavaraj S, Kandpal BK, Shouche Y, Rahi P. 2020. Pea (*Pisum sativum* L.) Plant Shapes Its Rhizosphere Microbiome for Nutrient Uptake and Stress Amelioration in Acidic Soils of the North-East Region of India. *Frontiers in Microbiology* 11:968.
5. Yuan Z-S, Liu F, Liu Z-Y, Huang Q-L, Zhang G-F, Pan H. 2021. Structural variability and differentiation of niches in the rhizosphere and endosphere bacterial microbiome of moso bamboo (*Phyllostachys edulis*). *Sci Rep* 11:1574.

- 551 6. Hestrin R, Hammer EC, Mueller CW, Lehmann J. 2019. Synergies between mycorrhizal
552 fungi and soil microbial communities increase plant nitrogen acquisition. *Commun Biol*
553 2:1–9.
- 554 7. Manzoni S, Trofymow JA, Jackson RB, Porporato A. 2010. Stoichiometric controls on
555 carbon, nitrogen, and phosphorus dynamics in decomposing litter. *Ecological Monographs*
556 80:89–106.
- 557 8. Gahan J, Schmalenberger A. 2014. The role of bacteria and mycorrhiza in plant sulfur
558 supply. *Frontiers in Plant Science* 5:723.
- 559 9. Garcia K, Doidy J, Zimmermann SD, Wipf D, Courty P-E. 2016. Take a Trip Through the
560 Plant and Fungal Transportome of Mycorrhiza. *Trends Plant Sci* 21:937–950.
- 561 10. Kamel L, Keller-Pearson M, Roux C, Ané J-M. 2017. Biology and evolution of arbuscular
562 mycorrhizal symbiosis in the light of genomics. *New Phytologist* 213:531–536.
- 563 11. Bais HP, Weir TL, Perry LG, Gilroy S, Vivanco JM. 2006. The Role of Root Exudates in
564 Rhizosphere Interactions with Plants and Other Organisms. *Annual Review of Plant*
565 *Biology* 57:233–266.
- 566 12. Pascale A, Proietti S, Pantelides IS, Stringlis IA. 2020. Modulation of the Root Microbiome
567 by Plant Molecules: The Basis for Targeted Disease Suppression and Plant Growth
568 Promotion. *Frontiers in Plant Science* 10:1741.
- 569 13. Sasse J, Martinoia E, Northen T. 2018. Feed Your Friends: Do Plant Exudates Shape the
570 Root Microbiome? *Trends in Plant Science* 23:25–41.

- 571 14. Pieterse CMJ, Zamioudis C, Berendsen RL, Weller DM, Van Wees SCM, Bakker PAHM.
572 2014. Induced Systemic Resistance by Beneficial Microbes. *Annual Review of*
573 *Phytopathology* 52:347–375.
- 574 15. Hiruma K, Gerlach N, Sacristán S, Nakano RT, Hacquard S, Kracher B, Neumann U,
575 Ramírez D, Bucher M, O’Connell RJ, Schulze-Lefert P. 2016. Root Endophyte
576 *Colletotrichum tofieldiae* Confers Plant Fitness Benefits that Are Phosphate Status
577 Dependent. *Cell* 165:464–474.
- 578 16. Caddell DF, Deng S, Coleman-Derr D. 2019. Role of the Plant Root Microbiome in Abiotic
579 Stress Tolerance, p. 273–311. *In* Verma, SK, White, J, James Francis (eds.), *Seed*
580 *Endophytes: Biology and Biotechnology*. Springer International Publishing, Cham.
- 581 17. Korenblum E, Dong Y, Szymanski J, Panda S, Jozwiak A, Massalha H, Meir S, Rogachev
582 I, Aharoni A. 2020. Rhizosphere microbiome mediates systemic root metabolite exudation
583 by root-to-root signaling. *PNAS* 117:3874–3883.
- 584 18. Krashevskaya V, Sandmann D, Maraun M, Scheu S. 2014. Moderate changes in nutrient input
585 alter tropical microbial and protist communities and belowground linkages. *ISME J*
586 8:1126–1134.
- 587 19. Zeng J, Liu X, Song L, Lin X, Zhang H, Shen C, Chu H. 2016. Nitrogen fertilization
588 directly affects soil bacterial diversity and indirectly affects bacterial community
589 composition. *Soil Biology and Biochemistry* 92:41–49.
- 590 20. Dai Z, Su W, Chen H, Barberán A, Zhao H, Yu M, Yu L, Brookes PC, Schadt CW, Chang
591 SX, Xu J. 2018. Long-term nitrogen fertilization decreases bacterial diversity and favors the

growth of Actinobacteria and Proteobacteria in agro-ecosystems across the globe. *Glob Chang Biol* 24:3452–3461.

21. Dai Z, Liu G, Chen H, Chen C, Wang J, Ai S, Wei D, Li D, Ma B, Tang C, Brookes PC, Xu J. 2020. Long-term nutrient inputs shift soil microbial functional profiles of phosphorus cycling in diverse agroecosystems. *ISME J* 14:757–770.

22. Fierer N, Lauber CL, Ramirez KS, Zaneveld J, Bradford MA, Knight R. 2012. Comparative metagenomic, phylogenetic and physiological analyses of soil microbial communities across nitrogen gradients. *ISME J* 6:1007–1017.

23. Mitchell PJ, Simpson AJ, Soong R, Schurman JS, Thomas SC, Simpson MJ. 2016. Biochar amendment and phosphorus fertilization altered forest soil microbial community and native soil organic matter molecular composition. *Biogeochemistry* 130:227–245.

24. Ramirez KS, Lauber CL, Knight R, Bradford MA, Fierer N. 2010. Consistent effects of nitrogen fertilization on soil bacterial communities in contrasting systems. *Ecology* 91:3463–3470.

25. Lebeis SL, Paredes SH, Lundberg DS, Breakfield N, Gehring J, McDonald M, Malfatti S, Glavina del Rio T, Jones CD, Tringe SG, Dangel JL. 2015. Salicylic acid modulates colonization of the root microbiome by specific bacterial taxa. *Science* 349:860–864.

26. Berg M, Koskella B. 2018. Nutrient- and Dose-Dependent Microbiome-Mediated Protection against a Plant Pathogen. *Current Biology* 28:2487-2492.e3.

- 611 27. Deng S, Wipf HM-L, Pierroz G, Raab TK, Khanna R, Coleman-Derr D. 2019. A Plant
612 Growth-Promoting Microbial Soil Amendment Dynamically Alters the Strawberry Root
613 Bacterial Microbiome. *Sci Rep* 9:17677.
- 614 28. Basak BB, Sarkar B, Naidu R. 2021. Environmentally safe release of plant available
615 potassium and micronutrients from organically amended rock mineral powder. *Environ*
616 *Geochem Health* 43:3273–3286.
- 617 29. Eisa AI, Taha MB, Abdalla AM. 2011. AMENDMENT OF SOIL FERTILITY AND
618 AUGMENTATION OF THE QUANTITY AND QUALITY OF SOYBEAN CROP BY
619 USING PHOSPHORUS AND MICRONUTRIENTS. *INTERNATIONAL JOURNAL OF*
620 *ACADEMIC RESEARCH* 3:10.
- 621 30. Siddiqui S, Alamri SA, Alrumman SA, Meghvansi MK, Chaudhary KK, Kilany M, Prasad
622 K. 2015. Role of Soil Amendment with Micronutrients in Suppression of Certain Soilborne
623 Plant Fungal Diseases: A Review, p. 363–380. *In* Meghvansi, MK, Varma, A (eds.),
624 Organic Amendments and Soil Suppressiveness in Plant Disease Management. Springer
625 International Publishing, Cham.
- 626 31. Datnoff LE, Elmer WH, Huber DM. 2007. Mineral nutrition and plant disease. Amer
627 Phytopathological Society, St. Paul.
- 628 32. Marschner P, Rengel Z. 2012. Chapter 12 - Nutrient Availability in Soils, p. 315–330. *In*
629 Marschner, P (ed.), Marschner's Mineral Nutrition of Higher Plants (Third Edition).
630 Academic Press, San Diego.

33. Boltz TP, Ferrel J, Bowen KM, Harding KL, Ayres VE, Moritz JS. 2021. The effect of a dacitic tuff breccia (Azomite) in corn, soybean, and dried distillers grains with solubles–based diets that vary in inorganic phosphate source on pellet mill production rate and pellet quality. *Journal of Applied Poultry Research* 30:100147.
34. Azad H, Poor A, Bakhshikhaniki G, Ebrahimi M. 2016. Physiological responses of two tomato (*Lycopersicon esculentum* M.) cultivars to Azomite fertilizer under drought stress. *Iranian Journal of Plant Physiology* 6:1835–1843.
35. Shade A, Stopnisek N. 2019. Abundance-occupancy distributions to prioritize plant core microbiome membership. *Current Opinion in Microbiology* 49:50–58.
36. Love MI, Huber W, Anders S. 2014. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biol* 15:550.
37. Abawi GS, Widmer TL. 2000. Impact of soil health management practices on soilborne pathogens, nematodes and root diseases of vegetable crops. *Applied Soil Ecology* 15:37–47.
38. Garbeva P, van Veen JA, van Elsas JD. 2004. MICROBIAL DIVERSITY IN SOIL: Selection of Microbial Populations by Plant and Soil Type and Implications for Disease Suppressiveness. *Annual Review of Phytopathology* 42:243–270.
39. Wakelin SA, Macdonald LM, Rogers SL, Gregg AL, Bolger TP, Baldock JA. 2008. Habitat selective factors influencing the structural composition and functional capacity of microbial communities in agricultural soils. *Soil Biology and Biochemistry* 40:803–813.

- 651 40. Trivedi P, Delgado-Baquerizo M, Jeffries TC, Trivedi C, Anderson IC, Lai K, McNee M,
652 Flower K, Singh BP, Minkey D, Singh BK. 2017. Soil aggregation and associated microbial
653 communities modify the impact of agricultural management on carbon content.
654 *Environmental Microbiology* 19:3070–3086.
- 655 41. Kandel S, Joubert P, Doty S. 2017. Bacterial Endophyte Colonization and Distribution
656 within Plants. *Microorganisms* 5:E77.
- 657 42. Callahan BJ, McMurdie PJ, Rosen MJ, Han AW, Johnson AJA, Holmes SP. 2016.
658 DADA2: High-resolution sample inference from Illumina amplicon data. *Nat Methods*
659 13:581–583.
- 660 43. McMurdie PJ, Holmes S. 2013. phyloseq: An R Package for Reproducible Interactive
661 Analysis and Graphics of Microbiome Census Data. *PLoS ONE* 8:e61217.
- 662 44. Sloan WT, Lunn M, Woodcock S, Head IM, Nee S, Curtis TP. 2006. Quantifying the roles
663 of immigration and chance in shaping prokaryote community structure. *Environ Microbiol*
664 8:732–740.
- 665 45. Sloan WT, Woodcock S, Lunn M, Head IM, Curtis TP. 2007. Modeling Taxa-Abundance
666 Distributions in Microbial Communities using Environmental Sequence Data. *Microb Ecol*
667 53:443–455.
- 668 46. Paradis E, Claude J, Strimmer K. 2004. APE: Analyses of Phylogenetics and Evolution in R
669 language. *Bioinformatics* 20:289–290.

47. Langille MGI, Zaneveld J, Caporaso JG, McDonald D, Knights D, Reyes JA, Clemente JC, Burkepile DE, Vega Thurber RL, Knight R, Beiko RG, Huttenhower C. 2013. Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. *Nat Biotechnol* 31:814–821.
48. Kanehisa M, Goto S. 2000. KEGG: Kyoto Encyclopedia of Genes and Genomes. *Nucleic Acids Research* 28:27–30.
49. Kanehisa M. 2019. Toward understanding the origin and evolution of cellular organisms. *Protein Sci* 28:1947–1951.
50. Kanehisa M, Furumichi M, Sato Y, Ishiguro-Watanabe M, Tanabe M. 2021. KEGG: integrating viruses and cellular organisms. *Nucleic Acids Research* 49:D545–D551.

Figure Legends

Figure 1: Microbial communities in soil, root and rhizosphere differentiate over time. A Bray-Curtis PCoA shows that microbial communities in soil, root and rhizosphere clustered primarily by compartment, and were relatively more distinct in later (week 18) sampling time than earlier (week 8) sampling time. The microbial community structure differentiated distinctly in the three compartments over the two sampling times, with a proportionally small effect of Azomite treatment on community similarity.

Figure 2: Shannon's alpha diversity between bacterial communities across Compartment, Treatment, and Sampling Time. Both, Compartment ($p < .001$) and Sampling Time ($p < .001$)

were identified as significant factors in an ANOVA, but no significant difference was seen between the control and Azomite treated plants. A Tukey Post Hoc test was performed on the samples at each timepoint, indicating that the roots had significantly lower diversity at 8 weeks than the soil ($p = 0.03$), and that the roots were significantly less diverse than soil ($p < 0.001$) and rhizosphere ($p < 0.001$) samples at 18 weeks.

Figure 3: Methods used to identify the Core taxa in each condition are illustrated. Differential abundance is calculated between the root and soil samples of each condition using DESeq2 (a). This allows us to determine which bacteria are present in both compartments (root and soil) but show significantly higher abundance within the root endosphere (green) than in the bulk soil (purple). In the second step, we fit the abundance-occupancy distribution to the Sloan neutral model (Sloan et al., 2006; 2007), which assumes that the taxa that have higher mean relative abundance will have more opportunities to disperse, and given the assumption of neutrality, will be able to occupy a larger proportion of samples across the metacommunity. Each taxation is plotted by its mean log₁₀ relative abundance across these samples against its frequency, or the percentage of samples in this condition in which it is present. We used a 95% confidence interval and consider the taxa that fall within the confidence interval to be neutrally selected (gray), while those that fall above or below are likely to be selected for (blue), or against (red), respectively by the plant or environment (b). The bacteria identified (a, green; and b, blue) are then cross referenced to select those that are significantly enriched and are above predicted frequency as the candidate “Core taxa” for the condition tested (c).

