THE HUMAN MICROBIOME AND SKIN AND SOFT-TISSUE INFECTIONS

by

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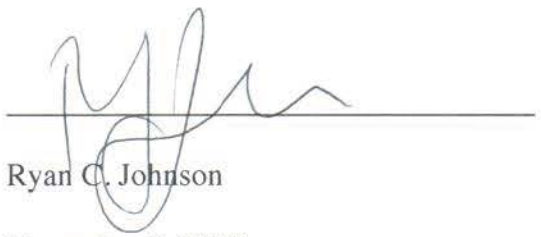
[Signature] 

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ABSTRACT

Title of Dissertation:

The Human Microbiome and Skin and Soft-Tissue Infections

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Skin and soft tissue infections (SSTIs) are among the most prevalent and complex infections observed in both the inpatient and outpatient settings. Clinically, SSTIs can range from mild (ex. folliculitis) to severe (ex. necrotizing fasciitis) and can present as either purulent (ex. cutaneous abscess) or non-purulent (ex. cellulitis). Furthermore, SSTIs can be caused by a wide array of bacterial pathogens such as *Staphylococcus aureus* and beta-hemolytic *Streptococci* (BHS). While SSTIs are frequently reported throughout the world, certain congregate populations, such as military trainees, are at increased risk for SSTI development. Indeed, the number of SSTI-related hospital admissions exceed even those for influenza and pneumonia during the first two years of service. Although nasal colonization with *S. aureus* is an established risk factor for SSTI development, it is still unclear why some colonized individuals develop disease while others do not. Given the recent association between the human microbiome and human health, we hypothesized that fluctuations in the nasal microbiome may be associated with

SSTI development. Furthermore, given the variability in SSTI presentation, we set out to determine if specific risk factors and/or microbial profiles were unique to either cutaneous abscess or cellulitis. Using a high-throughput sequencing approach, we found that the nasal microbiomes of trainees developed SSTI had significantly less Proteobacteria compared to trainees that did not harbor a SSTI. Additionally, we found that the abundance of *S. aureus* in the nares was inversely correlated with *Corynebacterium*. With respect to bacterial etiology, we found that while most cutaneous abscesses were dominated by *S. aureus*, polymicrobial infections were frequently observed. We also characterized a unique case of cutaneous abscess caused by a strain of *S. aureus* with decreased susceptibility to chlorhexidine. While *S. aureus* was typically associated with purulent abscess, cellulitis microbiomes were mostly composed of atypical bacteria such as *Rhodanobacter*. In addition to bacterial composition, we also observed differences in risk factors associated with either cutaneous abscess or cellulitis development. Together, these data not only demonstrate a correlation between the human microbiome and SSTIs, but also highlight important microbial and epidemiological differences between purulent and non-purulent SSTIs that should be considered when treating these complex infections.

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THE HUMAN MICROBIOME

Definition and Significance

The human body is a living ecosystem that contains trillions of bacteria, fungi, protozoans, and viruses. Collectively, these microbial communities make up what is known as the human microbiota. While basic culture techniques have provided a glimpse into the microbiota at specific body sites, the advent of high throughput DNA sequencing technologies has allowed researchers to characterize microbial communities with greater resolution. Indeed, the collective microbial genomes, or microbiome, at numerous anatomical locations have been described through a collaborative research consortium known as the Human Microbiome Project (HMP) (134). The HMP was established in 2008 with the primarily goal to characterize the human microbiome and elucidate its role in human health and disease. Since then, the number of studies that associate disease with the human microbiome has increased dramatically (Figure 1). Fluctuations in microbiome composition have been reported for various diseases that range in severity from acne to pancreatic cancer (91; 96). As we progress through the microbiome era, the identification of microbial differences between healthy and unhealthy microbiomes will become increasingly important.

The significant contribution of the human microbiota to human health is not surprising given that the number of human-associated bacterial cells far exceeds the 37.5 trillion cells of the human body by a factor of ~10 (27; 266). Additionally, the human

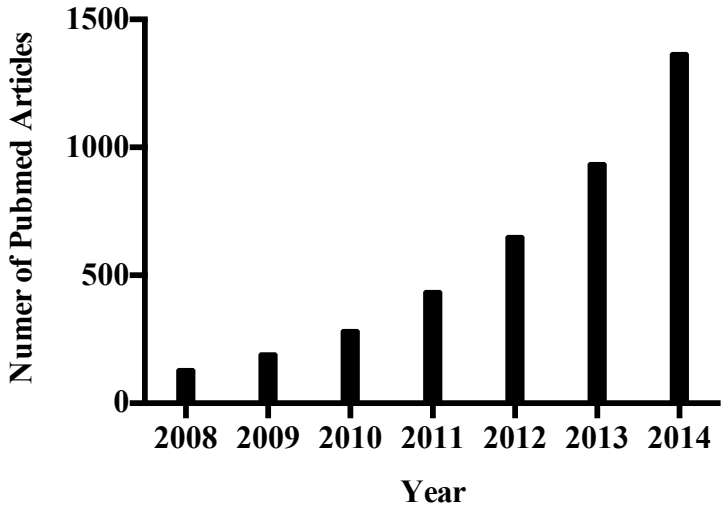

Figure 1. Microbiome and disease-related PubMed articles from 2008 to 2014. Data were downloaded from the National Center for Biotechnology Information (NCBI, http://www.ncbi.nlm.nih.gov/pubmed) after "microbiome disease" was entered as the search criteria.

microbiome contains hundreds of genes that have no functional homologs in the human genome (174; 245). Thus, microbes provide humans with essential biological processes that we have not acquired ourselves (116). In this regard, the human microbiota share numerous qualities similar to other organs within the body. Similar to how clinicians monitor organ function through clinical tests, scientists may potentially utilize the microbiome composition as a biomarker in the future to monitor disease progression or even assess disease susceptibilities.

Although disease presentation and subsequent microbiome dysbiosis (microbial imbalance) are important correlates, the idea of using microbiome reconstruction as a therapeutic has gained traction in the medical field as of late. The most well-documented instance of successful microbiome reconstruction to combat disease has been the implementation of fecal transplantation to replenish the gut microbiota during life-threatening *Clostridium difficile* infection (16). Since fecal transplantation is a novel and unappealing treatment option, other microbiome therapeutics such as probiotics have become increasingly popular (248). Fecal transplants and probiotics represent just two of the potentially limitless microbiome-related therapeutics. Current research is underway to determine which bacterial organism(s) can be supplemented at various body sites as a means to shift the microbiome from that of a diseased state to a healthy state.

Impact on Human Health

As early as the 1950's, it became evident that the human microbiota have a major impact on human health (293). However, the intricacies of which bacteria and other microbes influence our everyday life have only recently begun to come to light. Bacteria

are inherently given a bad reputation as agents that cause disease. However, thanks to the HMP and other studies, it is now clear that most bacterial species are nonpathogenic. In fact, some bacterial species engage in mutualistic behaviors with their human host (14). Perhaps the most well known example of bacteria-human mutualism is the intricate interaction of human metabolism with bacteria that reside within the gut. The human gut is an incredibly diverse microbial ecosystem comprised of over 1000 bacterial species (337). In return for a nutrient rich habitat provided by the human host, various gut bacteria can convert indigestible carbohydrates to digestible short-chain fatty acids (SCFAs) (253). This process is critical given that nearly 10-20% of all ingested carbohydrates are not solubilized by the intestinal tract (252). The bulk of bacteria-produced SCFAs are rapidly absorbed by the colon and serve as important energy sources for colonic-epithelial cells, promote tight-junction stability, and aid in epithelial cell repair and proliferation (253). In addition to SCFAs, the gut microbiota provide a plethora of vitamins that the human host is incapable of synthesizing *de novo*. These include vitamin K, thiamine, riboflavin, pyridoxine, panthotenic and nicotinc acids, biotin and folates (12; 167; 279). Additional studies have linked bacteria in the gut to other necessary physiological processes that include fat storage, glucose usage, and drug metabolism (13; 39; 327).

Interestingly, evidence suggests that the gut microbiota has a more global influence on human health. For example, the microbiota-gut-brain (MGB) axis is a concept that describes a bi-directional crosstalk between the central nervous system (CNS) and the gut microbiota. In support of the MGB axis hypothesis, a report in 2004 found that germfree mice exhibit an exaggerated hypothalamic-pituitary-adrenal (HPA)

stress response that is reversed when the mice are reconstituted with the gut bacterium *Bifidobacterium infantis* (285). The supplementation of gut microbiota in germfree mice has also been shown to alleviate anxiety-like behaviors (22; 215). Additionally, some gut microbiota are capable of neurotransmitter synthesis; *Bifidobacterium* and *Lactobacillus* both convert glutamate to γ-aminobutyric acid (GABA), an important inhibitory neurotransmitter required for proper CNS function (18; 128). Dysregulation of GABA has been linked to numerous neurological disorders including anxiety, epilepsy, and stiff-person syndrome (172; 181; 297). Consequently, modulation of the gut microbiota to treat neurological disorders has become an increasingly popular research field over the past decade.

There are fewer, but equally important studies and hypotheses that suggest that the CNS has the ability to alter the composition of the gut microbiome (15; 108). This is likely mediated by the direct brain-controlled secretion of signaling molecules that are detected by neurotransmitter receptors on enteric bacteria (118). Conversely, indirect CNS influence of the gut microbiota may occur through neuronal regulation of intestinal permeability, mucus secretion, and gut motility (17; 68; 249; 259). Preliminary work in our laboratory may also suggest an association between traumatic brain injury (TBI) and subsequent alteration of the gut microbiota (J. Singh, J.J. Gilbreath, M. Lagraoui, B.C. Schaefer, D.S. Merrell, unpublished results). While this facet of the MGB axis is a developing field of research, future studies will likely reveal additional CNS factors that influence the bacteria in the gut.

In addition to the MGB axis, there exists an expansive interplay between the gut microbiota and the human immune system. With respect to the innate immune response,

a healthy gut microbiota is required for proper NF-κB suppression, antimicrobial peptide secretion, neutrophil activity, and inflammatory homeostasis of intestinal epithelial cells via TLR9 signaling (40; 51; 119; 130; 272). The adaptive immune system's interaction with bacteria in the gut is complex given that microbes in the body are inherently foreign and should invoke an immune response. Rather than simply ignoring the gut microflora, the bacteria are utilized as an immunological training ground required for proper immune system maturation. Indeed, germfree mice exhibit numerous adaptive immunological defects that include reduced B cell and $CD4^+$/ $CD8^+$ T cell counts, insufficient Peyer's patch development, lack of Th17 cell induction, and reduced IgA secretion (122; 137; 143; 183; 240; 257). This immune system priming serves as the basis of what is known as the "microflora hypothesis." Similar to the hygiene hypothesis, the microflora hypothesis stipulates that limited microbial exposure results in suboptimal colonization of the infant gut, which in turn results in immune system deficiencies and subsequent allergy development (333). In support of the microflora hypothesis, numerous reports have associated gut dysbiosis with allergic diseases including atopic eczema, asthma, and rhinitis (2; 11; 28; 303).

Although microbial diversity in the gut is imperative for proper immune system function, studies have also linked the gut microbiota to autoimmune disorders. Inflammatory bowel disease (IBD), which includes Crohn's disease and ulcerative colitis, is an autoimmune disease characterized by chronic inflammation of the gastrointestinal tract. Interestingly, while IBD symptoms are primarily mediated by the immune system, antibiotic/probiotic therapy have proven beneficial (234; 309); a clear indication of microbial involvement. Moreover, the composition of the gut flora in IBD patients is

significantly altered compared to healthy patients (185). In addition to IBD, rheumatoid arthritis (RA) also appears to be influenced by the bacteria in the gut. In a T cell-mediated arthritis murine model (Il-1 receptor negative), gut colonized mice rapidly develop arthritis while germfree mice do not (1). Reconstitution of germfree mice with the gut bacterium *Lactobacillus bifidus* restored disease progression. Other autoimmune diseases associated with the gut microbiota include diabetes, systemic lupus erythematosus, and multiple sclerosis (37; 164; 341). Given the role of gut bacteria in both immune system maturation and disease, we now appreciate the delicate balance that must exist between bacteria and the immune system in healthy individuals.

Not surprisingly, the largest organ of the body, the skin, also plays host to a diverse array of bacterial species. Unlike the gut, the role of bacteria present on the skin has not been well characterized. What we do know, however, is that the microbial composition of the skin at various body sites is extremely variable and is further complicated by environmental and host factors (115). With respect to human health, the skin commensal, *Staphylococcus epidermidis*, actively secretes anti-microbial compounds against both *Staphylococcus aureus* and Group A *Streptococcus* (54; 55; 138). Interestingly, *S. epidermidis* is also capable of immune system suppression in response to skin injury via TLR3 inhibition (160). Despite its clear role in protecting the host from pathogenic organisms, *S. epidermidis* has also emerged as an important opportunistic pathogen. In fact, indwelling medical device contamination by *S. epidermidis* represents one of the leading causes of nosocomial infections (300). Similar to *S. epidermidis*, another common skin commensal, *Propionibacterium acnes*, harbors both mutualistic and pathogenic qualities. *P. acnes* is the predominant bacterium found

within skin pilosebacious units, or pores, and is known for its ability to produce propionic acid, which can suppress *S. aureus* growth and reduce the size of *S. aureus*-associated skin lesions in a mouse model (96; 273). On the other hand, *P. acnes* is associated with the adolescent malady acne vulgaris (175). Mechanistically, *P. acnes'* role in the pathogenesis of acne is multifactorial with both inflammatory and strain-specific components (25). Of particular interest, a recent report described a fermentation byproduct of *S. epidermidis*, succinic acid, which inhibits the growth of *P. acnes* (318). This byproduct may be a promising probiotic therapy for a condition that inflicts nearly 80% of all adolescents in the United States (35).

S. epidermidis and *P. acnes* represent two skin commensals that appear to play a role in both human health and disease. However, when the entire skin microbiota is considered, research has demonstrated that the microbial composition of the skin can change dramatically in response to human disease. In patients with atopic dermatitis (AD), a relapsing inflammatory skin disorder, disease severity is associated with a reduction in skin bacterial diversity (155). This lack of bacterial diversity is mainly driven by a stark increase in *S. aureus* abundance compared to healthy controls. Additionally, significant variations in bacterial abundance levels are also observed for *S. epidermidis, Streptococcus, Corynebacterium,* as well as *Propionibacterium,* which emphasizes the importance of comprehensive characterization of microbial communities during human disease (155).

Overall, our understanding of the human microbiome and how it influences human health has transformed the medical field. Researchers are rapidly uncovering the complex bacterial ecosystems that reside on the human body; however, the ability to

augment the microbial composition to prevent or treat specific diseases is an area of research that requires further exploration.

Defining the Human Microbiome

In 1973, Gilbert and Maxam successfully elucidated and published the sequence of the *lac* operator; the first ever published sequence of DNA (111). Four years later, the Sanger method of DNA sequencing was published and followed by the development of polymerase chain reaction (PCR) in 1983 (261; 265). In 2005, Life Sciences (a Roche company) introduced 454 high-throughput DNA sequencing technology, the first documented next-generation DNA sequencer. Since then, various other next-generation sequencing platforms have been introduced including Illumina/Solexa (2006), SOLiD (2007), Helicos (2009), Ion Torrent (2011) and PacBio Systems (2011). Together, next-generation DNA sequencing and PCR represent the two fundamental tools required for microbiome characterization. A brief overview of the steps required to analyze the microbial composition of a body site are as described below.

Whether it is a fecal sample, or a swab obtained from the axilla of patient, the first step to define a microbiome is to extract genomic DNA from the bacteria present in the sample. The genomic DNA then serves as template for PCR amplification of the 16S ribosomal RNA gene (*rrnA*). The 16S gene encodes a small subunit of the 30S prokaryotic ribosome and is not only present among all bacterial species, but is highly conserved as well. In other words, the 16S gene serves as molecular barcode. Indeed, phylogenetic mapping of the 16S gene, and the18S eukaryotic homologue, was used to establish the 3 domains of life: Archaea, Bacteria, and Eukaryota (330). The gene itself is

approximately 1.5 kb in length and consists of 9 variable regions (V1-V9) that allow for discrimination between bacterial species. Ideally, full-length 16S gene sequences would allow for the greatest resolution between species, but given the current limitations of next-generation sequencing, researchers are limited to specific regions of the 16S gene. Fortunately, the conserved regions of the 16S gene that flank the 9 variable regions are ideal for "universal" primer design and subsequent amplification by PCR. However, because the16S gene does not evolve evenly across its length, the region chosen for PCR amplification must be carefully considered (269). For example, it was determined that the V1 to V3 region is capable of discerning *S. aureus* from other coagulase-negative *Staphylococcus* species as well as *Streptococcus* species (42; 60). Of note, the HMP consortium also confirmed the significant resolution provided by the V1-V3 region (134).

Upon PCR amplification of the 16S gene variable region(s), the amplicons are subjected to high-throughput sequencing. Of the various sequencing platforms mentioned above, microbiome research currently most often utilizes either 454 or Illumina. 454 is advantageous given its long read length of up to 700 base pairs; however, the limited number of reads (1-2 million per sequencing reaction) may not sufficiently depict the total level of diversity represented in the sample. This is especially problematic if the sequencing reaction contains multiple samples (multiplexed). On the other hand, the Illumina platform is capable of generating over 30 million reads per run at a fraction of the price of 454. Although the read length of the Illumina platform is slightly reduced compared to 454 (~300-500 base pairs for MiSeq), the technology is rapidly advancing and will likely render 454 sequencing obsolete in the near future. Despite the advantages

and disadvantages of each platform, they each provide the researcher with millions of 16S amplicon sequences that are used to define the microbiome of the sample.

Microbiome data analysis relies primarily on the clustering of similar sequences together. As mentioned previously, because the 16S gene does not evolve uniformly along its length, a similarity threshold level must be established that will determine if two 16S reads are considered the same, even if they may not truly represent the same species. It was previously determined that species having 70% or greater DNA similarity routinely have more than 97% sequence identify between their 16S rRNA genes (278). Thus, a similarity level of 97% is frequently utilized to cluster sequences into operational taxonomic units (OTUs). Taxonomic information can be assigned for each sequence and/or OTU via alignment to a curated RNA database such as GreenGenes, Ribosomal Database Project, or SILVA (57; 191; 247). Alignment to a well-curated database is essential given that nearly five percent of all 16S rRNA sequences in GenBank may contain anomalies (9). OTU generation allows the researcher to perform various microbial diversity analyses to assess species richness and evenness. Currently, two commonly used software packages are in place that allow researchers to analyze their specific microbiome data sets: QIIME and Mothur (38; 270). Both analysis pipelines contain the molecular tools required for quality assessment, PCR chimera detection, contaminate removal, sequence clustering, taxonomic assignment, and diversity analyses of the 16S rRNA sequences.

While 16S rRNA PCR and sequencing has revolutionized the field of biology, important caveats exist that must be considered. One of the most overlooked problems in microbiome research is DNA contamination. The introduction of foreign DNA into the

PCR step that utilizes "universal" primers can result in amplification of the contaminating DNA and may dramatically influence downstream analyses. Indeed, this issue has been recognized by many groups and has been assigned the term "kitome", or the microbiome of the kits used to process the samples (262; 321). This is especially problematic if the bacterial load of the sample is low (262). The use of negative controls is therefore strongly encouraged. Another problem with "universal" primers is that, in some unique cases, they may not bind to a particular species' 16S gene. Furthermore, the PCR may be biased if the primers preferentially anneal to a specific bacterial species' 16S gene (152). In either case, the region that is amplified as well as the primers used must be carefully considered. Additionally, a single bacterial species can have up to 15 copies of the 16S gene on its genome, which may inflate the actual relative abundance of an organism in the sample (147; 150). Therefore, computational manipulation to correct for 16S rRNA copy number may be required to accurately characterize a microbiome.

The Nasal Microbiome

The nasal vestibule, or anterior nares (AN), is a semi-dry environment lined with squamous epithelium that contains tactile hair (vibrissae), sweat and sebaceous glands (110). As a major external entry point to the respiratory system, the AN is exposed to upwards of a million bacterial cells for every cubic meter of atmosphere (178). While many inhaled foreign bodies are actively expelled from the respiratory tract via the "mucocillary escalator" (308), select bacterial species are retained in the AN. Indeed, the AN is a clinically relevant habitat that harbors a diverse repertoire of bacterial inhabitants, both commensal and pathogenic (101; 223; 334). For example,

approximately 20-30% of the world's population carries the Gram-positive pathogen, *Staphylococcus aureus,* in their AN (154). In addition to *S. aureus,* other bacterial species have evolved to survive within the AN including *Corynebacterium* spp, *Staphylococcus epidermidis*, and *Propionibacterium* spp (328; 334). Although host factors can largely influence the colonization of bacteria in the AN, recent data suggest that the composition of the nasal microbiota is indeed environmentally determined (180). With respect to bacterial abundance, the bulk of the AN landscape is dominated by two phyla: Firmicutes and Actinobacteria. In fact, these two phyla alone typically represent over 90% of all bacterial species present in the AN (101; 334). To a lesser extent, the Proteobacteria and Bacteroidetes phyla are also present in the AN (≤10% abundance) (170; 223). The contribution of these four phyla to human health is still a very active field of research.

Numerous studies have attempted to characterize the "healthy" AN, however, it has become increasingly evident that the microbial composition of the AN is incredibly variable. For example, researchers found striking differences in the nasal microbial communities between children and adults (223). Interestingly, children appear to harbor more Proteobacteria and Bacteroidetes in their AN (223). In addition to age, the composition of the nasal microbioata fluctuates over time. In a longitudinal *S. aureus* colonization study of 43 patients that were initially *S. aureus* negative in the AN, over half (55.8%) became carriers 52 weeks later (6). Similarly, another study of 12 healthy adults that were sampled 4 times over a three-week period found that half of the patients were intermittently colonized with *S. aureus* while the remaining half were persistent carriers (334). Collectively, these studies not only emphasize the variable nature of the

nasal microbiota, but also suggest that a consensus "healthy" nasal microbiome may not be definable.

The observed microbial variation in the AN has prompted researchers to investigate specific correlations that may have future clinical implications. For instance, numerous reports have shown that nasal colonization with *S. aureus* is a risk factor for subsequent *S. aureus*-related disease (79; 153; 322). As such, treatments aimed at *S. aureus* clearance would prove beneficial to human health. A recurring phenomenon observed in the nares is the apparent inverse correlation between species of the *Corynebacterium* genus and *S. aureus* (170; 334). Indeed, 71% of *S. aureus* carriers became non-carriers after artificial implantation of *Corynebacterium* in the nares (302). While the mechanism behind this bacterial interference remains unknown, it represents yet another potential microbiome-altering probiotic therapy to prevent disease. Additional interactions of *S. aureus* with other bacterial inhabitants of the nose are shown in Figure 2 (31; 125; 149; 179; 228; 255).

Unlike the gut and skin, our understanding of how the microbial composition of the AN is altered in response to human disease is limited. This is largely due to the inability to discern between a diseased state and interpersonal microbiome variation. In a recent study that investigated fluctuations of the nasal microbiota associated with chronic rhinosinusitis (CRS), while the researchers observed a reduction in bacterial diversity in patients suffering from CRS compared to healthy controls, it was determined that the observed variation between individuals trumped variations associated with disease status (29). Therefore, further work is required in order to tease out how the nasal microbiome fluctuates at an intra as well as interpersonal level.

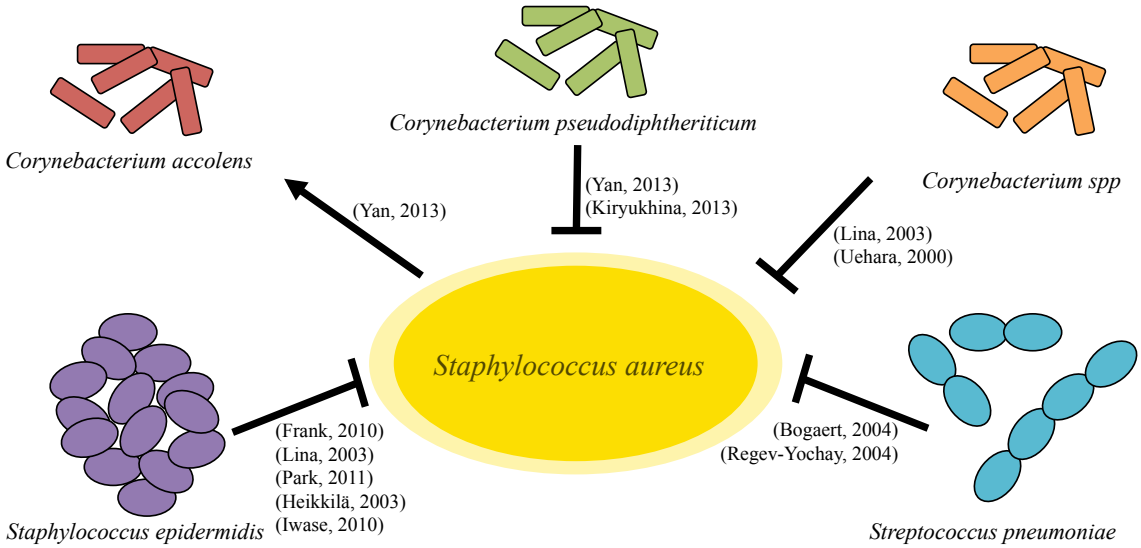

Figure 2. Interactions of *Staphylococcus aureus* with other common bacteria found within the anterior nares and nasal cavity.
Arrows indicate the promotion of growth while blunt ended lines indicate growth inhibition. Studies listed in parentheses support the interaction of the two organisms. spp = species.

SKIN AND SOFT-TISSUE INFECTIONS

Clinical Presentation and Etiology

Skin and soft-tissue infections (SSTIs) can be broadly defined as any microbial invasion of the skin or underlying soft tissue that invokes an immune response. These infections can range in clinical severity from mild and self-limiting to severe and life-threatening. As such, a classification system was implemented in 1998 by the US Food and Drug Administration that identifies SSTIs as either uncomplicated or complicated. Uncomplicated SSTIs, which include cellulitis, simple abscesses, erysipelas, and folliculitis, are superficial in nature and respond rapidly to antibiotic treatment, drainage, and debridement (281). A spectrum of uncomplicated SSTIs is depicted in Figure 3. Alternatively, complicated SSTIs, which include major abscesses, burns, infected ulcers and necrotizing fasciitis, involve deeper tissues that typically require surgical interventions (187). These severe infections are often accompanied by systemic maladies such as sepsis and neutropenia (70). SSTIs present on individuals with an underlying disease (*e.g.* immunocompromised, diabetes mellitus, obesity) that compromises treatment options may also be considered complicated (106).

The vast majority of SSTIs, both complicated and uncomplicated, are typically caused by the bacterial pathogen *S. aureus*. Indeed, the rate of *S. aureus*-associated SSTIs has risen with the emergence of methicillin-resistant *S. aureus* (MRSA) (284). In addition to beta-lactam antibiotics, *S. aureus* has evolved and/or acquired resistance to multiple classes of antibiotics and biocides such as quinolones, glycopeptides, aminoglycosides,

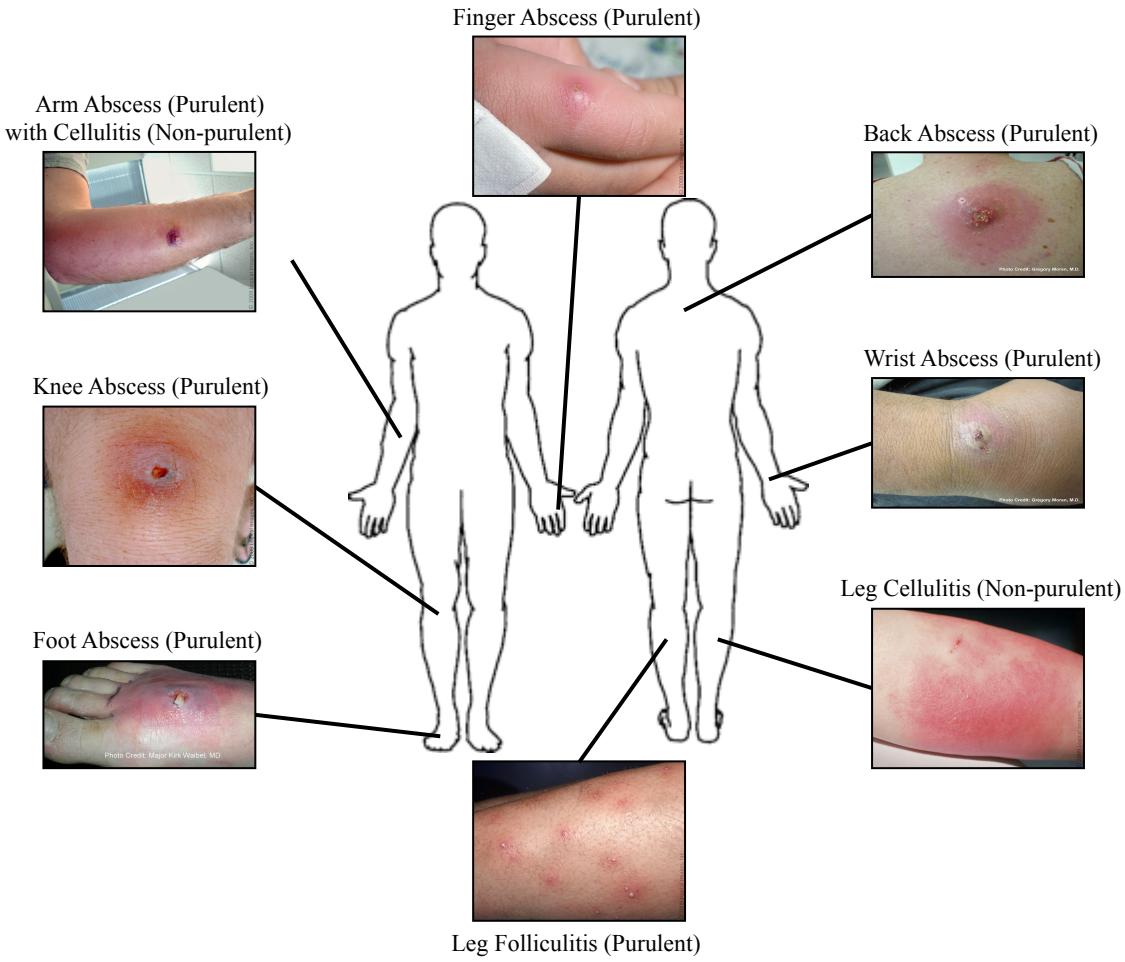

Figure 3. Clinical photographs of common skin and soft-tissue infections (SSTIs). SSTIs are noted as either purulent or non-purulent. All images are credited to Dr. Gregory Moran or Logical Images Incorporated. Body outline image courtesy of imgbuddy.com.

oxazolidinones, and quaternary ammonium compounds (30; 44; 109; 189; 256; 275; 290; 296; 298). While the vast majority of *S. aureus* resistance mechanisms have been molecularly elucidated, novel mechanisms are frequently identified. This rapid evolution of *S. aureus* continues to nullify even the newest of antimicrobial compounds and emphasizes the need for future antibiotic design.

Although *S. aureus* is associated with most SSTIs, other Gram-positive, as well as Gram-negative bacterial species, are also routinely isolated. These include beta-hemolytic streptococci (Groups A, B, C, and G), *Pseudomonas aeruginosa*, *Enterococcus* species, and *Escherichia coli* (201). Data suggest that the etiology of SSTIs is also influenced by any preexisting disease as evidenced by the increased prevalence of Group B streptococci SSTIs in diabetics and the elderly (86; 90). Furthermore, culture data can be difficult to obtain for SSTIs that are non-purulent, specifically for cellulitis infections. While serological data, syringe aspirates, and punch biopsies suggest that some cellulitis infections are caused by *S. aureus* and beta-hemolytic streptococci, in nearly 80% of all cases, no bacterium is isolated (71; 142; 171; 216; 235; 286). While culture remains the gold standard for SSTI etiology, researchers and clinicians would greatly benefit from increased sensitivity detection methods such as DNA sequencing.