Figure 4: Venn Diagram showing the overlap of the “Core” portion of the microbiome across treatments and time for the rhizosphere (a) and root endosphere (b). For the rhizosphere Control at 8 weeks had 2 core microbes, Control at 18 weeks had 13 core microbes, Azomite treated at 8 weeks notably had no core microbes identified and Azomite treated at 18 weeks had 13 core microbes. Control at 8 weeks and Control at 18 weeks share a single core microbe, while Control at 18 weeks and Azomite at 18 weeks share 2 core microbes. Notably, no core taxa are shared across all three conditions in the rhizosphere (a). For the root endosphere Control at 8 weeks had 21 core microbes, Control at 18 weeks had 29 core microbes, Azomite treated at 8 weeks had 13 core microbes and Azomite treated at 18 weeks had 26 core microbes. Control at 8 weeks and Control at 18 weeks share 6 core microbes, while Azomite treated at 8 weeks and Azomite treated at 18 weeks share only 1 core microbe. Control at 8 weeks and Azomite at 8 weeks share 4 core microbes and Control at 18 weeks and Azomite at 18 weeks share 8 core microbes.

Figure 5: Pie Charts showing the functional groups that are differentially abundant in each treatment and compartment as determined by DESeq2. Functions that were identified as more abundant in Control (left panel) and Azomite treated (right panel) samples at 8 weeks (a), and 18 weeks (b). Relatively large percentage of functions related to Glyoxylate / Dicarboxylase and Methane metabolism in Control samples. In contrast, relatively large percentage of functions related to Glycolysis / Gluconeogenesis and Citrate cycle (TCA cycle) in Azomite treated samples.

Figure 6: A working model showing the predicted impact of Azomite on root microbiome. It was determined that the core taxa composition in root endosphere changed differentially in

response to the soil amendment. The change in composition showed a relative shift in the majority of predicted core taxa functions, from metabolism of glyoxylate and dicarboxylate (shorter C-chain molecules) in control rhizosphere and roots, to majority of predicted core taxa functions linked to glycolysis / gluconeogenesis and citrate cycle (longer C-chain molecules) in rhizosphere and roots treated with Azomite. Based upon these observations, we predicted that the treated roots may have relatively higher levels of glucose or related sugar substrates. This change in biochemical composition may act to recruit and attract different bacteria from the surrounding soil. The underlying mechanisms involved are being investigated.

Supplemental Figure Legends

Supplemental Figure 1: The total number of tomatoes counted per plant weekly are plotted. Treatment with Azomite increased the number of tomatoes produced per plant. Weeks after sowing was determined from days after sowing, corresponding to the day of counting. Tomatoes were harvested in weeks 15 and 18 for additional analyses, resulting in the reduction in the number of tomatoes counted in the following weeks. Analyzed via ANOVA, N=16 plants/treatment ($p < 0.01$).

Supplemental Figure 2: Significantly differentially abundant taxa in each compartment across time (left panels) and Azomite treatment (right panels), as identified by DESeq2. For the comparison between 8 and 18 weeks the taxa in the highlighted green box are at increased abundance at 18 weeks compared to 8 weeks, and the taxa in the highlighted red box are at decreased abundance at 18 weeks when compared to 8 weeks. For the comparisons between

Azomite and Control the taxa in the green box are at increased abundance in the Azomite treatment samples, while the taxa in the red box are at decreased abundance compared to the controls. Overall, there are more differentially abundant taxa when comparing across time than Azomite treatment, with the greatest number of taxa differing in the roots over time. See SM Table 1 for the numbers of taxa that increased or decreased in abundance.

Supplemental Figure 3: Abundance occupancy relationship and associated mean (r^2) values within each compartment across time and Azomite treatment. The line represents the predicted values based on the sloan neutral model, with a 95% confidence interval highlighted in grey. The taxa that fall above (blue) and below (red) their predicted values are highlighted and represent deviations from the neutral model and the possibility that they may be actively selected for (above the line, blue) or against (below the line, red). The mean R^2 values which represent the goodness of fit for the data to the predict slope of the neutral model are roughly similar across compartments.

Supplemental Figure 4: The mean relative abundance of taxa that were found to be present in the sequenced Azomite fertilizer, but not in the bulk soil of control plants. There was no significant difference in the relative abundance of these taxa across any of the compartments. In total, there were 435 unique taxa identified in the sequenced Azomite and 443 unique taxa in the bulk soil of control plants. Of those taxa, 272 were shared by both Azomite and bulk soil. Duplicate samples of Azomite Granular and Azomite Ultrafine collected from the original bags that were used in this study were subjected to 16s rRNA amplification and sequencing as

described in Material and Methods. Genus level lists of the taxa present in Azomite Granular and Ultrafine are provided in SM Tables 2 and 3.

Supplemental Figure 5: Total number of taxa shared in each compartment across treatment and time. Grouped at the genus level there were 370 total taxa across all bulk soil and rhizosphere treatments and 404 in the roots. Approximately half of the taxa in each compartment were present across all treatments and timepoints.

Supplemental Table 1: Number of taxa exhibiting significant changes in their differential abundance in each compartment across time and in response to Azomite, as identified by DESeq2. Values of increase or decrease in abundance are plotted in SM Fig2.

Supplemental Table 2: List of taxa in the Azomite Granular product and the number of reads that match each sequence. Duplicate samples (AzG1 and AzG2) were analyzed. Taxa (ASV) are listed from highest to lowest number of reads obtained from the two samples.

Supplemental Table 3: List of taxa in the Azomite Granular product and the number of reads that match each sequence. Duplicate samples (AzU1 and AzU2) were analyzed. Taxa (ASV) are listed from highest to lowest number of reads obtained from the two samples.

Figures

Figure 1

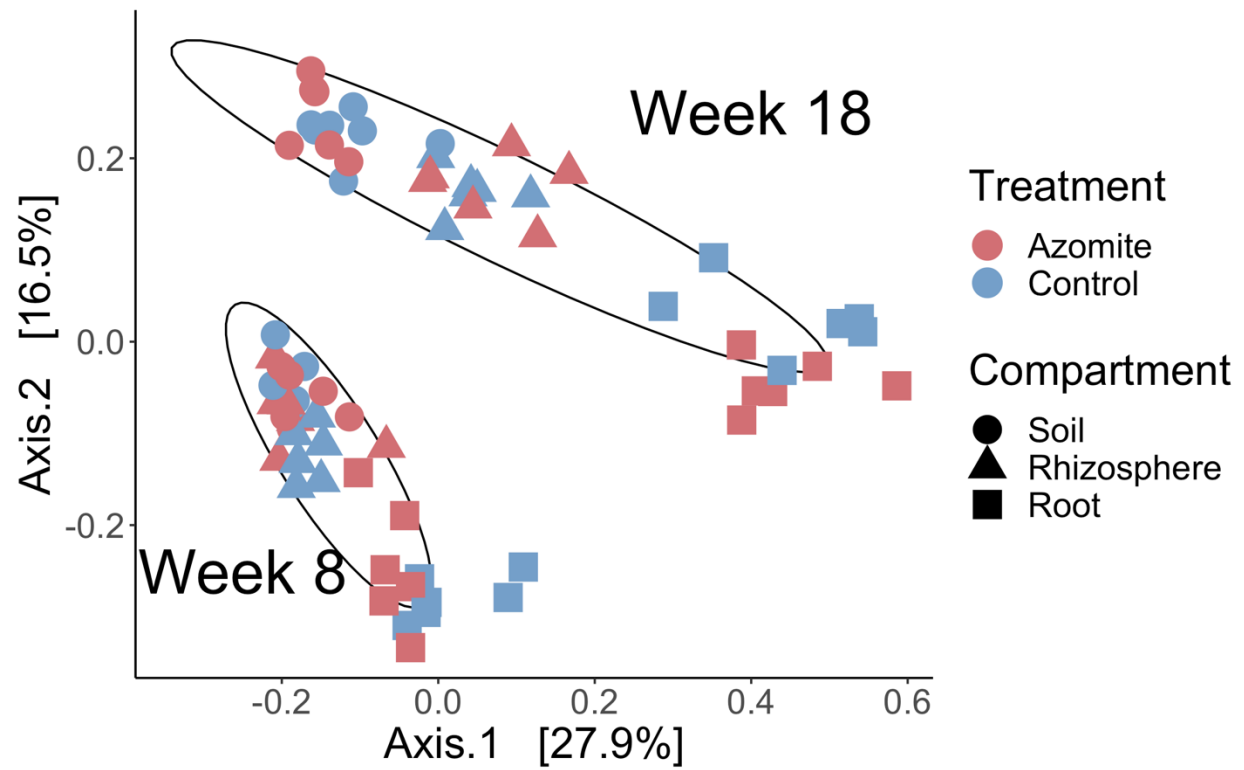


Figure 2

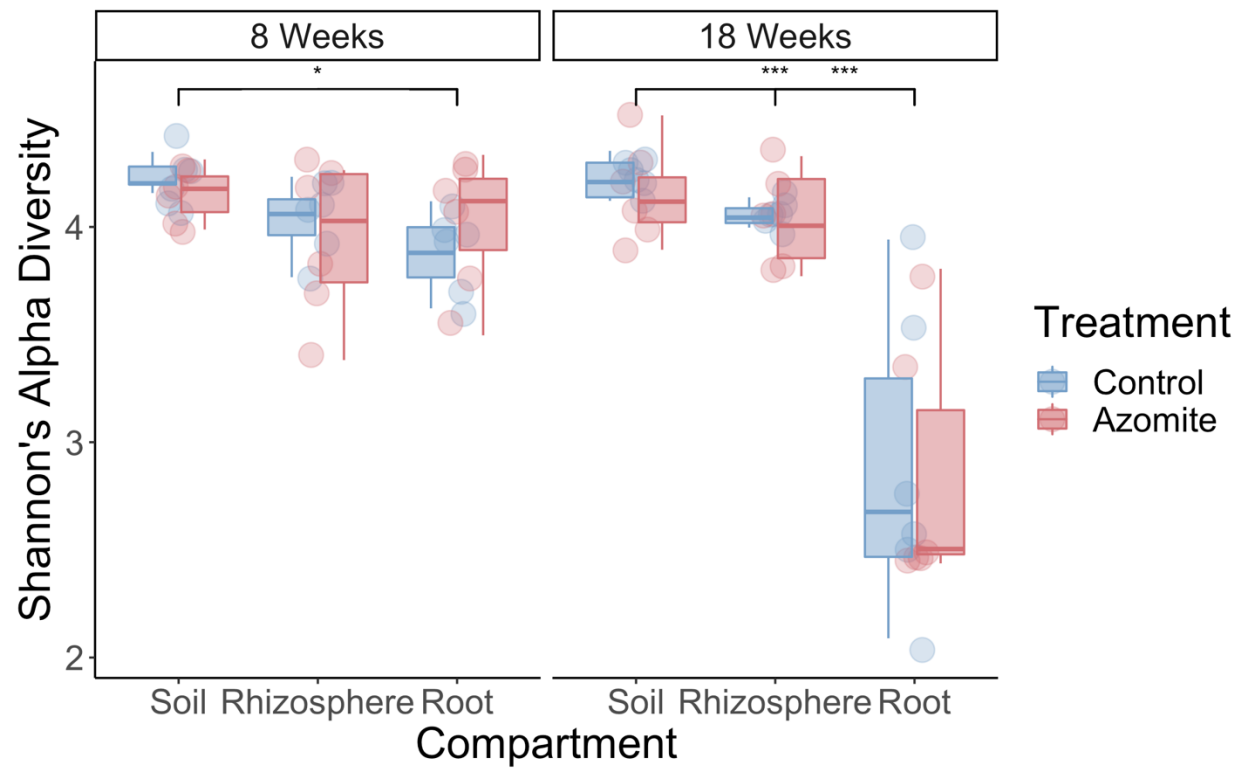


Figure 3

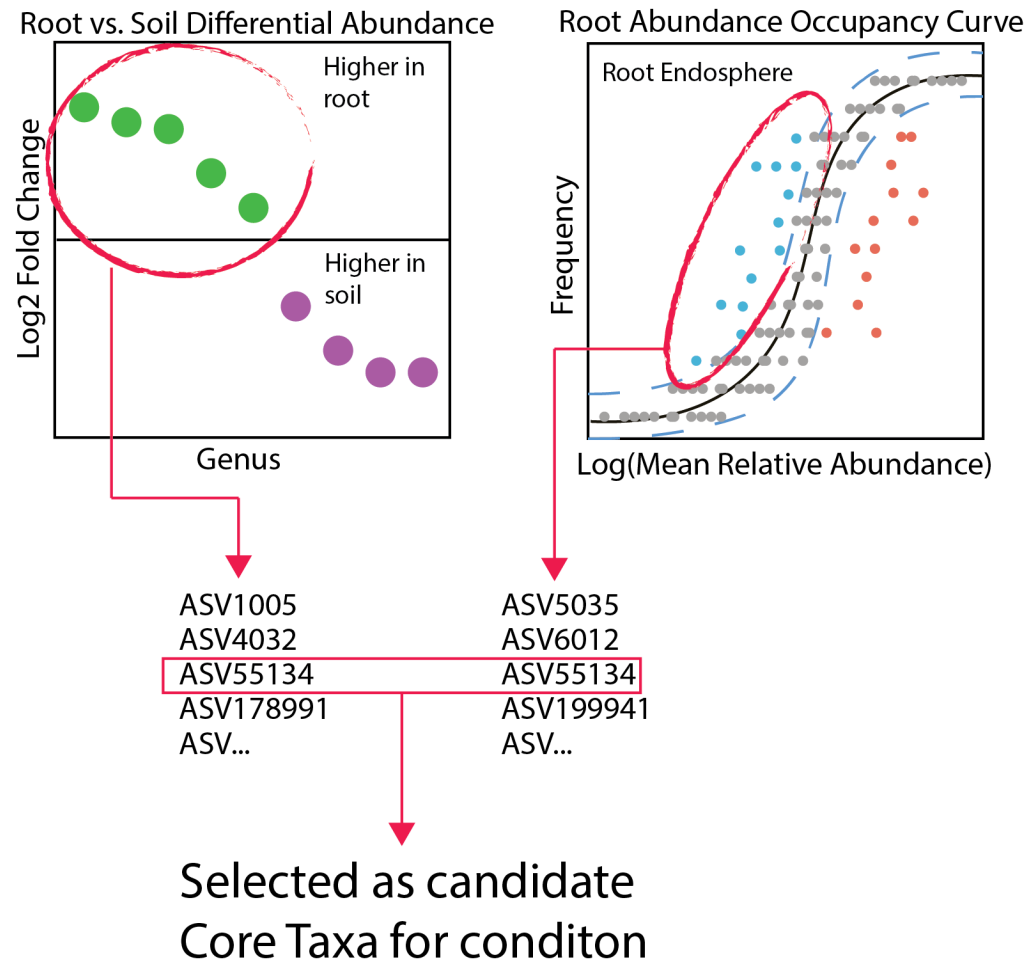


Figure 4

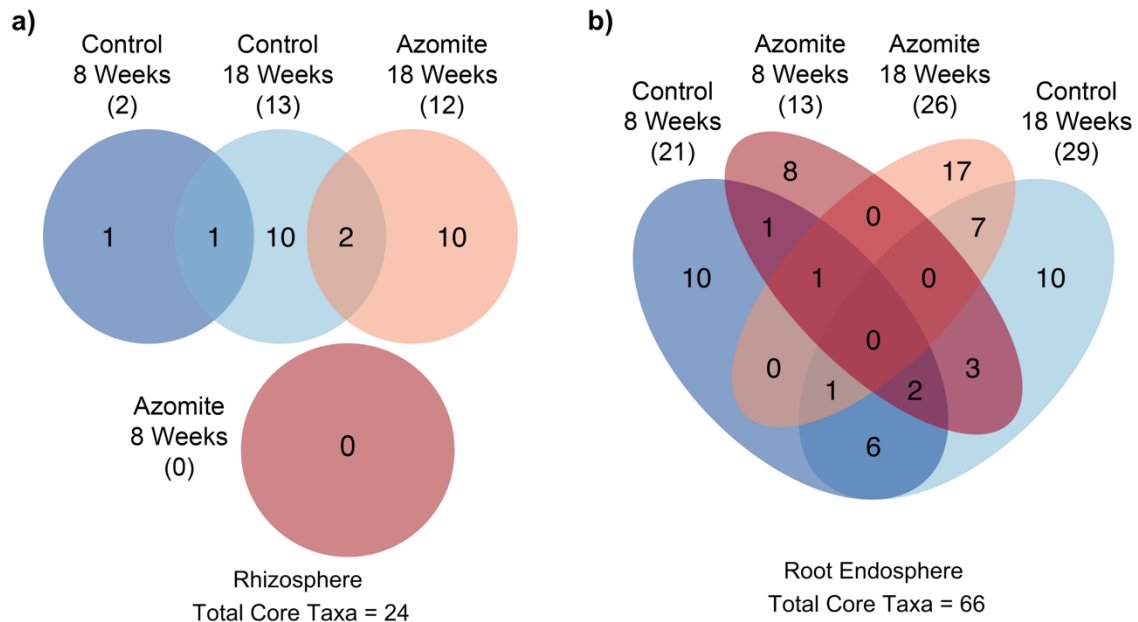
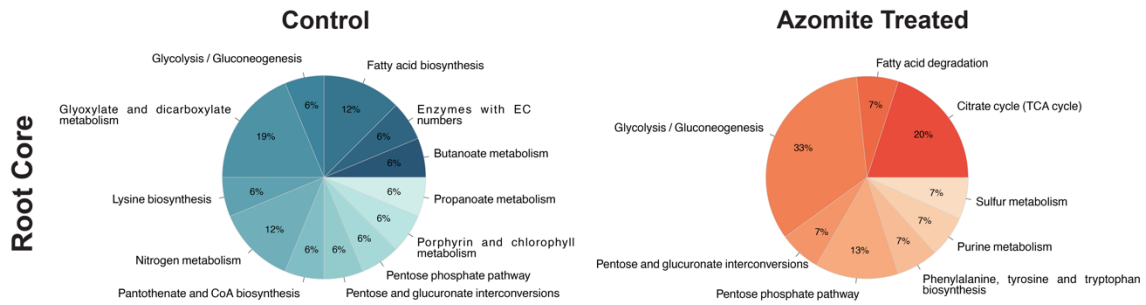


Figure 5

a) Functions that increase at 8 weeks



b) Functions that increase at 18 weeks

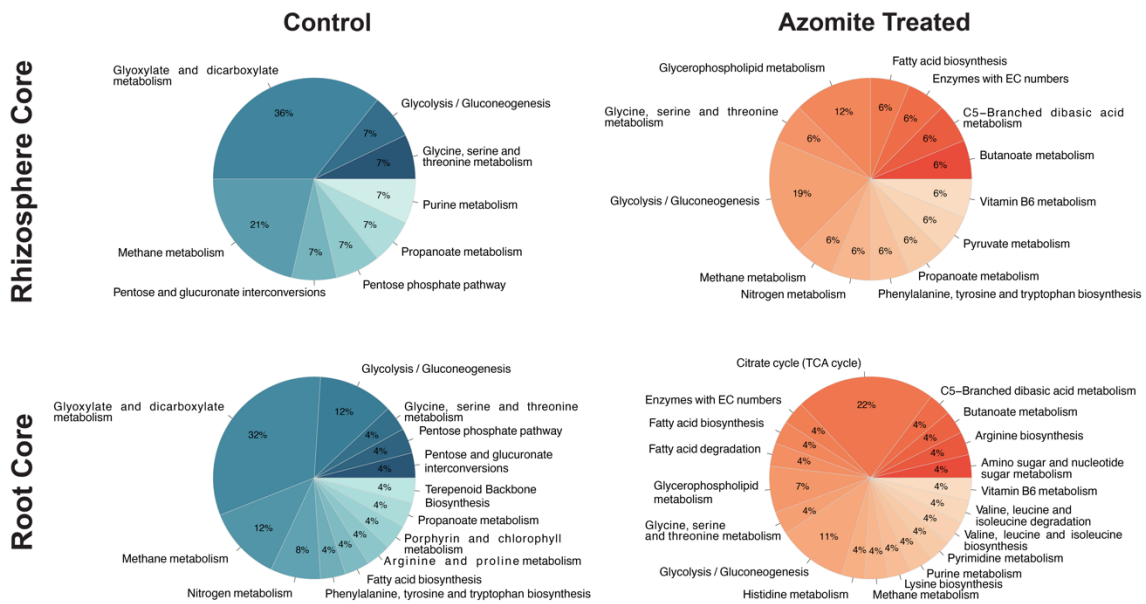
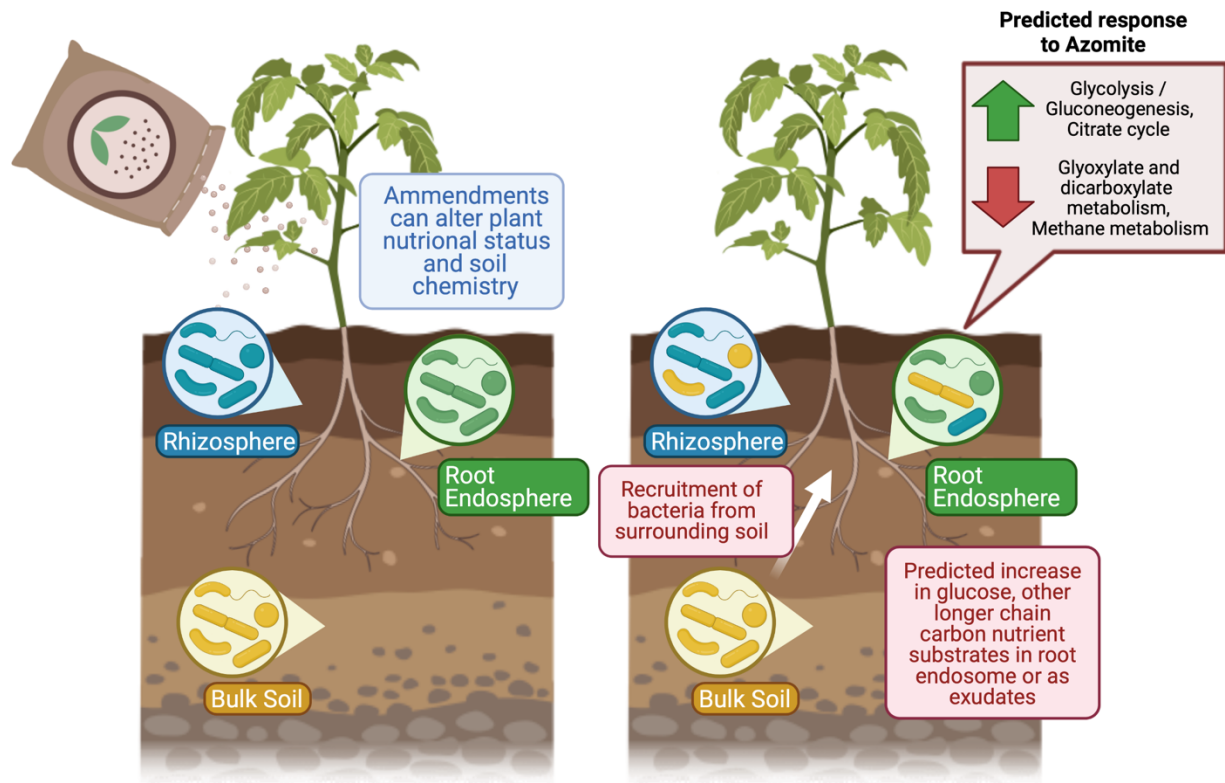


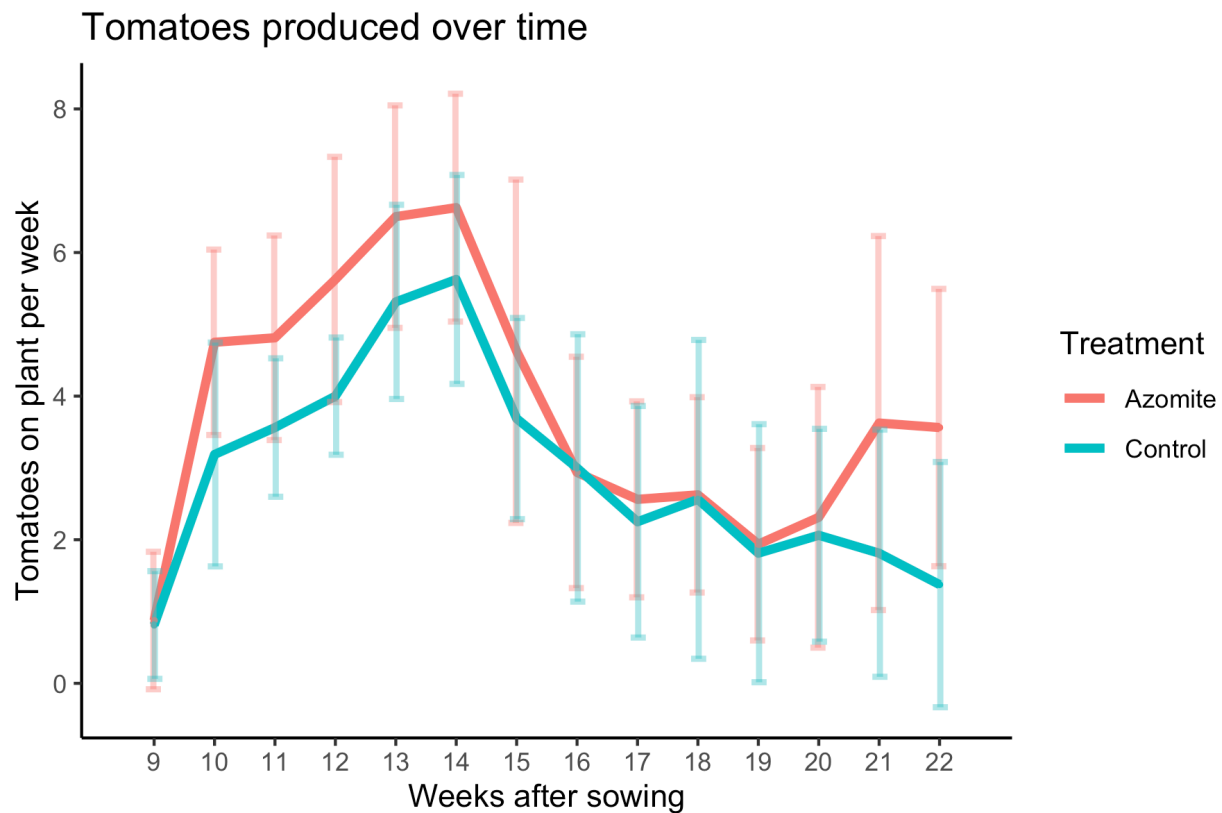
Figure 6



Supplemental Material

Mehlferber et al. (2021) Temporally selective modification of the tomato rhizosphere and root microbiome by a dacitic tuff breccia (volcanic ash) containing minerals and trace elements.