Treatment

Given the recent spread of MRSA and sharp rise in SSTI cases, the Infectious Diseases Society of America (IDSA) was forced to update their guidelines regarding SSTI treatment (281). Identification and targeted treatment of the infecting pathogen is the preferred practice, however, most clinicians are forced to treat empirically given the

difficulty associated with discerning bacterial etiology. This is especially worrisome given the rise in bacterial antibiotic resistance. Therefore, as emphasized by the IDSA, further research into the rapid identification of the causes of SSTIs, particularly cellulitis, is needed (281).

Per the IDSA's recommendations, the algorithm for SSTI management requires that the SSTI be initially identified as either purulent or non-purulent (281). For all purulent SSTIs, incision and drainage followed by culture and sensitivity testing should be performed. If forced to treat empirically, the recommended antibiotics for severe purulent SSTIs include vancomycin, daptomycin, linezolid, televancin, or ceftaroline. For moderate SSTIs, empiric antibiotic treatment should include trimethoprim/sulfamethoxazole (TMP/SMX) or doxycycline. Non-purulent SSTIs, such as cellulitis and erysipelas, can be treated with penicillin, cephalosporin, dicloxacillin, or clindamycin. Severe cases of non-purulent SSTI such as necrotizing fasciitis may require surgical debridement followed by empiric vancomycin plus piperacillin/tazobactam. These treatment options should be tailored accordingly if MRSA or another antibiotic resistant pathogen is identified (281).

While the IDSA recommendations were recently updated, there are additional complicating factors that make SSTI treatment exceptionally difficult. For instance, it has been shown that SSTIs can in fact be polymicrobial in nature (230; 320). Importantly, data suggest that mixed infections that involve *S. aureus* demonstrate enhanced pathogenesis (211). Also, the responsiveness of *S. aureus* to therapeutics in a polymicrobial setting has yet to be evaluated. Secondly, our basic understanding of cellulitis is limited. While most clinicians treat cellulitis with antibiotics, the use of anti-

inflammatories has also proven efficacious and suggests an immunological component to these infections that is currently unknown (65). These common oversights need to be considered in the future for the successful treatment of SSTIs.

Epidemiology and Military Impact

The ubiquity of *S. aureus* and the susceptibility of both healthy and non-healthy individuals makes SSTIs among the most prevalent infections in both community and hospital settings. In 2005 alone, there were over 14 million SSTI related hospitalizations in the United States, and the numbers continue to rise (127; 284). It is predicted that for every 1,000 physician, outpatient, or emergency room visits in the United States, over 48 of them are due to SSTI; a substantial increase from 32 visits per 1,000 people in 1997 (127). This surge in SSTI rates, as mentioned prior, is directly associated with the emergence of MRSA, particularly community-associated MRSA (CA-MRSA) (284). Indeed, the number of *S. aureus* associated SSTIs increased by a staggering 123% from 2001 to 2009 (284). SSTIs are not only a significant epidemiological issue, but also have a profound financial impact. From 2001 to 2008, the total cost of *S. aureus*-associated SSTI hospitalizations in the United States increased by 44%, which equated to over $4.8 billion (284). Thus, SSTIs represent a pressing public health issue that requires immediate attention.

While no individual is known to be immune to SSTI, there are established risk factors that increase one's susceptibility to future infection. Intuitively, repeated exposure and/or colonization with *S. aureus* increases the risk for SSTI development (156). This is especially true in hospitals and other health-care settings that foster an environment with

elevated *S. aureus* abundance levels. In addition to *S. aureus* exposure, individuals with underlying diseases such as diabetes and HIV are more likely to develop SSTIs than their non-diseased counterparts (64; 254). Other SSTI risk factors include obesity, prior SSTI, injection drug use, and poor hygiene (277; 288). Risk factors associated with specific SSTIs (*e.g.* abscess and cellulitis) have yet to be determined.

Given *S. aureus*' ability to survive on both biotic and abiotic surfaces, certain congregate settings where *S. aureus* can be efficiently transferred from one host to the next are routinely the site of localized SSTI outbreaks. Examples of such outbreaks include a French prison in 2010, a collegiate football team from 2002 to 2004, and a hospital nursery in 2010 (32; 258; 264). Furthermore, trainees in the military are disproportionately affected by SSTIs. Astonishingly, SSTI-related hospital admissions outnumber those for pneumonia and influenza within the first two years of military service (5). The increased prevalence of SSTIs in the military is also reflected by the numerous outbreaks reported at various military training facilities (36; 342). Indeed, it is predicted that at Fort Benning, one of the nation's largest Army training facilities, approximately 1 in 10 trainees will go on to develop an SSTI during their basic training (3). With about 20,000 new trainees per year, Fort Benning is a hotbed for SSTIs.

Although they are rarely fatal, SSTIs can cause significant morbidity. In the context of the military, this can greatly impair training participation and completion. In 2005, of the 4% of recruits at Fort Benning that were infected with CA-MRSA, 39% were placed on limited duty for approximately 5.3 days (206). Moreover, 10% of the CA-MRSA infected trainees required hospitalization. Because of the immense burden that SSTIs impose on military trainees at Fort Benning, researchers have attempted to reduce

SSTI rates via prophylactic hygiene strategies. In a recent cluster-randomized hygiene study at Fort Benning, researchers determined that chlorhexidine body wash did not reduce SSTI rates among military trainees (82). Given the potent anti-*S. aureus* effect of chlorhexidine and low prevalence of chlorhexidine resistance among *S. aureus* isolates in the U.S., the data from this clinical trial suggest that additional factors that will be key for reduction of SSTI rates have yet to be uncovered (52; 87; 190; 268).

Association of the Nasal Microbiome with SSTI

Currently, about 30% of the human population is either transiently or permanently colonized by *S. aureus* (85; 154). While this pathogen can inhabit various body sites, *S. aureus* preferentially colonizes the anterior nares (322). As mentioned previously, nasal colonization is a known risk factor for SSTI development (79; 105). It is hypothesized that the nares-colonizing strain of *S. aureus* can inoculate open cuts and wounds located at remote areas of the human body and cause SSTI. Indeed, in nearly 80% of cases, the infecting strain of *S. aureus* is identical to the individual's colonizing strain (67; 153; 236; 322). While nasal colonization with *S. aureus* increases SSTI risk, it does not guarantee subsequent infection (66). Furthermore, the anterior nares serve as a reservoir for other bacterial species that are routinely isolated from SSTIs such as coagulase-negative *Staphylococcus* and beta-hemolytic *Streptococcus* (251). Together, these data suggest a potential association of the bacteria in the nose with SSTIs. Characterization of this association could be useful for identification of individuals that are at increased risk for future SSTI development.

SSTI Associated Virulence Factors

S. aureus is not only a leading cause of SSTIs, but is also routinely associated with other diseases such as osteomyelitis, bacteremia, endocarditis, and toxic shock syndrome (93; 140; 209; 224). In order to establish infection, *S. aureus* is equipped with an impressive number of virulence factors that contribute to increased pathogenesis in the host as well as aid in immune system evasion. In the context of SSTIs, specific virulence factors are essential for disease progression and will be discussed below.

Of the most well characterized virulence factors, the prophage-encoded Panton-Valentine Leukocidin (PVL) protein is a beta-pore forming cytotoxin that has been shown to contribute to SSTI pathogenesis via keratinocyte apoptosis and leukocyte destruction (48; 112). The importance of PVL to *S. aureus* virulence with respect to SSTIs is exemplified by the low prevalence of PVL-positive strains isolated from healthy individuals (< 2%) as opposed to SSTI-associated isolates (> 30%) (19; 196; 243; 311). In addition to PVL, *S. aureus* produces other cytolytic toxins, which include delta toxin, alpha hemolysin, phenol soluble modulins (PSMs), leukocidins, and gamma hemolysin (26; 145; 207; 237). While the exact contribution of these various factors to SSTI pathogenesis is still an evolving area of research, these toxins are highly immunogenic and may be utilized as targets for vaccine development and immunotherapy (7). In fact, antagonism of alpha hemolysin with antibodies was shown to reduce SSTI severity in a mouse model (263). Although data suggest a contribution of the other cytotoxins to SSTI pathogenesis, the exact mechanisms have yet to be determined (24; 177).

In addition to cytotoxins, *S. aureus* has evolved additional mechanisms to avoid killing by the host immune system. Immune clearance of foreign cells is largely dependent on the ability to create antibodies that are specific to antigens on the surface of the cell. To overcome this defense, *S. aureus* is coated in a potent antiphagocytic protein known as capsular polysaccharide (CP) (214; 292). Similar to other bacterial capsules, CP obstructs the interaction between bound antibodies or complement factor C3b and the receptors on the phagocytic cell (222). *S. aureus* also inhibits phagocytosis via protein A (SpA) synthesis. SpA binds to antibodies, specifically IgG, and effectively inhibits the opsonization process (10; 239). Other immune modulators produced by *S. aureus* include the chemotaxis inhibitory protein of *S. aureus* (CHIPS) and extracellular adherence protein (Eap) (241; 329). Furthermore, *S. aureus* is notorious for its ability to create barricades that prevent immune cells from reaching the bacterium. For example, two clotting factors produced by *S. aureus*, coagulase and von Willebrand factor binding protein (vWbp), are necessary for kidney abscess formation in a mouse model (47). These two proteins activate host prothrombin, which catalyzes the conversion of fibrinogen to fibrin (227). This reaction results in the clotting of blood and plasma around the bacterium and provides protection from invading immune cells (47). Additionally, *S. aureus* is capable of biofilm formation, which not only protects the bacterium from phagocytosis, but also confers greater resistance to antibiotics (8; 294). Of interest, data suggest that *S. aureus* isolates from SSTIs are capable of biofilm formation, regardless of disease type (158). Whether SSTI pathogenesis is influenced by coagulase/vWbp expression or biofilm formation is still a debated topic and requires further elucidation.

Molecular Determinants of Methicillin Resistance

Of the numerous virulence factors associated with *S. aureus*, the ability to rapidly acquire resistance to antibiotics is indisputably the greatest threat to human health. Indeed, the Center for Disease Control and Prevention (CDC) lists both vancomycin resistant *S. aureus* (VRSA) and MRSA as two of the top 18 drug-resistant threats in the United States (276). Methicillin resistance, in particular, has resulted in a global pandemic of *S. aureus* infections that is ongoing to this day (195). At the molecular level, methicillin resistance is conferred by the *mecA* gene, which encodes the low-affinity penicillin-binding protein PBP2A that is carried on a mobile genetic element known as the staphylococcal chromosome cassette *mec* (SCC*mec*) (21). This cassette is variable from one strain to the next and can range in size from 21 to 60 kb in size (326). This variation has been exploited as a molecular typing technique that is used to characterize isolates of *S. aureus* (335). To date, there are 11 types of identified SCC*mec* cassettes (136). Despite the variability, all SCC*mec* cassettes have 4 unifying features: the *mecA* gene, the cassette chromosomal recombinase gene(s) (*ccr*), inverted and direct DNA repeats flanking each end, and integration into the *S. aureus* chromosome at the 3' end of a specific gene of unknown function designated *orfX* (136). Of note, the most prevalent clone of MRSA in the United States, USA300, typically carries the SCC*mec* type IV cassette (291).

Hospital-Acquired versus Community-Acquired MRSA

With increased use of methicillin in the hospital setting, MRSA was initially considered a strict nosocomial pathogen. However, in the early 1990's, isolates of MRSA

began to emerge in the community. These isolates infected healthy individuals with no prior association with health-care facilities (301). It was initially presumed that hospital-acquired MRSA (HA-MRSA) simply jumped from the health-care setting into the community. However, community-acquired MRSA (CA-MRSA) was deemed genetically distinct from HA-MRSA (301). Although it is hypothesized that CA-MRSA is the result of circulating MSSA strains that acquired the SCC*mec* cassette, why/how methicillin resistance emerged in a niche with little to no selective pressure remains a mystery.

At the genotypic level, CA-MRSA and HA-MRSA can be differentiated by two key features: SCC*mec* type and presence of genes encoding PVL. While CA-MRSA typically encodes a type IV SCC*mec* cassette, HA-MRSA strains harbor the larger type I, II, or III SCC*mec* element (94). Furthermore, PVL is highly prevalent in CA-MRSA isolates and is only rarely observed among strains of HA-MRSA (66). These genetic differences are also accompanied by epidemiological and clinical variations as well. Whereas HA-MRSA is routinely associated with multidrug resistance, CA-MRSA is susceptible to most non β-lactam antibiotics (210; 307). Moreover, while both MRSA types are capable of causing disease in both healthy and non-healthy people, CA-MRSA infections tend to present as SSTIs in younger, otherwise healthy individuals (66). Conversely, HA-MRSA infections afflict individuals with exposure to health-care facilities and typically manifest as pneumonia, bacteremia, and indwelling medical device infections (66). Although CA-MRSA has gained considerable attention due to its recent emergence and rapid spread, both MRSA types are capable of causing significant morbidity and mortality throughout the world and thus, should be monitored closely.

GOALS AND SPECIFIC AIMS

We now appreciate that colonization with *S. aureus*, particularly in the anterior nares, is a *bona fide* risk factor for SSTI development. However, it is still unclear why some carriers develop SSTI while others do not. This ambiguity is largely due to an incomplete understanding of host genetics, strain differences, immune response, and risk factors associated with SSTIs. Given the apparent link between the nasal microbiota and SSTI formation, we believe that the nose may harbor valuable clues regarding SSTI susceptibility that have yet to be discovered. To this end, the first goal of this dissertation was to correlate variations in the nasal microbiota with purulent abscess formation. This goal was divided into two aims: in Aim 1 we compared the nasal microbiomes of military trainees that either did or did not develop SSTI (described in Chapter 2). For Aim 2, we assessed the impact of *S. aureus,* both methicillin-resistant and methicillin-sensitive, on nasal and abscess microbiome composition. These studies not only highlight the complexity of the nasal and abscess microbiomes, but also indicate key SSTI-associated variations in the nasal microbiome that should prove useful for both clinicians and researchers alike.

Despite the medical and financial burden of SSTIs, remarkably little is known regarding the microbial etiology of SSTIs. While *S. aureus* is the main organism isolated from purulent SSTIs, other organisms are also frequently isolated. Furthermore, since bacteria are rarely isolated from cellulitis, their microbial composition remains largely unknown. Given the differences in clinical presentation between purulent and non-purulent SSTIs, we hypothesize that the microbial composition of each SSTI will vary.

Therefore, the second goal of this dissertation was to elucidate the microbial composition of both purulent and non-purulent (cellulitis) SSTIs. To address this goal, our first aim was to utilize high-throughput sequencing to analyze and compare the various SSTI microbiomes (described in Chapter 3). For aim 2, we characterized an SSTI caused by a clinically unique strain of *S. aureus* that was resistant to chlorhexidine (described in Chapter 4). Together, this dissertation provides insight into the nasal and SSTI microbiomes and will hopefully contribute to the treatment, as well as prevention, of SSTIs in the future.

CHAPTER TWO: Correlation Between Nasal Microbiome Composition and Remote Purulent Skin and Soft-Tissue Infections

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The work presented in this chapter is the sole work of R.C. Johnson with the following exceptions: abscess cultures were processed by Martin Army Community Hospital microbiology laboratory; study oversight at Fort Benning provided M.W. Ellis and C.D. Schlett; sample acquisition provided by J.B. Lanier; patient data collected by T. Cui.

ABSTRACT

The incidence of skin and soft-tissue infections (SSTIs) has dramatically increased over the past decade, resulting in significant morbidity in millions of otherwise healthy individuals worldwide. Certain groups, like military personnel, are at increased risk for SSTI development. Although nasal colonization with *Staphylococcus aureus* is an important risk factor for the development of SSTIs, it is not clear why some colonized individuals develop disease while others do not. Recent studies have revealed the importance of microbial diversity in human health. Therefore, we hypothesized that the nasal microbiome may provide valuable insight into SSTI development.

To examine this hypothesis, we obtained anterior nares samples from military trainees with cutaneous abscesses and from asymptomatic (Non-SSTI) participants. We also obtained samples from within abscess cavities. Specimens were analyzed by culture and the microbial community within each sample was characterized using a 16S sequencing-based approach.

We collected specimens from 46 Non-SSTI participants and from 40 participants with abscesses. We observed a significantly higher percent abundance of Proteobacteria in the anterior nares in Non-SSTI participants ($p<0.0001$) compared to participants with abscesses. Additionally, we noted a significant inverse correlation between *Corynebacterium* spp. and *S. aureus* ($p=0.0001$). The sensitivity of standard microbiological culture for abscesses was 71.4%. These data expand our knowledge of the complexity of the nasal and abscess microbiomes, and potentially pave the way for novel therapeutic and prophylactic countermeasures against SSTI.

INTRODUCTION

Staphylococcus aureus is a leading pathogen in both community and hospital settings. Infections with *S. aureus* range from invasive disease such as bacteremia and pneumonia to generally less severe skin and soft-tissue infections (SSTIs) (100; 202; 310). SSTIs, especially those caused by USA300 methicillin-resistant *Staphylococcus aureus* (MRSA) have emerged as a common, burdensome, and costly disease (127; 284; 289). Individuals in congregate settings (e.g., athletic teams, prison inmates, military trainees) are at increased risk for SSTI (151; 162; 166; 342).

Given that approximately one third of people may exhibit *S. aureus* carriage, it is unclear why some develop SSTI while others do not (154). While it is clear that host genetics, immune response, and strain differences contribute (33; 75; 132; 233; 260; 305), there are likely other important factors. As the anterior nares appears to be a critical *S. aureus* reservoir (310; 322; 323) and because antecedent nasal carriage increases the risk for infection (79; 102; 310) a better understanding of nasal microbial ecology may harbor valuable clues regarding SSTI susceptibility.

The anterior nares are a dynamic microbial battleground between pathogens and commensals (101; 223). The concept that changes in the host microbiome may influence human health is well documented (50); however, few studies have investigated how the nasal microbiome is altered in response to human disease (41; 92). Importantly, no study has investigated whether the microbial composition in the anterior nares can influence susceptibility to infection. Therefore, we hypothesized that variations in the nasal microbiome might be associated with purulent SSTIs and *S. aureus* colonization. The purpose of this study was to describe the microbial composition of the anterior nares in persons with and without cutaneous abscesses, as well as the microbial composition within cutaneous abscesses.

MATERIALS AND METHODS

Study participants and study design

This observational investigation was conducted from May 2010 to January 2012 in the setting of an ongoing prospective, field-based, cluster-randomized trial aimed at

preventing SSTI (83). Study participants were all male US Army soldiers age 17-39 who were undergoing Infantry training at Fort Benning, Georgia. The investigation was approved by the Uniformed Services University Infectious Diseases Institutional Review Board.

Enrollment and data collection

We enrolled two groups of participants: trainees with abscesses and asymptomatic (Non-SSTI) controls. Trainees who presented to the Troop Medical Clinic (TMC) with cutaneous abscesses that required incision and drainage were eligible to participate as abscess subjects. Trainees who presented with non-infectious complaints (e.g. ankle sprain) were eligible to participate as Non-SSTI subjects. After written informed consent, all participants underwent anterior nares sampling with two swabs (BD BBL CultureSwabs® (BD Diagnostic, Sparks MD)). One swab was used for microbiological culture and the other for microbiome analysis. Each swab was inserted about one centimeter into one nostril, rubbed in a circular/twirling fashion at least three times along the nasal septum and the superior, lateral, and inferior surfaces of the nare. The same swab was then used to sample the other nostril following the same procedure. For cutaneous abscesses, after skin was prepared with chlorhexidine, incision and drainage was performed in a standard fashion by TMC healthcare personnel. Two swabs were obtained from within the abscess cavity. One specimen was sent for standard microbiological culture, and the other for microbiome analysis. Within five minutes of collection, microbiome specimens were frozen at -20°C at the TMC. These samples were subsequently transported on dry ice and maintained at -80°C until molecular analysis.

Microbiological and molecular analysis

Abscess cultures were processed by the Martin Army Community Hospital microbiology laboratory according to standard protocols. Anterior nares specimens were processed as previously described (268). *S. aureus* isolates underwent PFGE to assess relatedness and PCR to assess for resistance and virulence determinants as previously described (83).

DNA extraction

Total genomic DNA was extracted from the samples using the GenElute Bacterial Genomic DNA kit (Sigma-Aldrich). Briefly, the swab heads were submerged in 500µL of Gram-Positive Lysis Solution consisting of lysozyme (45mg/mL), mutanolysin (125U/mL) and lysostaphin (0.16mg/mL) for 30 minutes at 37°C, followed by the addition of Proteinase K (0.95mg/mL) and 500µL of Lysis Solution C for 10 minutes at 55°C. Column purification of genomic DNA was conducted according to the manufacturer's recommendations.

DNA amplification and sequencing

Post DNA extraction, the V1-V3 region of the 16S rRNA gene was amplified from each sample using the universal 27F (5'-AGAGTTTGATCCTGGCTCAG-3') and 534R (5'-ATTACCGCGGCTGCTGG-3') primers (163). Briefly, 0.15µL of AccuPrime High Fidelity Taq DNA polymerase (Invitrogen) was added to a mixture containing 1X

AccuPrime PCR Buffer II, 0.2µM of each primer, and 15µL of genomic DNA to a final volume of 20µL. All reactions were performed minimally in triplicate and combined after amplicon verification on a 1% agarose gel. The combined reactions were cleaned using the Qiagen MinElute Reaction Cleanup Kit (per manufacturer's recommendation), quantified using a Nanodrop (NanoDrop 8000, Thermo Scientific), and added in a 1:1 ratio to a single 1.5mL eppendorf vial. 126 samples were multiplexed in two separate pyrosequencing runs (63 samples per run) using the Roche GS FLX Titanium 454 sequencer at the Tufts University Genomics Core Facility. Nasal and abscess samples were randomized between the two sequencing runs to reduce sequencing bias.

The reverse PCR primer contained a 6-nucleotide 'barcode' sequence that was unique to each sample, which allowed us to multiplex multiple reactions per pyrosequencing run. PCR reaction conditions were in accordance with the 16S 454 Sequencing Protocol of the Human Microbiome Consortium (http://www.hmpdacc.org/doc/16S_Sequencing_SOP_4.2.2.pdf).

Sequence processing

Sequences were processed according to the 454 standard operating procedure (SOP; http://www.mothur.org/wiki/454_SOP) using the open-source software program, mothur (v.1.31.2)(270). Sequences greater than 200 base pairs were de-noised using the mothur adapted PyroNoise algorithm (250) and aligned using the SILVA reference alignment (244). Any sequence containing more than 1 mismatch to the barcode and/or 2 mismatches to the primer sequence were discarded. Sequences within 2 base pairs of a more abundant sequence were pre-clustered together. PCR chimeras were identified and

removed using the mothur implementation of UCHIME (73). After de-nosing, trimming, and pre-clustering of raw sequences, all reads were classified using the Ribosomal Database Project (RDP) Bayesian classifier (315) using an 80% bootstrap confidence level over 100 iterations. Contaminant sequences, including mitochondria, chloroplasts, archaea, eukaryotes, and sequences classified as "unknown" at the Kingdom level, were removed from the study. All remaining sequences were clustered into operational taxonomic units (OTUs) defined by a 97% similarity level according to the average-neighbor algorithm. To avoid the effects of varying sequencing depths, all samples were rarefied to 2,245 reads per sample. Lastly, sequences were classified to the species level using the GreenGenes 16S rRNA gene database (May 2013 release) (69).

Diversity analysis and statistics

All alpha and beta-diversity analyses were computed using mothur. The inverse Simpson diversity estimator (invsimpson) was used for the alpha-diversity analyses since it can accurately assess diversity levels without being dramatically affected by sampling effort. Phylogenetic diversity was assessed using Faith's index (88). Statistical testing for percent abundance, invsimpson, Faith's index and observed Operational Taxonomic Unit (OTU) data were based on the Mann-Whitney test using GraphPad Prism. Linear regression analyses were also performed using GraphPad Prism. To determine if two populations (example: *S. aureus* carriers versus non-carriers) were significantly different based on bacterial composition, we used the analysis of molecular variance (AMOVA) test for the mothur generated Yue & Clayton (Θ_{YC}) and Jaccard distance matrices (139; 338). AMOVA was also used to test phylogenetic differences between communities

using the unweighted and weighted-Unifrac distances generated from a neighbor-joining tree containing all sequences. The neighbor-joining tree was created in mothur using the clearcut command and was also used when assessing phylogenetic diversity using Faith's index. The interrelationships between populations were spatially visualized by non-metric multidimensional scaling (NMDS) using R. When determining differentially represented OTUs between the communities, we utilized the mothur adapted Metastats software (324). OTUs that differed in abundance had a p and q value below 0.05, and were required to have a mean percent abundance greater than 0.1 in at least one of the communities.

RESULTS

Baseline participant characteristics

Overall, the study population consisted of 30,209 trainees, and 137 were enrolled in the microbiome portion of the study. Of these 137 subjects, 46 Non-SSTI, and 40 abscess participant samples were sequenced. Of the 40 abscess participants, 2 had received antimicrobials approximately 18-26 days prior to sampling and were subsequently removed from the analysis. We categorized Non-SSTI participants according to anterior nares culture results (15-MRSA, 15-methicillin-susceptible *S. aureus* (MSSA), 16-No *S. aureus* (NoSA)) and abscess participants based on anterior nares (11-MRSA, 16-MSSA, 11-NoSA) as well as abscess culture results (16-MRSA, 15-MSSA, 7-NoSA). Of the 31 *S. aureus* abscess participants, 15 (48%; 7-MRSA, 8-MSSA) had nasal-abscess concordant isolates as determined by PFGE. 15 of the 16 MRSA abscess isolates were

USA300. Study participant characteristics are outlined in Table 1. Age was shown to not have an influence on the nasal microbiome composition (Table 2). Additionally, the abscess microbiomes appeared similar in structure regardless of broadly defined anatomic location (Table 2).

Sequencing results

Sequencing of 86 participants' samples (46 Non-SSTI nasal; 40 abscess nasal, and 40 abscess cavities) were conducted in two separate pyrosequencing reactions yielding a total of 3,252,212 raw sequences; 66% of these reads remained after quality processing and contaminant removal. In addition to the two patient samples removed due to recent antimicrobial treatment, one abscess sample, which contained only 987 associated reads, was excluded from the analysis. On average, each remaining sample contained 16,538 (range 2,245-44,189) reads with an average read length of 194 (range 169-219) nucleotides. To obviate bias based on sequencing depth, 2,245 reads were randomly sub-sampled for each specimen. Good's coverage values (≥97%) as well as rarefaction curves (data not shown) suggested that this sampling size adequately represented the total observed biodiversity for each specimen. A table showing the percent abundance of each taxon for each sample is provided (Table 5 (S1)).

Phyla-level anterior nares microbiome

Analysis of the relative abundance of bacteria present within the 84 anterior nares samples revealed that the microbiome was largely composed of four phyla (Actinobacteria, Firmicutes, Proteobacteria, Bacteroidetes), and was predominantly composed of bacteria from the Actinobacteria and Firmicutes phyla (average percent abundance 56.8% and 39.7%, respectively; Figure 4A). The presence of Actinobacteria

Table 1. Study participant characteristics

	Abscess (n=38)	Non-SSTI (n=46)
Age		
Median years (range)	20 (17-33)	20.5 (18-39)
Race / Ethnicity[a]		
White, non-Hispanic	28 (74)	-[b]
Hispanic	5 (13.2)	-
Black, non-Hispanic	3 (7.9)	-
Other, non-Hispanic	1 (2.6)	-
Nasal Colonization		
MRSA	11 (28.9)	15 (32.6)
MSSA	16 (42.1)	15 (32.6)
NoSA	11 (28.9)	16 (34.8)
Abscess Colonization		
MRSA	16 (42.1)	NA
MSSA	15 (39.5)	NA
NoSA	7 (18.4)	NA
Site of Infection[c]		
Lower extremity	19 (50)	NA
Ankle	1 (2.6)	
Buttock	5 (13.2)	
Foot	1 (2.6)	
Knee	7 (18.4)	
Thigh	5 (13.2)	
Upper extremity	11 (28.9)	NA
Arm	2 (5.3)	
Elbow	5 (13.2)	
Finger	1 (2.6)	
Forearm	3 (7.9)	
Thorax	4 (10.5)	NA
Axilla	3 (7.9)	
Back	1 (2.6)	
Head and neck	3 (7.9)	NA
Neck	2 (5.3)	
Scalp	1 (2.6)	
Hygiene Study Group[d]		
Standard	8 (21)	20 (43.5)
Enhanced Standard	11 (28.9)	20 (43.5)
Chlorhexidine	19 (50)	6 (13)
Known/Suspected SSTI/MRSA Infection in the Past Year[e]	2 (5.3)	

Unless specified, numbers in parenthesis correspond to percentage of total individuals in either Abscess or Non-SSTI groups.

Abbreviations: Abscess, individuals that developed SSTI; Non-SSTI, individuals that did not develop SSTI; MRSA, Methicillin-Resistant *Staphylococcus aureus*; MSSA, Methicillin-Sensitive *Staphylococcus aureus*; NoSA, No *Staphylococcus aureus*; NA, Not Applicable

[a]Race / Ethnicity data for Non-SSTI individuals as well as one abscess individual was not obtained.

[b]Dashes correspond to data not available

[c]Site of Infection data for one individual was not obtained

[d]Military trainees were enrolled in an ongoing hygiene trial aimed at preventing SSTI prior to this study.

[e]Data for 2 individuals was not obtained.

Table 2. Microbiome composition differences

Community-1	Community-2	Jaccard p-value[a]	Φ_{yc} p-value[a]
Nasal microbiomes-<20 years old	Nasal microbiomes-Ages 20-29	0.180	0.490
Nasal microbiomes-Ages 20-29	Nasal microbiomes->29 years old	0.612	0.731
Nasal microbiomes-<20 years old	Nasal microbiomes->29 years old	0.276	0.675
Abscess microbiomes-Upper extremities	Abscess microbiomes-Lower extremities	0.378	0.257
Abscess microbiomes-Upper extremities	Abscess microbiomes-Thorax	0.486	0.515
Abscess microbiomes-Upper extremities	Abscess microbiomes-Head/Neck	0.536	0.725
Abscess microbiomes-Lower extremities	Abscess microbiomes-Thorax	0.305	0.379
Abscess microbiomes-Lower extremities	Abscess microbiomes-Head/Neck	0.519	0.512
Abscess microbiomes-Head/Neck	Abscess microbiomes-Thorax	0.435	0.063

[a]P-values are the result of performing analysis of molecular variance (AMOVA) on the Jaccard and Φ_{yc} distance matrices.