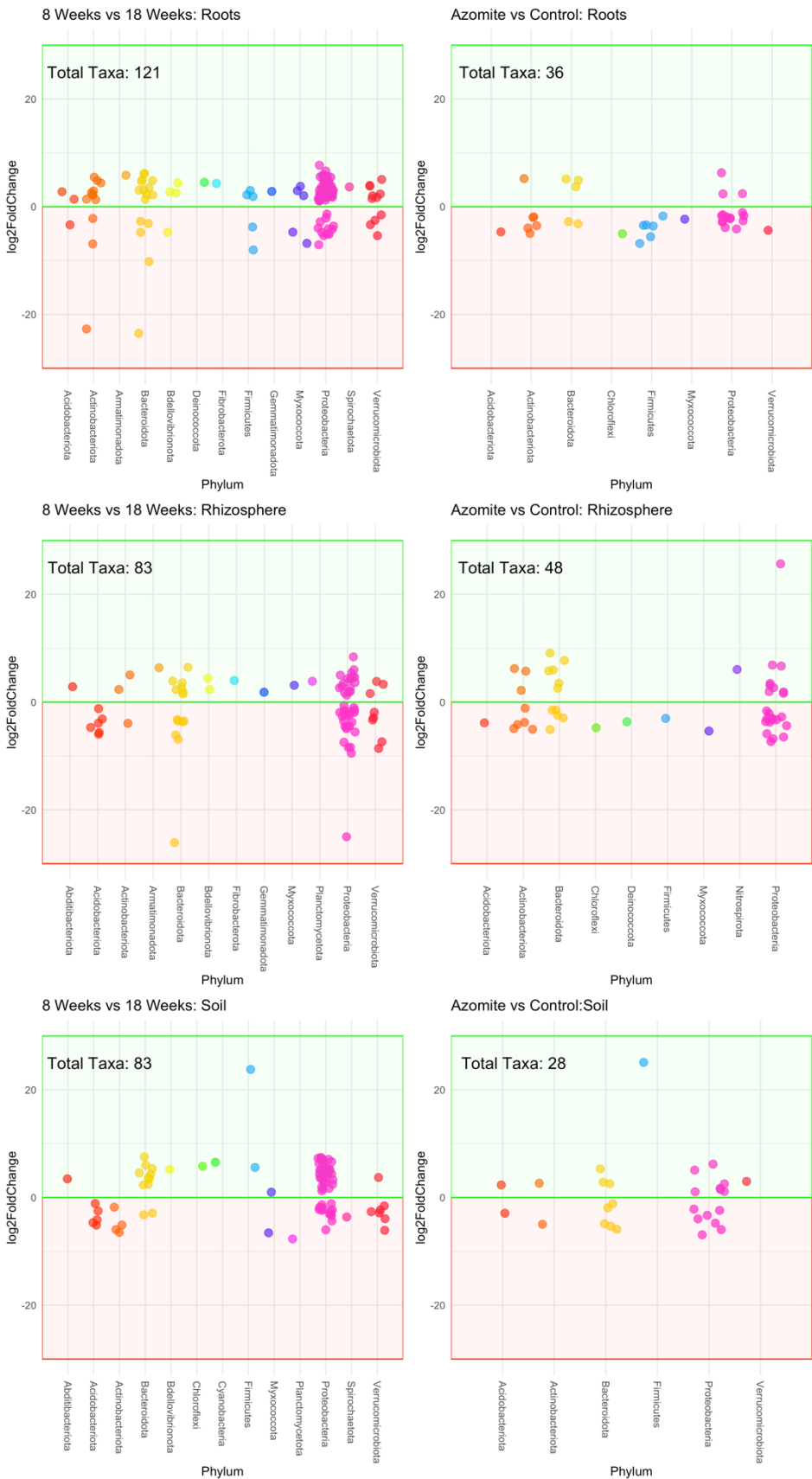
Supplemental Figure 1



SM Fig 1

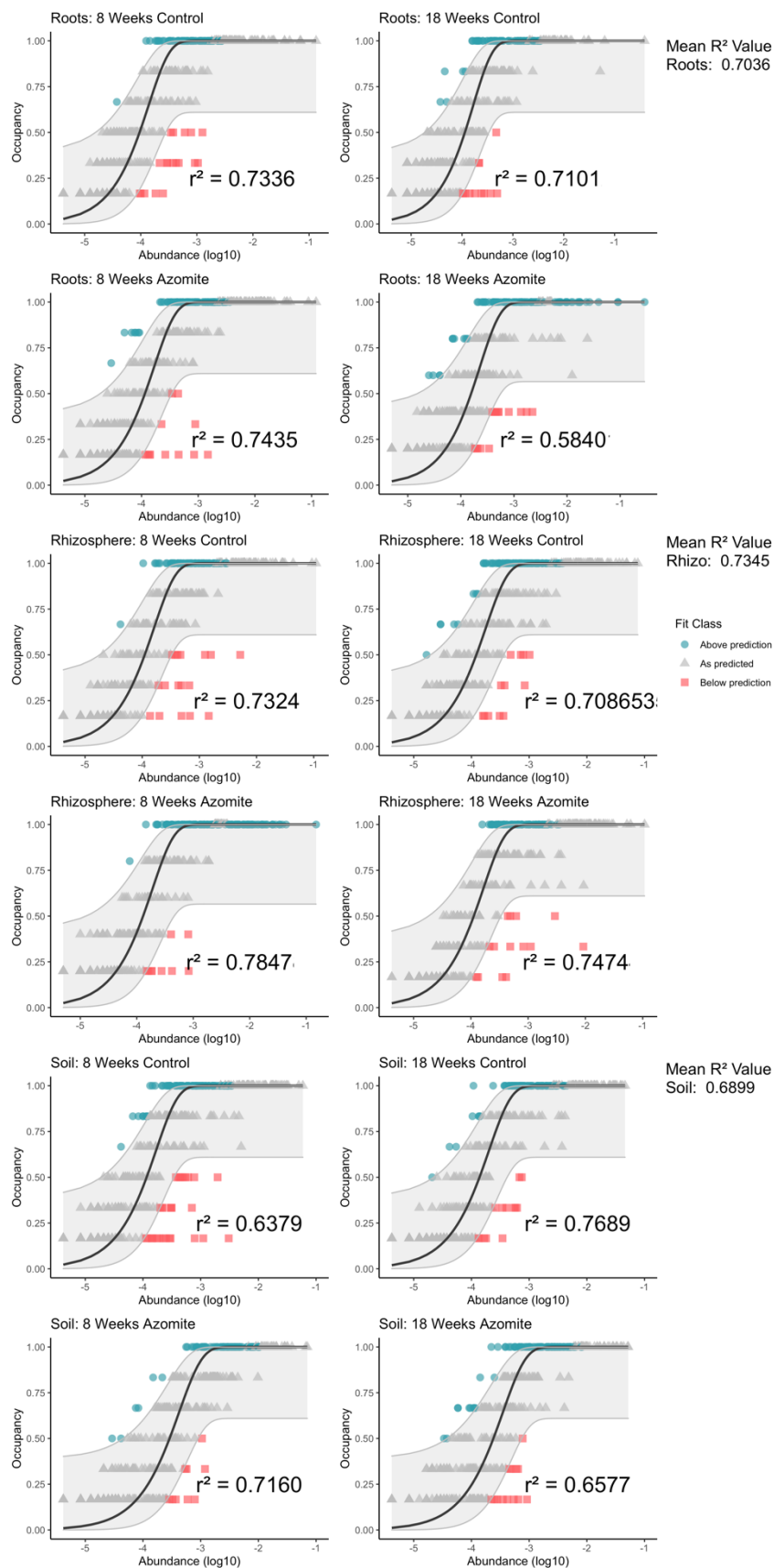
The total number of tomatoes counted per plant weekly are plotted. Treatment with Azomite increased the number of tomatoes produced per plant. Weeks after sowing was determined from days after sowing, corresponding to the day of counting. Tomatoes were harvested in weeks 15 and 18 for additional analyses, resulting in the reduction in the number of tomatoes counted in the following weeks. Analyzed via ANOVA, N=16 plants/treatment ($p < 0.01$).

Supplemental Figure 2



SM Fig 2
Significantly differentially abundant taxa in each compartment across time (left panels) and Azomite treatment (right panels), as identified by DESeq2. For the comparison between 8 and 18 weeks the taxa in the highlighted green box are at increased abundance at 18 weeks compared to 8 weeks, and the taxa in the highlighted red box are at decreased abundance at 18 weeks when compared to 8 weeks. For the comparisons between Azomite and Control the taxa in the green box are at increased abundance in the Azomite treatment samples, while the taxa in the red box are at decreased abundance compared to the controls. Overall, there are more differentially abundant taxa when comparing across time than Azomite treatment, with the greatest number of taxa differing in the roots over time. See SM Table 1 for the numbers of taxa that increased or decreased in abundance.

Supplemental Figure 3

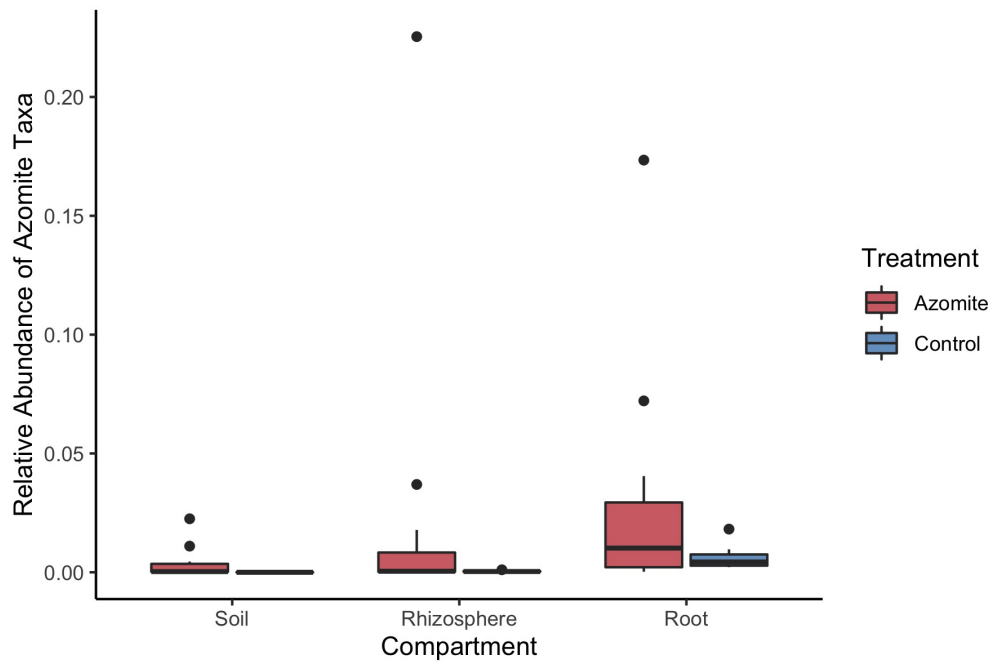


SM Fig 3

Abundance occupancy relationship and associated mean (r^2) values within each compartment across time and Azomite treatment. The line represents the predicted values based on the sloan neutral model, with a 95% confidence interval highlighted in grey. The taxa that fall above (blue) and below (red) their predicted values are highlighted and represent deviations from the neutral model and the possibility that they may be actively selected for (above the line, blue) or against (below the line, red). The mean R^2 values which represent the goodness of fit for the data to the predict slope of the neutral model are roughly similar across compartments.

Supplemental Figure 4

Relative abundance of taxa found in Azomite fertilizer but not bulk soil of control plants.

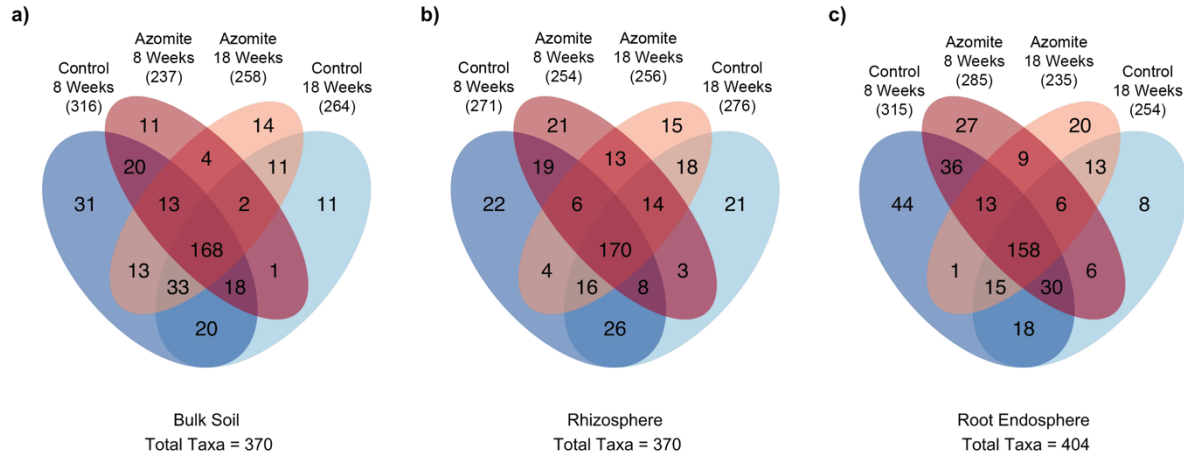


SM Fig 4

The mean relative abundance of taxa that were found to be present in the sequenced Azomite fertilizer, but not in the bulk soil of control plants. There was no significant difference in the relative abundance of these taxa across any of the compartments. In total, there were 435 unique taxa identified in the sequenced Azomite and 443 unique taxa in the bulk soil of control plants. Of those taxa, 272 were shared by both Azomite and bulk soil. Duplicate samples of Azomite Granular and Azomite Ultrafine collected from the original bags that were used in this study were subjected to 16s rRNA amplification and sequencing as described in Material and Methods. Genus level lists of the taxa present in Azomite Granular and Ultrafine are provided in SM Tables 2 and 3.

Supplemental Figure 5

Overlap between microbes in different compartments between control and treated samples at the two time points tested



SM Fig 5

Total number of taxa shared in each compartment across treatment and time. Grouped at the genus level there were 370 total taxa across all bulk soil (a) and Rhizosphere treatments (b), and 404 in the Roots (c). Approximately half of the taxa in each compartment were present across all treatments and timepoints.

Supplemental Table 1.

Compartment	Comparison	Compared Across	Increased	Decreased	Total
Roots	Time	18 Weeks vs 8 Weeks	30	91	121
	Treatment	Azomite vs Control	7	29	36
Rhizosphere	Time	18 Weeks vs 8 Weeks	45	38	83
	Treatment	Azomite vs Control	19	29	48
Soil	Time	18 Weeks vs 8 Weeks	34	49	83
	Treatment	Azomite vs Control	14	14	28

Number of taxa exhibiting significant changes in their differential abundance in each compartment across time and in response to Azomite, as identified by DESeq2. Values of increase or decrease in abundance are plotted in SM Fig2.

Supplemental Table 2.

List of taxa in the Azomite Granular product and the number of reads that match each sequence. Duplicate samples (AzG1 and AzG2) were analyzed. Taxa (ASV) are listed from highest to lowest number of reads obtained from the two samples.

Supplemental Table 3.

List of taxa in the Azomite Granular product and the number of reads that match each sequence. Duplicate samples (AzU1 and AzU2) were analyzed. Taxa (ASV) are listed from highest to lowest number of reads obtained from the two samples.

Supplemental Table 2

List of taxa in the Azomite Granular product and the number of reads that match to each sequence. Duplicate samples (AzG1 and AzG2) were analyzed. Taxa (ASV) are listed from highest to lowest number of reads obtained from the two samples.

	ASV	AzG1	AzG2	Kingdom	Phylum	Class	Order	Family	Genus
8	ASV13	48564	54891	Bacteria	Actinobacteriota	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Saccharopolyspora
101	ASV685	5896	7115	Bacteria	Actinobacteriota	Actinobacteria	Propionibacteriales	Nocardioidaceae	Nocardioides
66	ASV313	4452	6507	Bacteria	Actinobacteriota	Actinobacteria	Micromonosporales	Micromonosporaceae	Micromonospora
51	ASV196	2979	3010	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylobacterium-Methylorubrum
2	ASV3	2038	2575	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
7	ASV11	1775	2398	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Micrococcaceae	Pseudarthrobacter
17	ASV37	1425	1123	Bacteria	Actinobacteriota	Actinobacteria	Streptomycetales	Streptomycetaceae	Streptomyces
11	ASV24	1594	873	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus
132	ASV1150	2098	86	Bacteria	Proteobacteria	Gammaproteobacteria	Steroidobacterales	Steroidobacteraceae	Steroidobacter
200	ASV3047	844	793	Bacteria	Actinobacteriota	Thermoleophilia	Solirubrobacterales	Solirubrobacteraceae	Solirubrobacter
158	ASV1738	731	725	Bacteria	Actinobacteriota	Actinobacteria	Streptosporangiales	Thermomonosporaceae	Actinomadura
99	ASV660	496	769	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	Cupriavidus
76	ASV383	1117	145	Bacteria	Firmicutes	Bacilli	Paenibacillales	Paenibacillaceae	Paenibacillus
221	ASV4146	1170	83	Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	Anaerolinea
159	ASV1744	322	836	Bacteria	Actinobacteriota	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Pseudonocardia
164	ASV1820	549	522	Bacteria	Actinobacteriota	Actinobacteria	Corynebacteriales	Nocardiaceae	Nocardia
111	ASV782	211	832	Bacteria	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	Halomonas
71	ASV330	697	275	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium
172	ASV1975	437	526	Bacteria	Actinobacteriota	Actinobacteria	Propionibacteriales	Nocardioidaceae	Marmoricola
202	ASV3095	424	515	Bacteria	Actinobacteriota	Thermoleophilia	Gaiellales	Gaiellaceae	Gaiella
118	ASV940	673	112	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Oxalobacteraceae	Noviherbaspirillum
120	ASV957	328	396	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Promicromonosporaceae	Promicromonospora
42	ASV156	163	506	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
196	ASV2776	512	153	Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylocaldum
1	ASV1	430	186	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Micrococcaceae	Arthrobacter
193	ASV2668	282	282	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Yonghaparkia
84	ASV445	525	0	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Verrucomicrobiales	Rubritaleaceae	Luteolibacter
137	ASV1208	252	259	Bacteria	Actinobacteriota	Actinobacteria	Frankiales	Geodermatophilaceae	Blastococcus
14	ASV31	159	302	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter
31	ASV107	216	214	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
203	ASV3195	358	54	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Dermabacteraceae	Brachybacterium
98	ASV629	144	258	Bacteria	Acidobacteriota	Acidobacteriae	Acidobacteriales	Acidobacteriaceae_(Subgroup_1)	Granulicella
74	ASV362	306	89	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Chthoniobacterales	Chthoniobacteraceae	Chthoniobacter
61	ASV271	137	255	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia
109	ASV760	141	239	Bacteria	Actinobacteriota	Actinobacteria	Propionibacteriales	Nocardioidaceae	Aeromicrobium
154	ASV1671	126	254	Bacteria	Actinobacteriota	Thermoleophilia	Solirubrobacterales	Solirubrobacteraceae	Conexibacter
70	ASV328	126	238	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Ellin6055
90	ASV545	161	202	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Geobacillus
35	ASV129	269	89	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Opitutales	Opitutaceae	Opitutus
75	ASV371	167	176	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Mesorhizobium
242	ASV5390	342	0	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Micrococcaceae	Citricoccus
107	ASV741	42	298	Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Microscillaceae	Chryseolinea
261	ASV6344	51	288	Bacteria	Actinobacteriota	Rubrobacteria	Rubrobacterales	Rubrobacteriaceae	Rubrobacter
65	ASV307	113	223	Bacteria	Proteobacteria	Alphaproteobacteria	Reyranellales	Reyraneliaceae	Reyranella
40	ASV148	333	0	Bacteria	Gemmatimonadota	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
243	ASV5391	333	0	Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Cyclobacteriaceae	Marinoscillum
82	ASV422	155	167	Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	Rheinheimera
222	ASV4166	320	0	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Rhodocyclaceae	Azoarcus
189	ASV2565	239	70	Bacteria	Firmicutes	Bacilli	Paenibacillales	Paenibacillaceae	Cohnella
224	ASV4240	214	94	Bacteria	Firmicutes	Clostridia	Clostridia_or	Hungateiclostridiaceae	HN-HF0106
289	ASV8544	218	88	Bacteria	Actinobacteriota	Actinobacteria	Micromonosporales	Micromonosporaceae	Longispora
46	ASV171	187	109	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas
100	ASV679	224	72	Bacteria	Actinobacteriota	Acidimicrobiia	Microtrichales	Iamiaceae	Iamia
155	ASV1713	87	201	Bacteria	Actinobacteriota	Actinobacteria	Propionibacteriales	Nocardioidaceae	Kribbella
215	ASV3863	190	97	Bacteria	Myxococcota	Myxococcia	Myxococcales	Vulgatibacteraceae	Vulgatibacter
249	ASV5583	269	0	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Paraliobacillus
254	ASV6042	194	61	Bacteria	Actinobacteriota	Actinobacteria	Micromonosporales	Micromonosporaceae	Luedemannella
150	ASV1554	85	168	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Microbacterium
97	ASV608	93	158	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Roseomonas
129	ASV1087	214	25	Bacteria	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Pseudohongiellaceae	Blyi10
106	ASV736	193	41	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Pseudogracilibacillus
29	ASV102	233	0	Bacteria	Acidobacteriota	Acidobacteriae	Solibacterales	Solibacteraceae	Candidatus_Solibacter
32	ASV114	10	221	Bacteria	Myxococcota	Polyangia	Haliangiales	Haliangiaceae	Haliangium
39	ASV141	122	106	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Galbitalea
18	ASV38	226	0	Bacteria	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_Ince	Unknown_Family	Acidibacter
140	ASV1231	144	80	Bacteria	Actinobacteriota	Actinobacteria	Corynebacteriales	Mycobacteriaceae	Mycobacterium
131	ASV1116	45	173	Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planomicrobium

87	ASV462	0	217	Bacteria	Bacteroidota	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
281	ASV7931	149	68	Bacteria	Bacteroidota	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Anseongella
235	ASV4903	216	0	Bacteria	Chloroflexi	Chloroflexia	Thermomicrobiales	Thermomicrobiaceae	Sphaerobacter
269	ASV6817	5	204	Bacteria	Proteobacteria	Alphaproteobacteria	Kiloniellales	Kiloniellaceae	Pelagibius
170	ASV1935	93	111	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Microvirga
252	ASV6013	36	164	Bacteria	Actinobacteriota	Actinobacteria	Propionibacteriales	Nocardiodaceae	Actinopolymorpha
72	ASV339	177	22	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Rhodoplanes
247	ASV5531	0	199	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Nitrobacter
236	ASV4921	155	43	Bacteria	Actinobacteriota	Actinobacteria	Streptosporangiales	Nocardiodaceae	Nocardiosis
64	ASV296	185	0	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingopyxis
88	ASV472	185	0	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Altererythrobacter
260	ASV6297	17	167	Bacteria	Actinobacteriota	Actinobacteria	Propionibacteriales	Nocardiodaceae	Tenggerimyces
24	ASV76	179	0	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Opitutales	Opitaceae	Lacunisphaera
183	ASV2437	172	5	Bacteria	Bdellovibrionota	Bdellovibrionia	Bdellovibrionales	Bdellovibrionaceae	OM27_clade
190	ASV2609	176	0	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Arachidicoccus
208	ASV3398	108	68	Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Hymenobacteraceae	Adhaeribacter
21	ASV48	68	107	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Lelliottia
95	ASV605	70	96	Bacteria	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_Ince	Unknown_Family	Candidatus_Ovatusbacter
244	ASV5451	31	134	Bacteria	Firmicutes	Bacilli	Paenibacillales	Paenibacillaceae	Thermobacillus
20	ASV44	148	13	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Dokdonella
52	ASV200	77	81	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiales_Incertae_Sedis	Bauldia
86	ASV461	143	10	Bacteria	Actinobacteriota	Acidimicrobia	Microtrichales	Ilumatobacteraceae	CL500-29_marine_group
209	ASV3665	52	101	Bacteria	Gemmatimonadota	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Roseisolibacter
176	ASV2101	0	152	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Roseimicrobium
37	ASV134	107	43	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Methylophilaceae	Methylobacillus
96	ASV606	124	26	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Nitrosomonadaceae	MND1
186	ASV2482	127	21	Bacteria	Myxococcota	Polyangia	Polyangiales	Polyangiaceae	Pajaroellobacter
4	ASV7	132	15	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Devosiaceae	Devosia
267	ASV6694	103	43	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Filomicrobium
28	ASV99	111	30	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Pseudolabrys
218	ASV4091	138	3	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium
265	ASV6654	105	36	Bacteria	Acidobacteriota	Vicinamibacteria	Vicinamibacterales	Vicinamibacteraceae	Luteitalea
53	ASV204	121	18	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium
143	ASV1387	135	0	Bacteria	Sumerlaeota	Sumerlaeia	Sumerlaeales	Sumerlaeaceae	Sumerlaea
91	ASV549	132	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Pedomicrobium
283	ASV8168	60	70	Bacteria	Actinobacteriota	Actinobacteria	Propionibacteriales	Propionibacteriaceae	Jiangella
299	ASV10347	130	0	Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Cyclobacteriaceae	Imperialibacter
226	ASV4337	53	75	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Intrasporangiaceae	Lapillicoccus
94	ASV581	83	41	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Dyella
113	ASV824	45	77	Bacteria	Firmicutes	Bacilli	Staphylococcales	Staphylococcaceae	Staphylococcus
284	ASV8195	83	39	Bacteria	Acidobacteriota	Vicinamibacteria	Vicinamibacterales	Vicinamibacteraceae	Vicinamibacter
296	ASV9436	0	120	Bacteria	Methyломirabilota	Methyломirabilia	Methyломirabiales	Methyломirabillaceae	MIZ17
12	ASV25	57	62	Bacteria	Bacteroidota	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
278	ASV7736	115	0	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	Spirochaetaceae	Spirochaeta
27	ASV90	41	72	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Luteimonas
204	ASV3196	61	52	Bacteria	Acidobacteriota	Blastocatellia	Pyrinomonadales	Pyrinomonadaceae	RB41
133	ASV1172	79	31	Bacteria	Actinobacteriota	Actinobacteria	Streptosporangiales	Streptosporangiaceae	Nonomurea
285	ASV8377	110	0	Bacteria	Desulfobacterota	Syntrophobacteria	Syntrophobacterales	Syntrophobacteraceae	Syntrophobacter
237	ASV5063	43	65	Bacteria	Actinobacteriota	Actinobacteria	Streptosporangiales	Thermomonosporaceae	Actinoallomurus
135	ASV1197	107	0	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
308	ASV13174	58	47	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methyloiligellaceae	Methyloceanibacter
191	ASV2636	104	0	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Demequinaceae	Demequina
212	ASV3726	0	103	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Alcaligenaceae	Candidimonas
251	ASV5804	0	103	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Aurantimonas
168	ASV1880	52	49	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Intrasporangiaceae	Ornithinimicrobium
207	ASV3271	49	52	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Ureibacillus
274	ASV7321	87	14	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Chthoniobacterales	Chthoniobacteraceae	Candidatus_Udaebacter
149	ASV1500	25	75	Bacteria	Actinobacteriota	Actinobacteria	Propionibacteriales	Propionibacteriaceae	Cutibacterium
174	ASV2072	100	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Pseudorhodoplanes
180	ASV2292	83	17	Bacteria	Actinobacteriota	Actinobacteria	Frankiales	Sporichthyaceae	Sporichthya
316	ASV15716	100	0	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Marinilabiliaceae	Ruminofilibacter
264	ASV6558	0	99	Bacteria	Actinobacteriota	Thermoleophilina	Solirubrobacterales	Solirubrobacteraceae	JCM_18997
287	ASV8437	99	0	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Micrococcaceae	Nesterenkonia
290	ASV8545	25	73	Bacteria	Actinobacteriota	Actinobacteria	Micromonosporales	Micromonosporaceae	Phytohabitans
26	ASV81	97	0	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Ramlibacter
230	ASV4679	96	1	Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Lysinibacillus
119	ASV948	25	71	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Caenimonas
263	ASV6493	68	28	Bacteria	Actinobacteriota	Actinobacteria	Pseudonocardiales	Pseudonocardaceae	Actinophytocola
136	ASV1198	0	94	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Parafilimonas
93	ASV561	83	9	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Taibaiella
181	ASV2299	16	76	Bacteria	Nitrospirota	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira