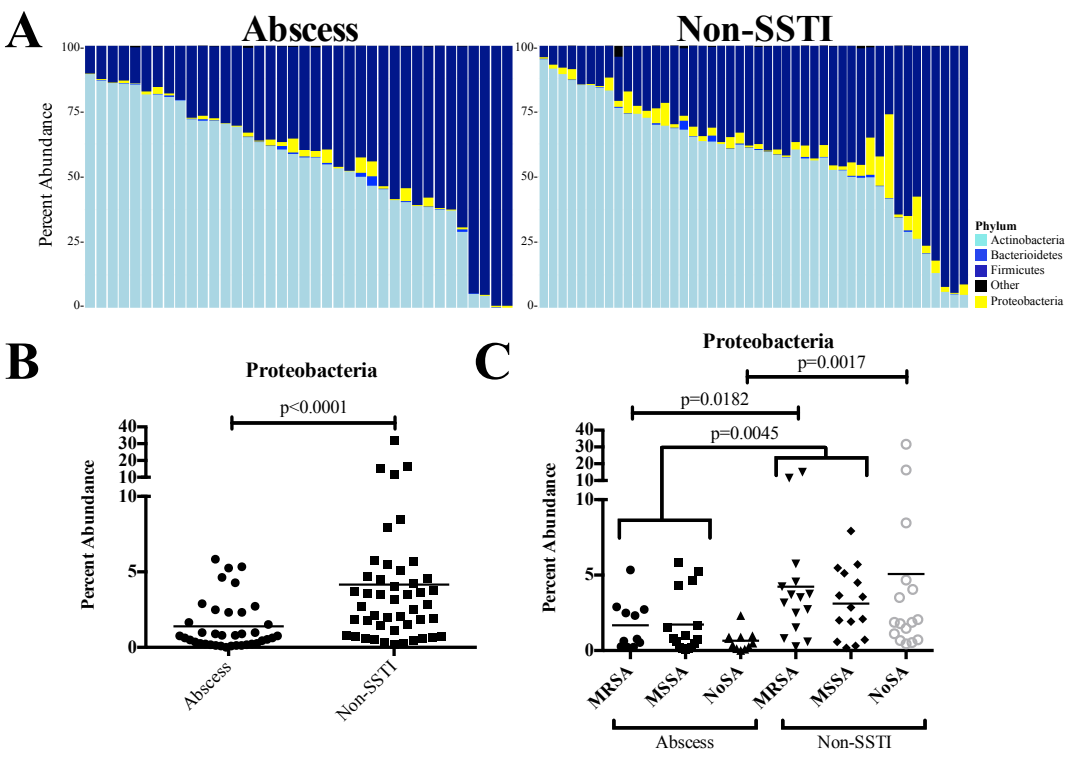

Figure 4. Characterization of the nasal microbiomes for those that did (Abscess) and did not develop SSTI (Non-SSTI).
A, Breakdown of each nasal specimen by phyla. Each column represents one swab. **B**, Percent abundance of Proteobacteria in the nose for the Abscess and Non-SSTI groups. **C**, Proteobacteria abundance broken down by nasal culture results (MRSA, MSSA, and NoSA) for the Abscess and Non-SSTI groups. Horizontal lines represent the average percent abundance. Significant comparisons were calculated using the Mann-Whitney statistical test.

and Firmicutes was inversely correlated in the anterior nares (Figure 5A). There was a significantly higher percent abundance of Proteobacteria in the anterior nares of the Non-SSTI group compared to the abscess participants (average percent abundance 1.4% vs 4.1%; $p<0.0001$; Figure 4B). This increase in Proteobacteria was not attributed to any single bacterium, but was due to an overall increase in multiple genera including *Neisseria* and *Haemophilus* (Table 3). When analyzed based on *S. aureus* nasal carriage status (MRSA, MSSA, or NoSA), we found that the Non-SSTI participants that did not carry *S. aureus* (NoSA) showed a significantly higher abundance of Proteobacteria compared to the NoSA abscess participants ($p=0.0017$; Figure 4C). The NoSA abscess participants showed exceptionally low levels of nasal Proteobacteria. A significant difference was not observed when the MSSA groups were compared between the Non-SSTI and abscess groups ($p>0.05$); however, MRSA carriers showed a significantly higher percent abundance of Proteobacteria in the Non-SSTI group ($p=0.0182$; Figure 4C). Additionally, *S. aureus* carriers (MRSA + MSSA) had a significantly greater percent abundance of Proteobacteria in the Non-SSTI group ($p=0.0045$; Figure 4C).

Genus and species-level anterior nares microbiome

Visualization of the predominant phyla, genera, and species across nasal samples suggested significant differences between the abscess and Non-SSTI samples (Figure 6). Indeed, we observed a significantly higher abundance of *Propionibacteria* ($p=0.0292$) and *S. epidermidis* ($p=0.0221$) in the Non-SSTI NoSA group as compared to the NoSA abscess group (Figure 7A, B). Additionally, among the abscess participants, we found that the NoSA group contained a significantly higher percentage of *Corynebacterium* as

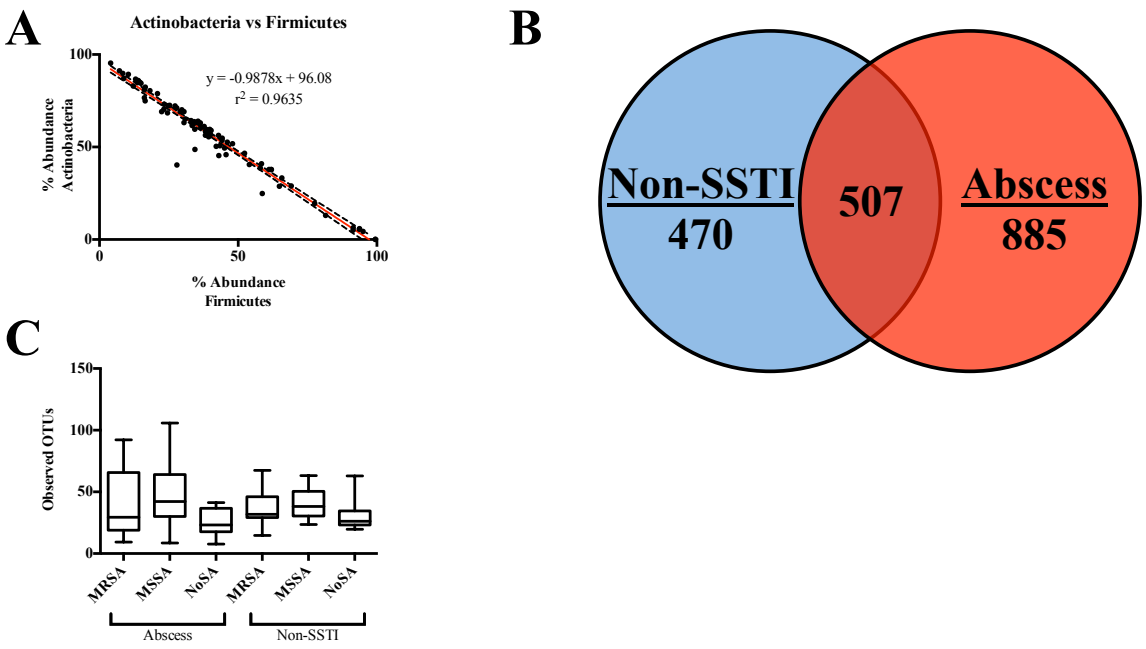

Figure 5. Characterization of the nasal microbiomes.

A, Inverse correlation between Actinobacteria and Firmicutes for all nasal samples (slope (m) = -0.9878). Red line and inset equation represent the best fit line (y = slope (x) + y-intercept). Dashed lines show the 95% confidence interval. r^2 = Coefficient of determination. **B**, Venn-diagram representing the number of Operational Taxonomic Units (OTUs) that were unique as well as shared between the Non-SSTI and abscess nasal groups. **C**, The number of OTUs for individuals colonized (MRSA and MSSA) or not colonized (NoSA) with *S. aureus* that either did (Abscess) or did not develop SSTI (Non-SSTI). Each box represents the interquartile range with the mean shown within. The whiskers spread from the minimum to maximum values.

Table 3. Abundance of Proteobacteria in the nares

	Average Percent Abundance (% ± SD)	
Genus[a]	**Abscess**[b]	**Non-SSTI**[c]
Dyella	0.41 ± 0.88	1.08 ± 2.63
Rhodanobacter	0.28 ± 0.49	0.99 ± 1.04
Haemophilus	0.01 ± 0.05	0.46 ± 2.09
Vitreoscilla	0.16 ± 0.43	0.79 ± 2.42
Neisseria	0.06 ± 0.15	0.24 ± 0.54
Moraxella	0.02 ± 0.11	0.15 ± 0.36
Burkholderia	0.03 ± 0.05	0.10 ± 0.14

SD = Standard Deviation.
[a]As determined by GreenGenes database.
[b]Individuals that developed skin and soft-tissue infections.
[c]Individuals that did not develop skin and soft-tissue infections.

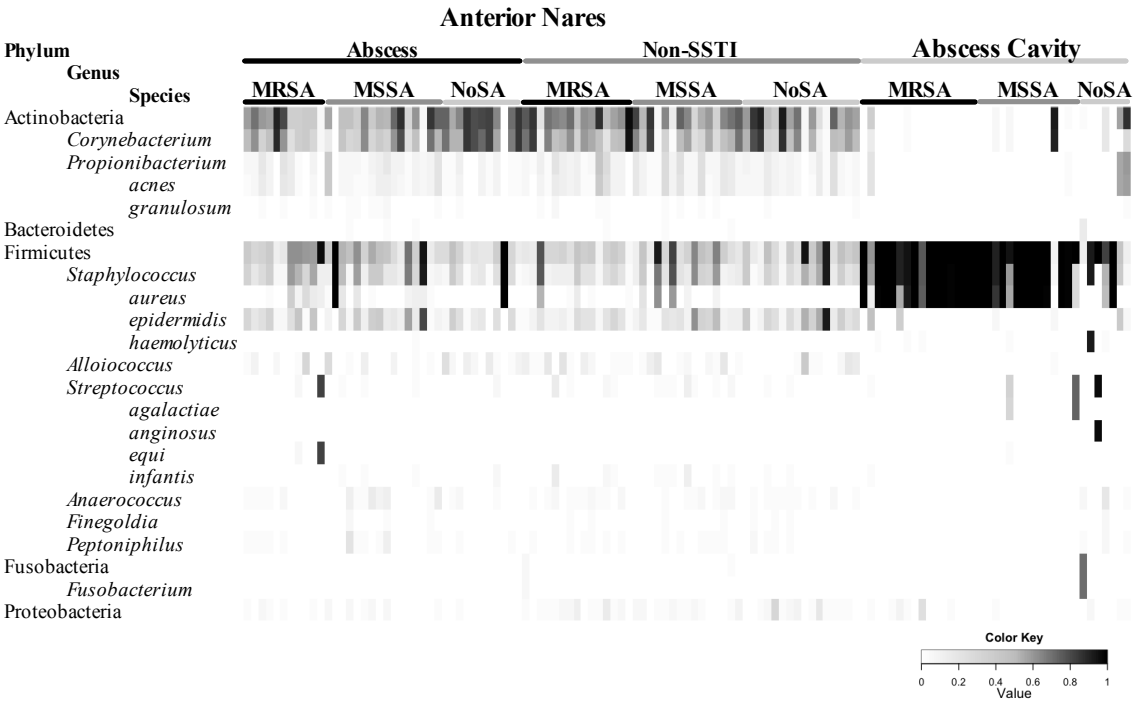

Figure 6. Heatmap showing the percent abundance for the predominant phyla, genera and species for all nasal and abscess cavity samples.
The anterior nares specimens are separated by those that did (Abscess) and did not develop SSTI (Non-SSTI). Additional sub-groupings are based on nasal culture results (MRSA, MSSA, or no *S. aureus* (NoSA)). The darker the shading, the more abundant the taxa. Each column represents a single sample.

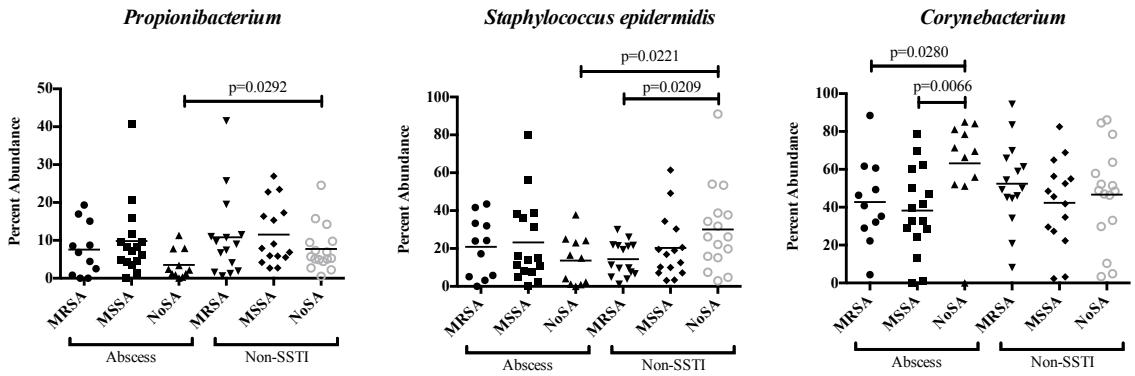

Figure 7. Percent abundance in the anterior nares for *Propionibacterium, Staphylococcus epidermidis*, and *Corynebacterium* (**A, B,** and **C**, respectively). Samples are categorized based on SSTI status (Abscess or Non-SSTI) as well as *S. aureus* nasal culture results (MRSA, MSSA, NoSA). Horizontal lines represent the average percent abundance. Significant comparisons were calculated using the Mann-Whitney statistical test.

compared to the MRSA and MSSA groups (Figure 7C). However, this correlation was not observed for the Non-SSTI groups.

Nasal microbiome composition analysis

We next investigated the overall variation in bacterial composition between the Non-SSTI and abscess participants' nasal microbiomes. Among the Non-SSTI and abscess participants, we observed a total of 977 and 1392 OTUs, respectively. Only 507 OTUs were shared across the groups (Figure 5B). In keeping with this, we observed a significant difference in the Jaccard distance matrix (AMOVA, $p<0.001$), which suggests a difference in OTU membership between the Non-SSTI and abscess participants' nasal microbiomes. This OTU membership difference was present between the Non-SSTI and abscess MRSA groups (Jaccard AMOVA, $p=0.023$; Θ_{YC} AMOVA, $p=0.152$), MSSA groups (Jaccard AMOVA, $p=0.01$; Θ_{YC} AMOVA, $p=0.928$), and NoSA groups (Jaccard AMOVA, $p=0.014$; Θ_{YC} AMOVA, $p=0.225$), suggesting that there is a bacterial membership difference between the abscess and Non-SSTI groups' nasal microbiomes, regardless of *S. aureus* colonization status. Metastats analysis of the differentially represented OTUs between the abscess and Non-SSTI nasal microbiomes showed that many were very low in abundance. However, a substantial proportion of them were from the Proteobacteria phylum (Table 4). Phylogenetic analysis using the unweighted-UniFrac distances supported the bacterial membership difference between the abscess and Non-SSTI nasal microbiomes (unweighted-Unifrac AMOVA, $p<0.001$). However, when the relative abundance of OTUs was considered, we did not detect differences

Table 4. Differential abundance of OTUs using Metastats

OTU[a]	Taxonomy[b]	Community-1 (Mean Percent Abundance)	Community-2 (Mean Percent Abundance)	p-value	q-value
0001	*Staphylococcus* (g)	*S. aureus* positive nares (34.78)	*S. aureus* negative nares (20.63)	0.004	0.018
0003	*Corynebacterium* (g)	*S. aureus* positive nares (2.19)	*S. aureus* negative nares (9.15)	0.002	0.009
0014	Proteobacteria (p)	Abscess nares (0.29)	Non-SSTI nares (0.99)	0.002	0.005
0022	Proteobacteria (p)	Abscess nares (0.005)	Non-SSTI nares (0.45)	0.021	0.041
0029	Proteobacteria (p)	Abscess nares (0.02)	Non-SSTI nares (0.17)	0.005	0.011

[a]Operational Taxonomic Unit (OTU) designation as assigned by mothur
[b](g), Genus; (p), Phylum

between the abscess and Non-SSTI nasal communities (Θ_{YC} AMOVA, p=0.825; weighted-Unifrac, p=0.603).

Although we did not detect any differences in bacterial diversity between the abscess and Non-SSTI nasal microbiomes using the inverse Simpson calculator (data not shown), at the phylogenetic level, we found that the abscess group was significantly more diverse than the Non-SSTI nasal communities (Figure 8A). However, we did not detect any significant differences when the MRSA, MSSA and NoSA groups were compared individually between the abscess and Non-SSTI groups (Figure 8B).

S. aureus impact on anterior nares bacterial composition

Given that our data suggested that *S. aureus* colonization affects the nasal architecture (Figures 6, 7), we next assessed the overall impact of *S. aureus* carriage on the nasal microbiome. As determined by the Jaccard and Θ_{yc} distances, we did not observe significant differences in anterior nares microbiome structure between MRSA and MSSA carriers among the abscess and Non-SSTI participants (data not shown). Therefore, we grouped all participants together (abscess and Non-SSTI) and subsequently reorganized them into *S. aureus*-positive and *S. aureus*-negative based on the sequencing results (> 0% abundance = *S. aureus* positive). Upon visual observation of the most abundant phyla, genera, and species, there appeared to be a higher abundance of bacteria from the Actinobacteria phylum, particularly from the genus *Corynebacterium* present in the anterior nares of *S. aureus*-negative participants (Figure 9A, B). This inverse correlation was confirmed by regression analysis (coefficient of determination (r^2) = 0.2859, slope (m) = -0.6791, p <0.0001; Figure 9C). Of note, the inverse correlation was also present between *S. epidermidis* and *Corynebacterium* (r^2 = 0.2373, m = -0.6524, p

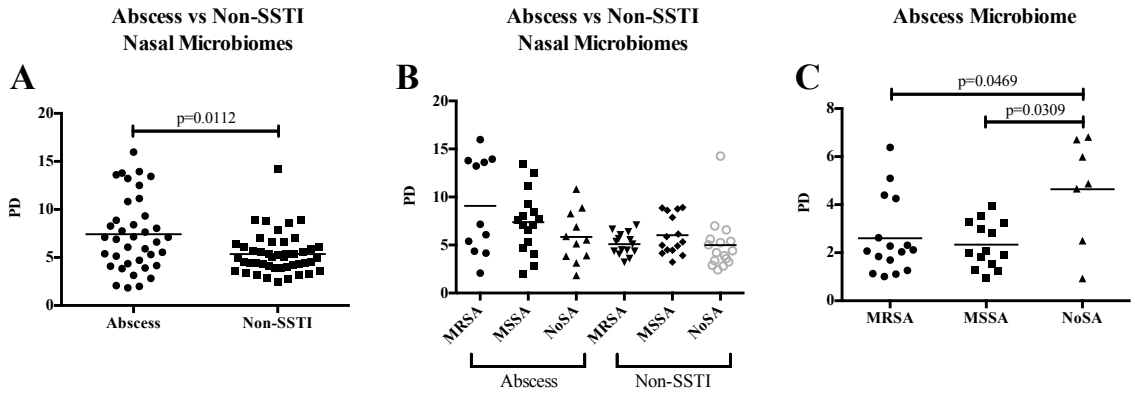

Figure 8. Phylogenetic diversity (PD) as determined using Faith's index between the **A,** abscess and Non-SSTI nasal microbiomes and **B,** various nasal microbiome subgroupings as determined by *S. aureus* colonization status (MRSA, MSSA, NoSA).
C, PD was also computed for the abscess cavity microbiomes. The various subgrouping are based on infecting *S. aureus* strain (MRSA, MSSA, NoSA).

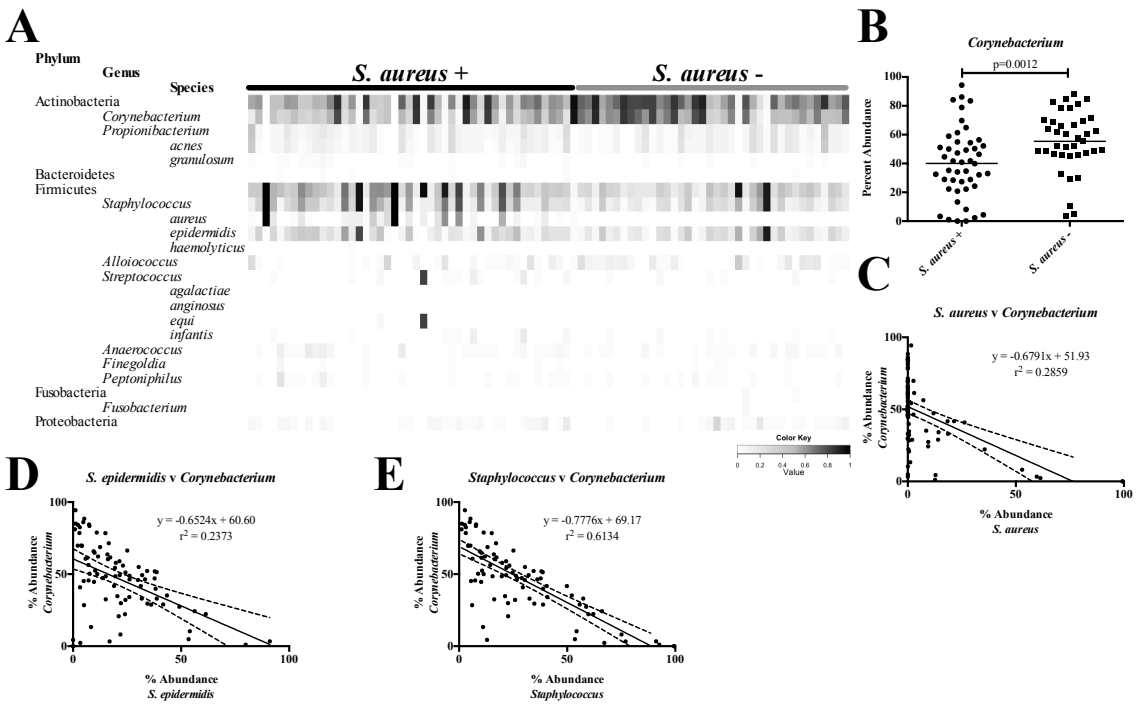

Figure 9. Impact of *Staphylococcus* on the nasal microbiome.

A, Heatmap showing the percent abundance for the predominant phyla, genera and species for nasal samples separated by *S. aureus* colonization status (based on sequencing results). The darker the shading, the more abundant the taxa. Each column represents a single sample. **B**, Percent abundance of *Corynebacterium* in the nose for individuals that were sequence positive or negative for *S. aureus*. Horizontal lines represent average percent abundance. **C**, Inverse correlation between *Corynebacterium* and *S. aureus*, **D,** *S. epidermidis*, **E**, and *Staphylococcus*. Solid lines and inset equations represent the best fit line (y = slope (x) + y-intercept). Dashed lines represent the 95% confidence interval. r^2 = Coefficient of determination.

<0.0001), but was strongest when all species of *Staphylococcus* were considered (r^2 = 0.6134, m = -0.7776, p<0.0001; Figure 9D, E). Thus, *Staphylococcus* and *Corynebacterium* appear to compete for nasal landscape.

When we analyzed the overall bacterial composition between *S. aureus*-negative and positive nasal microbiomes using the Θ_{YC} and weighted-Unifrac distance matrices, we observed a significant difference in OTU abundance levels between *S. aureus*-positive and *S. aureus*-negative groups (Θ_{YC} AMOVA, p=0.003; weighted-Unifrac AMOVA, p<0.001). This difference could be visualized by non-metric multidimensional scaling (NMDS; Figure 10), and was shown by Metastats analysis to be largely driven by differential representation of Staphylococcal and Corynebacterial OTUs (Table 4). These data support our finding that *Staphylococcus* and *Corynebacterium* presence are inversely correlated (Figure 9) and suggests that these two genera alone can greatly impact the overall diversity of the anterior nares.

Abscess microbiome

We next characterized the 37 abscess swabs obtained from abscess participants. As shown in Figure 11A, we found that the majority of bacteria present within the abscess belonged to the Firmicutes phylum (87.6% average abundance). Of note, many of the abscesses were polymicrobial; 10 of the 37 abscesses had no single bacterial species reach more than 90% abundance (Figures 6 and 11A). At the species level, *S. aureus* dominated the majority of abscesses (73.7% average abundance). Other common bacteria found within the abscesses included: *Staphylococcus haemolyticus, Streptococcus agalactiae, Streptococcus anginosus, Propionibacterium acnes,* and *Corynebacterium*. We observed one sample highly rich in *Fusobacterium* (Figure 6). For the seven NoSA

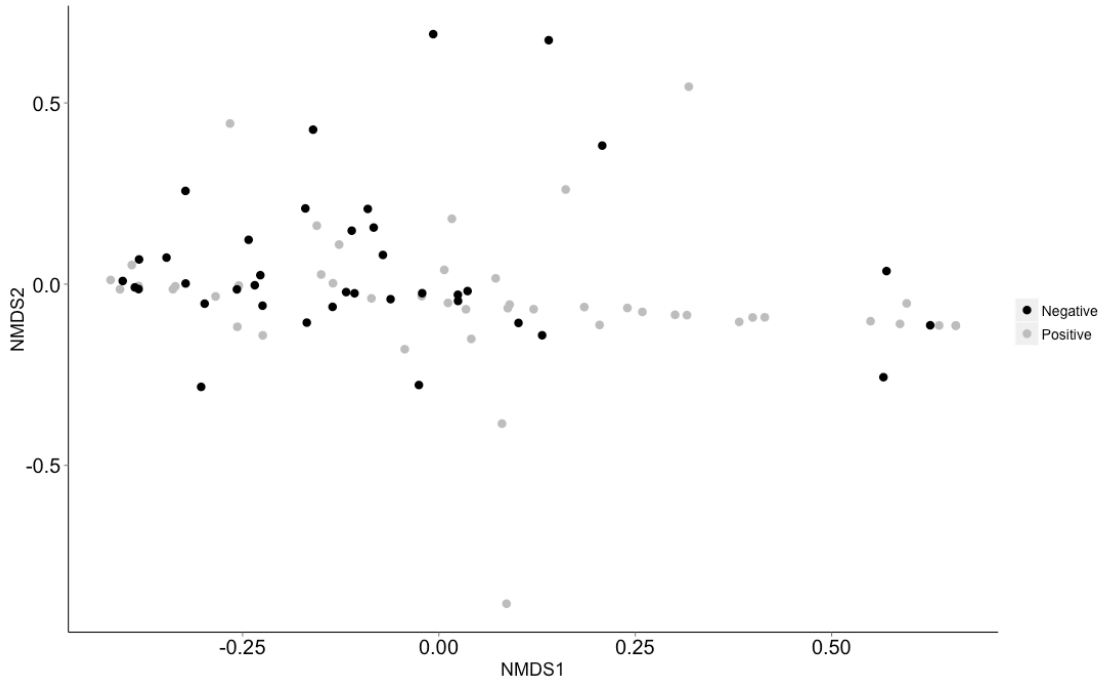

Figure 10. Non-metric multidimensional scaling (NMDS) plot showing the spatial variation between *S. aureus* positive and negative nasal communities using the Θ_{YC} distances, indicating that these communities are compositionally distinct. The spatial separation between the positive and negative groups is statistically significant (AMOVA, $p<0.001$).

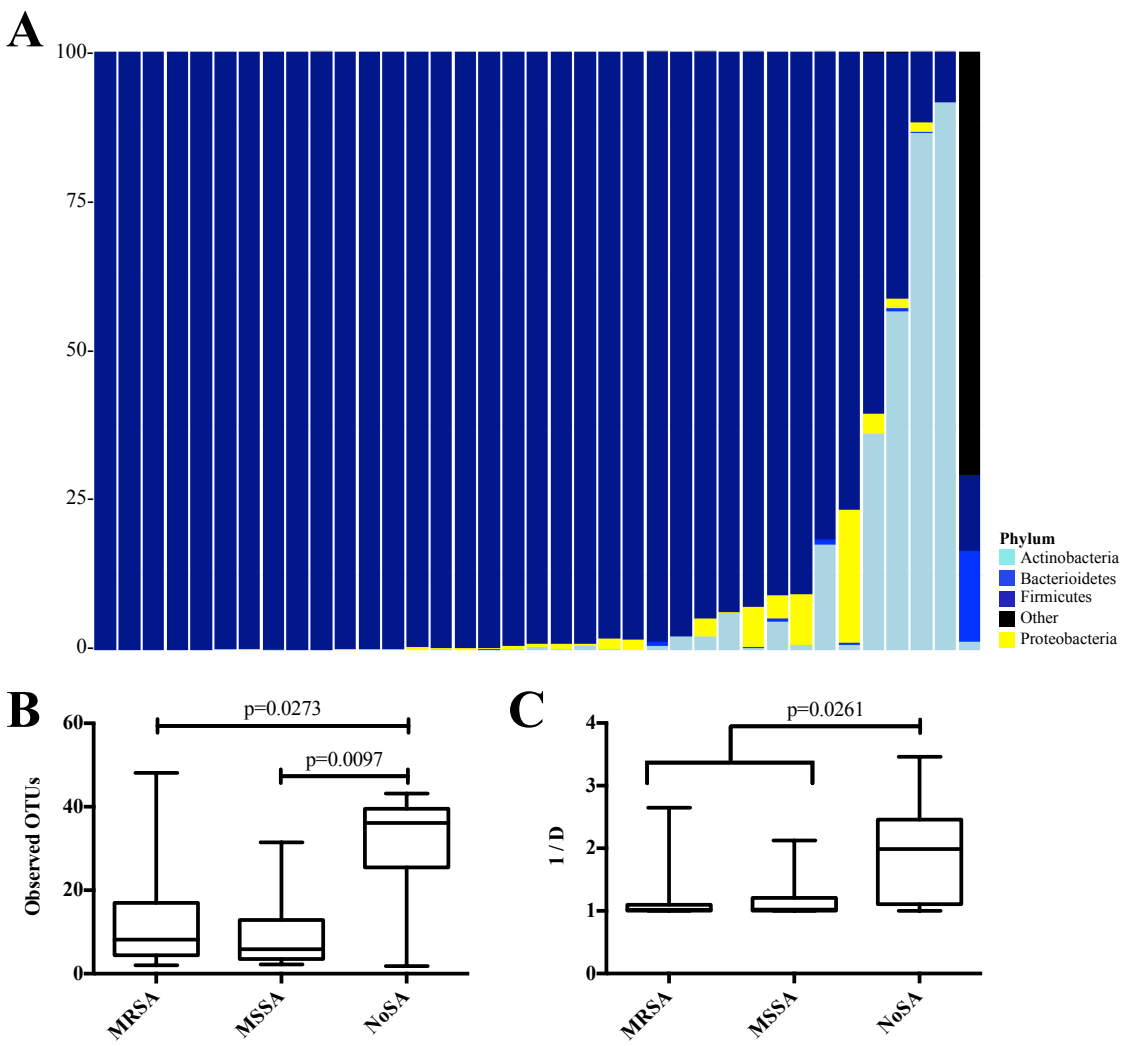

Figure 11. Characterization of the abscess cavity microbiomes.
A, Breakdown of each abscess cavity specimen by phyla. Each column represents one abscess swab. **B**, The number of observed OTUs for each abscess is shown as well as the **C**, inverse simpson index (1/D). Each box represents the interquartile range with the mean shown within. The whiskers spread from the minimum to maximum values. Significant comparisons were calculated using the Mann-Whitney statistical test.

abscesses, we collected basic microbiological information for the organisms that were cultured from the abscess cavity. These included coagulase-negative *Staphylococcus*, *Escherichia coli*, Group A and G *Streptococcus,* and *Enterobacter*. Although it is difficult to draw any correlations between nasal and abscess colonization, we note that for the individual in which Group A *Streptococcus* was cultured from the abscess, we observed an exceptionally high level of *Streptococcus* in the nares (>80 percent abundance).

Our study design allowed us to also directly compare the microbiomes of MRSA, MSSA, and no *S. aureus* (NoSA) abscesses. This analysis revealed that NoSA abscesses showed a significantly greater number of observed OTUs compared to the MRSA ($p=0.0273$) and MSSA abscesses ($p=0.0097$; Figure 11B). In addition, the NoSA group was significantly more diverse than the *S. aureus* positive abscesses (MRSA + MSSA; $p=0.0261$; Figure 11C). Using Faith's index, we also found that at the phylogenetic level, the NoSA groups were more diverse than the MRSA ($p=0.0469$) and MSSA ($p=0.0309$) abscesses (Figure 8C). Comparison of the Θ_{YC} and weighted-Unifrac distances among groups revealed that the NoSA abscesses were significantly different from the MRSA (Θ_{YC} AMOVA, $p<0.001$; weighted-Unifrac AMOVA, $p=0.002$) and MSSA (Θ_{YC} AMOVA, $p=0.004$; weighted-Unifrac AMOVA, $p=0.035$) abscesses. This suggests that bacteria found among the *S. aureus*-positive and negative abscess communities were different in abundance levels. There were no OTU abundance differences between the MRSA and MSSA abscesses. Membership-based Jaccard and unweighted-Unifrac distance analysis revealed that the MRSA and MSSA abscesses were significantly different from that of the NoSA abscesses in regards to which OTUs were present

(Jaccard AMOVA, p=0.005 and p=0.021, respectively; unweighted-Unifrac AMOVA, p=0.002 and p=0.001, respectively).

Sensitivity of culture for *S. aureus* detection

For individuals that were considered *S. aureus*-negative (NoSA) by anterior nares culture, we observed a high level of concordance with sequencing data. Only one out of the 27 culture-negative anterior nares specimens demonstrated a *S. aureus* abundance level greater than 0.1% in the sequencing results. On the other hand, abscess culture appeared significantly less reliable; 2 of the 7 culture negative abscesses were sequence positive and showed a relatively high abundance level of *S. aureus* (>49% abundance). Thus, this culture sensitivity of 71.4% for abscess samples may indicate that standard microbiology culture alone has limitations for determining abscess etiology.

DISCUSSION

In this investigation involving a large community-based population at high risk for SSTI, we made several significant observations that help describe a healthy nasal microbial composition and may help inform future prevention strategies. We observed a greater abundance of Proteobacteria in the anterior nares of the Non-SSTI participants compared to those who had developed cutaneous abscesses. Additionally, with regard to anterior nares carriage, we noted an inverse correlation between *Corynebacterium* spp and *S. aureus*.

S. aureus nasal colonization is a risk factor for the development of SSTIs (67; 322; 323); however, as demonstrated in our investigation, it is not always associated with

SSTI. Therefore, we set out to classify the nasal microbiomes of people who did or did not develop cutaneous abscess in order to identify a "marker" microbiome associated with abscess development. In agreement with other nasal microbiome studies that have primarily looked at healthy individuals (101; 170; 223; 334), we found that Actinobacteria and Firmicutes dominated the nares of all patients (Figure 4A). In particular, *Corynebacterium* and *Staphylococcus* were the most abundant genera present (Figure 5). Intriguingly, we found that participants without abscesses carried a higher abundance of Proteobacteria in their anterior nares (Figure 4B). This finding suggests that a loss of Proteobacteria in the nares may either be associated with development of SSTI or may be a "marker" of the SSTI state. While the most significant reduction of Proteobacteria was seen in NoSA abscess individuals, lower abundance was also seen in *S. aureus* colonized abscess participants (Figure 4C). Thus, even in the presence of *S. aureus* carriage, low levels of Proteobacteria appear to correlate with SSTI. In a recent study by Lemon, *et al*., an inverse correlation between Firmicutes and Proteobacteria abundance was observed in the oropharynx (170). Their finding suggests that Proteobacteria may inhibit Firmicutes colonization in that niche. However, when we compared abundance of Proteobacteria to Firmicutes in our patients, we did not find any significant correlations (data not shown). Thus, SSTI incidence is not solely due to increased abundance of *S. aureus* (Figure 4C). For those individuals who are not *S. aureus* carriers, it is intriguing to speculate that Proteobacteria occupy the nasal niche in such a way as to prevent colonization by other pathogenic microbes. Therefore, it would be interesting to determine if Proteobacteria in the nares may in fact be protective against SSTI and could be used prophylactically to prevent SSTI.

We observed a significant inverse correlation between *S. aureus* and *Corynebacterium* abundance in the nares (Figure 9C). A similar finding has been documented by other studies (170; 302; 334). Indeed, *Corynebacterium* has been shown to directly inhibit *S. aureus* growth (170), as well as to foster clearance of *S. aureus* from the anterior nares (302). The molecular mechanism by which this occurs is not clear. Perhaps *Corynebacterium* produces a product that is toxic to *S. aureus*. Alternatively, *Corynebacterium* may successfully compete for limited nutrients required for *S. aureus* growth. If the former is the case, and the toxic molecule can be isolated and purified, it could potentially serve as a novel therapeutic agent to prevent *S. aureus* colonization.

Our data indicate that *S. aureus* colonization has a major impact on the overall composition of the nasal microbiota in our study population (Figure 10). However, our cross-sectional sampling limits our ability to discern between persistently or non-persistently colonized individuals. In a recent study that monitored the nasal microbiome of 12 healthy individuals over a course of three weeks, it was determined that while *S. aureus* carriers and non-carriers had similar nasal microbiomes, non-persistent carriers displayed a significant drop in bacterial diversity (334). Proteobacteria levels in the nares were also shown to significantly vary among persistent and non-persistent carriers (334). Additionally, microbiota changes at other body locations (axilla, groin, perianal), as well as the site of infection prior to abscess formation, may also contribute to SSTI susceptibility (336).

Although vaccine studies have been largely ineffective at preventing *S. aureus* carriage in humans (33; 62; 267), a greater understanding of the nature of the apparent competition between *S. aureus* and other taxa may hold promise for future therapeutic

design to prevent *S. aureus* carriage and SSTI development. Although bacterial antagonism against *S. aureus* has previously been investigated (138; 228; 302; 334), our data suggests that there are additional variables to consider when designing prophylactic countermeasures; in order to lower the risk of development of SSTI, one must lower *S. aureus* colonization levels, but must be cognizant about other nasal bacterial inhabitants, especially from the Proteobacteria phylum. Additionally, a reduction of specific bacteria in non-carriers, including *Propionibacterium* and *S. epidermidis,* correlates with SSTI development (Figure 7). Given these data, nasal administration of a single bacterium may not be sufficient to protect against SSTIs; a medley of bacteria may be needed.

Given that culture has been the primary method used to identify the etiological agent of abscesses (282), our study provides the first in-depth characterization of abscesses from individuals infected with MRSA, MSSA and NoSA. Not surprisingly, we found that the vast majority of MRSA and MSSA culture-positive abscesses were dominated by *S. aureus* (Figure 6). Interestingly, we identified a high number of polymicrobial infections, especially in the NoSA abscess group (Figures 6 and 11). It is possible that bacteria within a polymicrobial infection may possess a distinct transcriptional profile compared to a monomicrobial abscess. Indeed, *S. aureus* in the context of a polymicrobial infection displays enhanced pathogenesis when compared to a *S. aureus* monoinfection (212).

There are limitations to our investigation. First, this study was conducted in the context of a prospective cluster-randomized trial that involved hygiene measures. Although we did not detect any differences in the nasal microbiomes of the participants in different study groups (data not shown), it is possible that the hygiene interventions

(287), especially chlorhexidine use, may have impacted the anterior nares microbiome. However, given that some of our findings are congruent with other studies (the inverse correlation between *S. aureus* and *Corynebacterium* in the nares has also been observed elsewhere (170; 302; 334)), this suggests that chlorhexidine use did not have a major impact on the nasal microbiome. Nevertheless, our large sample provides a firm hypothesis-generating foundation upon which to build. Second, because all abscesses were drained based on clinical criteria, these culture swabs were processed in the microbiology lab using standard techniques, which is different from the enriched technique employed for the anterior nares specimens. This may in part explain the discrepancy between culture-negative and sequence-positive abscesses.

In summary, we have characterized the nasal microbiome of over 80 individuals and have described significant differences in microbial composition in the anterior nares between those with and without abscesses, and between *S. aureus* carriers and non-carriers. We also used high-throughput sequencing techniques to unveil the microbiome of abscesses. These observations expand our understanding of the complexity of the nasal and abscess microbiomes, and will potentially be useful in the design of future therapeutic and prophylactic countermeasures against *S. aureus* carriage and subsequent disease.

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Table 5 (S1). Percent abundance of each taxon per sample according to the GreenGenes database.
Each column represents one sample and is labeled with sample ID, sample location (abscess cavity or nasal), and SSTI/*S. aureus* colonization status (Abscess or Non-SSTI; MRSA, MSSA, or NoSA). The total number of reads associated with each sample is included at the bottom of each column.

Sample ID	1712R	1717R	1742R	1749R	1751R	1978R	2012R	2040R	2046R	2123R	2171R	1683R	1715R	1716R	1737R	1761R	1767R	1781R	1790R
Sample Location	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose
SSTI/*S. aureus* colonization status	MRSA Abscess	MRSA Abscess	MRSA Abscess	MRSA Abscess	MRSA Abscess	MRSA Abscess	MRSA Abscess	MRSA Abscess	MRSA Abscess	MRSA Abscess	MRSA Abscess	MSSA Abscess	MSSA Abscess	MSSA Abscess	MSSA Abscess	MSSA Abscess	MSSA Abscess	MSSA Abscess	MSSA Abscess
Taxon																			
p__Acidobacteria	0.222717149	0	0.222717149	0	0	0.08908686	0.08908686	0	0.04454343	0.04454343	0	0.04454343	0	0.04454343	0	0	0	0.222717149	0.08908686
c__Acidobacteria-5	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
c__Acidobacteria-6	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0.04454343	0
o__iii1-15	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0.04454343	0
c__Acidobacteriia	0.08908686	0	0.178173719	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0.13363029	0
o__Acidobacteriales	0.08908686	0	0.178173719	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0.13363029	0
f__Acidobacteriaceae	0.04454343	0	0.08908686	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0.08908686	0
g__Edaphobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__modestum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Terriglobus	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0.04454343	0	0.08908686	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.08908686	0
unclassified	0.04454343	0	0.08908686	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.08908686	0
f__Koribacteraceae	0.04454343	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Candidatus_Koribacter	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Chloracidobacteria	0.04454343	0	0.04454343	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343
o__DS-100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__PK29	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
o__RB41	0.04454343	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343
f__Ellin6075	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343
unclassified	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343
unclassified	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__DA052	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
o__Ellin6513	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
c__RB25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Solibacteres	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Solibacterales	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__MVS-65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__PK34	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Sva0725	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Sva0725	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__iii1-8	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
o__DS-18	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Actinobacteria	57.95100223	69.08685969	59.64365256	56.83741648	89.30957684	80.8908686	37.86191537	37.77282851	40.97995546	38.6636971	4.365256125	55.54565702	0.08908686	46.63697105	45.87973274	37.9064588	64.32071269	40.53452116	51.75946548
c__Acidimicrobiia	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Acidimicrobiales	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__C111	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__EB1017	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Actinobacteria	57.77282851	69.04231626	59.42093541	56.83741648	89.30957684	80.84632517	37.86191537	37.77282851	40.97995546	38.48552339	4.365256125	55.50111359	0.08908686	46.63697105	45.83518931	37.86191537	64.32071269	40.35634744	51.75946548
o__Actinomycetales	57.77282851	68.99777283	59.42093541	56.83741648	89.30957684	80.84632517	37.86191537	37.77282851	40.97995546	38.48552339	4.365256125	55.50111359	0.08908686	46.63697105	45.83518931	37.86191537	64.32071269	40.35634744	51.75946548
f__Actinomycetaceae	0	0	0	0	0	0.08908686	0	0	0	0.04454343	0	0.08908686	0	0	0.04454343	0	0.222717149	0.04454343	0
g__Actinobaculum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Actinomyces	0	0	0	0	0	0.08908686	0	0	0	0.04454343	0	0.08908686	0	0	0	0	0.222717149	0.04454343	0
s__europaeus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__hyovaginalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.08908686	0	0	0	0.04454343	0	0.08908686	0	0	0	0	0.222717149	0.04454343	0
g__Mobiluncus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Varibaculum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Actinosynnemataceae	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343	0
g__Actinoalloteichus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kutzneria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lentzea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__violacea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Saccharothrix	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
f__Beutenbergiaceae	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
f__Bogoriellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Georgenia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Brevibacteriaceae	0	0.04454343	0.08908686	0	0	0.04454343	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0.13363029	0
g__Brevibacterium	0	0.04454343	0.08908686	0	0	0.04454343	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0.13363029	0
s__aureum	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0.04454343	0
s__casei	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
s__paucivorans	0	0.04454343	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0
f__Cellulomonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinotalea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Cellulomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__uda	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Corynebacteriaceae	49.30957684	61.6481069	32.11581292	46.36971047	88.46325167	60.66815145	22.22717149	35.23385301	40.84632517	28.99777283	4.365256125	13.31848552	0.04454343	41.69265033	28.46325167	33.00668151	62.31625835	28.86414254	39.86636971
g__Corynebacterium	49.30957684	61.6481069	32.11581292	46.36971047	88.46325167	60.66815145	22.22717149	35.23385301	40.84632517	28.99777283	4.365256125	13.31848552	0.04454343	41.69265033	28.46325167	33.00668151	62.31625835	28.86414254	39.86636971
s__durum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__kroppenstedtii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__lubricantis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mastitidis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__pilosum	0.178173719	0.04454343	0.04454343	0.489977728	0.08908686	0.04454343	0.267260579	0	0.178173719	0	0	0	0	0.04454343	4.855233853	0.08908686	0	0	0.13363029
s__renale	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
s__simulans	0	0	0.222717149	0	0	0.13363029	0	0.178173719	0	0.267260579	0	0.08908686	0	0.04454343	0	0	0.04454343	0.356347439	0.04454343
s__stationis	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	49.13140312	61.60356347	31.84855234	45.87973274	88.37416481	60.48997773	21.95991091	35.05567929	40.66815145	28.73051225	4.365256125	13.1403118	0.04454343	41.60356347	23.60801782	32.91759465	62.27171492	28.5077951	39.68819599
f__Dermabacteraceae	0.04454343	0	0.08908686	0.04454343	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0.04454343
g__Brachybacterium	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
s__conglomeratum	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Dermabacter	0.04454343	0	0.08908686	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0.04454343	0	0.08908686	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343
f__Dermacoccaceae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dermacoccus	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Dermatophilaceae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dermatophilus	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Dietziaceae	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dietzia	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Frankiaceae	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0.04454343	0
g__Frankia	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Geodermatophilaceae	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Blastococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aggregatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Geodermatophilus	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
s__obscurus	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Modestobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Gordoniaceae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Gordonia	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Intrasporangiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Knoellia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__subterranea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Phycicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Serinicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Kineosporiaceae	0	0.04454343	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Kineococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kineosporia	0	0.04454343	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
f__Microbacteriaceae	0.13363029	0.04454343	0.356347439	0	0	0.178173719	0.04454343	0	0	0.13363029	0	0.222717149	0	0	0	0.13363029	0	0.08908686	0.04454343
g__Agrococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__jenensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Clavibacter	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__michiganensis	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Cryocola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Curtobacterium	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Frigoribacterium	0	0	0	0	0	0.08908686	0	0	0	0.04454343	0	0.13363029	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.08908686	0	0	0	0.04454343	0	0.13363029	0	0	0	0	0	0	0
g__Leucobacter	0	0.04454343	0.267260579	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0.04454343
unclassified	0	0.04454343	0.267260579	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0.04454343
g__Microbacterium	0	0	0.08908686	0	0	0.08908686	0.04454343	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0
s__chocolatum	0	0	0.04454343	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0
s__maritypicum	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0
g__Mycetocola	0.08908686	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0.08908686	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Pseudoclavibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0
s__bifida	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0
g__Yonghaparkia	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Micrococcaceae	0.356347439	0.13363029	0.445434298	0.801781737	0.04454343	0.13363029	0.267260579	0	0.04454343	0	0	0.222717149	0	0.08908686	0.13363029	0	0.08908686	0.979955457	0.04454343
g__Arthrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__crystallopoietes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__psychrolactophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Citricoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__alkalitolerans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kocuria	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0
s__palustris	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0
s__rhizophila	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Microbispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__rosea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Micrococcus	0.356347439	0.13363029	0.400890869	0	0.04454343	0.13363029	0.267260579	0	0.04454343	0	0	0.13363029	0	0.08908686	0.13363029	0	0.08908686	0.890868597	0.04454343
s__luteus	0.356347439	0.13363029	0.400890869	0	0.04454343	0.13363029	0.267260579	0	0.04454343	0	0	0.13363029	0	0.08908686	0.13363029	0	0.08908686	0.890868597	0.04454343
g__Nesterenkonia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Renibacterium	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0
g__Rothia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aeria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mucilaginosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Zhihengliuella	0	0	0	0.801781737	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.801781737	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Micromonosporaceae	3.118040089	0.04454343	8.864142539	0	0	0.04454343	0.04454343	0	0	0.04454343	0	0	0	0	10.95768374	0.08908686	0	0.267260579	0
g__Actinocatenispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Catellatospora	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
g__Couchioplanes	3.118040089	0.04454343	8.864142539	0	0	0	0	0	0	0	0	0	0	0	10.95768374	0.08908686	0	0.222717149	0
s__caeruleus	3.118040089	0.04454343	8.864142539	0	0	0	0	0	0	0	0	0	0	0	10.95768374	0.08908686	0	0.222717149	0
g__Solwaraspora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Verrucosispora	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__gifhornensis	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
f__Mycobacteriaceae	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0
g__Mycobacterium	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0
s__celatum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__gordonae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__vaccae	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
f__Nakamurellaceae	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343	0
unclassified	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343	0
unclassified	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343	0
f__Nocardiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nocardia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__fascians	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__globerulus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nocardioidaceae	0.08908686	0.222717149	0.178173719	0.04454343	0	0.222717149	0.08908686	0	0.04454343	0.222717149	0	0.04454343	0	0	0	0.222717149	0.13363029	0.08908686	0.04454343
g__Actinopolymorpha	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Aeromicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Friedmanniella	0	0	0.04454343	0	0	0	0.04454343	0	0	0.08908686	0	0.04454343	0	0	0	0	0.04454343	0.08908686	0
unclassified	0	0	0.04454343	0	0	0	0.04454343	0	0	0.08908686	0	0.04454343	0	0	0	0	0.04454343	0.08908686	0
g__Nocardioides	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
g__Pimelobacter	0.08908686	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0.04454343	0	0	0.04454343
unclassified	0.08908686	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0.04454343	0	0	0.04454343
g__Propionicimonas	0	0.222717149	0.04454343	0.04454343	0	0.222717149	0	0	0.04454343	0.04454343	0	0	0	0	0	0.178173719	0.08908686	0	0
unclassified	0	0.222717149	0.04454343	0.04454343	0	0.222717149	0	0	0.04454343	0.04454343	0	0	0	0	0	0.178173719	0.08908686	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nocardiopsaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nocardiopsis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__composta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Promicromonosporaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Cellulosimicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Promicromonospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Propionibacteriaceae	4.454342984	6.815144766	16.97104677	8.730512249	0.801781737	19.33184855	15.10022272	2.538975501	0	8.55233853	0	40.80178174	0.04454343	4.855233853	6.191536748	4.409799555	1.514476615	9.665924276	11.71492205
g__Luteococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Microlunatus	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Propionibacterium	4.454342984	6.815144766	16.97104677	8.730512249	0.801781737	19.33184855	15.05567929	2.538975501	0	8.5077951	0	40.80178174	0.04454343	4.855233853	6.191536748	4.409799555	1.469933185	9.665924276	11.71492205
s__acnes	3.919821826	6.191536748	15.76837416	7.928730512	0.712694878	18.30734967	14.4766147	2.405345212	0	6.057906459	0	38.6636971	0.04454343	4.632516704	5.033407572	2.93986637	1.158129176	6.681514477	10.20044543
s__granulosum	0.534521158	0.623608018	1.202672606	0.801781737	0.08908686	1.024498886	0.579064588	0.13363029	0	2.449888641	0	2.138084633	0	0.222717149	1.158129176	1.469933185	0.311804009	2.9844098	1.514476615
g__Tessaracoccus	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343	0	0
f__Pseudonocardiaceae	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
g__Actinomycetospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
g__Pseudonocardia	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Sporichthyaceae	0.08908686	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Sporichthya	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.08908686	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0.08908686	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0
f__Streptomycetaceae	0.178173719	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0.08908686	0
g__Kitasatospora	0.178173719	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.178173719	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Streptomyces	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0.08908686	0
s__lanatus	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0	0
s__mashuensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__scabrisporus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
f__Streptosporangiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nonomuraea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__roseoviolacea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphaerisporangium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermomonosporaceae	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0
g__Actinomadura	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0
s__vinacea	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0
f__Tsukamurellaceae	0	0	0	0.846325167	0	0	0	0	0	0.178173719	0	0.400890869	0	0	0	0	0	0	0
g__Tsukamurella	0	0	0	0.846325167	0	0	0	0	0	0.178173719	0	0.400890869	0	0	0	0	0	0	0
unclassified	0	0	0	0.846325167	0	0	0	0	0	0.178173719	0	0.400890869	0	0	0	0	0	0	0
o__Micrococcales	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Coriobacteriia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
o__Coriobacteriales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
f__Coriobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Adlercreutzia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Atopobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
s__rimae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Collinsella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aerofaciens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Slackia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__MB-A2-108	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__0319-7L14	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__OPB41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Rubrobacteria	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
o__Rubrobacterales	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
f__Rubrobacteraceae	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Rubrobacter	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
c__Thermoleophilia	0.13363029	0.04454343	0.178173719	0	0	0.04454343	0	0	0	0.13363029	0	0.04454343	0	0	0	0.04454343	0	0.178173719	0
o__Gaiellales	0.08908686	0	0.04454343	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
f__Gaiellaceae	0.08908686	0	0.04454343	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0.08908686	0	0.04454343	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0.08908686	0	0.04454343	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
o__Solirubrobacterales	0.04454343	0.04454343	0.13363029	0	0	0	0	0	0	0.08908686	0	0.04454343	0	0	0	0.04454343	0	0.178173719	0
f__Conexibacteraceae	0	0	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0.04454343	0
g__Conexibacter	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
f__Patulibacteraceae	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
f__Solirubrobacteraceae	0	0.04454343	0.04454343	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0.08908686	0
g__Solirubrobacter	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0.08908686	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0.08908686	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Armatimonadetes	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Armatimonadia	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Armatimonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Armatimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__CL0-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__FW68	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Chthonomonadetes	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Chthonomonadales	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Chthonomonadaceae	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Fimbriimonadia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Fimbriimonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Fimbriimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Fimbriimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__OPB50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__BRC1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__PRR-11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Bacteroidetes	0.178173719	0.13363029	0.311804009	0.356347439	0	0.267260579	0.04454343	0.04454343	0	0.13363029	0	0.668151448	0	0.222717149	3.207126949	0	0.222717149	0.311804009	0.04454343
c__Bacteroidia	0	0	0.04454343	0	0	0	0	0	0	0	0	0.08908686	0	0.178173719	3.162583519	0	0.222717149	0.04454343	0
o__Bacteroidales	0	0	0.04454343	0	0	0	0	0	0	0	0	0.08908686	0	0.178173719	3.162583519	0	0.222717149	0.04454343	0
f__Bacteroidaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bacteroides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__caccae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ovatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__uniformis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Paraprevotellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0.178173719	0	0
g__Prevotella	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0.08908686	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0.08908686	0	0
g__YRC22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0
f__Porphyromonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	3.118040089	0	0	0.04454343	0
g__Porphyromonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	3.118040089	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	3.118040089	0	0	0.04454343	0
g__Tannerella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Prevotellaceae	0	0	0.04454343	0	0	0	0	0	0	0	0	0.08908686	0	0	0.04454343	0	0.04454343	0	0
g__Prevotella	0	0	0.04454343	0	0	0	0	0	0	0	0	0.08908686	0	0	0.04454343	0	0.04454343	0	0
s__copri	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0.04454343	0	0
s__melaninogenica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__nanceiensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ruminicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__stercorea	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
f__Rikenellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Blvii28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__S24-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Cytophagia	0.04454343	0	0.08908686	0.04454343	0	0.04454343	0.04454343	0	0	0.04454343	0	0.04454343	0	0.04454343	0.04454343	0	0	0	0
o__Cytophagales	0.04454343	0	0.08908686	0.04454343	0	0.04454343	0.04454343	0	0	0.04454343	0	0.04454343	0	0.04454343	0.04454343	0	0	0	0
f__Cytophagaceae	0.04454343	0	0.08908686	0.04454343	0	0.04454343	0.04454343	0	0	0.04454343	0	0.04454343	0	0.04454343	0.04454343	0	0	0	0
g__Adhaeribacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dyadobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Hymenobacter	0.04454343	0	0.08908686	0.04454343	0	0.04454343	0	0	0	0.04454343	0	0.04454343	0	0.04454343	0.04454343	0	0	0	0
unclassified	0.04454343	0	0.08908686	0.04454343	0	0.04454343	0	0	0	0.04454343	0	0.04454343	0	0.04454343	0.04454343	0	0	0	0
g__Rhodocytophaga	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
c__Flavobacteriia	0	0.08908686	0.08908686	0.311804009	0	0.04454343	0	0.04454343	0	0.04454343	0	0.445434298	0	0	0	0	0	0.222717149	0
o__Flavobacteriales	0	0.08908686	0.08908686	0.311804009	0	0.04454343	0	0.04454343	0	0.04454343	0	0.445434298	0	0	0	0	0	0.222717149	0
f__Cryomorphaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Fluviicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Flavobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Algibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__lectus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Capnocytophaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ochracea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Flavobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__succinicans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Myroides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__odoratimimus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Weeksellaceae	0	0.08908686	0.08908686	0.311804009	0	0.04454343	0	0.04454343	0	0.04454343	0	0.445434298	0	0	0	0	0	0.222717149	0
g__Chryseobacterium	0	0.04454343	0	0.311804009	0	0	0	0	0	0.04454343	0	0.267260579	0	0	0	0	0	0.04454343	0
unclassified	0	0.04454343	0	0.311804009	0	0	0	0	0	0.04454343	0	0.267260579	0	0	0	0	0	0.04454343	0
g__Cloacibacterium	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Elizabethkingia	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.08908686	0
s__meningoseptica	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.08908686	0
g__Ornithobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Riemerella	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Wautersiella	0	0	0.04454343	0	0	0	0	0	0	0	0	0.178173719	0	0	0	0	0	0.04454343	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0.178173719	0	0	0	0	0	0.04454343	0
g__Weeksella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Saprospirae	0.13363029	0.04454343	0.08908686	0	0	0.13363029	0	0	0	0.04454343	0	0.08908686	0	0	0	0	0	0	0.04454343
o__Saprospirales	0.13363029	0.04454343	0.08908686	0	0	0.13363029	0	0	0	0.04454343	0	0.08908686	0	0	0	0	0	0	0.04454343
f__Chitinophagaceae	0.13363029	0.04454343	0.08908686	0	0	0.13363029	0	0	0	0.04454343	0	0.08908686	0	0	0	0	0	0	0.04454343
g__Chitinophaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__arvensicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Flavihumibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Flavisolibacter	0.04454343	0.04454343	0.08908686	0	0	0.08908686	0	0	0	0.04454343	0	0.08908686	0	0	0	0	0	0	0.04454343
unclassified	0.04454343	0.04454343	0.08908686	0	0	0.08908686	0	0	0	0.04454343	0	0.08908686	0	0	0	0	0	0	0.04454343

g__Niabella	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Niastella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sediminibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Segetibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Terrimonas	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Sphingobacteriia	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
o__Sphingobacteriales	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
f__Sphingobacteriaceae	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Olivibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pedobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__cryoconitis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphingobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__faecium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mizutaii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__multivorum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Chloroflexi	0.08908686	0	0	0	0	0	0.08908686	0	0	0.08908686	0	0	0	0	0	0.04454343	0	0.04454343	0
c__Anaerolineae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Caldilineales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Caldilineaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SBR1031	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__A4b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SJA-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__C0119	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0
c__Chloroflexi	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
o__AKIW781	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Chloroflexales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__FFCH7168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Roseiflexales	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
f__Roseiflexaceae	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Roseiflexus	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
c__Ktedonobacteria	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__B12-WMSP1	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Thermogemmatisporales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermogemmatisporaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__SHA-26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__TK10	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
o__B07_WMSP1	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
f__FFCH4570	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
c__Thermomicrobia	0	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0
o__JG30-KF-CM45	0	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0
p__Cyanobacteria	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
c__4C0d-2	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
o__MLE1-12	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Chloroplast	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
o__Stramenopiles	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Streptophyta	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
p__FBP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Firmicutes	39.02004454	30.46770601	34.34298441	40.04454343	10.42316258	16.16926503	61.15812918	61.95991091	58.44097996	57.99554566	95.01113586	39.37639198	99.46547884	52.29398664	45.65701559	61.91536748	33.05122494	54.0311804	47.97327394
c__Bacilli	33.80846325	25.5233853	26.8596882	36.25835189	10.33407572	6.993318486	60.22271715	61.3363029	58.26280624	57.28285078	95.01113586	38.21826281	99.46547884	52.07126949	7.082405345	57.72828508	26.14699332	39.59910913	39.1091314
o__Bacillales	32.33853007	17.32739421	26.05790646	36.21380846	5.256124722	6.458797327	59.82182628	52.11581292	29.48775056	55.85746102	12.91759465	11.13585746	99.42093541	49.93318486	6.013363029	57.41648107	11.9376392	38.93095768	38.88641425
f__Alicyclobacillaceae	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Alicyclobacillus	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bacillaceae	0.13363029	0	0	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Alkalibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Anoxybacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__kestanbolensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bacillus	0.13363029	0	0	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__acidicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__flexus	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
s__foraminis	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__horikoshii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__muralis	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__trypoxylicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Geobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__vulcani	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Marinibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Marinococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Exiguobacteraceae	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Exiguobacterium	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Paenibacillaceae	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Ammoniphilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__oxalaticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Paenibacillus	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__amylolyticus	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__edaphicus	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
s__stellifer	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
f__Planococcaceae	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lysinibacillus	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
s__boronitolerans	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Planomicrobium	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sporosarcina	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Sporolactobacillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sporolactobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Staphylococcaceae	32.11581292	17.32739421	25.92427617	36.21380846	5.256124722	6.191536748	59.82182628	52.11581292	29.48775056	55.81291759	12.91759465	11.13585746	99.42093541	49.93318486	6.013363029	57.41648107	11.9376392	38.84187082	38.88641425
g__Jeotgalicoccus	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0
s__psychrophilus	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Salinicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Staphylococcus	32.11581292	17.32739421	25.92427617	36.21380846	5.256124722	6.191536748	59.82182628	52.11581292	29.48775056	55.81291759	12.91759465	11.09131403	99.42093541	49.88864143	6.013363029	57.41648107	11.9376392	38.84187082	38.88641425
s__aureus	0.04454343	0	0.579064588	2.628062361	0	0	35.59020045	8.55233853	26.23608018	14.0311804	12.87305122	1.113585746	99.37639198	18.39643653	0.668151448	18.61915367	0	2.048997773	0.445434298
s__epidermidis	31.98218263	17.19376392	24.23162584	33.31848552	5.167037862	5.79064588	24.00890869	43.47438753	3.251670379	41.69265033	0.04454343	8.329621381	0	31.35857461	5.077951002	38.75278396	11.58129176	36.1247216	38.21826281
s__equorum	0	0	0.178173719	0	0	0	0	0.04454343	0	0	0	0.08908686	0	0.04454343	0.08908686	0	0	0	0
s__haemolyticus	0.08908686	0.13363029	0.935412027	0.04454343	0	0.400890869	0.04454343	0.04454343	0	0	0	0.445434298	0.04454343	0.04454343	0.178173719	0	0.311804009	0.13363029	0.222717149