292	ASV8908	92	0	Bacteria	Firmicutes	Clostridia	Clostridia_or	Hungateiclostridiaceae	Hungateiclostridium
25	ASV77	90	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Bradyrhizobium
114	ASV846	23	65	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacterales	Pectobacteriaceae	Pectobacterium
127	ASV1069	0	88	Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Sporosarcina
50	ASV194	45	42	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Oceanobacillus
220	ASV4126	61	25	Bacteria	Myxococcota	Polyangia	Nannocystales	Nannocystaceae	Nannocystis
6	ASV10	85	0	Bacteria	Proteobacteria	Gammaproteobacteria	Cellvibrionales	Cellvibrionaceae	Cellvibrio
102	ASV690	11	74	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	PMMR1
282	ASV8103	84	0	Bacteria	Actinobacteriota	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Saccharothrix
295	ASV9377	0	84	Bacteria	Actinobacteriota	Actinobacteria	Kineosporiales	Kineosporiaceae	Kineococcus
175	ASV2081	55	28	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Intrasporangiaceae	Janibacter
62	ASV277	82	0	Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Microscillaceae	Ohtaekwangia
79	ASV410	81	0	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	Limnobacter
141	ASV1290	81	0	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Chitinophaga
146	ASV1419	6	75	Bacteria	Actinobacteriota	Actinobacteria	Corynebacterales	Dietziaceae	Dietzia
234	ASV4843	81	0	Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planococcus
266	ASV6671	34	47	Bacteria	Actinobacteriota	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Amycolatopsis
134	ASV1184	0	79	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Citrobacter
298	ASV10184	78	0	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Cellulomonadaceae	Actinotalea
80	ASV412	72	0	Bacteria	Actinobacteriota	Actinobacteria	Corynebacterales	Nocardiaceae	Rhodococcus
54	ASV223	38	33	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Rhodoferax
128	ASV1081	63	8	Bacteria	Bdellovibrionota	Bdellovibrionia	Bacteriovoracales	Bacteriovoracaceae	Peredibacter
43	ASV159	70	0	Bacteria	Proteobacteria	Alphaproteobacteria	Ferrovibrionales	Ferrovibrionaceae	Ferrovibrio
122	ASV968	70	0	Bacteria	Chloroflexi	Chloroflexia	Chloroflexales	Herpetosiphonaceae	Herpetosiphon
139	ASV1228	28	42	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter
276	ASV7567	0	70	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylovirgula
5	ASV9	0	69	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Pelomonas
19	ASV42	69	0	Bacteria	Proteobacteria	Alphaproteobacteria	Dongiales	Dongiaceae	Dongia
147	ASV1442	69	0	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Cerasibacillus
30	ASV105	68	0	Bacteria	Acidobacteriota	Acidobacteriae	Bryobacterales	Bryobacteraceae	Bryobacter
36	ASV131	50	18	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium
130	ASV1091	68	0	Bacteria	Acidobacteriota	Thermoanaerobaculia	Thermoanaerobaculales	Thermoanaerobaculaceae	Subgroup_10
73	ASV347	67	0	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Rhizobacter
199	ASV2943	67	0	Bacteria	Actinobacteriota	Actinobacteria	Frankiales	Frankiaceae	Jatrophihabitans
303	ASV11544	67	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhodobiaceae	Tepidamorphus
160	ASV1766	51	14	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Cellulomonadaceae	Cellulomonas
108	ASV757	50	14	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Micrococcaceae	Kocuria
49	ASV191	62	0	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Nitrosomonadaceae	Nitrosospira
227	ASV4372	0	62	Bacteria	Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	Aerococcus
163	ASV1809	49	10	Bacteria	Actinobacteriota	Actinobacteria	Frankiales	Nakamurellaceae	Nakamurella
194	ASV2669	59	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Ochrobactrum
312	ASV14434	59	0	Bacteria	Actinobacteriota	Actinobacteria	Euzebyales	Euzebyaceae	Euzebya
156	ASV1734	14	44	Bacteria	Acidobacteriota	Blastocatellia	Blastocatellales	Blastocatellaceae	JGI_0001001-H03
253	ASV6031	57	0	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Alcaligenaceae	Bordetella
305	ASV11898	56	0	Bacteria	Actinobacteriota	Actinobacteria	Frankiales	Frankiaceae	Frankia
58	ASV239	55	0	Bacteria	Bdellovibrionota	Bdellovibrionia	Bdellovibrionales	Bdellovibrionaceae	Bdellovibrio
311	ASV14429	40	15	Bacteria	Actinobacteriota	Thermoleophilia	Solirubrobacterales	Solirubrobacteraceae	Parviterribacter
152	ASV1581	53	0	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Rhodoglobus
179	ASV2220	12	39	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Promicromonosporaceae	Cellulosimicrobium
286	ASV8392	51	0	Bacteria	Firmicutes	Bacilli	Thermoactinomycetales	Thermoactinomycetaceae	Lihuaxuella
59	ASV246	9	41	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Flavisolibacter
280	ASV7812	50	0	Bacteria	Actinobacteriota	Actinobacteria	Streptosporangiales	Thermomonosporaceae	Thermostaphylospora
306	ASV12707	0	50	Bacteria	Actinobacteriota	Actinobacteria	Streptomycetales	Streptomycetaceae	Allostreptomyces
44	ASV161	0	49	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Terrimonas
201	ASV3053	49	0	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Segetibacter
48	ASV178	0	48	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Porphyrobacter
250	ASV5785	48	0	Bacteria	Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	Haemophilus
307	ASV13171	47	0	Bacteria	Firmicutes	Clostridia	Eubacteriales	Garciellaceae	Rhabdanaerobium
9	ASV18	46	0	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Leptothrix
77	ASV393	46	0	Bacteria	Proteobacteria	Alphaproteobacteria	Micropepsales	Micropepsaceae	Micropepsis
121	ASV958	46	0	Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Cytophagaceae	Sporocytophaga
184	ASV2456	45	0	Bacteria	Actinobacteriota	Actinobacteria	Streptosporangiales	Streptosporangiaceae	Sphaerisporangium
288	ASV8503	44	0	Bacteria	Proteobacteria	Gammaproteobacteria	Cellvibrionales	Porticoccaceae	C1-B045
310	ASV13682	44	0	Bacteria	Proteobacteria	Gammaproteobacteria	Granulosicoccales	Granulosicoccales_fa	Methylohalomonas
47	ASV177	43	0	Bacteria	Acidobacteriota	Acidobacteriae	Acidobacteriae_or	Acidobacteriae_fa	Paludibaculum
293	ASV9216	43	0	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Bogoriellaceae	Georgenia
125	ASV1032	0	42	Bacteria	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Alcanivoracaceae1	Alcanivorax
83	ASV444	40	0	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Amnibacterium
144	ASV1398	0	40	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Alcaligenaceae	Achromobacter
271	ASV7019	40	0	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Saprospiraceae	Aureispira
63	ASV281	39	0	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Opitutales	Opitutaceae	Alterococcus

166	ASV1876	0	39	Bacteria	Actinobacteriota	Actinobacteria	Micromonosporales	Micromonosporaceae	Dactylosporangium
173	ASV2038	39	0	Bacteria	Firmicutes	Clostridia	Peptostreptococcales-Tissie	Peptostreptococcales-Tissierellales_fa	Tepidimicrobium
337	ASV111	0	39	Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Spirosomaceae	Arcicella
214	ASV3826	38	0	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Craurococcus-Caldovatus
313	ASV14829	38	0	Bacteria	Actinobacteriota	Actinobacteria	Propionibacteriales	Propionibacteriaceae	Haloactinopolyspora
126	ASV1061	37	0	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Plot4-2H12
177	ASV2168	32	5	Bacteria	Deinococcota	Deinococci	Deinococcales	Trueperaceae	Truepera
178	ASV2192	37	0	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Tahibacter
258	ASV6259	0	37	Bacteria	Firmicutes	Bacilli	Paenibacillales	Paenibacillaceae	Ammoniphilus
259	ASV6271	36	0	Bacteria	Firmicutes	Bacilli	Thermoactinomycetales	Thermoactinomycetaceae	Melghirimyces
22	ASV66	35	0	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Niastella
55	ASV224	35	0	Bacteria	Bdellovibrionota	Oligoflexia	Oligoflexales	Oligoflexales_fa	Oligoflexus
182	ASV2307	0	35	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Micrococcaceae	Enteractinococcus
187	ASV2490	12	22	Bacteria	Actinobacteriota	Actinobacteria	Glycomycetales	Glycomycetaceae	Glycomyces
188	ASV2495	0	34	Bacteria	Proteobacteria	Gammaproteobacteria	Salinisphaerales	Solimonadaceae	Solimonas
56	ASV225	33	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Hyphomicrobium
138	ASV1218	33	0	Bacteria	Firmicutes	Bacilli	Paenibacillales	Paenibacillaceae	Ammoniiibacillus
34	ASV126	32	0	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Caulobacter
85	ASV459	0	32	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Afipia
195	ASV2672	0	32	Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Psychrobacillus
229	ASV4656	32	0	Bacteria	Actinobacteriota	Actinobacteria	Streptosporangiales	Thermomonosporaceae	Actinocorallia
302	ASV11097	32	0	Bacteria	Firmicutes	Clostridia	Peptostreptococcales-Tissie	Sedimentibacteraceae	Sedimentibacter
318	ASV16175	0	32	Bacteria	Chloroflexi	Chloroflexia	Thermomicrobiales	Thermomicrobiaceae	Nitrolancea
3	ASV6	0	31	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas
162	ASV1804	12	19	Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter
185	ASV2457	0	31	Bacteria	Actinobacteriota	Actinobacteria	Frankiales	Geodermatophilaceae	Modestobacter
238	ASV5178	31	0	Bacteria	Firmicutes	Bacilli	Lactobacillales	Vagococcaceae	Vagococcus
245	ASV5484	31	0	Bacteria	Actinobacteriota	Actinobacteria	Streptosporangiales	Thermomonosporaceae	Thermobispora
23	ASV71	30	0	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Chitinimonadaceae	Chitinimonas
157	ASV1735	21	9	Bacteria	Acidobacteriota	Blastocatellia	Blastocatellales	Blastocatellaceae	Stenotrophobacter
217	ASV3995	7	23	Bacteria	Actinobacteriota	Acidimicrobiia	Microtrichales	Ilumatobacteraceae	Ilumatobacter
319	ASV16724	0	30	Bacteria	Planctomycetota	Planctomycetes	Planctomycetales	Rubinisphaeraceae	Planctomicrobium
69	ASV319	29	0	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Rhodovastum
151	ASV1560	29	0	Bacteria	Acidobacteriota	Blastocatellia	Blastocatellales	Blastocatellaceae	Blastocatella
256	ASV6152	10	19	Bacteria	Actinobacteriota	Actinobacteria	Frankiales	Geodermatophilaceae	Geodermatophilus
89	ASV520	28	0	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacterales	Yersiniaceae	Serratia
145	ASV1416	14	14	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnoclostridium
320	ASV17247	28	0	Bacteria	Proteobacteria	Gammaproteobacteria	Nitrosococcales	Nitrosococcaceae	wb1-P19
105	ASV731	13	14	Bacteria	Deinococcota	Deinococci	Thermales	Thermaceae	Thermus
110	ASV777	26	0	Bacteria	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	Myxococcus
223	ASV4203	26	0	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Gryllotalpicola
45	ASV169	25	0	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Prosthecobacter
115	ASV858	25	0	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Dinghuibacter
213	ASV3791	25	0	Bacteria	Actinobacteriota	Actinobacteria	Frankiales	Acidothermaceae	Acidothermus
10	ASV23	23	0	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Methylophilaceae	Methylothenera
211	ASV3685	0	23	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Alkanindiges
68	ASV318	22	0	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Parafrigoribacterium
248	ASV5562	22	0	Bacteria	Firmicutes	Bacilli	Paenibacillales	Paenibacillaceae	Saccharibacillus
255	ASV6071	22	0	Bacteria	Actinobacteriota	Actinobacteria	Kineosporiales	Kineosporiaceae	Quadrisphaera
262	ASV6452	22	0	Bacteria	Firmicutes	Bacilli	Alicyclobacillales	Alicyclobacillaceae	Alicyclobacillus
171	ASV1968	21	0	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Nitrosomonadaceae	Ellin6067
324	ASV19502	21	0	Bacteria	Chloroflexi	Ktedonobacteria	Ktedonobacterales	Ktedonobacteraceae	1959-1
112	ASV818	20	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Paracoccus
148	ASV1456	20	0	Bacteria	Planctomycetota	Phycisphaerae	Phycisphaerales	Phycisphaeraceae	CL500-3
325	ASV19902	20	0	Bacteria	Firmicutes	Clostridia	Oscillospirales	Oscillospiraceae	Sporobacter
67	ASV315	9	10	Bacteria	Bacteroidota	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Mucilagibacter
123	ASV976	19	0	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Demequinaceae	Lysinimicrobium
206	ASV3229	19	0	Bacteria	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae	Weissella
277	ASV7569	0	19	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Agrococcus
294	ASV9349	19	0	Bacteria	Firmicutes	Bacilli	Thermoactinomycetales	Thermoactinomycetaceae	Thermoactinomyces
60	ASV257	18	0	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Opituales	Puniceicoccaceae	Cerasicoccus
124	ASV1001	18	0	Bacteria	Deinococcota	Deinococci	Deinococcales	Deinococcaceae	Deinococcus
321	ASV17972	18	0	Bacteria	Firmicutes	Clostridia	Peptostreptococcales-Tissie	Peptostreptococcales-Tissierellales_fa	Tissierella
326	ASV20789	18	0	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Dysgonomonadaceae	Fermentimonas
16	ASV35	17	0	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Asticcacaulis
153	ASV1656	0	17	Bacteria	Proteobacteria	Gammaproteobacteria	Coxiellales	Coxiellaceae	Coxiella
205	ASV3224	0	17	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylocystis
228	ASV4636	17	0	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacterium
304	ASV11647	17	0	Bacteria	Actinobacteriota	Actinobacteria	Micromonosporales	Micromonosporaceae	Plantactinospora
315	ASV15640	17	0	Bacteria	Actinobacteriota	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Saccharomonospora
327	ASV21292	0	17	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Glaciibacter

117	ASV931	16	0	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Pedosphaerales	Pedosphaeraceae	Ellin516
291	ASV8794	16	0	Bacteria	Firmicutes	Bacilli	Bacillales	Salisediminibacteriaceae	Salipaludibacillus
329	ASV21769	0	16	Bacteria	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Marinilactibacillus
273	ASV7219	15	0	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Methylophilaceae	UBA6140
142	ASV1334	14	0	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Polaromonas
167	ASV1879	0	14	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylocella
192	ASV2653	14	0	Bacteria	Planctomycetota	Planctomycetes	Pirellulales	Pirellulaceae	Pirellula
225	ASV4334	0	14	Bacteria	Actinobacteriota	Actinobacteria	Micromonosporales	Micromonosporaceae	Asanoa
241	ASV5266	14	0	Bacteria	Firmicutes	Clostridia	Oscillospirales	Ruminococcaceae	Ruminococcus
165	ASV1862	13	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Devosiaceae	Arsenicitalea
233	ASV4784	13	0	Bacteria	Firmicutes	Bacilli	Brevibacillales	Brevibacillaceae	Brevibacillus
257	ASV6159	13	0	Bacteria	Firmicutes	Bacilli	Alicyclobacillales	Alicyclobacillaceae	Tumebacillus
328	ASV21654	13	0	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Alcaligenaceae	Advenella
13	ASV28	12	0	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Puia
33	ASV122	12	0	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	SWB02
92	ASV558	12	0	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Variovorax
270	ASV6993	0	12	Bacteria	Proteobacteria	Alphaproteobacteria	Tistrellales	Geminicoccaceae	Candidatus_Alysiosphaera
322	ASV18041	0	12	Bacteria	Actinobacteriota	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Crossiella
323	ASV19040	12	0	Bacteria	Firmicutes	Bacilli	Thermoactinomycetales	Thermoactinomycetaceae	Shimazuella
330	ASV24315	0	12	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Neisseriaceae	Kingella
15	ASV34	0	11	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Sinibacillus
309	ASV13198	11	0	Bacteria	Firmicutes	Desulfotomaculia	Desulfotomaculales	Desulfotomaculales_fa	Pelotomaculum
332	ASV25047	0	11	Bacteria	Proteobacteria	Gammaproteobacteria	Nitrosococcales	Nitrosococcaceae	SZB85
78	ASV395	10	0	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Edaphobaculum
232	ASV4771	10	0	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Intrasporangiaceae	Ornithinococcus
331	ASV24327	10	0	Bacteria	Firmicutes	Desulfitobacteriia	Desulfitobacteriales	Desulfitobacteriaceae	Desulfosporosinus
333	ASV25812	10	0	Bacteria	Actinobacteriota	Actinobacteria	Streptosporangiales	Streptosporangiaceae	Sinosporangium
300	ASV10892	9	0	Bacteria	Planctomycetota	Planctomycetes	Pirellulales	Pirellulaceae	Pir4_lineage
314	ASV15077	9	0	Bacteria	Firmicutes	Clostridia	Eubacteriales	Garciellaceae	Garciella
334	ASV26671	0	9	Bacteria	Cyanobacteria	Cyanobacteriia	Cyanobacteriales	Chroococciidiopsaceae	Crinalium_SAG_22.89
216	ASV3978	0	8	Bacteria	Bacteroidota	Bacteroidia	Flavobacteriales	Weeksellaceae	Empedobacter
219	ASV4107	0	8	Bacteria	Acidobacteriota	Acidobacteriae	Acidobacteriales	Acidobacteriaceae_(Subgroup_1)	Acidipila
161	ASV1802	7	0	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Humibacter
169	ASV1889	7	0	Bacteria	Firmicutes	Bacilli	Staphylococcales	Staphylococcaceae	Macrococcus
246	ASV5505	0	7	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Aminobacter
38	ASV136	6	0	Bacteria	Firmicutes	Bacilli	Exiguobacterales	Exiguobacteraceae	Exiguobacterium
57	ASV227	6	0	Bacteria	Bacteroidota	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Sphingobacterium
104	ASV726	0	6	Bacteria	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Skermanella
198	ASV2911	6	0	Bacteria	Gemmatimonadota	Longimicrobia	Longimicrobiales	Longimicrobiaceae	YC-ZSS-LKJ147
297	ASV9620	6	0	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Chthoniobacterales	Xiphinematobacteraceae	Candidatus_Xiphinematobacter
240	ASV5221	5	0	Bacteria	Chloroflexi	Chloroflexia	Thermobaculales	Thermobaculaceae	Thermobaculum
272	ASV7129	5	0	Bacteria	Proteobacteria	Gammaproteobacteria	Diplorickettsiales	Diplorickettsiaceae	Aquicella
279	ASV7754	5	0	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Flaviaesturariibacter
335	ASV28309	5	0	Bacteria	Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae	Litorilinea
336	ASV29461	0	5	Bacteria	Bacteroidota	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Galbibacter
197	ASV2814	4	0	Bacteria	Patescibacteria	Saccharimonadia	Saccharimonadales	Saccharimonadaceae	TM7a
268	ASV6727	4	0	Bacteria	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Atopostipes
275	ASV7402	4	0	Bacteria	Actinobacteriota	Actinobacteria	Propionibacteriales	Propionibacteriaceae	Microlunatus
301	ASV11062	0	4	Bacteria	Bacteroidota	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Myroides
41	ASV149	3	0	Bacteria	Bacteroidota	Bacteroidia	Flavobacteriales	Weeksellaceae	Chryseobacterium
81	ASV420	3	0	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	Spirochaetaceae	Spirochaeta_2
103	ASV719	0	3	Bacteria	Planctomycetota	Phycisphaerae	Phycisphaerales	Phycisphaeraceae	SM1A02
210	ASV3684	3	0	Bacteria	Firmicutes	Bacilli	Thermoactinomycetales	Thermoactinomycetaceae	Planifilum
231	ASV4713	3	0	Bacteria	Planctomycetota	Planctomycetes	Gemmatales	Gemmataceae	Gemmata
317	ASV16089	3	0	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Prevotellaceae	Alloprevotella
116	ASV922	2	0	Bacteria	Proteobacteria	Alphaproteobacteria	Caedibacterales	Caedibacteraceae	Candidatus_Nucleicultrix
239	ASV5183	0	2	Bacteria	Bacteroidota	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Salinimicrobium

Supplemental Table 3.

List of taxa in the Azomite Granular product and the number of reads that match to each sequence. Duplicate samples (AzU1 and AzU2) were analyzed. Taxa (ASV) are listed from highest to lowest number of reads obtained from the two samples.

	ASV	AzU1	AzU2	Kingdom	Phylum	Class	Order	Family	Genus
12	ASV25	0	7936	Bacteria	Bacteroidota	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
2	ASV3	141	6317	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
15	ASV35	0	3952	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Asticcacaulis
9	ASV18	0	3794	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Leptothrix
49	ASV149	62	3529	Bacteria	Bacteroidota	Bacteroidia	Flavobacteriales	Weeksellaceae	Chryseobacterium
43	ASV129	0	3343	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Opitutales	Opitutaceae	Opitutus
116	ASV551	0	3060	Bacteria	Bacteroidota	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Nubsella
100	ASV445	0	2941	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Verrucomicrobiales	Rubritaleaceae	Luteolibacter
63	ASV204	0	2824	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium
6	ASV10	0	2821	Bacteria	Proteobacteria	Gammaproteobacteria	Cellvibrionales	Cellvibrionaceae	Cellvibrio
98	ASV443	0	2737	Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Spirosomaceae	Dyadobacter
28	ASV87	0	2449	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium
44	ASV131	0	2421	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium
10	ASV23	0	2258	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Methylophilaceae	Methylotenera
4	ASV7	67	2124	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Devosiaceae	Devosia
117	ASV561	0	1407	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Taibaiella
169	ASV1580	0	1373	Bacteria	Bacteroidota	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Arcticibacter
42	ASV126	14	1347	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Caulobacter
127	ASV685	1192	88	Bacteria	Actinobacteriota	Actinobacteria	Propionibacteriales	Nocardioideaceae	Nocardioides
149	ASV1085	0	1252	Bacteria	Armatimonadota	Fimbriimonadia	Fimbriimonadales	Fimbriimonadaceae	Fimbriimonas
92	ASV395	0	1228	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Edaphobaculum
7	ASV11	1001	58	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Micrococcaceae	Pseudarthrobacter
48	ASV148	28	948	Bacteria	Gemmatimonadota	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
53	ASV169	0	945	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Prostheco bacter
71	ASV266	0	941	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Opitutales	Opitutaceae	IMCC26134
36	ASV107	145	792	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
84	ASV330	0	915	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium
54	ASV171	14	877	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas
51	ASV159	0	841	Bacteria	Proteobacteria	Alphaproteobacteria	Ferrovibrionales	Ferrovibrionaceae	Ferrovibrio
248	ASV17	0	833	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacterales	Erwiniaceae	Pantoea
69	ASV239	0	826	Bacteria	Bdellovibrionota	Bdellovibrionia	Bdellovibrionales	Bdellovibrionaceae	Bdellovibrio
145	ASV968	0	789	Bacteria	Chloroflexi	Chloroflexia	Chloroflexales	Herpetosiphonaceae	Herpetosiphon
78	ASV296	0	705	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingopyxis
37	ASV108	0	695	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Methylophilaceae	Methylophilus
88	ASV362	18	665	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Chthoniobacterales	Chthoniobacteraceae	Chthoniobacter
163	ASV1333	0	683	Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Legionella
16	ASV37	496	173	Bacteria	Actinobacteriota	Actinobacteria	Streptomycetales	Streptomycetaceae	Streptomyces
24	ASV76	8	651	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Opitutales	Opitutaceae	Lacunisphaera
22	ASV60	0	645	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Oxalobacteraceae	Duganella
31	ASV95	0	631	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Aquabacterium
33	ASV99	129	484	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Pseudolabrys
104	ASV462	153	457	Bacteria	Bacteroidota	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
91	ASV391	0	564	Bacteria	Fibrobacterota	Fibrobacteria	Fibrobacterales	Fibrobacteraceae	possible_genus_04
35	ASV105	16	536	Bacteria	Acidobacteriota	Acidobacteriae	Bryobacterales	Bryobacteraceae	Bryobacter
39	ASV117	0	542	Bacteria	Bacteroidota	Bacteroidia	Flavobacteriales	Crocinitomicaceae	Fluviicola
45	ASV134	0	523	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Methylophilaceae	Methylobacillus
52	ASV161	10	495	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Terrimonas
121	ASV608	21	463	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Roseomonas
106	ASV480	0	431	Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Spirosomaceae	Runella
138	ASV826	0	412	Bacteria	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Azospirillum
55	ASV177	0	409	Bacteria	Acidobacteriota	Acidobacteriae	Acidobacteriae_or	Acidobacteriae_fa	Paludibaculum
57	ASV179	0	394	Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Spirosomaceae	Emticicia
77	ASV292	0	377	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	Hirschia
102	ASV460	0	365	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Pedosphaerales	Pedosphaeraceae	SH3-11
29	ASV90	0	357	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Luteimonas
152	ASV1098	0	350	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Gemmobacter
154	ASV1131	0	332	Bacteria	Bacteroidota	Bacteroidia	Flavobacteriales	Crocinitomicaceae	Crocinitomix
164	ASV1398	0	315	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Alcaligenaceae	Achromobacter
182	ASV1931	0	315	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Paucibacter
3	ASV6	0	307	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas
46	ASV137	0	307	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Methylibium
203	ASV3047	167	137	Bacteria	Actinobacteriota	Thermoleophilla	Solirubrobacterales	Solirubrobacteraceae	Solirubrobacter

94	ASV410	0	293	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	Limnobacter
150	ASV1087	0	287	Bacteria	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Pseudohongiellaceae	Blyi10
5	ASV9	0	272	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Pelomonas
79	ASV307	31	236	Bacteria	Proteobacteria	Alphaproteobacteria	Reyranellales	Reyranellaceae	Reyranella
122	ASV642	0	265	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Hydrogenophaga
1	ASV1	247	9	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Micrococcaceae	Arthrobacter
62	ASV200	20	229	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiales_Incertae_Sedis	Bauldia
189	ASV2202	0	249	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Pseudacidovorax
86	ASV347	0	248	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Rhizobacter
109	ASV505	0	243	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Pedosphaerales	Pedosphaeraceae	DEV008
67	ASV225	5	235	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Hyphomicrobium
178	ASV1820	231	8	Bacteria	Actinobacteriota	Actinobacteria	Corynebacteriales	Nocardiaceae	Nocardia
40	ASV118	0	239	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Shinella
125	ASV673	0	234	Bacteria	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	KD3-10
14	ASV32	13	217	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Nitrosomonadaceae	IS-44
105	ASV472	15	203	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Altererythrobacter
59	ASV185	29	174	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Ferruginibacter
27	ASV81	0	201	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Ramlibacter
212	ASV3771	0	200	Bacteria	Myxococcota	Polyangia	Polyangiales	Polyangiaceae	Jahnella
26	ASV79	0	196	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Lacibacter
50	ASV156	0	194	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
131	ASV735	0	193	Bacteria	Proteobacteria	Gammaproteobacteria	Salinisphaerales	Solimonadaceae	Panacagrimonas
108	ASV496	0	187	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Oxalobacteraceae	Herminiimonas
18	ASV42	22	159	Bacteria	Proteobacteria	Alphaproteobacteria	Dongiales	Dongiaceae	Dongia
60	ASV191	0	180	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Nitrosomonadaceae	Nitrosospira
76	ASV286	0	180	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Pedosphaerales	Pedosphaeraceae	Ellin517
114	ASV545	62	117	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Geobacillus
38	ASV114	14	165	Bacteria	Myxococcota	Polyangia	Haliangiales	Haliangiaceae	Haliangium
47	ASV141	0	176	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Galbitalea
113	ASV539	0	176	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Thermomonas
228	ASV6671	168	0	Bacteria	Actinobacteriota	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Amycolatopsis
183	ASV1975	167	0	Bacteria	Actinobacteriota	Actinobacteria	Propionibacteriales	Nocardiodiaceae	Marmoricola
13	ASV31	51	116	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter
87	ASV352	0	162	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Rhodopseudomonas
142	ASV944	0	159	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Pseudorhodoferax
210	ASV3692	0	151	Bacteria	Abditibacteriota	Abditibacteria	Abditibacteriales	Abditibacteriaceae	Abditibacterium
126	ASV679	39	108	Bacteria	Actinobacteriota	Acidimicrobiia	Microtrichales	Iamiaceae	Iamia
58	ASV182	0	144	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Acidovorax
144	ASV958	0	144	Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Cytophagaceae	Sporocytophaga
61	ASV196	143	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylobacterium-Methylorubrum
25	ASV77	9	119	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Bradyrhizobium
225	ASV5858	0	128	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Verrucomicrobium
112	ASV533	0	123	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Rubrivivax
11	ASV24	101	19	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus
20	ASV47	37	81	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Comamonas
64	ASV216	0	116	Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Cytophagaceae	Cytophaga
162	ASV1282	29	82	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	alpha_cluster
165	ASV1416	61	47	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnoclostridium
136	ASV818	0	107	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Paracoccus
215	ASV3958	0	106	Bacteria	Proteobacteria	Alphaproteobacteria	Paracaedibacterales	Paracaedibacteraceae	Candidatus_Captivus
175	ASV1744	105	0	Bacteria	Actinobacteriota	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Pseudonocardia
219	ASV4679	104	0	Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Lysinibacillus
72	ASV271	20	84	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia
101	ASV459	37	63	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Afipia
120	ASV606	97	0	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Nitrosomonadaceae	MND1
194	ASV2485	0	96	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Parasegetibacter
8	ASV13	89	6	Bacteria	Actinobacteriota	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Saccharopolyspora
83	ASV328	19	74	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Ellin6055
81	ASV318	0	93	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Parafrigoribacterium
231	ASV8168	91	0	Bacteria	Actinobacteriota	Actinobacteria	Propionibacteriales	Propionibacteriaceae	Jiangella
74	ASV277	0	90	Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Microscillaceae	Ohtaekwangia
193	ASV2437	0	90	Bacteria	Bdellovibrionota	Bdellovibrionia	Bdellovibrionales	Bdellovibrionaceae	OM27_clade
207	ASV3325	0	88	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Rurimicrobium
107	ASV486	0	87	Bacteria	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42
211	ASV3765	0	87	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Rhodovarius
172	ASV1623	0	86	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	UKL13-1
148	ASV1081	0	84	Bacteria	Bdellovibrionota	Bdellovibrionia	Bacteriovoracales	Bacteriovoracaceae	Peredibacter