s__lugdunensis	0	0	0	0.222717149	0.08908686	0	0.178173719	0	0	0.04454343	0	1.113585746	0	0.04454343	0	0.04454343	0.04454343	0.534521158	0
s__pettenkoferi	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__sciuri	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermoactinomycetaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Planifilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Gemellales	0	0.04454343	0	0	0	0	0.04454343	0	0	0.04454343	0.04454343	0	0	0.13363029	0	0	0.356347439	0.04454343	0
f__Gemellaceae	0	0.04454343	0	0	0	0	0.04454343	0	0	0.04454343	0.04454343	0	0	0.13363029	0	0	0.356347439	0.04454343	0
g__Gemella	0	0.04454343	0	0	0	0	0.04454343	0	0	0.04454343	0.04454343	0	0	0.13363029	0	0	0.356347439	0.04454343	0
unclassified	0	0.04454343	0	0	0	0	0.04454343	0	0	0.04454343	0.04454343	0	0	0.13363029	0	0	0.356347439	0.04454343	0
o__Lactobacillales	1.469933185	8.151447661	0.801781737	0.04454343	5.077951002	0.534521158	0.356347439	9.220489978	28.77505568	1.380846325	82.04899777	27.08240535	0.04454343	2.004454343	1.069042316	0.311804009	13.85300668	0.623608018	0.222717149
f__Aerococcaceae	1.380846325	8.062360802	0.579064588	0	5.077951002	0.356347439	0.04454343	2.9844098	28.55233853	0.890868597	0	26.8596882	0	0.08908686	1.069042316	0	10.28953229	0.13363029	0.13363029
g__Abiotrophia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Aerococcus	0	0.08908686	0.08908686	0	0.04454343	0.222717149	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0.08908686	0.08908686	0.08908686
unclassified	0	0.08908686	0.08908686	0	0.04454343	0.222717149	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0.08908686	0.08908686	0.08908686
g__Alloiococcus	1.380846325	7.928730512	0.311804009	0	5.033407572	0.13363029	0	2.9844098	28.55233853	0.846325167	0	26.8596882	0	0	1.069042316	0	10.20044543	0	0
s__otitis	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	1.380846325	7.884187082	0.311804009	0	5.033407572	0.13363029	0	2.9844098	28.55233853	0.846325167	0	26.8596882	0	0	1.069042316	0	10.20044543	0	0
g__Facklamia	0	0.04454343	0.178173719	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0.04454343
unclassified	0	0.04454343	0.178173719	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0.04454343
f__Carnobacteriaceae	0.04454343	0	0.04454343	0	0	0.08908686	0.04454343	0	0.08908686	0.04454343	0	0.04454343	0	0.356347439	0	0.04454343	0.13363029	0.04454343	0
g__Carnobacterium	0	0	0	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0
s__viridans	0	0	0	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0
g__Desemzia	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Granulicatella	0.04454343	0	0.04454343	0	0	0.04454343	0.04454343	0	0.04454343	0.04454343	0	0	0	0.356347439	0	0.04454343	0.13363029	0.04454343	0
unclassified	0.04454343	0	0.04454343	0	0	0.04454343	0.04454343	0	0.04454343	0.04454343	0	0	0	0.356347439	0	0.04454343	0.13363029	0.04454343	0
f__Enterococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Enterococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__casseliflavus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__cecorum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Lactobacillaceae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0
g__Lactobacillus	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0
s__delbrueckii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__helveticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
s__manihotivorans	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__salivarius	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Leuconostocaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Leuconostoc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Streptococcaceae	0.04454343	0.08908686	0.13363029	0.04454343	0	0.08908686	0.267260579	6.236080178	0.13363029	0.445434298	82.04899777	0.178173719	0.04454343	1.559020045	0	0.267260579	3.385300668	0.400890869	0.08908686
g__Lactococcus	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0
g__Streptococcus	0.04454343	0.08908686	0.13363029	0.04454343	0	0.08908686	0.267260579	6.236080178	0.13363029	0.445434298	82.04899777	0.13363029	0.04454343	1.559020045	0	0.267260579	3.340757238	0.400890869	0.08908686
s__agalactiae	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
s__anginosus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__equi	0	0	0	0	0	0	0	6.191536748	0	0	82.00445434	0	0	0	0	0	0	0	0
s__infantis	0.04454343	0.08908686	0.13363029	0.04454343	0	0.08908686	0.267260579	0	0.08908686	0.356347439	0.04454343	0.04454343	0.04454343	1.514476615	0	0.267260579	3.340757238	0.400890869	0.08908686
unclassified	0	0	0	0	0	0	0	0	0.04454343	0.08908686	0	0.08908686	0	0.04454343	0	0	0	0	0
o__Turicibacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Turicibacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Turicibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Clostridia	5.211581292	4.944320713	7.483296214	3.786191537	0.08908686	9.175946548	0.935412027	0.623608018	0.178173719	0.712694878	0	1.158129176	0	0.222717149	38.57461024	4.187082405	6.904231626	14.38752784	8.864142539
o__Clostridiales	5.211581292	4.944320713	7.483296214	3.786191537	0.08908686	9.175946548	0.935412027	0.623608018	0.178173719	0.712694878	0	1.158129176	0	0.222717149	38.57461024	4.187082405	6.904231626	14.38752784	8.864142539
f__Christensenellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Clostridiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0
g__02d06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Caloramator	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Clostridium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0
g__Oxobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Dehalobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dehalobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Eubacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Anaerofustis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
f__Lachnospiraceae	0	0.04454343	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0.13363029	0	0
g__Blautia	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__obeum	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__producta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Coprococcus	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0.08908686	0	0
s__catus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__eutactus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0.08908686	0	0
g__Dorea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__formicigenerans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lachnobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Moryella	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
s__indoligenes	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
g__Roseburia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__faecis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ruminococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__gnavus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__torques	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Shuttleworthia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Mogibacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
g__Mogibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
f__Peptococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
g__Peptococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
g__WCHB1-84	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Peptostreptococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Filifactor	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Peptostreptococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__anaerobius	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Ruminococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Faecalibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__prausnitzii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oscillospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ruminococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__bromii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__callidus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Symbiobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Symbiobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__thermophilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Tissierellaceae	5.167037862	4.855233853	7.349665924	3.741648107	0.08908686	9.175946548	0.890868597	0.623608018	0.178173719	0.668151448	0	1.158129176	0	0	36.16926503	4.187082405	6.325167038	14.25389755	8.864142539
g__1-68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Anaerococcus	3.741648107	1.781737194	3.296213808	2.227171492	0.08908686	5.523385301	0.846325167	0.445434298	0.13363029	0.668151448	0	0.489977728	0	0	11.26948775	1.870824053	2.76169265	14.20935412	7.082405345
unclassified	3.741648107	1.781737194	3.296213808	2.227171492	0.08908686	5.523385301	0.846325167	0.445434298	0.13363029	0.668151448	0	0.489977728	0	0	11.26948775	1.870824053	2.76169265	14.20935412	7.082405345
g__Finegoldia	0.178173719	0.489977728	0.356347439	0.178173719	0	0.846325167	0	0.08908686	0	0	0	0.668151448	0	0	5.345211581	0.846325167	0.979955457	0	0.178173719
unclassified	0.178173719	0.489977728	0.356347439	0.178173719	0	0.846325167	0	0.08908686	0	0	0	0.668151448	0	0	5.345211581	0.846325167	0.979955457	0	0.178173719
g__GW-34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Gallicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Parvimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Peptoniphilus	1.247216036	2.538975501	3.697104677	1.336302895	0	2.76169265	0.04454343	0.08908686	0	0	0	0	0	0	19.5545657	1.469933185	2.583518931	0	1.603563474
unclassified	1.247216036	2.538975501	3.697104677	1.336302895	0	2.76169265	0.04454343	0.08908686	0	0	0	0	0	0	19.5545657	1.469933185	2.583518931	0	1.603563474
g__WAL_1855D	0	0.04454343	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__ph2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Veillonellaceae	0.04454343	0.04454343	0.08908686	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0.13363029	2.405345212	0	0.356347439	0	0
g__Dialister	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	2.405345212	0	0.08908686	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	2.405345212	0	0.08908686	0	0
g__Megasphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0
g__Pelosinus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Propionispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Selenomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__noxia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Succiniclasticum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Veillonella	0.04454343	0.04454343	0.04454343	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0.13363029	0	0	0.178173719	0	0
s__dispar	0.04454343	0.04454343	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0.08908686	0	0	0.04454343	0	0
s__parvula	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0.13363029	0	0

c__Erysipelotrichi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
o__Erysipelotrichales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
f__Erysipelotrichaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Bulleidia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__moorei	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Eubacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__biforme	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Fusobacteria	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0.04454343	0	0	0.846325167	0	0
c__Fusobacteriia	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0.04454343	0	0	0.846325167	0	0
o__Fusobacteriales	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0.04454343	0	0	0.846325167	0	0
f__Fusobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0.534521158	0	0
g__Fusobacterium	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0.534521158	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0.534521158	0	0
f__Leptotrichiaceae	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0.311804009	0	0
g__Leptotrichia	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0.222717149	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0.222717149	0	0
g__Streptobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0
s__moniliformis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0
p__Gemmatimonadetes	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0.08908686	0.04454343
c__Gemm-1	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
c__Gemmatimonadetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0.04454343
o__Ellin5290	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0
o__Gemmatimonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Ellin5301	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__KD8-87	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
o__N1423WL	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__MVP-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Nitrospirae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Nitrospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Nitrospirales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nitrospiraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nitrospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermodesulfovibrionaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Candidatus_Magnetoovum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__OD1	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__ZB2	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__OP3	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__koll11	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__GIF10	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__kpj58rc	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Planctomycetes	0.08908686	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Phycisphaerae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__WD2101	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Planctomycetia	0.08908686	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Gemmatales	0.08908686	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Gemmataceae	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Gemmata	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Isosphaeraceae	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Proteobacteria	2.316258352	0.267260579	5.345211581	2.71714922	0.222717149	2.494432071	0.757238307	0.222717149	0.534521158	2.89532294	0.623608018	4.276169265	0.445434298	0.757238307	5.256124722	0.13363029	1.514476615	4.632516704	0.08908686
c__Alphaproteobacteria	0.489977728	0.04454343	0.534521158	0.04454343	0.04454343	0.13363029	0.13363029	0	0.04454343	0.445434298	0	0.222717149	0	0	0.08908686	0	0.04454343	0.222717149	0
o__Caulobacterales	0	0	0.04454343	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0.08908686	0
f__Caulobacteraceae	0	0	0.04454343	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0.08908686	0
g__Brevundimonas	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0.08908686	0
s__diminuta	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0.08908686	0
g__Phenylobacterium	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Ellin329	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
o__Rhizobiales	0.267260579	0	0.222717149	0.04454343	0	0.08908686	0.08908686	0	0	0.267260579	0	0.04454343	0	0	0	0	0.04454343	0.04454343	0
f__Aurantimonadaceae	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0
f__Bartonellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bartonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Beijerinckiaceae	0	0	0.13363029	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0
g__Methylocella	0	0	0.13363029	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
unclassified	0	0	0.13363029	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
f__Bradyrhizobiaceae	0.04454343	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Balneimonas	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
g__Bosea	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__genosp.	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
f__Hyphomicrobiaceae	0.13363029	0	0.04454343	0.04454343	0	0	0.04454343	0	0	0.08908686	0	0	0	0	0	0	0	0	0
g__Hyphomicrobium	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
s__sulfonivorans	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodoplanes	0.13363029	0	0.04454343	0.04454343	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0
unclassified	0.13363029	0	0.04454343	0.04454343	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0
f__Methylobacteriaceae	0.04454343	0	0	0	0	0.04454343	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0
g__Methylobacterium	0.04454343	0	0	0	0	0.04454343	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0
s__komagatae	0.04454343	0	0	0	0	0.04454343	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0
f__Phyllobacteriaceae	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Mesorhizobium	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__huakuii	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nitratireductor	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Xanthobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Blastochloris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rhodobacterales	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.04454343	0
f__Rhodobacteraceae	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Rubellimicrobium	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.04454343	0
o__Rhodospirillales	0.13363029	0.04454343	0.178173719	0	0	0.04454343	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0.04454343	0
f__Acetobacteraceae	0.13363029	0	0.13363029	0	0	0.04454343	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0.04454343	0
g__Acetobacter	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Acidisphaera	0	0	0.08908686	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.08908686	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Acidocella	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Roseococcus	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__mucosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Swaminathania	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Rhodospirillaceae	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oleomonas	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Sphingomonadales	0.08908686	0	0.08908686	0	0.04454343	0	0	0	0	0.13363029	0	0.04454343	0	0	0.08908686	0	0	0	0
f__Sphingomonadaceae	0.08908686	0	0.08908686	0	0.04454343	0	0	0	0	0.13363029	0	0.04454343	0	0	0.08908686	0	0	0	0
g__Kaistobacter	0.08908686	0	0.08908686	0	0	0	0	0	0	0.08908686	0	0	0	0	0.08908686	0	0	0	0
unclassified	0.08908686	0	0.08908686	0	0	0	0	0	0	0.08908686	0	0	0	0	0.08908686	0	0	0	0
g__Novosphingobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__resinovorum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphingobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__yanoikuyae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphingomonas	0	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0
s__azotifigens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

s__echinoides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__wittichii	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__yabuuchiae	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0
c__Betaproteobacteria	1.024498886	0	0.579064588	2.004454343	0.04454343	0.623608018	0.311804009	0	0.08908686	0.267260579	0	0.623608018	0.13363029	0.445434298	1.781737194	0	0.712694878	0.267260579	0.08908686	
o__A21b	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__EB1003	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Burkholderiales	0.178173719	0	0.489977728	0.04454343	0.04454343	0.623608018	0.267260579	0	0.04454343	0.178173719	0	0.579064588	0.13363029	0.13363029	0.04454343	0	0.04454343	0.222717149	0.04454343	
f__Alcaligenaceae	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0.04454343	0	
g__Achromobacter	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0	0	
g__Denitrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Oligella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Tetrathiobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	
s__kashmirensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Burkholderiaceae	0	0.04454343	0	0	0	0	0.08908686	0	0.04454343	0.13363029	0	0.222717149	0	0	0.04454343	0	0	0.13363029	0	
g__Burkholderia	0	0	0.04454343	0	0	0	0.08908686	0	0.04454343	0.13363029	0	0.222717149	0	0	0.04454343	0	0	0.13363029	0	
s__andropogonis	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	
s__bryophila	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__graminis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__tuberum	0	0	0.04454343	0	0	0	0.04454343	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0.08908686	0	
unclassified	0	0	0	0	0	0	0.04454343	0	0.04454343	0.08908686	0	0.13363029	0	0	0.04454343	0	0	0.04454343	0	
g__Lautropia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Salinispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__tropica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Comamonadaceae	0.04454343	0	0.222717149	0	0	0.08908686	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343		
g__Acidovorax	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__delafieldii	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Alicycliphilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Aquabacterium	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Azohydromonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Comamonas	0	0	0.08908686	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	
s__terrigena	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0.08908686	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	
g__Delftia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Diaphorobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	
g__Glesbergeria	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Hylemonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Leptothrix	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Methylibium	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__petroleiphilum	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Paucibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Pelomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__puraquae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Ramlibacter	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Rubrivivax	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__gelatinosus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Schlegelella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Tepidimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Variovorax	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	
s__paradoxus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	
f__Oxalobacteraceae	0.13363029	0	0.222717149	0.04454343	0.04454343	0.534521158	0.13363029	0	0	0.04454343	0	0.222717149	0.13363029	0.13363029	0	0	0.04454343	0	0	
g__Collimonas	0.13363029	0	0.04454343	0	0	0.222717149	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0	
unclassified	0.13363029	0	0.04454343	0	0	0.222717149	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0	
g__Cupriavidus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__gilardii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Herbaspirillum	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Herminiimonas	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Janthinobacterium	0	0	0.04454343	0	0	0.267260579	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	
s__lividum	0	0	0.04454343	0	0	0.267260579	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	
g__Oxalobacter	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	
s__formigenes	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	
g__Polynucleobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__cosmopolitanus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0.08908686	0.04454343	0	0.04454343	0.04454343	0	0	0	0	0.178173719	0.13363029	0.08908686	0	0	0.04454343	0	0	
unclassified	0	0	0.08908686	0.04454343	0	0.04454343	0.04454343	0	0	0	0	0.178173719	0.13363029	0.08908686	0	0	0.04454343	0	0	
o__Ellin6067	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__MND1	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__Neisseriales	0.757238307	0	0	1.959910913	0	0	0.04454343	0	0.04454343	0.08908686	0	0.04454343	0	0.311804009	1.692650334	0	0.668151448	0.04454343	0.04454343	
f__Neisseriaceae	0.757238307	0	0	1.959910913	0	0	0.04454343	0	0.04454343	0.08908686	0	0.04454343	0	0.311804009	1.692650334	0	0.668151448	0.04454343	0.04454343	
g__Aquitalea	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	
s__magnusonii	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	
g__Eikenella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Kingella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	
g__Microvirgula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__aerodenitrificans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Neisseria	0	0	0	0	0	0	0	0	0.04454343	0.08908686	0	0.04454343	0	0.311804009	0	0	0.623608018	0	0.04454343	
s__cinerea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	
s__subflava	0	0	0	0	0	0	0	0	0.04454343	0.08908686	0	0.04454343	0	0.08908686	0	0	0.222717149	0	0.04454343	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.222717149	0	0	0.311804009	0	0	
g__Vitreoscilla	0.757238307	0	0	1.959910913	0	0	0	0	0	0	0	0	0	0	1.692650334	0	0	0	0	
unclassified	0.757238307	0	0	1.959910913	0	0	0	0	0	0	0	0	0	0	1.692650334	0	0	0	0	
o__Rhodocyclales	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Rhodocyclaceae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Azospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Dok59	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Methyloversatilis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Propionivibrio	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Zoogloea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__SBla14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__SC-I-84	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
c__Deltaproteobacteria	0.08908686	0	0.04454343	0	0	0	0.04454343	0	0	0.04454343	0	0.04454343	0	0	0.04454343	0	0	0.04454343	0	
o__Desulfovibrionales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Desulfovibrionaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Desulfovibrio	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__cavernae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__FAC87	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__MIZ46	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	
unclassified	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	
unclassified	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	
unclassified	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	
o__Myxococcales	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0	
f__Cystobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Cystobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Haliangiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
g__Haliangium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
f__Myxococcaceae	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	
g__Anaeromyxobacter	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	
o__SAR324	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	
o__Syntrophobacterales	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	
f__Syntrophobacteraceae	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	
g__Syntrophobacter	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	
c__Epsilonproteobacteria	0	0	0.178173719	0	0	0.04454343	0	0	0	0	0	0	0	0	1.870824053	0	0.311804009	0	0	
o__Campylobacterales	0	0	0.178173719	0	0	0.04454343	0	0	0	0	0	0	0	0	1.870824053	0	0.311804009	0	0	
f__Campylobacteraceae	0	0	0.178173719	0	0	0	0	0	0	0	0	0	0	0	1.870824053	0	0.311804009	0	0	

g__Campylobacter	0	0	0.178173719	0	0	0	0	0	0	0	0	0	0	0	1.870824053	0	0.311804009	0	0
s__rectus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ureolyticus	0	0	0.178173719	0	0	0	0	0	0	0	0	0	0	0	1.870824053	0	0.311804009	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Helicobacteraceae	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Helicobacter	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
s__pylori	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Nautiliales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nautiliaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nautilia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Gammaproteobacteria	0.712694878	0.222717149	4.008908686	0.668151448	0.13363029	1.692650334	0.267260579	0.222717149	0.400890869	2.138084633	0.623608018	3.385300668	0.311804009	0.311804009	1.469933185	0.13363029	0.445434298	4.097995546	0
o__Alteromonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Shewanellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Shewanella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__pacifica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Enterobacteriales	0	0	0	0	0.04454343	0.04454343	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0
f__Enterobacteriaceae	0	0	0	0	0.04454343	0.04454343	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0
g__Citrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Enterobacter	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
s__cowanii	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
g__Erwinia	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__dispersa	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Klebsiella	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
s__oxytoca	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Salmonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__enterica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Legionellales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Coxiellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Legionellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Legionella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Oceanospirillales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Halomonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Halomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Oceanospirillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Marinomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__primoryensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Pasteurellales	0	0	0	0	0	0	0.04454343	0	0	0	0.222717149	0.04454343	0	0	0	0	0	0	0
f__Pasteurellaceae	0	0	0	0	0	0	0.04454343	0	0	0	0.222717149	0.04454343	0	0	0	0	0	0	0
g__Actinobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__parahaemolyticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Haemophilus	0	0	0	0	0	0	0.04454343	0	0	0	0.222717149	0.04454343	0	0	0	0	0	0	0
s__influenzae	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
s__parainfluenzae	0	0	0	0	0	0	0	0	0	0	0.222717149	0.04454343	0	0	0	0	0	0	0
o__Pseudomonadales	0.04454343	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0.04454343	0.04454343	0	0.04454343	0.13363029	0
f__Moraxellaceae	0.04454343	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343	0.08908686	0
g__Acinetobacter	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__guillouiae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__lwoffii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__rhizosphaerae	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
s__schindleri	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__venetianus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Alkanindiges	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Enhydrobacter	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0
g__Moraxella	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ovis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Pseudomonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0.04454343	0
g__Pseudomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0.04454343	0
s__alcaligenes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__fragi	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0
s__umsongensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__veronii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__viridiflava	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Xanthomonadales	0.668151448	0.222717149	4.008908686	0.668151448	0.08908686	1.603563474	0.178173719	0.178173719	0.400890869	2.093541203	0.400890869	3.340757238	0.311804009	0.267260579	1.425389755	0.13363029	0.356347439	3.964365256	0
f__Sinobacteraceae	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Hydrocarboniphaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__effusa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Xanthomonadaceae	0.623608018	0.222717149	4.008908686	0.668151448	0.08908686	1.603563474	0.178173719	0.178173719	0.400890869	2.093541203	0.400890869	3.340757238	0.311804009	0.267260579	1.425389755	0.13363029	0.356347439	3.964365256	0
g__Dokdonella	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Dyella	0.534521158	0.04454343	3.429844098	0	0.04454343	0.13363029	0	0	0.267260579	1.425389755	0.356347439	0.13363029	0.04454343	0.04454343	1.158129176	0	0.04454343	3.118040089	0
s__ginsengisoli	0.534521158	0.04454343	3.429844098	0	0.04454343	0.13363029	0	0	0.267260579	1.425389755	0.356347439	0.13363029	0.04454343	0.04454343	1.158129176	0	0.04454343	3.118040089	0
g__Luteimonas	0	0	0.13363029	0	0	0	0.04454343	0	0	0.08908686	0	0.579064588	0	0	0	0	0	0.04454343	0
unclassified	0	0	0.13363029	0	0	0	0.04454343	0	0	0.08908686	0	0.579064588	0	0	0	0	0	0.04454343	0
g__Lysobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0
g__Pseudoxanthomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mexicana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodanobacter	0.08908686	0.178173719	0.445434298	0.623608018	0.04454343	1.380846325	0.13363029	0.178173719	0.13363029	0.579064588	0.04454343	2.538975501	0.267260579	0.222717149	0.267260579	0.08908686	0.267260579	0.712694878	0
s__lindaniclasticus	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0
unclassified	0.08908686	0.178173719	0.445434298	0.623608018	0.04454343	1.380846325	0.13363029	0.178173719	0.13363029	0.489977728	0.04454343	2.538975501	0.267260579	0.222717149	0.267260579	0.08908686	0.267260579	0.712694878	0
g__Stenotrophomonas	0	0	0	0.04454343	0	0.08908686	0	0	0	0	0	0.04454343	0	0	0	0	0	0.08908686	0
s__acidaminiphila	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__geniculata	0	0	0	0	0	0.08908686	0	0	0	0	0	0.04454343	0	0	0	0	0	0.08908686	0
s__retroflexus	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__fusca	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Xanthomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Spirochaetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Spirochaetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Borreliales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Borreliaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Spironema	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Spirochaetales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Spirochaetaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Treponema	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Synergistetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Synergistia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Synergistales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Dethiosulfovibrionaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pyramidobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__piscolens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermovirgaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermovirga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__TM7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__TM7-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__TM7-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__EW055	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Tenericutes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
c__Mollicutes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
o__RF39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
p__Thermi	0	0.04454343	0	0.04454343	0	0.04454343	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0.08908686	0
c__Deinococci	0	0.04454343	0	0.04454343	0	0.04454343	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0.08908686	0
o__Deinococcales	0	0.04454343	0	0.04454343	0	0.04454343	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0.08908686	0
f__Deinococcaceae	0	0.04454343	0	0.04454343	0	0.04454343	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0.08908686	0
g__Deinococcus	0	0.04454343	0	0.04454343	0	0.04454343	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0.08908686	0
s__alpinitundrae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aquatilis	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__geothermalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0.08908686	0
o__Thermales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Verrucomicrobia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Pedosphaerae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Pedosphaerales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Pedosphaeraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pedosphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Spartobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Chthoniobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Chthoniobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ellin506	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__WPS-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
Total Number of Reads	11649	19350	12925	10137	44032	16206	26150	32057	27228	21823	22096	9720	14787	14373	16825	19695	32118	10235	18419

Sample ID	1852R	1859R	1863R	1899R	1977R	1993R	2000R	2051R	1674R	1766R	1858R	1867R	1920R	1933R	1990R	2010R	2050R	2139R	2168R
Sample Location	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose
SSTI/*S. aureus* colonization status	MSSA Abscess	MSSA Abscess	MSSA Abscess	MSSA Abscess	MSSA Abscess	MSSA Abscess	MSSA Abscess	MSSA Abscess	NoSA Abscess	NoSA Abscess	NoSA Abscess	NoSA Abscess	NoSA Abscess	NoSA Abscess	NoSA Abscess	NoSA Abscess	NoSA Abscess	NoSA Abscess	NoSA Abscess
Taxon																			
p__Acidobacteria	0	0.04454343	0	0.13363029	0	0	0.04454343	0.04454343	0.04454343	0.08908686	0	0	0	0	0.04454343	0	0	0	0.04454343
c__Acidobacteria-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Acidobacteria-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__iii1-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Acidobacteriia	0	0.04454343	0	0.08908686	0	0	0	0	0.04454343	0.08908686	0	0	0	0	0	0	0	0	0.04454343
o__Acidobacteriales	0	0.04454343	0	0.08908686	0	0	0	0	0.04454343	0.08908686	0	0	0	0	0	0	0	0	0.04454343
f__Acidobacteriaceae	0	0.04454343	0	0.08908686	0	0	0	0	0.04454343	0.08908686	0	0	0	0	0	0	0	0	0.04454343
g__Edaphobacter	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0
s__modestum	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0
g__Terriglobus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0.08908686	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0.04454343	0	0.08908686	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343
f__Koribacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Candidatus_Koribacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Chloracidobacteria	0	0	0	0.04454343	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0
o__DS-100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__PK29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__RB41	0	0	0	0.04454343	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0
f__Ellin6075	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__DA052	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Ellin6513	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__RB25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Solibacteres	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Solibacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__MVS-65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__PK34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Sva0725	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Sva0725	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__iii1-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__DS-18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Actinobacteria	50.33407572	71.09131403	86.68151448	28.99777283	60.62360802	5.879732739	84.85523385	72.51670379	72.24944321	54.78841871	63.07349666	85.9688196	78.88641425	80.4454343	82.36080178	63.91982183	0.04454343	70.155902	85.61247216
c__Acidimicrobiia	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Acidimicrobiales	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__C111	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__EB1017	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Actinobacteria	50.33407572	71.0467706	86.68151448	28.90868597	60.53452116	5.879732739	84.85523385	72.51670379	72.24944321	54.78841871	63.07349666	85.9688196	78.88641425	80.40089087	82.36080178	63.91982183	0.04454343	70.155902	85.61247216
o__Actinomycetales	50.33407572	71.0467706	86.68151448	28.90868597	60.53452116	5.879732739	84.85523385	72.51670379	72.24944321	54.78841871	63.07349666	85.9688196	78.88641425	80.35634744	82.36080178	63.91982183	0.04454343	70.155902	85.61247216
f__Actinomycetaceae	0.08908686	0.04454343	0.04454343	0.13363029	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0
g__Actinobaculum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinomyces	0.08908686	0.04454343	0.04454343	0.13363029	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0
s__europaeus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
s__hyovaginalis	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.08908686	0.04454343	0.04454343	0.13363029	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
g__Mobiluncus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Varibaculum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Actinosynnemataceae	0	0.04454343	0	0	0	0	1.069042316	0.400890869	0	0	0.267260579	0	0	0	0	0	0	0	0
g__Actinoalloteichus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kutzneria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lentzea	0	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
s__violacea	0	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
g__Saccharothrix	0	0	0	0	0	0	1.069042316	0.400890869	0	0	0.222717149	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	1.069042316	0.400890869	0	0	0.222717149	0	0	0	0	0	0	0	0
f__Beutenbergiaceae	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bogoriellaceae	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Georgenia	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Brevibacteriaceae	0.04454343	0	0.04454343	0	1.559020045	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Brevibacterium	0.04454343	0	0.04454343	0	1.559020045	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aureum	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__casei	0	0	0	0	0.178173719	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__paucivorans	0.04454343	0	0	0	1.380846325	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Cellulomonadaceae	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinotalea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Cellulomonas	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__uda	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Corynebacteriaceae	32.51670379	60.40089087	78.84187082	24.27616927	47.26057906	1.069042316	69.79955457	50.28953229	69.62138085	51.98218263	51.13585746	85.03340757	78.48552339	71.44766147	81.11358575	55.94654788	0	66.36971047	84.23162584
g__Corynebacterium	32.51670379	60.40089087	78.84187082	24.27616927	47.26057906	1.069042316	69.79955457	50.28953229	69.62138085	51.98218263	51.13585746	85.03340757	78.48552339	71.44766147	81.11358575	55.94654788	0	66.36971047	84.23162584
s__durum	0.04454343	0	0	0	0.08908686	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
s__kroppenstedtii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__lubricantis	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mastitidis	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
s__pilosum	0.178173719	0.222717149	0.178173719	0	0.356347439	0	0.267260579	0.04454343	3.875278396	0.222717149	0.267260579	0.04454343	0	0.13363029	0.04454343	0.178173719	0	0.04454343	0
s__renale	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__simulans	0.489977728	0	0.13363029	0.13363029	5.389755011	0	0.400890869	0	0	0	0.04454343	0	0.178173719	0.13363029	0	0.13363029	0	0	0
s__stationis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	31.80400891	60.13363029	78.53006682	24.14253898	41.3363029	1.069042316	69.13140312	50.20044543	65.70155902	51.75946548	50.82405345	84.98886414	78.30734967	71.18040089	81.06904232	55.63474388	0	66.32516704	84.23162584
f__Dermabacteraceae	0.13363029	0	0.08908686	0.13363029	0.222717149	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0
g__Brachybacterium	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
s__conglomeratum	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
g__Dermabacter	0.08908686	0	0.08908686	0.13363029	0.222717149	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0.08908686	0	0.08908686	0.13363029	0.222717149	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
f__Dermacoccaceae	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0.08908686	0	0	0	0	0
g__Dermacoccus	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0.08908686	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0.08908686	0	0	0	0	0
f__Dermatophilaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dermatophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Dietziaceae	0	0	0	0	0.178173719	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dietzia	0	0	0	0	0.178173719	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.178173719	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Frankiaceae	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
g__Frankia	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Geodermatophilaceae	0	0	0	0	0.04454343	0	0	0.13363029	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Blastococcus	0	0	0	0	0.04454343	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0
s__aggregatus	0	0	0	0	0.04454343	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0
g__Geodermatophilus	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__obscurus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Modestobacter	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
f__Gordoniaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Gordonia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Intrasporangiaceae	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
g__Knoellia	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__subterranea	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Phycicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Serinicoccus	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
f__Kineosporiaceae	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0
g__Kineococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kineosporia	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0
f__Microbacteriaceae	0.08908686	0.178173719	0	0.08908686	0.04454343	0.04454343	0.04454343	0.08908686	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343
g__Agrococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__jenensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Clavibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__michiganensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Cryocola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Curtobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Frigoribacterium	0.08908686	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.08908686	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Leucobacter	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Microbacterium	0	0.04454343	0	0	0	0	0.04454343	0.08908686	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343
s__chocolatum	0	0	0	0	0	0	0	0.08908686	0	0	0.04454343	0	0	0	0	0	0	0	0
s__maritypicum	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Mycetocola	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pseudoclavibacter	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__bifida	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Yonghaparkia	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Micrococcaceae	0.846325167	0.267260579	0.400890869	0.712694878	2.004454343	0.08908686	0	0.178173719	0.04454343	0.311804009	0.13363029	0.04454343	0.08908686	0.668151448	0	0	0	0.13363029	0
g__Arthrobacter	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__crystallopoietes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__psychrolactophilus	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Citricoccus	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__alkalitolerans	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kocuria	0	0	0	0	0.222717149	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
s__palustris	0	0	0	0	0.222717149	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__rhizophila	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Microbispora	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__rosea	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Micrococcus	0.757238307	0.222717149	0.400890869	0.668151448	1.692650334	0.08908686	0	0.178173719	0	0.311804009	0.13363029	0.04454343	0.08908686	0.623608018	0	0	0	0.13363029	0
s__luteus	0.757238307	0.222717149	0.400890869	0.668151448	1.692650334	0.08908686	0	0.178173719	0	0.311804009	0.13363029	0.04454343	0.08908686	0.623608018	0	0	0	0.13363029	0
g__Nesterenkonia	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Renibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rothia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aeria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mucilaginosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Zhihengliuella	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Micromonosporaceae	0.267260579	0.222717149	0	0.04454343	0	0	5.567928731	0.356347439	0	0.222717149	0	0	0	0.311804009	0	0	0	0.13363029	0
g__Actinocatenispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Catellatospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Couchioplanes	0.267260579	0.222717149	0	0.04454343	0	0	5.567928731	0.356347439	0	0.222717149	0	0	0	0.311804009	0	0	0	0.13363029	0
s__caeruleus	0.267260579	0.222717149	0	0.04454343	0	0	5.567928731	0.356347439	0	0.222717149	0	0	0	0.311804009	0	0	0	0.13363029	0
g__Solwaraspora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Verrucosispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__gifhornensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Mycobacteriaceae	0	0	0.04454343	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Mycobacterium	0	0	0.04454343	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__celatum	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__gordonae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__vaccae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nakamurellaceae	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nocardiaceae	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Nocardia	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Rhodococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__fascians	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__globerulus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nocardioidaceae	0.222717149	0.08908686	0	0	0.400890869	0	0.13363029	0.04454343	0.04454343	0.04454343	0.04454343	0	0	0	0	0	0	0.08908686	0.08908686
g__Actinopolymorpha	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Aeromicrobium	0	0	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Friedmanniella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nocardioides	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Pimelobacter	0	0	0	0	0.13363029	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.13363029	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Propionicimonas	0.222717149	0.08908686	0	0	0.13363029	0	0.13363029	0	0	0	0.04454343	0	0	0	0	0	0	0.08908686	0.08908686
unclassified	0.222717149	0.08908686	0	0	0.13363029	0	0.13363029	0	0	0	0.04454343	0	0	0	0	0	0	0.08908686	0.08908686
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nocardiopsaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nocardiopsis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__composta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Promicromonosporaceae	0	0	0	0	0.311804009	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Cellulosimicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Promicromonospora	0	0	0	0	0.311804009	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.311804009	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Propionibacteriaceae	16.08017817	9.710467706	7.171492205	3.385300668	8.285077951	4.632516704	8.240534521	20.71269488	2.405345212	2.182628062	11.31403118	0.890868597	0.311804009	7.839643653	1.247216036	7.884187082	0.04454343	3.385300668	1.247216036
g__Luteococcus	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Microlunatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Propionibacterium	16.03563474	9.710467706	7.171492205	3.385300668	8.195991091	4.632516704	8.240534521	20.71269488	2.405345212	2.182628062	11.31403118	0.890868597	0.311804009	7.839643653	1.247216036	7.884187082	0.04454343	3.385300668	1.247216036
s__acnes	11.31403118	9.042316258	6.414253898	2.76169265	7.661469933	4.543429844	7.661469933	19.51002227	1.870824053	1.915367483	9.799554566	0.668151448	0.13363029	7.750556793	1.158129176	7.616926503	0.04454343	3.162583519	1.202672606
s__granulosum	4.721603563	0.668151448	0.757238307	0.623608018	0.534521158	0.08908686	0.579064588	1.202672606	0.534521158	0.267260579	1.514476615	0.222717149	0.178173719	0.08908686	0.08908686	0.267260579	0	0.222717149	0.04454343
g__Tessaracoccus	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Pseudonocardiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinomycetospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pseudonocardia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Sporichthyaceae	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Sporichthya	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343	0
f__Streptomycetaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
g__Kitasatospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Streptomyces	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
s__lanatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mashuensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__scabrisporus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
f__Streptosporangiaceae	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nonomuraea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__roseoviolacea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphaerisporangium	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermomonosporaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinomadura	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__vinacea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Tsukamurellaceae	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0
g__Tsukamurella	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0
o__Micrococcales	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
c__Coriobacteriia	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Coriobacteriales	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Coriobacteriaceae	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Adlercreutzia	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Atopobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__rimae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Collinsella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aerofaciens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Slackia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__MB-A2-108	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__0319-7L14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__OPB41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