201	ASV2894	0	81	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Lactococcus
188	ASV2168	68	9	Bacteria	Deinococcota	Deinococci	Deinococcales	Trueperaceae	Truepera
187	ASV2150	0	77	Bacteria	Myxococcota	Myxococcia	Myxococcales	Anaeromyxobacteraceae	Anaeromyxobacter
223	ASV5474	74	0	Bacteria	Cyanobacteria	Cyanobacteriia	Cyanobacteriales	Nostocaceae	Calothrix_PCC-6303
85	ASV339	0	74	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Rhodoplanes
68	ASV227	0	72	Bacteria	Bacteroidota	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Sphingobacterium
118	ASV577	0	71	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Pedosphaerales	Pedosphaeraceae	DEV114
192	ASV2371	0	71	Bacteria	Actinobacteriota	Actinobacteria	Streptosporangiales	Nocardiopeceae	Thermobifida
103	ASV461	20	50	Bacteria	Actinobacteriota	Acidimicrobiia	Microtrichales	Ilumatobacteraceae	CL500-29_marine_group
90	ASV383	19	48	Bacteria	Firmicutes	Bacilli	Paenibacillales	Paenibacillaceae	Paenibacillus
66	ASV223	5	61	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Rhodoferrax
89	ASV371	0	66	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Mesorhizobium
227	ASV6654	20	43	Bacteria	Acidobacteriota	Vicinamibacteria	Vicinamibacterales	Vicinamibacteraceae	Luteitalea
168	ASV1560	61	0	Bacteria	Acidobacteriota	Blastocatellia	Blastocatellales	Blastocatellaceae	Blastocatella
56	ASV178	0	61	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Porphyrobacter
146	ASV976	0	60	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Demequinaceae	Lysinimicrobium
153	ASV1116	59	0	Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planomicrobium
204	ASV3095	59	0	Bacteria	Actinobacteriota	Thermoleophilina	Gaiellales	Gaiellaceae	Gaiella
158	ASV1228	55	4	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter
82	ASV319	0	59	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Rhodovastum
181	ASV1888	0	59	Bacteria	Proteobacteria	Alphaproteobacteria	Parvibaculales	Parvibaculaceae	Parvibaculum
218	ASV4636	58	0	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacterium
30	ASV93	0	57	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Sediminibacterium
93	ASV400	0	55	Bacteria	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Niveispirillum
155	ASV1135	0	55	Bacteria	Proteobacteria	Alphaproteobacteria	Ferrovibrionales	Ferrovibrionales_fa	Taonella
233	ASV9613	0	55	Bacteria	Spirochaetota	Leptospirae	Leptospirales	Leptospiraceae	Leptospira
198	ASV2636	0	54	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Demequinaceae	Demequina
97	ASV435	0	53	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Flavitalea
232	ASV9439	0	52	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Dermacoccaceae	Dermacoccus
217	ASV4211	0	51	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Bosea
129	ASV705	0	49	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Leifsonia
134	ASV760	48	0	Bacteria	Actinobacteriota	Actinobacteria	Propionibacteriales	Nocardioideaceae	Aeromicrobium
199	ASV2697	48	0	Bacteria	Cyanobacteria	Cyanobacteriia	Cyanobacteriales	Chroococcidiopsaceae	Chroococcidiopsis_SAG_2023
75	ASV281	47	0	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Opitutales	Opitutaceae	Alterococcus
19	ASV44	0	47	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Dokdonella
143	ASV957	46	0	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Promicromonosporaceae	Promicromonospora
229	ASV7931	46	0	Bacteria	Bacteroidota	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Anseongella
239	ASV1364	45	0	Bacteria	Cyanobacteria	Cyanobacteriia	Cyanobacteriales	Nostocaceae	Scytonema_UTEX_2349
196	ASV2565	0	45	Bacteria	Firmicutes	Bacilli	Paenibacillales	Paenibacillaceae	Cohnella
124	ASV662	0	43	Bacteria	Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae	Aeromonas
202	ASV2939	0	43	Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae	Candidatus_Megaira
34	ASV102	0	41	Bacteria	Acidobacteriota	Acidobacteriae	Solibacterales	Solibacteraceae	Candidatus_Solibacter
173	ASV1712	40	0	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Erwiniaceae	Erwinia
216	ASV3995	37	0	Bacteria	Actinobacteriota	Acidimicrobiia	Microtrichales	Ilumatobacteraceae	Ilumatobacter
70	ASV246	6	30	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Flavisolibacter
171	ASV1618	0	36	Bacteria	Actinobacteriota	Actinobacteria	Corynebacteriales	Nocardiaceae	Gordonia
32	ASV97	35	0	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Enterobacter
151	ASV1091	35	0	Bacteria	Acidobacteriota	Thermoanaerobaculia	Thermoanaerobaculales	Thermoanaerobaculaceae	Subgroup_10
221	ASV4771	35	0	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Intrasporangiaceae	Ornithinococcus
132	ASV736	0	35	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Pseudogracilibacillus
140	ASV912	0	35	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Inhella
147	ASV1069	34	0	Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Sporosarcina
23	ASV71	0	34	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Chitinimonadaceae	Chitinimonas
195	ASV2495	0	34	Bacteria	Proteobacteria	Gammaproteobacteria	Salinisphaerales	Solimonadaceae	Solimonas
157	ASV1208	32	0	Bacteria	Actinobacteriota	Actinobacteria	Frankiales	Geodermatophilaceae	Blastococcus
222	ASV4903	32	0	Bacteria	Chloroflexi	Chloroflexia	Thermomicrobiales	Thermomicrobiaceae	Sphaerobacter
21	ASV48	29	0	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Lelliottia
128	ASV690	0	28	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	PMMR1
110	ASV520	27	0	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Yersiniaceae	Serratia
166	ASV1454	0	27	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Micrococcaceae	Micrococcus
176	ASV1754	0	27	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Labraceae	Labrys
235	ASV1029	0	27	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Thioclava
115	ASV549	26	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Pedomicrobium
180	ASV1862	25	0	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Devosiaceae	Arsenicitalea
190	ASV2292	25	0	Bacteria	Actinobacteriota	Actinobacteria	Frankiales	Sporichthyaceae	Sporichthya
119	ASV605	0	24	Bacteria	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_Incertae_Sedis	Unknown_Family	Candidatus_Ovatusbacter
123	ASV660	0	24	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	Cupriavidus

156	ASV1197	0	24	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
185	ASV2101	0	24	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Roseimicrobium
230	ASV8103	23	0	Bacteria	Actinobacteriota	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Saccharothrix
96	ASV422	0	23	Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	Rheinheimera
186	ASV2123	0	23	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Alcaligenaceae	Pusillimonas
224	ASV5785	0	23	Bacteria	Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	Haemophilus
241	ASV1701	22	0	Bacteria	Proteobacteria	Gammaproteobacteria	Cardiobacteriales	Wohlfahrtiimonadaceae	Ignatzschineria
73	ASV276	0	22	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Flavihumibacter
243	ASV1915	0	22	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Devosiaceae	Youhaiella
133	ASV757	21	0	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Micrococcaceae	Kocuria
197	ASV2581	21	0	Bacteria	Actinobacteriota	Actinobacteria	Corynebacteriales	Nocardiaceae	Williamsia
41	ASV122	0	20	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	SWB02
95	ASV420	0	20	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	Spirochaetaceae	Spirochaeta_2
111	ASV524	19	0	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Arenimonas
174	ASV1713	17	0	Bacteria	Actinobacteriota	Actinobacteria	Propionibacteriales	Nocardiodiaceae	Kribbella
220	ASV4713	0	17	Bacteria	Planctomycetota	Planctomycetes	Gemmatales	Gemmataceae	Gemmata
141	ASV931	0	15	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Pedosphaerales	Pedosphaeraceae	Ellin516
65	ASV222	0	14	Bacteria	Spirochaetota	Spirochaetia	Spirochaetales	Spirochaetaceae	Salinispira
237	ASV1240	0	14	Bacteria	Verrucomicrobiota	Chlamydiae	Chlamydiales	Parachlamydiaceae	Candidatus_Proteochlamydia
200	ASV2800	0	13	Bacteria	Proteobacteria	Alphaproteobacteria	Paracaedibacterales	Paracaedibacteraceae	Candidatus_Paracaedibacter
213	ASV3773	0	13	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Micrococcaceae	Rothia
234	ASV1021	0	13	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Beijerinckia
160	ASV1243	0	12	Bacteria	Verrucomicrobiota	Chlamydiae	Chlamydiales	Parachlamydiaceae	Neochlamydia
244	ASV2432	0	12	Bacteria	Firmicutes	Desulfitobacteriia	Desulfitobacteriales	Desulfitobacteriaceae	Desulfosporosinus
139	ASV846	11	0	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacterales	Pectobacteriaceae	Pectobacterium
209	ASV3665	0	11	Bacteria	Gemmatimonadota	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Roseisolibacter
159	ASV1231	10	0	Bacteria	Actinobacteriota	Actinobacteria	Corynebacteriales	Mycobacteriaceae	Mycobacterium
238	ASV1252	10	0	Bacteria	Actinobacteriota	Actinobacteria	Micromonosporales	Micromonosporaceae	Rhizocola
167	ASV1500	7	3	Bacteria	Actinobacteriota	Actinobacteria	Propionibacteriales	Propionibacteriaceae	Cutibacterium
170	ASV1603	0	10	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Roseococcus
206	ASV3196	9	0	Bacteria	Acidobacteriota	Blastocatellia	Pyrinomonadales	Pyrinomonadaceae	RB41
242	ASV1755	9	0	Bacteria	Firmicutes	Desulfitobacteriia	Desulfitobacteriales	Desulfitobacteriaceae	Desulfitobacterium
191	ASV2298	0	9	Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Spirosomaceae	Larkinella
245	ASV2832	8	0	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacterales	Morganellaceae	Proteus
179	ASV1854	0	8	Bacteria	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	Archangium
161	ASV1259	7	0	Bacteria	Myxococcota	Polyangia	Polyangiales	Phaselicystidaceae	Phaselicystis
99	ASV444	0	7	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Amnibacterium
240	ASV1455	0	7	Bacteria	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Pseudohongiellaceae	Pseudohongiella
246	ASV2873	0	7	Bacteria	Firmicutes	Clostridia	Peptostreptococcales-Tissierellales	Peptostreptococcales-Tissie	Brassicibacter
247	ASV2873	0	7	Bacteria	Firmicutes	Thermoanaerobacteria	Caldicellulosiruptorales	Caldicellulosiraptoraceae	Caldicellulosiruptor
135	ASV777	6	0	Bacteria	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	Myxococcus
208	ASV3398	6	0	Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Hymenobacteraceae	Adhaeribacter
226	ASV6344	6	0	Bacteria	Actinobacteriota	Rubrobacteria	Rubrobacterales	Rubrobacteriaceae	Rubrobacter
80	ASV309	5	0	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
214	ASV3863	5	0	Bacteria	Myxococcota	Myxococcia	Myxococcales	Vulgatibacteraceae	Vulgatibacter
184	ASV2038	0	5	Bacteria	Firmicutes	Clostridia	Peptostreptococcales-Tissierellales	Peptostreptococcales-Tissie	Tepidimicrobium
205	ASV3195	4	0	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Dermabacteraceae	Brachybacterium
236	ASV1106	4	0	Bacteria	Bacteroidota	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Myroides
130	ASV731	0	4	Bacteria	Deinococcota	Deinococci	Thermales	Thermaceae	Thermus
177	ASV1804	3	0	Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter
137	ASV824	0	3	Bacteria	Firmicutes	Bacilli	Staphylococcales	Staphylococcaceae	Staphylococcus
17	ASV38	2	0	Bacteria	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_Incertae_Sedis	Unknown_Family	Acidibacter