c__Rubrobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rubrobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Rubrobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rubrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Thermoleophilia	0	0.04454343	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
o__Gaiellales	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
f__Gaiellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
o__Solirubrobacterales	0	0.04454343	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Conexibacteraceae	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Conexibacter	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Patulibacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Solirubrobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Solirubrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Armatimonadetes	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
c__Armatimonadia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
o__Armatimonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
f__Armatimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
g__CL0-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
o__FW68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Chthonomonadetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Chthonomonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Chthonomonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Fimbriimonadia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Fimbriimonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Fimbriimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Fimbriimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__OPB50	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__BRC1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__PRR-11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Bacteroidetes	1.559020045	0.13363029	0.08908686	0.979955457	1.514476615	0.13363029	0.445434298	0.445434298	0.08908686	0.04454343	0.13363029	0.04454343	0.04454343	0.445434298	0.08908686	0.08908686	0	0	0.08908686
c__Bacteroidia	1.247216036	0	0	0.534521158	0.178173719	0	0.400890869	0.178173719	0.04454343	0	0	0.04454343	0	0.04454343	0	0.08908686	0	0	0
o__Bacteroidales	1.247216036	0	0	0.534521158	0.178173719	0	0.400890869	0.178173719	0.04454343	0	0	0.04454343	0	0.04454343	0	0.08908686	0	0	0
f__Bacteroidaceae	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bacteroides	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__caccae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ovatus	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__uniformis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Paraprevotellaceae	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0
g__Prevotella	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0
g__YRC22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Porphyromonadaceae	0	0	0	0	0.08908686	0	0.13363029	0	0	0	0	0	0	0	0	0.04454343	0	0	0
g__Porphyromonas	0	0	0	0	0.08908686	0	0.13363029	0	0	0	0	0	0	0	0	0.04454343	0	0	0
unclassified	0	0	0	0	0.08908686	0	0.13363029	0	0	0	0	0	0	0	0	0.04454343	0	0	0
g__Tannerella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Prevotellaceae	1.247216036	0	0	0.311804009	0.08908686	0	0.267260579	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Prevotella	1.247216036	0	0	0.311804009	0.08908686	0	0.267260579	0	0.04454343	0	0	0	0	0	0	0	0	0	0
s__copri	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
s__melaninogenica	0	0	0	0.267260579	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__nanceiensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ruminicola	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0
s__stercorea	0	0	0	0.04454343	0	0	0.178173719	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	1.247216036	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Rikenellaceae	0	0	0	0.178173719	0	0	0	0.13363029	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0
g__Blvii28	0	0	0	0.178173719	0	0	0	0.13363029	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0.178173719	0	0	0	0.13363029	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0
f__S24-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Cytophagia	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Cytophagales	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Cytophagaceae	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Adhaeribacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dyadobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Hymenobacter	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodocytophaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Flavobacteriia	0.311804009	0.08908686	0.08908686	0.356347439	1.069042316	0.04454343	0.04454343	0.178173719	0.04454343	0	0.13363029	0	0	0.356347439	0.08908686	0	0	0	0.08908686
o__Flavobacteriales	0.311804009	0.08908686	0.08908686	0.356347439	1.069042316	0.04454343	0.04454343	0.178173719	0.04454343	0	0.13363029	0	0	0.356347439	0.08908686	0	0	0	0.08908686
f__Cryomorphaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
g__Fluviicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
f__Flavobacteriaceae	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Algibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__lectus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Capnocytophaga	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ochracea	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Flavobacterium	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__succinicans	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Myroides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__odoratimimus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Weeksellaceae	0.311804009	0.04454343	0.08908686	0.311804009	1.069042316	0.04454343	0.04454343	0.178173719	0.04454343	0	0.13363029	0	0	0.267260579	0.08908686	0	0	0	0.08908686
g__Chryseobacterium	0.311804009	0.04454343	0	0.178173719	0.846325167	0	0	0	0.04454343	0	0.13363029	0	0	0.08908686	0.04454343	0	0	0	0.04454343
unclassified	0.311804009	0.04454343	0	0.178173719	0.846325167	0	0	0	0.04454343	0	0.13363029	0	0	0.08908686	0.04454343	0	0	0	0.04454343
g__Cloacibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0
g__Elizabethkingia	0	0	0.04454343	0.13363029	0.178173719	0.04454343	0.04454343	0.178173719	0	0	0	0	0	0.13363029	0	0	0	0	0.04454343
s__meningoseptica	0	0	0.04454343	0.13363029	0.178173719	0.04454343	0.04454343	0.178173719	0	0	0	0	0	0.13363029	0	0	0	0	0.04454343
g__Ornithobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Riemerella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Wautersiella	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Weeksella	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Saprospirae	0	0.04454343	0	0.08908686	0.08908686	0	0	0.04454343	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0
o__Saprospirales	0	0.04454343	0	0.08908686	0.08908686	0	0	0.04454343	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0
f__Chitinophagaceae	0	0.04454343	0	0.08908686	0.08908686	0	0	0.04454343	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0
g__Chitinophaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__arvensicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Flavihumibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Flavisolibacter	0	0.04454343	0	0.08908686	0.04454343	0	0	0.04454343	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0
unclassified	0	0.04454343	0	0.08908686	0.04454343	0	0	0.04454343	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0
g__Niabella	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Niastella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sediminibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Segetibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Terrimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Sphingobacteriia	0	0	0	0	0.13363029	0.04454343	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0	0	0
o__Sphingobacteriales	0	0	0	0	0.13363029	0.04454343	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0	0	0
f__Sphingobacteriaceae	0	0	0	0	0.08908686	0.04454343	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Olivibacter	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pedobacter	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
s__cryoconitis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
g__Sphingobacterium	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__faecium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mizutaii	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__multivorum	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Chloroflexi	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
c__Anaerolineae	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Caldilineales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Caldilineaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SBR1031	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__A4b	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SJA-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__C0119	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Chloroflexi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__AKIW781	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Chloroflexales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__FFCH7168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Roseiflexales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Roseiflexaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseiflexus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Ktedonobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__B12-WMSP1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Thermogemmatisporales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermogemmatisporaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__SHA-26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__TK10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__B07_WMSP1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__FFCH4570	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Thermomicrobia	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
o__JG30-KF-CM45	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
p__Cyanobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
c__4C0d-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
o__MLE1-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
c__Chloroplast	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Stramenopiles	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Streptophyta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__FBP	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Firmicutes	42.0935412	27.88418708	13.05122494	69.13140312	36.61469933	93.76391982	13.67483296	25.30066815	27.26057906	44.23162584	34.43207127	13.98663697	20.93541203	18.17371938	16.52561247	35.54565702	99.46547884	29.71046771	13.36302895
c__Bacilli	17.50556793	26.45879733	11.62583519	67.75055679	33.80846325	92.91759465	6.681514477	9.220489978	26.81514477	43.07349666	25.74610245	13.67483296	20.66815145	17.59465479	16.43652561	32.33853007	99.46547884	27.52783964	12.33853007
o__Bacillales	16.74832962	16.5701559	11.35857461	66.4142539	30.02227171	92.60579065	5.300668151	8.864142539	4.276169265	38.08463252	24.81069042	1.291759465	15.10022272	17.06013363	1.113585746	23.25167038	99.46547884	25.12249443	2.628062361
f__Alicyclobacillaceae	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Alicyclobacillus	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bacillaceae	0.08908686	0.04454343	0	0.13363029	0.222717149	0	0.04454343	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Alkalibacillus	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Anoxybacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__kestanbolensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bacillus	0.04454343	0.04454343	0	0.13363029	0.222717149	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0	0
s__acidicola	0	0	0	0	0.178173719	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__flexus	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__foraminis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__horikoshii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__muralis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__trypoxylicola	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0.08908686	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0	0
g__Geobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__vulcani	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Marinibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Marinococcus	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Exiguobacteraceae	0	0	0	0.13363029	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Exiguobacterium	0	0	0	0.13363029	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.13363029	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Paenibacillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ammoniphilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__oxalaticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Paenibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__amylolyticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__edaphicus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__stellifer	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Planococcaceae	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lysinibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__boronitolerans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Planomicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sporosarcina	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Sporolactobacillaceae	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sporolactobacillus	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Staphylococcaceae	16.65924276	16.52561247	11.35857461	66.05790646	29.62138085	92.56124722	5.256124722	8.819599109	4.231625835	38.08463252	24.81069042	1.291759465	15.10022272	17.06013363	1.113585746	23.25167038	99.46547884	25.12249443	2.628062361
g__Jeotgalicoccus	0.267260579	0.04454343	0	0	0.400890869	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__psychrophilus	0.13363029	0.04454343	0	0	0.222717149	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.13363029	0	0	0	0.178173719	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Salinicoccus	0.13363029	0	0	0	0.178173719	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
unclassified	0.13363029	0	0	0	0.178173719	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
g__Staphylococcus	16.25835189	16.48106904	11.35857461	66.05790646	29.04231626	92.56124722	5.256124722	8.819599109	4.231625835	38.08463252	24.81069042	1.291759465	15.05567929	17.06013363	1.113585746	23.25167038	99.46547884	25.12249443	2.628062361
s__aureus	0.445434298	0	0.08908686	9.398663697	11.89309577	12.65033408	2.628062361	0.13363029	0	0	0.04454343	0	0	0	0	0	99.37639198	0	0.04454343
s__epidermidis	15.14476615	16.1247216	10.95768374	56.25835189	13.76391982	79.86636971	2.182628062	7.616926503	4.142538976	37.81737194	24.23162584	1.202672606	14.96659243	16.52561247	0.935412027	23.07349666	0	25.077951	2.271714922
s__equorum	0.04454343	0	0	0.08908686	0.04454343	0	0.04454343	0.178173719	0	0	0.13363029	0	0	0.13363029	0.04454343	0	0.04454343	0	0.04454343
s__haemolyticus	0.400890869	0.222717149	0.13363029	0.222717149	2.628062361	0	0.400890869	0.757238307	0.08908686	0.267260579	0.178173719	0.08908686	0	0.356347439	0.13363029	0.178173719	0.04454343	0.04454343	0.178173719
s__lugdunensis	0.222717149	0.13363029	0.178173719	0.08908686	0	0.04454343	0	0.13363029	0	0	0.222717149	0	0.08908686	0.04454343	0	0	0	0	0.08908686
s__pettenkoferi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__sciuri	0	0	0	0	0.712694878	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermoactinomycetaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Planifilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Gemellales	0	0.08908686	0	0.04454343	0.13363029	0.08908686	0	0	0	0	0	0	0	0	0	0.890868597	0	0	0
f__Gemellaceae	0	0.08908686	0	0.04454343	0.13363029	0.08908686	0	0	0	0	0	0	0	0	0	0.890868597	0	0	0
g__Gemella	0	0.08908686	0	0.04454343	0.13363029	0.08908686	0	0	0	0	0	0	0	0	0	0.890868597	0	0	0
unclassified	0	0.08908686	0	0.04454343	0.13363029	0.08908686	0	0	0	0	0	0	0	0	0	0.890868597	0	0	0
o__Lactobacillales	0.757238307	9.799554566	0.267260579	1.291759465	3.608017817	0.222717149	1.380846325	0.356347439	22.5389755	4.988864143	0.935412027	12.3830735	5.567928731	0.534521158	15.32293987	8.195991091	0	2.405345212	9.710467706
f__Aerococcaceae	0.178173719	9.532293987	0.04454343	0.890868597	2.227171492	0	1.202672606	0.04454343	22.5389755	4.944320713	0.890868597	11.80400891	5.122494432	0.13363029	15.32293987	3.340757238	0	2.405345212	9.621380846
g__Abiotrophia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Aerococcus	0.08908686	0.04454343	0.04454343	0.801781737	0.13363029	0	0	0.04454343	0	0	0	0.04454343	0.08908686	0.13363029	0	0.04454343	0	0	0
unclassified	0.08908686	0.04454343	0.04454343	0.801781737	0.13363029	0	0	0.04454343	0	0	0	0.04454343	0.08908686	0.13363029	0	0.04454343	0	0	0
g__Alloiococcus	0.04454343	9.487750557	0	0	1.425389755	0	1.202672606	0	22.5389755	4.944320713	0.890868597	11.75946548	5.033407572	0	15.32293987	3.296213808	0	2.405345212	9.621380846
s__otitis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.311804009	0	0	0
unclassified	0.04454343	9.487750557	0	0	1.425389755	0	1.202672606	0	22.5389755	4.944320713	0.890868597	11.75946548	5.033407572	0	15.32293987	2.9844098	0	2.405345212	9.621380846
g__Facklamia	0.04454343	0	0	0.08908686	0.668151448	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0.08908686	0.668151448	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Carnobacteriaceae	0	0.04454343	0	0	0.13363029	0.08908686	0	0.08908686	0	0	0	0	0	0	0	0.13363029	0	0	0
g__Carnobacterium	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__viridans	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0

g__Desemzia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Granulicatella	0	0.04454343	0	0	0.08908686	0.08908686	0	0.08908686	0	0	0	0	0	0	0	0	0.13363029	0	0	0
unclassified	0	0.04454343	0	0	0.08908686	0.08908686	0	0.08908686	0	0	0	0	0	0	0	0	0.13363029	0	0	0
f__Enterococcaceae	0.08908686	0	0.04454343	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0.178173719	0	0	0	0	0
g__Enterococcus	0.08908686	0	0.04454343	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0.178173719	0	0	0	0	0
s__casseliflavus	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__cecorum	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
unclassified	0.08908686	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0
f__Lactobacillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lactobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__delbrueckii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__helveticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__manihotivorans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__salivarius	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Leuconostocaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Leuconostoc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Streptococcaceae	0.489777728	0.222717149	0.178173719	0.356347439	1.202672606	0.13363029	0.178173719	0.222717149	0	0.04454343	0.04454343	0.579064588	0.445434298	0.222717149	0	4.721603563	0	0	0.08908686	
g__Lactococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Streptococcus	0.489777728	0.222717149	0.178173719	0.356347439	1.202672606	0.13363029	0.178173719	0.222717149	0	0.04454343	0.04454343	0.579064588	0.445434298	0.222717149	0	4.721603563	0	0	0.08908686	
s__agalactiae	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__anginosus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__equi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__infantis	0.445434298	0.178173719	0.178173719	0.267260579	1.202672606	0.13363029	0.13363029	0.222717149	0	0.04454343	0.04454343	0.579064588	0.400890869	0	0	4.587973274	0	0	0.08908686	
unclassified	0	0.04454343	0	0.08908686	0	0	0.04454343	0	0	0	0	0	0.04454343	0.222717149	0	0.13363029	0	0	0	
o__Turicibacterales	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Turicibacteraceae	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Turicibacter	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
c__Clostridia	24.58797327	1.425389755	1.425389755	1.380846325	2.806236608	0.846325167	6.993318486	16.08017817	0.445434298	1.158129176	8.68596882	0.311804009	0.267260579	0.579064588	0.08908686	3.207126949	0	2.182628062	1.024498886	
o__Clostridiales	24.58797327	1.425389755	1.425389755	1.380846325	2.806236608	0.846325167	6.993318486	16.08017817	0.445434298	1.158129176	8.68596882	0.311804009	0.267260579	0.579064588	0.08908686	3.207126949	0	2.182628062	1.024498886	
f__Christensenellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Clostridiaceae	0	0	0	0.178173719	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
g__02d06	0	0	0	0.178173719	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0.178173719	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Caloramator	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Clostridium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Oxobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
f__Dehalobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Dehalobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Eubacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Anaerofustis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Lachnospiraceae	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	
g__Blautia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__obeum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__producta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Coprococcus	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	
s__catus	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	
s__eutactus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Dorea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__formicigenerans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Lachnobacterium	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	
g__Moryella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__indoligenes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Roseburia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__faecis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Ruminococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__gnavus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__torques	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Shuttleworthia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Mogibacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Mogibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Peptococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Peptococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__WCHB1-84	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Peptostreptococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Filifactor	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Peptostreptococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__anaerobius	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Ruminococcaceae	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Faecalibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__prausnitzii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Oscillospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Ruminococcus	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__bromii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__callidus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Symbiobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Symbiobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__thermophilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Tissierellaceae	23.74164811	1.425389755	1.380846325	0.979955457	2.628062361	0.846325167	6.592427617	16.08017817	0.400890869	1.158129176	8.59688196	0.311804009	0.267260579	0.579064588	0.04454343	2.9844098	0	2.182628062	0.979955457	
g__1-68	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Anaerococcus	10.06681514	0.801781737	0.801781737	0.712694878	0.979955457	0.801781737	2.093541203	13.89755011	0.356347439	1.069042316	5.300668151	0.311804009	0.267260579	0.534521158	0.04454343	1.781737194	0	0.935412027	0.489777728	
unclassified	10.06681514	0.801781737	0.801781737	0.712694878	0.979955457	0.801781737	2.093541203	13.89755011	0.356347439	1.069042316	5.300668151	0.311804009	0.267260579	0.534521158	0.04454343	1.781737194	0	0.935412027	0.489777728	
g__Finegoldia	2.271714922	0.13363029	0.13363029	0.267260579	0.801781737	0	1.915367483	0.04454343	0	0	0.801781737	0	0	0	0	0.311804009	0	0.08908686	0.08908686	
unclassified	2.271714922	0.13363029	0.13363029	0.267260579	0.801781737	0	1.915367483	0.04454343	0	0	0.801781737	0	0	0	0	0.311804009	0	0.08908686	0.08908686	
g__GW-34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Gallicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Parvimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Peptoniphilus	11.40311804	0.489777728	0.356347439	0	0.668151448	0.04454343	2.583518931	2.093541203	0.04454343	0.08908686	2.494432071	0	0	0.04454343	0	0.890868597	0	1.113585746	0.400890869	
unclassified	11.40311804	0.489777728	0.356347439	0	0.668151448	0.04454343	2.583518931	2.093541203	0.04454343	0.08908686	2.494432071	0	0	0.04454343	0	0.890868597	0	1.113585746	0.400890869	
g__WAL_18SSD	0	0	0.04454343	0	0.178173719	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343	0	
unclassified	0	0	0.04454343	0	0.178173719	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343	0	
g__ph2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Veillonellaceae	0.846325167	0	0.04454343	0.222717149	0.08908686	0	0.400890869	0	0	0	0.04454343	0	0	0	0	0.222717149	0	0	0.04454343	
g__Dialister	0.846325167	0	0	0	0	0	0.267260579	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0.846325167	0	0	0	0	0	0.267260579	0	0	0	0	0	0	0	0	0	0	0	0	
g__Megasphaera	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	
g__Pelosinus	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Propionispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Selenomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	
s__noxia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	
g__Succiniclasticum	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	
g__Veillonella	0	0	0	0.222717149	0.08908686	0	0	0	0	0	0.04454343	0	0	0	0	0.222717149	0	0	0	
s__dispar	0	0	0	0.222717149	0.04454343	0	0	0	0	0	0.04454343	0	0	0	0	0.13363029	0	0	0	
s__parvula	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	
c__Erysipelotrichi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__Erysipelotrichales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Erysipelotrichaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Bulleidia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__moorei	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Eubacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__biforme	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
p__Fusobacteria	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	
c__Fusobacteriia	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	
o__Fusobacteriales	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	
f__Fusobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Fusobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Leptotrichiaceae	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	
g__Leptotrichia	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	
g__Streptobacillus	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__moniliformis	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
p__Gemmatimonadetes	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	
c__Gemm-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Gemmatimonadetes	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Ellin5290	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Gemmatimonadales	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Ellin5301	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__KD8-87	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__N1423WL	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__MVP-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Nitrospirae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Nitrospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Nitrospirales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nitrospiraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nitrospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermodesulfovibrionaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Candidatus_Magnetoovum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__OD1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__ZB2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__OP3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__koll11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__GIF10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__kpj58rc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Planctomycetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Phycisphaerae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__WD2101	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Planctomycetia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Gemmatales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Gemmataceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Gemmata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Isosphaeraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Proteobacteria	5.83518931	0.801781737	0.178173719	0.623608018	0.979955457	0.13363029	0.178173719	1.648106904	0.267260579	0.801781737	2.316258352	0	0.08908686	0.890868597	0.979955457	0.356347439	0.489977728	0.13363029	0.890868597
c__Alphaproteobacteria	0.267260579	0.178173719	0	0.178173719	0.267260579	0	0.08908686	0.178173719	0	0.178173719	0	0	0	0.04454343	0.04454343	0	0	0.04454343	0
o__Caulobacterales	0.13363029	0	0	0	0.178173719	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0
f__Caulobacteraceae	0.13363029	0	0	0	0.178173719	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0
g__Brevundimonas	0.13363029	0	0	0	0.178173719	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0
s__diminuta	0.13363029	0	0	0	0.178173719	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0
g__Phenylobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Ellin329	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
o__Rhizobiales	0.08908686	0.08908686	0	0.08908686	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343	0
f__Aurantimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bartonellaceae	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bartonella	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Beijerinckiaceae	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Methylocella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bradyrhizobiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Balneimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bosea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__genosp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Hyphomicrobiaceae	0	0.04454343	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Hyphomicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__sulfonivorans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodoplanes	0	0.04454343	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0.04454343	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
f__Methylobacteriaceae	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
g__Methylobacterium	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
s__komagatae	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
f__Phyllobacteriaceae	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Mesorhizobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__huakuii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nitratireductor	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Xanthobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Blastochloris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rhodobacterales	0	0.08908686	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
f__Rhodobacteraceae	0	0.08908686	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
g__Rubellimicrobium	0	0.08908686	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.08908686	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
o__Rhodospirillales	0	0	0	0.08908686	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
f__Acetobacteraceae	0	0	0	0.08908686	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Acetobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Acidisphaera	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Acidocella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseomonas	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mucosa	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Swaminathania	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
f__Rhodospirillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oleomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Sphingomonadales	0.04454343	0	0	0	0.04454343	0	0.08908686	0.04454343	0	0.08908686	0	0	0	0	0.04454343	0	0	0	0
f__Sphingomonadaceae	0.04454343	0	0	0	0.04454343	0	0.08908686	0.04454343	0	0.08908686	0	0	0	0	0.04454343	0	0	0	0
g__Kaistobacter	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0
g__Novosphingobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__resinovorum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphingobium	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__yanoikuyae	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Sphingomonas	0.04454343	0	0	0	0.04454343	0	0.08908686	0.04454343	0	0	0	0	0	0	0	0	0	0	0
s__azotifigens	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__echinoides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__wittichii	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__yabuuchiae	0	0	0	0	0	0	0.08908686	0.04454343	0	0	0	0	0	0	0	0	0	0	0
c__Betaproteobacteria	1.113585746	0.489977728	0.13363029	0.267260579	0.534521158	0.13363029	0	1.113585746	0.13363029	0.04454343	0.668151448	0	0	0.668151448	0.222717149	0.222717149	0.04454343	0.08908686	0.13363029
o__A21b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__EB1003	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Burkholderiales	0.445434298	0.311804009	0.13363029	0.222717149	0.356347439	0.04454343	0	0.222717149	0.13363029	0.04454343	0.13363029	0	0	0.668151448	0.08908686	0.04454343	0.04454343	0.04454343	0.13363029
f__Alcaligenaceae	0	0	0.04454343	0	0.08908686	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
g__Achromobacter	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Denitrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
g__Oligella	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Tetrathiobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__kashmirensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Burkholderiaceae	0.222717149	0.04454343	0	0	0.04454343	0	0	0.08908686	0.04454343	0	0.04454343	0	0	0.04454343	0.08908686	0	0.04454343	0	0.04454343
g__Burkholderia	0	0.04454343	0	0	0.04454343	0	0	0.08908686	0.04454343	0	0.04454343	0	0	0.04454343	0.08908686	0	0.04454343	0	0.04454343

s__andropogonis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__bryophila	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__graminis	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0	0	0
s__tuberum	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0.04454343	
unclassified	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0.08908686	0	0	0	0
g__Lautropia	0.222717149	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.222717149	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Salinispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__tropica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Comamonadaceae	0	0.04454343	0	0.08908686	0.13363029	0	0	0.04454343	0	0	0	0	0	0.445434298	0	0.04454343	0	0	0.04454343
g__Acidovorax	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__delafieldii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Alicycliphilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Aquabacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0
g__Azohydromonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Comamonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__terrigena	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Delftia	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0
g__Diaphorobacter	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.178173719	0	0.04454343	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.178173719	0	0.04454343	0	0	0
g__Giesbergeria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Hylemonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Leptothrix	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Methylibium	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__petroleiphilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Paucibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pelomonas	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
s__puraquae	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
g__Ramlibacter	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rubrivivax	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__gelatinosus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Schlegelella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Tepidimonas	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Variovorax	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	
s__paradoxus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	
f__Oxalobacteraceae	0.222717149	0.222717149	0.08908686	0.13363029	0.08908686	0.04454343	0	0.08908686	0.08908686	0.04454343	0.08908686	0	0	0.08908686	0	0	0	0.04454343	0.04454343
g__Collimonas	0.08908686	0.08908686	0.04454343	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0.08908686	0.08908686	0.04454343	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Cupriavidus	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__gilardii	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Herbaspirillum	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Herminiimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Janthinobacterium	0	0.08908686	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
s__lividum	0	0.08908686	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oxalobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__formigenes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Polynucleobacter	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__cosmopolitanus	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.13363029	0.04454343	0.04454343	0	0.04454343	0	0	0.04454343	0.04454343	0	0.08908686	0	0	0.08908686	0	0	0	0	0
unclassified	0.13363029	0.04454343	0.04454343	0	0.04454343	0	0	0.04454343	0.04454343	0	0.08908686	0	0	0.08908686	0	0	0	0	0
o__Ellin6067	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__MND1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Neisseriales	0.668151448	0.13363029	0	0.04454343	0.178173719	0.04454343	0	0.890868597	0	0	0.534521158	0	0	0	0.13363029	0.178173719	0	0.04454343	0
f__Neisseriaceae	0.668151448	0.13363029	0	0.04454343	0.178173719	0.04454343	0	0.890868597	0	0	0.534521158	0	0	0	0.13363029	0.178173719	0	0.04454343	0
g__Aquitalea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__magnusonii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Eikenella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kingella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Microvirgula	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aerodenitrificans	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Neisseria	0.668151448	0.04454343	0	0	0.178173719	0	0	0.178173719	0	0	0	0	0	0	0	0.178173719	0	0	0
s__cinerea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__subflava	0.04454343	0.04454343	0	0	0.08908686	0	0	0.178173719	0	0	0	0	0	0	0	0.178173719	0	0	0
unclassified	0.623608018	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Vitreoscilla	0	0.08908686	0	0	0	0.04454343	0	0.712694878	0	0	0.534521158	0	0	0	0.13363029	0	0	0.04454343	0
unclassified	0	0.08908686	0	0	0	0.04454343	0	0.712694878	0	0	0.534521158	0	0	0	0.13363029	0	0	0.04454343	0
o__Rhodocyclales	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Rhodocyclaceae	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Azospira	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dok59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Methyloversatilis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Propionivibrio	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Zoogloea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SBla14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SC-I-84	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Deltaproteobacteria	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0
o__Desulfovibrionales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Desulfovibrionaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Desulfovibrio	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__cavernae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__FAC87	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__MIZ46	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0
o__Myxococcales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Cystobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Cystobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Haliangiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Haliangium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Myxococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Anaeromyxobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SAR324	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Syntrophobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Syntrophobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Syntrophobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Epsilonproteobacteria	0	0	0	0	0	0	0	0	0	0	0.222717149	0	0	0	0	0	0	0	0.04454343
o__Campylobacterales	0	0	0	0	0	0	0	0	0	0	0.222717149	0	0	0	0	0	0	0	0.04454343
f__Campylobacteraceae	0	0	0	0	0	0	0	0	0	0	0.222717149	0	0	0	0	0	0	0	0.04454343
g__Campylobacter	0	0	0	0	0	0	0	0	0	0	0.222717149	0	0	0	0	0	0	0	0.04454343
s__rectus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ureolyticus	0	0	0	0	0	0	0	0	0	0	0.222717149	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Helicobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Helicobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__pylori	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Nautiliales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nautiliaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nautilia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Gammaproteobacteria	4.454342984	0.08908686	0.04454343	0.178173719	0.178173719	0	0.08908686	0.356347439	0.13363029	0.534521158	1.380846325	0	0.08908686	0.178173719	0.712694878	0.13363029	0.445434298	0	0.712694878
o__Alteromonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Shewanellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Shewanella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__pacifica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Enterobacteriales	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Enterobacteriaceae	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Citrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Enterobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

s__cowanii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Erwinia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__dispersa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Klebsiella	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__oxytoca	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Salmonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__enterica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Legionellales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Coxiellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Legionellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Legionella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Oceanospirillales	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0
f__Halomonadaceae	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
g__Halomonas	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
f__Oceanospirillaceae	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
g__Marinomonas	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
s__primoryensis	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
o__Pasteurellales	0	0	0	0	0	0	0	0	0	0.222717149	0	0	0	0	0	0	0	0	0
f__Pasteurellaceae	0	0	0	0	0	0	0	0	0	0.222717149	0	0	0	0	0	0	0	0	0
g__Actinobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__parahaemolyticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Haemophilus	0	0	0	0	0	0	0	0	0	0.222717149	0	0	0	0	0	0	0	0	0
s__influenzae	0	0	0	0	0	0	0	0	0	0.222717149	0	0	0	0	0	0	0	0	0
s__parainfluenzae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Pseudomonadales	0	0.04454343	0	0.04454343	0.08908686	0	0.04454343	0.178173719	0.04454343	0.13363029	0	0	0	0.13363029	0	0	0	0	0.712694878
f__Moraxellaceae	0	0.04454343	0	0	0	0	0	0	0.04454343	0.08908686	0	0	0	0.13363029	0	0	0	0	0.712694878
g__Acinetobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0
s__guillouiae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__lwoffii	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
s__rhizosphaerae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__schindleri	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__venetianus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Alkanindiges	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Enhydrobacter	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Moraxella	0	0.04454343	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0.712694878
s__ovis	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0.712694878
f__Pseudomonadaceae	0	0	0	0.04454343	0.08908686	0	0.04454343	0.178173719	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Pseudomonas	0	0	0	0.04454343	0.08908686	0	0.04454343	0.178173719	0	0.04454343	0	0	0	0	0	0	0	0	0
s__alcaligenes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__fragi	0	0	0	0.04454343	0.04454343	0	0.04454343	0.13363029	0	0	0	0	0	0	0	0	0	0	0
s__umsongensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__veronii	0	0	0	0	0.04454343	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0
s__viridiflava	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Xanthomonadales	4.409799555	0.04454343	0.04454343	0.13363029	0.08908686	0	0.04454343	0.08908686	0.08908686	0.178173719	1.380846325	0	0.08908686	0.04454343	0.712694878	0.13363029	0.445434298	0	0
f__Sinobacteraceae	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Hydrocarboniphaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__effusa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Xanthomonadaceae	4.409799555	0	0.04454343	0.13363029	0.08908686	0	0.04454343	0.08908686	0.08908686	0.178173719	1.380846325	0	0.08908686	0.04454343	0.712694878	0.13363029	0.445434298	0	0
g__Dokdonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dyella	3.028953229	0	0	0.04454343	0	0	0	0	0	0.08908686	1.158129176	0	0.04454343	0	0.534521158	0.04454343	0.04454343	0	0
s__ginsengisoli	3.028953229	0	0	0.04454343	0	0	0	0	0	0.08908686	1.158129176	0	0.04454343	0	0.534521158	0.04454343	0.04454343	0	0
g__Luteimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lysobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pseudoxanthomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mexicana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodanobacter	1.380846325	0	0.04454343	0	0.04454343	0	0.04454343	0	0.08908686	0	0.222717149	0	0.04454343	0	0.178173719	0.08908686	0.400890869	0	0
s__lindaniclasticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	1.380846325	0	0.04454343	0	0.04454343	0	0.04454343	0	0.08908686	0	0.222717149	0	0.04454343	0	0.178173719	0.08908686	0.400890869	0	0
g__Stenotrophomonas	0	0	0	0.08908686	0.04454343	0	0	0.08908686	0	0.08908686	0	0	0	0.04454343	0	0	0	0	0
s__acidaminiphila	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__geniculata	0	0	0	0.08908686	0.04454343	0	0	0.04454343	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0
s__retroflexus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
g__Thermomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__fusca	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Xanthomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Spirochaetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Spirochaetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Borreliales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Borreliaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Spironema	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Spirochaetales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Spirochaetaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Treponema	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Synergistetes	0	0	0	0	0.04454343	0	0.801781737	0	0	0	0	0	0	0	0	0	0	0	0
c__Synergistia	0	0	0	0	0.04454343	0	0.801781737	0	0	0	0	0	0	0	0	0	0	0	0
o__Synergistales	0	0	0	0	0.04454343	0	0.801781737	0	0	0	0	0	0	0	0	0	0	0	0
f__Dethiosulfovibrionaceae	0	0	0	0	0	0	0.801781737	0	0	0	0	0	0	0	0	0	0	0	0
g__Pyramidobacter	0	0	0	0	0	0	0.801781737	0	0	0	0	0	0	0	0	0	0	0	0
s__piscolens	0	0	0	0	0	0	0.801781737	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermovirgaceae	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermovirga	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__TM7	0.178173719	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__TM7-1	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__TM7-3	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__EW055	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Tenericutes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Mollicutes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__RF39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Thermi	0	0	0	0	0.08908686	0	0	0	0.08908686	0.04454343	0.04454343	0	0	0	0	0	0	0	0
c__Deinococci	0	0	0	0	0.08908686	0	0	0	0.08908686	0.04454343	0.04454343	0	0	0	0	0	0	0	0
o__Deinococcales	0	0	0	0	0.08908686	0	0	0	0.08908686	0.04454343	0.04454343	0	0	0	0	0	0	0	0
f__Deinococcaceae	0	0	0	0	0.08908686	0	0	0	0.08908686	0.04454343	0.04454343	0	0	0	0	0	0	0	0
g__Deinococcus	0	0	0	0	0.08908686	0	0	0	0.08908686	0.04454343	0.04454343	0	0	0	0	0	0	0	0
s__alpinitundrae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aquatilis	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0
s__geothermalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.08908686	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0
o__Thermales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Verrucomicrobia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Pedosphaerae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Pedosphaerales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Pedosphaeraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pedosphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Spartobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Chthoniobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Chthoniobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ellin506	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__WPS-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Total Number of Reads	5413	12070	3629	2245	8812	31740	5284	15256	10115	20328	33592	36997	21991	2662	30131	20983	12584	29787	19584

Sample ID	5949R	5952R	5973R	6020R	6094R	6131R	6145R	6160R	6178R	6201R	6206R	6208R	6228R	6292R	6333R	5918R	5919R
Sample Location	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**
SSTI/*S. aureus* colonization status	**MRSA Non-SSTI**	**MRSA Non-SSTI**	**MRSA Non-SSTI**	**MRSA Non-SSTI**	**MRSA Non-SSTI**	**MRSA Non-SSTI**	**MRSA Non-SSTI**	**MRSA Non-SSTI**	**MRSA Non-SSTI**	**MRSA Non-SSTI**	**MRSA Non-SSTI**	**MRSA Non-SSTI**	**MRSA Non-SSTI**	**MRSA Non-SSTI**	**MRSA Non-SSTI**	**MSSA Non-SSTI**	**MSSA Non-SSTI**
Taxon																	
p__Acidobacteria	0.04454343	0	0	0.04454343	0	0	0.04454343	0	0	0.04454343	0.04454343	0	0	0	0	0.08908686	0
c__Acidobacteria-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Acidobacteria-6	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__iii1-15	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Acidobacteriia	0	0	0	0.04454343	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0
o__Acidobacteriales	0	0	0	0.04454343	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0
f__Acidobacteriaceae	0	0	0	0.04454343	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0
g__Edaphobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__modestum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Terriglobus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0
f__Koribacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Candidatus_Koribacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Chloracidobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__DS-100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__PK29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__RB41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Ellin6075	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__DA052	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Ellin6513	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__RB25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Solibacteres	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
o__Solibacterales	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
f__MVS-65	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
f__PK34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Sva0725	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
o__Sva0725	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
c__iii1-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
o__DS-18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
p__Actinobacteria	76.61469933	84.98886414	19.51002227	69.13140312	65.16703786	62.0935412	70.33407572	45.38975501	61.11358575	58.57461024	87.08240535	48.68596882	56.16926503	61.6481069	95.3674833	82.9844098	50.69042316
c__Acidimicrobiia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Acidimicrobiales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__C111	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__EB1017	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Actinobacteria	76.61469933	84.98886414	19.51002227	69.13140312	65.077951	62.0935412	70.28953229	45.38975501	61.06904232	58.53006682	87.03786192	48.55233853	56.16926503	61.6481069	95.3674833	82.9844098	50.69042316
o__Actinomycetales	76.61469933	84.98886414	19.51002227	69.13140312	65.077951	62.0935412	70.28953229	45.38975501	61.06904232	58.53006682	87.03786192	48.55233853	56.16926503	61.6481069	95.3674833	82.9844098	50.69042316
f__Actinomycetaceae	0	0	0	0	0.08908686	0	0	0.08908686	0	0	0.08908686	0.267260579	0	0.04454343	0	0.222717149	0
g__Actinobaculum	0	0	0	0	0.08908686	0	0	0	0	0	0.08908686	0	0	0	0	0	0
unclassified	0	0	0	0	0.08908686	0	0	0	0	0	0.08908686	0	0	0	0	0	0
g__Actinomyces	0	0	0	0	0	0	0	0.08908686	0	0	0	0.267260579	0	0.04454343	0	0.222717149	0
s__europaeus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__hyovaginalis	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.08908686	0	0	0	0.222717149	0	0.04454343	0	0.222717149	0
g__Mobiluncus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Varibaculum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Actinosynnemataceae	0	0.08908686	0	0.04454343	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0.04454343	0.178173719
g__Actinoalloteichus	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kutzneria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lentzea	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0.178173719
s__violacea	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0.178173719
g__Saccharothrix	0	0.08908686	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0.08908686	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
f__Beutenbergiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bogoriellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Georgenia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Brevibacteriaceae	0	0	0	0	0	0.08908686	0.04454343	0	0	0	0.04454343	0	0	0	0	0.04454343	0.08908686
g__Brevibacterium	0	0	0	0	0	0.08908686	0.04454343	0	0	0	0.04454343	0	0	0	0	0.04454343	0.08908686
s__aureum	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0
s__casei	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0.08908686
s__paucivorans	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0
f__Cellulomonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Actinotalea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Cellulomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__uda	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Corynebacteriaceae	69.844098	83.4298441	8.106904232	65.87973274	44.6325167	50.06681514	61.3363029	34.16481069	58.93095768	54.34298441	45.16703786	20.80178174	45.9688196	49.26503341	94.34298441	64.89977728	41.82628062
g__Corynebacterium	69.844098	83.4298441	8.106904232	65.87973274	44.6325167	50.06681514	61.3363029	34.16481069	58.93095768	54.34298441	45.16703786	20.80178174	45.9688196	49.26503341	94.34298441	64.89977728	41.82628062
s__durum	0	0	0	0	0.08908686	0	0.400890869	0.04454343	0	0	0	0.13363029	0	0	0	0.04454343	0
s__kroppenstedtii	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0.08908686
s__lubricantis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0
s__mastitidis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__pilosum	0.13363029	0.178173719	0	0.178173719	0.04454343	0.04454343	0.04454343	0	0.222717149	0.445434298	0	0	0.04454343	0.04454343	0.04454343	0.935412027	19.33184855
s__renale	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
s__simulans	0	0	0	0	0	0	0.08908686	0	0	0	0	0.04454343	0	0	0.04454343	0	0
s__stationis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	69.71046771	83.25167038	8.106904232	65.70155902	44.49888641	50.02227171	60.80178174	34.07572383	58.6636971	53.89755011	45.16703786	20.62360802	45.92427617	49.22048998	94.25389755	63.83073497	22.40534521
f__Dermabacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Brachybacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__conglomeratum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dermabacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Dermacoccaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dermacoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Dermatophilaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dermatophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Dietziaceae	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Dietzia	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
f__Frankiaceae	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0.04454343
g__Frankia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
f__Geodermatophilaceae	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Blastococcus	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
s__aggregatus	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Geodermatophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__obscurus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Modestobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Gordoniaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Gordonia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Intrasporangiaceae	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Knoellia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__subterranea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

g__Phycicoccus	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Serinicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Kineosporiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kineococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kineosporia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Microbacteriaceae	0	0	0.04454343	0	0.04454343	0	0.04454343	0	0.04454343	0	0	0.04454343	0.04454343	0.04454343	0	0	0	0.04454343
g__Agrococcus	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__jenensis	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Clavibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__michiganensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Cryocola	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Curtobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Frigoribacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Leucobacter	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
g__Microbacterium	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0.04454343
s__chocolatum	0	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0
s__maritypicum	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Mycetocola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pseudoclavibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__bifida	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Yonghaparkia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Micrococcaceae	0.04454343	0.08908686	0	0	0.222717149	0.04454343	0.311804009	0.13363029	0.178173719	0.04454343	0	0.178173719	0.222717149	0.04454343	0.04454343	0.13363029	0	0
g__Arthrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
s__crystallopoietes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__psychrolactophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
g__Citricoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__alkalitolerans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kocuria	0	0	0	0	0.08908686	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__palustris	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__rhizophila	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Microbispora	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
s__rosea	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Micrococcus	0.04454343	0	0	0	0.13363029	0.04454343	0.311804009	0.13363029	0.13363029	0.04454343	0	0.13363029	0.222717149	0	0.04454343	0.08908686	0	0
s__luteus	0.04454343	0	0	0	0.13363029	0.04454343	0.311804009	0.13363029	0.13363029	0.04454343	0	0.13363029	0.222717149	0	0.04454343	0.08908686	0	0
g__Nesterenkonia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Renibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rothia	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
s__aeria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mucilaginosa	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
g__Zhihengliuella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Micromonosporaceae	0	0.08908686	0.178173719	1.291759465	0	0	0.979955457	0.222717149	0.178173719	0	0	1.247216036	0	2.85077951	0.311804009	0.311804009	0.534521158	0
g__Actinocatenispora	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Catellatospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Couchioplanes	0	0.08908686	0.178173719	1.247216036	0	0	0.979955457	0.222717149	0.13363029	0	0	1.247216036	0	2.85077951	0.311804009	0.311804009	0.534521158	0
s__caeruleus	0	0.08908686	0.178173719	1.247216036	0	0	0.979955457	0.222717149	0.13363029	0	0	1.247216036	0	2.85077951	0.311804009	0.311804009	0.534521158	0
g__Solwaraspora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Verrucosispora	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__gifhornensis	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
f__Mycobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Mycobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__celatum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__gordonae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__vaccae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nakamurellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nocardiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nocardia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__fascians	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__globerulus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nocardioidaceae	0	0.04454343	0	0	0.489977728	0.356347439	0.08908686	0.04454343	0.13363029	0.04454343	0.178173719	0.13363029	0.13363029	0.400890869	0	0.04454343	0.04454343	0
g__Actinopolymorpha	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Aeromicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Friedmanniella	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0.08908686	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0.08908686	0	0	0	0	0
g__Nocardioides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pimelobacter	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0
g__Propionicimonas	0	0.04454343	0	0	0.489977728	0.356347439	0.08908686	0.04454343	0.13363029	0	0.08908686	0.13363029	0.04454343	0.400890869	0	0.04454343	0	0
unclassified	0	0.04454343	0	0	0.489977728	0.356347439	0.08908686	0.04454343	0.13363029	0	0.08908686	0.13363029	0.04454343	0.400890869	0	0.04454343	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
f__Nocardiopsaceae	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0
g__Nocardiopsis	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0
s__composta	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0
f__Promicromonosporaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
g__Cellulosimicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
g__Promicromonospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Propionibacteriaceae	6.681514477	1.247216036	11.00222717	1.915367483	19.51002227	11.4922049	7.394209354	10.73496659	1.559020045	4.053452116	41.55902004	25.70155902	9.710467706	8.997772829	0.623608018	17.28285078	7.884187082	0
g__Luteococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Microlunatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Propionibacterium	6.681514477	1.247216036	11.00222717	1.915367483	19.51002227	11.4922049	7.394209354	10.73496659	1.559020045	4.053452116	41.55902004	25.70155902	9.710467706	8.997772829	0.623608018	17.28285078	7.884187082	0
s__acnes	6.681514477	0.935412027	9.977728285	1.826280624	15.14476615	11.13585746	7.037861915	10.155902	1.469933185	3.385300668	40.48997773	24.6325167	9.576837416	8.329621381	0.623608018	16.65924276	7.884187082	0
s__granulosum	0	0.311804009	1.024498886	0.08908686	4.365256125	0.356347439	0.356347439	0.579064588	0.08908686	0.668151448	1.069042316	1.069042316	0.13363029	0.668151448	0	0.623608018	0	0
g__Tessaracoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Pseudonocardiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinomycetospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pseudonocardia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Sporichthyaceae	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sporichthya	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Streptomycetaceae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
g__Kitasatospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Streptomyces	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
s__lanatus	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__mashuensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__scabrisporus	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
f__Streptosporangiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nonomuraea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__roseoviolacea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphaerisporangium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermomonosporaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinomadura	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__vinacea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Tsukamurellaceae	0	0	0	0	0.08908686	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
g__Tsukamurella	0	0	0	0	0.08908686	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.08908686	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
o__Micrococcales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Coriobacteriia	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0
o__Coriobacteriales	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0
f__Coriobacteriaceae	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0
g__Adlercreutzia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Atopobium	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0
s__rimae	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
g__Collinsella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aerofaciens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Slackia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__MB-A2-108	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__0319-7L14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__OPB41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Rubrobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rubrobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Rubrobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rubrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Thermoleophilia	0	0	0	0	0.08908686	0	0.04454343	0	0.04454343	0.04454343	0	0.08908686	0	0	0	0	0
o__Gaiellales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Gaiellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Solirubrobacterales	0	0	0	0	0.08908686	0	0.04454343	0	0.04454343	0.04454343	0	0.08908686	0	0	0	0	0
f__Conexibacteraceae	0	0	0	0	0.08908686	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0
g__Conexibacter	0	0	0	0	0.08908686	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.08908686	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
f__Patulibacteraceae	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
f__Solirubrobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
g__Solirubrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Armatimonadetes	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
c__Armatimonadia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Armatimonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Armatimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__CL0-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__FW68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Chthonomonadetes	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
o__Chthonomonadales	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
f__Chthonomonadaceae	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
c__Fimbriimonadia	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Fimbriimonadales	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Fimbriimonadaceae	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Fimbriimonas	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
c__OPB50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__BRC1	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
c__PRR-11	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
p__Bacteroidetes	0.400890869	0.08908686	0.13363029	0.13363029	0.178173719	0.08908686	0.534521158	0.13363029	0.04454343	0.04454343	0.267260579	1.069042316	0.13363029	0.356347439	0.04454343	0.13363029	0.13363029
c__Bacteroidia	0.311804009	0.04454343	0.04454343	0.04454343	0.08908686	0.04454343	0.267260579	0	0	0	0.08908686	0.846325167	0	0.311804009	0	0.08908686	0
o__Bacteroidales	0.311804009	0.04454343	0.04454343	0.04454343	0.08908686	0.04454343	0.267260579	0	0	0	0.08908686	0.846325167	0	0.311804009	0	0.08908686	0
f__Bacteroidaceae	0	0	0	0	0	0	0.04454343	0	0	0	0.08908686	0	0	0.13363029	0	0	0
g__Bacteroides	0	0	0	0	0	0	0.04454343	0	0	0	0.08908686	0	0	0.13363029	0	0	0
s__caccae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ovatus	0	0	0	0	0	0	0.04454343	0	0	0	0.08908686	0	0	0	0	0	0
s__uniformis	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Paraprevotellaceae	0.267260579	0	0	0.04454343	0.08908686	0.04454343	0.13363029	0	0	0	0	0.712694878	0	0.08908686	0	0	0
g__Prevotella	0.267260579	0	0	0	0.08908686	0.04454343	0.13363029	0	0	0	0	0.712694878	0	0	0	0	0
unclassified	0.267260579	0	0	0	0.08908686	0.04454343	0.13363029	0	0	0	0	0.712694878	0	0	0	0	0
g__YRC22	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0
f__Porphyromonadaceae	0.04454343	0	0	0	0	0	0.08908686	0	0	0	0	0.13363029	0	0	0	0	0
g__Porphyromonas	0.04454343	0	0	0	0	0	0.08908686	0	0	0	0	0.13363029	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0.08908686	0	0	0	0	0.13363029	0	0	0	0	0
g__Tannerella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Prevotellaceae	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0.08908686	0
g__Prevotella	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0.08908686	0
s__copri	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__melaninogenica	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0
s__nanceiensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ruminicola	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__stercorea	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Rikenellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Blvii28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__S24-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Cytophagia	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0
o__Cytophagales	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0
f__Cytophagaceae	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0
g__Adhaeribacter	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Dyadobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Hymenobacter	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
g__Rhodocytophaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Flavobacteriia	0.08908686	0	0.08908686	0	0.04454343	0	0.222717149	0.13363029	0	0	0.04454343	0.178173719	0	0.04454343	0.04454343	0.04454343	0.13363029
o__Flavobacteriales	0.08908686	0	0.08908686	0	0.04454343	0	0.222717149	0.13363029	0	0	0.04454343	0.178173719	0	0.04454343	0.04454343	0.04454343	0.13363029
f__Cryomorphaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Fluviicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Flavobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0
g__Algibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__lectus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Capnocytophaga	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__ochracea	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Flavobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__succinicans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Myroides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__odoratimimus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Weeksellaceae	0.08908686	0	0.08908686	0	0.04454343	0	0.222717149	0.13363029	0	0	0.04454343	0.13363029	0	0.04454343	0.04454343	0	0.13363029
g__Chryseobacterium	0.08908686	0	0.08908686	0	0	0	0.08908686	0.13363029	0	0	0	0.08908686	0	0.04454343	0.04454343	0	0.08908686
unclassified	0.08908686	0	0.08908686	0	0	0	0.08908686	0.13363029	0	0	0	0.08908686	0	0.04454343	0.04454343	0	0.08908686
g__Cloacibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Elizabethkingia	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0.04454343	0.04454343	0	0	0	0	0
s__meningoseptica	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0.04454343	0.04454343	0	0	0	0	0
g__Ornithobacterium	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Riemerella	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Wautersiella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Weeksella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Saprospirae	0	0	0	0.04454343	0	0.04454343	0.04454343	0	0.04454343	0.04454343	0.08908686	0	0.08908686	0	0	0	0
o__Saprospirales	0	0	0	0.04454343	0	0.04454343	0.04454343	0	0.04454343	0.04454343	0.08908686	0	0.08908686	0	0	0	0
f__Chitinophagaceae	0	0	0	0.04454343	0	0.04454343	0.04454343	0	0.04454343	0.04454343	0.08908686	0	0.08908686	0	0	0	0
g__Chitinophaga	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
s__arvensicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Flavihumibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Flavisolibacter	0	0	0	0.04454343	0	0	0	0	0	0.04454343	0.08908686	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0.04454343	0.08908686	0	0	0	0	0	0
g__Niabella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Niastella	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
g__Sediminibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Segetibacter	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
g__Terrimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
c__Sphingobacteriia	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0
o__Sphingobacteriales	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0
f__Sphingobacteriaceae	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Olivibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pedobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__cryoconitis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphingobacterium	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__faecium	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0

s__mizutaii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__multivorum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Chloroflexi	0	0	0	0	0	0	0	0	0	0	0.04454343	0.222717149	0.04454343	0.04454343	0	0	0
c__Anaerolineae	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
o__Caldilineales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Caldilineaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SBR1031	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__A4b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SJA-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
c__C0119	0	0	0	0	0	0	0	0	0	0	0.04454343	0.13363029	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0.13363029	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0.13363029	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0.13363029	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0.13363029	0	0	0	0	0
c__Chloroflexi	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
o__AKIW781	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Chloroflexales	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
f__FFCH7168	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
o__Roseiflexales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Roseiflexaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseiflexus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Ktedonobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
o__B12-WMSP1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Thermogemmatisporales	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
f__Thermogemmatisporaceae	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
c__SHA-26	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
c__TK10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__B07_WMSP1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__FFCH4570	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Thermomicrobia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__JG30-KF-CM45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Cyanobacteria	0	0	0	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0
c__4C0d-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__MLE1-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Chloroplast	0	0	0	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0
o__Stramenopiles	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
o__Streptophyta	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
p__FBP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Firmicutes	16.21380846	14.61024499	77.59465479	29.08685969	30.95768374	33.54120267	23.20712695	43.02895323	37.72828508	38.17371938	8.730512249	34.43207127	39.82182628	33.40757238	4.008908686	12.20489978	43.4298441
c__Bacilli	15.94654788	9.576837416	77.55011136	27.43875278	24.94432071	32.56124722	15.14476615	41.02449889	34.12026726	28.32962138	6.013363029	28.86414254	38.57461024	24.76614699	4.008908686	11.40311804	41.82628062
o__Bacillales	4.276169265	7.750556793	75.14476615	9.576837416	10.20044543	11.35857461	10.46770601	40.80178174	21.73719376	21.87082405	5.70155902	22.93986637	30.51224944	21.78173719	2.672605791	10.33407572	40.53452116
f__Alicyclobacillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Alicyclobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bacillaceae	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0.04454343	0
g__Alkalibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Anoxybacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__kestanbolensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bacillus	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0.04454343	0
s__acidicola	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0
s__flexus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__foraminis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__horikoshii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__muralis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__trypoxylicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0.04454343	0
g__Geobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__vulcani	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Marinibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Marinococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Exiguobacteraceae	0	0	0	0	0	0	0.13363029	0	0	0	0.04454343	0	0	0.04454343	0	0	0
g__Exiguobacterium	0	0	0	0	0	0	0.13363029	0	0	0	0.04454343	0	0	0.04454343	0	0	0
unclassified	0	0	0	0	0	0	0.13363029	0	0	0	0.04454343	0	0	0.04454343	0	0	0
f__Paenibacillaceae	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0.04454343	0	0	0	0
g__Ammoniphilus	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0
s__oxalaticus	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0
g__Paenibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
s__amylolyticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__edaphicus	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
s__stellifer	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Planococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Lysinibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__boronitolerans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Planomicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sporosarcina	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
f__Sporolactobacillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sporolactobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Staphylococcaceae	4.276169265	7.750556793	75.14476615	9.576837416	10.20044543	11.35857461	10.33407572	40.80178174	21.73719376	21.87082405	5.523385301	22.80623608	30.42316258	21.73719376	2.672605791	10.28953229	40.53452116
g__Jeotgalicoccus	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
s__psychrophilus	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Salinicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Staphylococcus	4.276169265	7.750556793	75.14476615	9.576837416	10.20044543	11.35857461	10.33407572	40.80178174	21.73719376	21.87082405	5.523385301	22.71714922	30.42316258	21.73719376	2.672605791	10.28953229	40.53452116
s__aureus	0	0.08908686	52.91759465	0	0.178173719	0.04454343	2.9844098	14.25389755	0.04454343	1.603563474	0	0.579064588	0	0	1.559020045	0.04454343	21.42538976
s__epidermidis	3.875278396	7.572383073	21.91536748	9.532293987	9.710467706	11.18040089	6.592427617	26.01336303	21.46993318	19.42093541	4.899777283	21.15812918	30.02227171	21.60356347	1.113585746	9.977728285	18.97550111
s__equorum	0.04454343	0	0	0.04454343	0	0.04454343	0	0.04454343	0	0	0	0.08908686	0.04454343	0	0	0.04454343	0.04454343
s__haemolyticus	0.356347439	0	0.178173719	0	0.311804009	0.08908686	0.311804009	0.400890869	0.222717149	0	0.623608018	0.668151448	0.267260579	0.13363029	0	0.178173719	0
s__lugdunensis	0	0.08908686	0.13363029	0	0	0	0.445434298	0.08908686	0	0.846325167	0	0.222717149	0.08908686	0	0	0.04454343	0.08908686
s__pettenkoferi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__sciuri	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermoactinomycetaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Planifilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Gemellales	0	0.08908686	0.222717149	0.04454343	0.178173719	0.311804009	0.04454343	0	0.04454343	0	0	0.267260579	2.004454343	0	0	0.08908686	0
f__Gemellaceae	0	0.08908686	0.222717149	0.04454343	0.178173719	0.311804009	0.04454343	0	0.04454343	0	0	0.267260579	2.004454343	0	0	0.08908686	0
g__Gemella	0	0.08908686	0.222717149	0.04454343	0.178173719	0.311804009	0.04454343	0	0.04454343	0	0	0.267260579	2.004454343	0	0	0.08908686	0
unclassified	0	0.08908686	0.222717149	0.04454343	0.178173719	0.311804009	0.04454343	0	0.04454343	0	0	0.267260579	2.004454343	0	0	0.08908686	0
o__Lactobacillales	11.67037862	1.737193764	2.182628062	17.81737194	14.56570156	20.8908686	4.632516704	0.222717149	12.33853007	6.458797327	0.311804009	5.65701559	6.057906459	2.9844098	1.336302895	0.979955457	1.291759465
f__Aerococcaceae	11.62583519	1.514476615	1.737193764	17.50556793	0	20.31180401	3.162583519	0	11.53674833	6.369710468	0.08908686	0	4.097995546	2.449888641	1.247216036	0	1.113585746
g__Abiotrophia	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686
g__Aerococcus	0	0	0	0	0	0.04454343	0.13363029	0	0.04454343	0	0	0	0.13363029	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0.13363029	0	0.04454343	0	0	0	0.13363029	0	0	0	0
g__Alloiococcus	11.62583519	1.514476615	1.692650334	17.50556793	0	20.26726058	3.028953229	0	11.4922049	6.369710468	0.04454343	0	3.919821826	2.449888641	1.247216036	0	1.024498886
s__otitis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	11.62583519	1.514476615	1.692650334	17.50556793	0	20.26726058	3.028953229	0	11.4922049	6.369710468	0.04454343	0	3.919821826	2.449888641	1.247216036	0	1.024498886
g__Facklamia	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0
f__Carnobacteriaceae	0	0.04454343	0	0	0.267260579	0	0.08908686	0	0	0	0	1.069042316	0.04454343	0	0	0.04454343	0

g__Carnobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
s__viridans	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Desemzia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Granulicatella	0	0.04454343	0	0	0.267260579	0	0.08908686	0	0	0	0	1.069042316	0	0	0	0.04454343	0
unclassified	0	0.04454343	0	0	0.267260579	0	0.08908686	0	0	0	0	1.069042316	0	0	0	0.04454343	0
f__Enterococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Enterococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__casseliflavus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__cecorum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
f__Lactobacillaceae	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
g__Lactobacillus	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
s__delbrueckii	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
s__helveticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__manihotivorans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__salivarius	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Leuconostocaceae	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
g__Leuconostoc	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
f__Streptococcaceae	0.04454343	0.178173719	0.445434298	0.311804009	14.25389755	0.579064588	1.380846325	0.222717149	0.757238307	0.08908686	0.222717149	4.587973274	1.915367483	0.534521158	0.08908686	0.890868597	0.178173719
g__Lactococcus	0	0	0	0	0.04454343	0	0.222717149	0	0	0	0	0	0	0.04454343	0	0	0
unclassified	0	0	0	0	0.04454343	0	0.222717149	0	0	0	0	0	0	0.04454343	0	0	0
g__Streptococcus	0.04454343	0.178173719	0.445434298	0.311804009	14.20935412	0.579064588	1.158129176	0.222717149	0.757238307	0.08908686	0.222717149	4.587973274	1.915367483	0.489977728	0.08908686	0.890868597	0.178173719
s__agalactiae	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__anginosus	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
s__equi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__infantis	0	0.178173719	0.311804009	0.222717149	13.94209354	0.579064588	0.979955457	0.04454343	0.712694878	0.08908686	0	4.320712695	1.870824053	0.445434298	0.04454343	0.712694878	0.04454343
unclassified	0	0	0.08908686	0.08908686	0.267260579	0	0.178173719	0.178173719	0.04454343	0	0.222717149	0.222717149	0.04454343	0.04454343	0.04454343	0.178173719	0.13363029
o__Turicibacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Turicibacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Turicibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Clostridia	0.267260579	5.033407572	0.04454343	1.648106904	6.013363029	0.979955457	8.062360802	2.004454343	3.608017817	9.844097996	2.71714922	5.523385301	1.247216036	8.64142539	0	0.801781737	1.603563474
o__Clostridiales	0.267260579	5.033407572	0.04454343	1.648106904	6.013363029	0.979955457	8.062360802	2.004454343	3.608017817	9.844097996	2.71714922	5.523385301	1.247216036	8.64142539	0	0.801781737	1.603563474
f__Christensenellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Clostridiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__02d06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Caloramator	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Clostridium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oxobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Dehalobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dehalobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Eubacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Anaerofustis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Lachnospiraceae	0	0	0	0	0	0	0	0	0	0.04454343	0	0.178173719	0	0.400890869	0	0	0
g__Blautia	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0
s__obeum	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
s__producta	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Coprococcus	0	0	0	0	0	0	0	0	0	0	0	0.178173719	0	0.08908686	0	0	0
s__catus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__eutactus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.178173719	0	0.08908686	0	0	0
g__Dorea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__formicigenerans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lachnobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0.222717149	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.222717149	0	0	0
g__Moryella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__indoligenes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseburia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__faecis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ruminococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
s__gnavus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__torques	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
g__Shuttleworthia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Mogibacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Mogibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Peptococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Peptococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__WCHB1-84	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Peptostreptococcaceae	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Filifactor	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Peptostreptococcus	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__anaerobius	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Ruminococcaceae	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0	0.267260579	0	0	0
g__Faecalibacterium	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0	0.178173719	0	0	0
s__prausnitzii	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0	0.178173719	0	0	0
g__Oscillospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ruminococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0
s__bromii	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
s__callidus	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Symbiobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
g__Symbiobacterium	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
s__thermophilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
f__Tissierellaceae	0.13363029	4.766146993	0.04454343	1.648106904	5.924276169	0.935412027	7.706013363	2.004454343	3.563474388	9.532293987	2.672605791	4.855233853	1.247216036	7.839643653	0	0.712694878	1.469933185
g__1-68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Anaerococcus	0	2.227171492	0.04454343	1.202672606	4.855233853	0.935412027	3.608017817	1.380846325	1.024498886	4.187082405	1.469933185	2.360801782	0.623608018	5.879732739	0	0.712694878	0.846325167
unclassified	0	2.227171492	0.04454343	1.202672606	4.855233853	0.935412027	3.608017817	1.380846325	1.024498886	4.187082405	1.469933185	2.360801782	0.623608018	5.879732739	0	0.712694878	0.846325167
g__Finegoldia	0	0.801781737	0	0.08908686	0.356347439	0	1.158129176	0.13363029	0.489977728	1.469933185	0.400890869	0.534521158	0.178173719	0.222717149	0	0	0.311804009
unclassified	0	0.801781737	0	0.08908686	0.356347439	0	1.158129176	0.13363029	0.489977728	1.469933185	0.400890869	0.534521158	0.178173719	0.222717149	0	0	0.311804009
g__GW-34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Gallicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Parvimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Peptoniphilus	0.13363029	1.737193764	0	0.356347439	0.712694878	0	2.93986637	0.489977728	2.004454343	3.875278396	0.801781737	1.959910913	0.445434298	1.737193764	0	0	0.311804009
unclassified	0.13363029	1.737193764	0	0.356347439	0.712694878	0	2.93986637	0.489977728	2.004454343	3.875278396	0.801781737	1.959910913	0.445434298	1.737193764	0	0	0.311804009
g__WAL_1855D	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
g__ph2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Veillonellaceae	0	0.267260579	0	0	0.08908686	0.04454343	0.222717149	0	0.04454343	0.267260579	0.04454343	0.400890869	0	0.13363029	0	0.08908686	0.13363029
g__Dialister	0	0.267260579	0	0	0	0	0.222717149	0	0	0.267260579	0.04454343	0.222717149	0	0.04454343	0	0	0
unclassified	0	0.267260579	0	0	0	0	0.222717149	0	0	0.267260579	0.04454343	0.222717149	0	0.04454343	0	0	0
g__Megasphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0
g__Pelosinus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Propionispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Selenomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__noxia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Succiniclasticum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Veillonella	0	0	0	0	0.08908686	0.04454343	0	0	0.04454343	0	0	0.178173719	0	0	0	0.08908686	0.13363029
s__dispar	0	0	0	0	0.08908686	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0
s__parvula	0	0	0	0	0	0.04454343	0	0	0	0	0	0.13363029	0	0	0	0.08908686	0.13363029
c__Erysipelotrichi	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
o__Erysipelotrichales	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
f__Erysipelotrichaceae	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Bulleidia	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__moorei	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Eubacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__biforme	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Fusobacteria	4.187082405	0	0	0	0.08908686	0	0.13363029	0	0.222717149	0	0	0.400890869	0	0	0	0.08908686	0
c__Fusobacteriia	4.187082405	0	0	0	0.08908686	0	0.13363029	0	0.222717149	0	0	0.400890869	0	0	0	0.08908686	0
o__Fusobacteriales	4.187082405	0	0	0	0.08908686	0	0.13363029	0	0.222717149	0	0	0.400890869	0	0	0	0.08908686	0
f__Fusobacteriaceae	4.187082405	0	0	0	0	0	0	0	0.178173719	0	0	0.400890869	0	0	0	0.08908686	0
g__Fusobacterium	4.187082405	0	0	0	0	0	0	0	0.178173719	0	0	0.400890869	0	0	0	0.08908686	0
unclassified	4.187082405	0	0	0	0	0	0	0	0.178173719	0	0	0.400890869	0	0	0	0.08908686	0
f__Leptotrichiaceae	0	0	0	0	0.08908686	0	0.13363029	0	0.04454343	0	0	0	0	0	0	0	0
g__Leptotrichia	0	0	0	0	0.08908686	0	0.13363029	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.08908686	0	0.13363029	0	0	0	0	0	0	0	0	0	0
g__Streptobacillus	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
s__moniliformis	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
p__Gemmatimonadetes	0	0	0.04454343	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0
c__Gemm-1	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0

unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Gemmatimonadetes	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0
o__Ellin5290	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0
o__Gemmatimonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Ellin5301	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__KD8-87	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__N1423WL	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__MVP-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Nitrospirae	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
c__Nitrospira	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
o__Nitrospirales	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
f__Nitrospiraceae	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Nitrospira	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
f__Thermodesulfovibrionaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Candidatus_Magnetoovum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__OD1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__ZB2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__OP3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__koll11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__GIF10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__kpj58rc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Planctomycetes	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
c__Phycisphaerae	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
o__WD2101	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
c__Planctomycetia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Gemmatales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Gemmataceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Gemmata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Isosphaeraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Proteobacteria	2.494432071	0.267260579	2.71714922	1.514476615	3.518930958	4.231625835	5.74610245	11.44766147	0.801781737	3.162583519	3.741648107	15.01113586	3.697104677	4.543429844	0.579064588	4.498886414	5.70155902
c__Alphaproteobacteria	0	0.04454343	0	0.178173719	0	0.04454343	0.13363029	0.08908686	0	0	0.178173719	0.13363029	0.13363029	0.04454343	0	0	0.04454343
o__Caulobacterales	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0.08908686	0.04454343	0.13363029	0	0	0	0
f__Caulobacteraceae	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0.08908686	0.04454343	0.13363029	0	0	0	0
g__Brevundimonas	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0.08908686	0.04454343	0.13363029	0	0	0	0
s__diminuta	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0.08908686	0.04454343	0.13363029	0	0	0	0
g__Phenylobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Ellin329	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rhizobiales	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0.08908686	0.04454343	0	0	0	0	0
f__Aurantimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bartonellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bartonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Beijerinckiaceae	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
g__Methylocella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
f__Bradyrhizobiaceae	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0
g__Balneimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bosea	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0
s__genosp.	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0
f__Hyphomicrobiaceae	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Hyphomicrobium	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
s__sulfonivorans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodoplanes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Methylobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Methylobacterium	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__komagatae	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
f__Phyllobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Mesorhizobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__huakuii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nitratireductor	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Xanthobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Blastochloris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rhodobacterales	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0
f__Rhodobacteraceae	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0
g__Rubellimicrobium	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0
o__Rhodospirillales	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
f__Acetobacteraceae	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Acetobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Acidisphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Acidocella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseococcus	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mucosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Swaminathania	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Rhodospirillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oleomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Sphingomonadales	0	0	0	0.04454343	0	0	0	0.08908686	0	0	0	0.04454343	0	0.04454343	0	0	0
f__Sphingomonadaceae	0	0	0	0.04454343	0	0	0	0.08908686	0	0	0	0.04454343	0	0.04454343	0	0	0
g__Kaistobacter	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Novosphingobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__resinovorum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphingobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__yanoikuyae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphingomonas	0	0	0	0	0	0	0	0.08908686	0	0	0	0.04454343	0	0.04454343	0	0	0
s__azotifigens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__echinoides	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__wittichii	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
s__yabuuchiae	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0
c__Betaproteobacteria	0.178173719	0.04454343	0.178173719	0	0.935412027	0.08908686	2.449888641	7.661469933	0.04454343	2.004454343	0.356347439	1.158129176	1.915367483	0.400890869	0	0.489977728	0.08908686
o__A21b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__EB1003	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Burkholderiales	0.13363029	0	0.13363029	0	0.579064588	0.04454343	0.712694878	0.400890869	0.04454343	0.04454343	0.311804009	0.400890869	0.400890869	0.400890869	0	0	0.08908686
f__Alcaligenaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Achromobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Denitrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oligella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Tetrathiobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__kashmirensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

f__Burkholderiaceae	0	0	0	0	0.356347439	0	0.534521158	0.400890869	0.04454343	0	0.13363029	0.267260579	0.04454343	0.178173719	0	0	0
g__Burkholderia	0	0	0	0	0.356347439	0	0.534521158	0.400890869	0.04454343	0	0.13363029	0.267260579	0.04454343	0.178173719	0	0	0
s__andropogonis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__bryophila	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__graminis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__tuberum	0	0	0	0	0.178173719	0	0.178173719	0.08908686	0	0	0	0.13363029	0	0.13363029	0	0	0
unclassified	0	0	0	0	0.178173719	0	0.356347439	0.311804009	0.04454343	0	0.13363029	0.13363029	0.04454343	0.04454343	0	0	0
g__Lautropia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Salinispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__tropica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Comamonadaceae	0.08908686	0	0.04454343	0	0.178173719	0	0.13363029	0	0	0	0.13363029	0	0.04454343	0.178173719	0	0	0
g__Acidovorax	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__delafieldii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Alicycliphilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Aquabacterium	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Azohydromonas	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Comamonas	0.04454343	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
s__terrigena	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
g__Delftia	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0.178173719	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0.178173719	0	0	0
g__Diaphorobacter	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
g__Giesbergeria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Hylemonella	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Leptothrix	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Methylibium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__petroleiphilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Paucibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pelomonas	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
s__puraquae	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Ramlibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rubrivivax	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__gelatinosus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Schlegelella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Tepidimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Variovorax	0	0	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0
s__paradoxus	0	0	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0
f__Oxalobacteraceae	0.04454343	0	0.08908686	0	0.04454343	0.04454343	0.04454343	0	0	0.04454343	0.04454343	0.13363029	0.311804009	0.04454343	0	0	0.08908686
g__Collimonas	0	0	0	0	0.04454343	0	0	0	0	0	0	0.08908686	0.222717149	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0.08908686	0.222717149	0	0	0	0
g__Cupriavidus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__gilardii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Herbaspirillum	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
g__Herminiimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Janthinobacterium	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
s__lividum	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oxalobacter	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
s__formigenes	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Polynucleobacter	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
s__cosmopolitanus	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0.04454343	0	0.04454343	0	0	0.04454343	0.04454343	0	0	0.04454343	0	0.04454343	0	0	0	0	0.04454343
unclassified	0.04454343	0	0.04454343	0	0	0.04454343	0.04454343	0	0	0.04454343	0	0.04454343	0	0	0	0	0.04454343
o__Ellin6067	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__MND1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Neisseriales	0.04454343	0.04454343	0.04454343	0	0.356347439	0.04454343	1.692650334	7.260579065	0	1.959910913	0.04454343	0.757238307	1.514476615	0	0	0.489977728	0
f__Neisseriaceae	0.04454343	0.04454343	0.04454343	0	0.356347439	0.04454343	1.692650334	7.260579065	0	1.959910913	0.04454343	0.757238307	1.514476615	0	0	0.489977728	0
g__Aquitalea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__magnusonii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Eikenella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kingella	0	0	0	0	0	0	0	0.08908686	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.08908686	0	0	0	0.04454343	0	0	0	0	0
g__Microvirgula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aerodenitrificans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Neisseria	0.04454343	0.04454343	0.04454343	0	0.356347439	0.04454343	0.178173719	0	0	0	0.04454343	0.712694878	0	0	0	0.267260579	0
s__cinerea	0	0	0	0	0.04454343	0.04454343	0.178173719	0	0	0	0	0.400890869	0	0	0	0	0
s__subflava	0	0	0	0	0.311804009	0	0	0	0	0	0.04454343	0.311804009	0	0	0	0.267260579	0
unclassified	0.04454343	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Vitreoscilla	0	0	0	0	0	0	1.514476615	7.171492205	0	1.959910913	0	0	1.514476615	0	0	0.222717149	0
unclassified	0	0	0	0	0	0	1.514476615	7.171492205	0	1.959910913	0	0	1.514476615	0	0	0.222717149	0
o__Rhodocyclales	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
f__Rhodocyclaceae	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Azospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dok59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Methyloversatilis	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Propionivibrio	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Zoogloea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SBla14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SC-I-84	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Deltaproteobacteria	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0	0	0	0
o__Desulfovibrionales	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
f__Desulfovibrionaceae	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
g__Desulfovibrio	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
s__cavernae	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
o__FAC87	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__MI246	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Myxococcales	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
f__Cystobacteraceae	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
g__Cystobacter	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
f__Haliangiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Haliangium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Myxococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Anaeromyxobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SAR324	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Syntrophobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Syntrophobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Syntrophobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Epsilonproteobacteria	0	0.04454343	0	0	0	0	0	0	0	0.846325167	0.178173719	0.08908686	0	0.13363029	0	0	0
o__Campylobacterales	0	0.04454343	0	0	0	0	0	0	0	0.846325167	0.178173719	0.08908686	0	0.13363029	0	0	0
f__Campylobacteraceae	0	0.04454343	0	0	0	0	0	0	0	0.846325167	0.178173719	0.08908686	0	0.13363029	0	0	0
g__Campylobacter	0	0.04454343	0	0	0	0	0	0	0	0.846325167	0.178173719	0.08908686	0	0.13363029	0	0	0
s__rectus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ureolyticus	0	0.04454343	0	0	0	0	0	0	0	0.846325167	0	0.08908686	0	0.13363029	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.178173719	0	0	0	0	0	0
f__Helicobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Helicobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__pylori	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Nautiliales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nautiliaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nautilia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Gammaproteobacteria	2.316258352	0.13363029	2.538975501	1.336302895	2.538975501	4.097995546	3.162583519	3.697104677	0.757238307	0.311804009	2.9844098	13.63028953	1.648106904	3.964365256	0.579064588	4.008908686	5.567928731
o__Alteromonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Shewanellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Shewanella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__pacifica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Enterobacteriales	0	0	0.04454343	0	0.04454343	0	0.04454343	0.13363029	0	0	0.178173719	0	0	0	0	0	0
f__Enterobacteriaceae	0	0	0.04454343	0	0.04454343	0	0.04454343	0.13363029	0	0	0.178173719	0	0	0	0	0	0
g__Citrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Enterobacter	0	0	0.04454343	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__cowanii	0	0	0.04454343	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Erwinia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__dispersa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Klebsiella	0	0	0	0	0	0	0.04454343	0.08908686	0	0	0.04454343	0	0	0	0	0	0
s__oxytoca	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Salmonella	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0
s__enterica	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0
o__Legionellales	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
f__Coxiellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Legionellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Legionella	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
o__Oceanospirillales	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0
f__Halomonadaceae	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0
g__Halomonas	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0
f__Oceanospirillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Marinomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__primoryensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Pasteurellales	0.08908686	0	0	0	0	0.04454343	0.04454343	0	0	0	0.08908686	0.178173719	0.08908686	0	0	0	0.04454343
f__Pasteurellaceae	0.08908686	0	0	0	0	0.04454343	0.04454343	0	0	0	0.08908686	0.178173719	0.08908686	0	0	0	0.04454343
g__Actinobacillus	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0.08908686	0	0	0	0
s__parahaemolyticus	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0.08908686	0	0	0	0
g__Haemophilus	0.08908686	0	0	0	0	0.04454343	0.04454343	0	0	0	0.08908686	0.13363029	0	0	0	0	0.04454343
s__influenzae	0.08908686	0	0	0	0	0	0.04454343	0	0	0	0.08908686	0.04454343	0	0	0	0	0.04454343
s__parainfluenzae	0	0	0	0	0	0.04454343	0	0	0	0	0	0.08908686	0	0	0	0	0
o__Pseudomonadales	1.380846325	0	0.04454343	0	0	0	0.04454343	0.13363029	0.534521158	0.13363029	0.04454343	0	0.445434298	0.222717149	0	0	0.04454343
f__Moraxellaceae	1.336302895	0	0.04454343	0	0	0	0.04454343	0.04454343	0.489977728	0.13363029	0.04454343	0	0.445434298	0.222717149	0	0	0
g__Acinetobacter	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
s__guillouiae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__lwoffii	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
s__rhizosphaerae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__schindleri	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__venetianus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Alkanindiges	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Enhydrobacter	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0
g__Moraxella	1.336302895	0	0.04454343	0	0	0	0	0	0.489977728	0.13363029	0	0	0.400890869	0.222717149	0	0	0
s__ovis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	1.336302895	0	0.04454343	0	0	0	0	0	0.489977728	0.13363029	0	0	0.400890869	0.222717149	0	0	0
f__Pseudomonadaceae	0.04454343	0	0	0	0	0	0	0.08908686	0.04454343	0	0	0	0	0	0	0	0.04454343
g__Pseudomonas	0.04454343	0	0	0	0	0	0	0.08908686	0.04454343	0	0	0	0	0	0	0	0.04454343
s__alcaligenes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__fragi	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__umsongensis	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__veronii	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0.04454343
s__viridiflava	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
o__Xanthomonadales	0.846325167	0.13363029	2.449888641	1.336302895	2.494432071	4.053452116	3.028953229	3.340757238	0.222717149	0.178173719	2.672605791	13.45211581	1.069042316	3.741648107	0.579064588	4.008908686	5.478841871
f__Sinobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Hydrocarboniphaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__effusa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Xanthomonadaceae	0.846325167	0.13363029	2.449888641	1.336302895	2.494432071	4.053452116	3.028953229	3.340757238	0.222717149	0.178173719	2.672605791	13.45211581	1.069042316	3.741648107	0.579064588	4.008908686	5.478841871
g__Dokdonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dyella	0.08908686	0	1.915367483	1.069042316	0.311804009	3.251670379	0.400890869	0.178173719	0	0	0.445434298	10.6013363	0.13363029	3.118040089	0.445434298	3.429844098	4.899777283
s__ginsengisoli	0.08908686	0	1.915367483	1.069042316	0.311804009	3.251670379	0.400890869	0.178173719	0	0	0.445434298	10.6013363	0.13363029	3.118040089	0.445434298	3.429844098	4.899777283
g__Luteimonas	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
g__Lysobacter	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pseudoxanthomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mexicana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodanobacter	0.757238307	0.08908686	0.489977728	0.267260579	2.182628062	0.712694878	2.628062361	3.028953229	0.222717149	0.178173719	2.182628062	2.80623608	0.890868597	0.623608018	0.13363029	0.579064588	0.534521158
s__lindaniclasticus	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0.757238307	0.08908686	0.489977728	0.267260579	2.182628062	0.712694878	2.583518931	3.028953229	0.222717149	0.178173719	2.182628062	2.80623608	0.890868597	0.623608018	0.13363029	0.579064588	0.534521158
g__Stenotrophomonas	0	0	0.04454343	0	0	0.08908686	0	0.13363029	0	0	0	0.04454343	0.04454343	0	0	0	0.04454343
s__acidaminiphila	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__geniculata	0	0	0.04454343	0	0	0.08908686	0	0.08908686	0	0	0	0.04454343	0.04454343	0	0	0	0.04454343
s__retroflexus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__fusca	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Xanthomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Spirochaetes	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0
c__Spirochaetes	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0
o__Borreliales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Borreliaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Spironema	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Spirochaetales	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0
f__Spirochaetaceae	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0
g__Treponema	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0
p__Synergistetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Synergistia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Synergistales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Dethiosulfovibrionaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pyramidobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__piscolens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermovirgaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermovirga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__TM7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__TM7-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__TM7-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__EW055	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Tenericutes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Mollicutes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__RF39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Thermi	0.04454343	0.04454343	0	0	0.04454343	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0.04454343
c__Deinococci	0.04454343	0.04454343	0	0	0.04454343	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0.04454343
o__Deinococcales	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343
f__Deinococcaceae	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343
g__Deinococcus	0.04454343	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343
s__alpinitundrae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aquatilis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__geothermalis	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343
o__Thermales	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0
f__Thermaceae	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Thermus	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0
p__Verrucomicrobia	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
c__Pedosphaerae	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
o__Pedosphaerales	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
f__Pedosphaeraceae	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Pedosphaera	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
c__Spartobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Chthoniobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Chthoniobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ellin506	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__WPS-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Total Number of Reads	7137	6493	9276	10315	2934	10658	3417	4270	13461	13652	3456	4399	8901	10148	28007	11210	9392

Sample ID	5920R	5921R	5922R	5925R	5926R	5944R	5948R	5961R	5977R	5985R	5986R	5987R	6430R	5927R	5931R	5933R	5936R
Sample Location	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose	Nose
SSTI/*S. aureus* colonization status	MSSA Non-SSTI	MSSA Non-SSTI	MSSA Non-SSTI	MSSA Non-SSTI	MSSA Non-SSTI	MSSA Non-SSTI	MSSA Non-SSTI	MSSA Non-SSTI	MSSA Non-SSTI	MSSA Non-SSTI	MSSA Non-SSTI	MSSA Non-SSTI	MSSA Non-SSTI	NoSA Non-SSTI	NoSA Non-SSTI	NoSA Non-SSTI	NoSA Non-SSTI
Taxon																	
p__Acidobacteria	0.04454343	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0.08908686	0	0	0	0.13363029
c__Acidobacteria-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Acidobacteria-6	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
o__iii1-15	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
c__Acidobacteriia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029
o__Acidobacteriales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029
f__Acidobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Edaphobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__modestum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Terriglobus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Koribacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029
g__Candidatus_Koribacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029
c__Chloracidobacteria	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
o__DS-100	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
o__PK29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__RB41	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Ellin6075	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__DA052	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Ellin6513	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__RB25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Solibacteres	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
o__Solibacterales	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
f__MVS-65	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
f__PK34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Sva0725	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Sva0725	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__iii1-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__DS-18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Actinobacteria	85.43429844	5.033407572	63.20712695	13.05122494	72.33853007	63.69710468	28.81959911	53.5857461	59.51002227	33.27394209	63.02895323	68.41870824	74.96659243	58.97550111	84.45434298	89.79955457	49.48775056
c__Acidimicrobiia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Acidimicrobiales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__C111	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__EB1017	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Actinobacteria	85.43429844	5.033407572	63.20712695	13.05122494	72.33853007	63.69710468	28.81959911	53.5857461	59.51002227	33.27394209	62.9844098	68.41870824	74.922049	58.97550111	84.45434298	89.79955457	49.48775056
o__Actinomycetales	85.43429844	5.033407572	63.20712695	13.05122494	72.33853007	63.69710468	28.81959911	53.5857461	59.51002227	33.27394209	62.9844098	68.41870824	74.922049	58.97550111	84.45434298	89.79955457	49.48775056
f__Actinomycetaceae	0	0	0.445434298	0.04454343	0.04454343	0	0	0	0	0.400890869	0	0.267260579	0.04454343	0.04454343	0	0.04454343	0.178173719
g__Actinobaculum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinomyces	0	0	0.445434298	0	0.04454343	0	0	0	0	0.400890869	0	0.267260579	0.04454343	0.04454343	0	0.04454343	0.178173719
s__europaeus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__hyovaginalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686
unclassified	0	0	0.445434298	0	0.04454343	0	0	0	0	0.400890869	0	0.267260579	0.04454343	0.04454343	0	0.04454343	0.08908686
g__Mobiluncus	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Varibaculum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Actinosynnemataceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
g__Actinoalloteichus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kutzneria	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
g__Lentzea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__violacea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Saccharothrix	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Beutenbergiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bogoriellaceae	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Georgenia	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
f__Brevibacteriaceae	0	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0
g__Brevibacterium	0	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0
s__aureum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__casei	0	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0
s__paucivorans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Cellulomonadaceae	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
g__Actinotalea	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
g__Cellulomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__uda	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Corynebacteriaceae	82.5389755	2.271714922	34.74387528	3.251670379	48.5077951	56.34743875	22.27171492	29.57683742	54.96659243	27.34966592	45.61247216	52.47216036	68.81959911	51.40311804	78.53006682	84.49888641	33.05122494
g__Corynebacterium	82.5389755	2.271714922	34.74387528	3.251670379	48.5077951	56.34743875	22.27171492	29.57683742	54.96659243	27.34966592	45.61247216	52.47216036	68.81959911	51.40311804	78.53006682	84.49888641	33.05122494
s__durum	0	0.08908686	0.08908686	0.04454343	0	0.08908686	0	0	0	0.08908686	0.04454343	0	0.04454343	0	0	0	0.13363029
s__kroppenstedtii	0	0	0	0	0	0.04454343	0	0	0	0.08908686	0	0	0	0	0	0	0
s__lubricantis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mastitidis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__pilosum	0.222717149	0	0.04454343	0	0.04454343	0.04454343	0	0.04454343	0.04454343	0.178173719	0	0.04454343	0.178173719	0.222717149	0.267260579	0.178173719	0.08908686
s__renale	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__simulans	0.13363029	0.08908686	0	0.08908686	0	0.08908686	0.489977728	0.04454343	0	0	0	0.178173719	0.04454343	0	0.04454343	0	0.445434298
s__stationis	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	82.18262806	2.093541203	34.61024499	3.118040089	48.46325167	56.03563474	21.78173719	29.48775056	54.922049	26.99331849	45.56792873	52.24944321	68.55233853	51.18040089	78.21826281	84.32071269	32.3830735
f__Dermabacteraceae	0	0	0	0	0.08908686	0.222717149	0	0.04454343	0	0	0	0.08908686	0	0	0	0	0
g__Brachybacterium	0	0	0	0	0	0.178173719	0	0	0	0	0	0	0	0	0	0	0
s__conglomeratum	0	0	0	0	0	0.178173719	0	0	0	0	0	0	0	0	0	0	0
g__Dermabacter	0	0	0	0	0.08908686	0.04454343	0	0.04454343	0	0	0	0.08908686	0	0	0	0	0
unclassified	0	0	0	0	0.08908686	0.04454343	0	0.04454343	0	0	0	0.08908686	0	0	0	0	0
f__Dermacoccaceae	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Dermacoccus	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
f__Dermatophilaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dermatophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Dietziaceae	0	0	0	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0
g__Dietzia	0	0	0	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0
f__Frankiaceae	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Frankia	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Geodermatophilaceae	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Blastococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aggregatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Geodermatophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__obscurus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Modestobacter	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
f__Gordoniaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Gordonia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Intrasporangiaceae	0	0	0	0	0	0	0	0	0.04454343	0	0.178173719	0	0	0	0	0	0
g__Knoellia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__subterranea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

g__Phycicoccus	0	0	0	0	0	0	0	0	0.04454343	0	0.178173719	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0.178173719	0	0	0	0	0	0
g__Serinicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Kineosporiaceae	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0
g__Kineococcus	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0
g__Kineosporia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Microbacteriaceae	0	0.04454343	0	0.04454343	0.04454343	0.04454343	0	0.04454343	0.04454343	0	0.08908686	0.04454343	0.04454343	0	0	0	0
g__Agrococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__jenensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Clavibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__michiganensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Cryocola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Curtobacterium	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
g__Frigoribacterium	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0
g__Leucobacter	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
g__Microbacterium	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0.04454343	0.04454343	0	0	0	0	0
s__chocolatum	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0
s__maritypicum	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
g__Mycetocola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pseudoclavibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__bifida	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Yonghaparkia	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
f__Micrococcaceae	0	0.04454343	0.08908686	0	0.04454343	0.04454343	0.222717149	0.08908686	0	0	0	0	0	0.13363029	0.04454343	0	0.08908686
g__Arthrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__crystallopoietes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__psychrolactophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Citricoccus	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0
s__alkalitolerans	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Kocuria	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__palustris	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__rhizophila	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Microbispora	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
s__rosea	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
g__Micrococcus	0	0	0	0	0.04454343	0	0.13363029	0.04454343	0	0	0	0	0	0.13363029	0	0	0.08908686
s__luteus	0	0	0	0	0.04454343	0	0.13363029	0.04454343	0	0	0	0	0	0.13363029	0	0	0.08908686
g__Nesterenkonia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Renibacterium	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0
g__Rothia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aeria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mucilaginosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Zhihengliuella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Micromonosporaceae	0.04454343	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Actinocatenispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Catellatospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Couchioplanes	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__caeruleus	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Solwaraspora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Verrucosispora	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
s__glhomensis	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
f__Mycobacteriaceae	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
g__Mycobacterium	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
s__celatum	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
s__gordonae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__vaccae	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nakamurellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nocardiaceae	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Nocardia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodococcus	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__fascians	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__globerulus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nocardioidaceae	0.08908686	0	0.579064588	0.222717149	0.801781737	0	0.04454343	0.311804009	0.178173719	0	0.668151448	0.04454343	0.04454343	0.04454343	0.178173719	0	0.178173719
g__Actinopolymorpha	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Aeromicrobium	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0
g__Friedmanniella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nocardioides	0.04454343	0	0	0.08908686	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0
unclassified	0.04454343	0	0	0.08908686	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0
g__Pimelobacter	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0
g__Propionicimonas	0.04454343	0	0.579064588	0.13363029	0.801781737	0	0	0.267260579	0.13363029	0	0.534521158	0.04454343	0.04454343	0	0.178173719	0	0.178173719
unclassified	0.04454343	0	0.579064588	0.13363029	0.801781737	0	0	0.267260579	0.13363029	0	0.534521158	0.04454343	0.04454343	0	0.178173719	0	0.178173719
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
f__Nocardiopsaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nocardiopsis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__composta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Promicromonosporaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Cellulosimicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Promicromonospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Propionibacteriaceae	2.71714922	2.672605791	26.94877506	9.175946548	22.80623608	6.859688196	6.057906459	23.47438753	4.187082405	5.523385301	16.34743875	15.32293987	5.924276169	7.305122494	5.70155902	5.256124722	15.76837416
g__Luteococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Microlunatus	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Propionibacterium	2.71714922	2.672605791	26.94877506	9.086859688	22.80623608	6.859688196	5.924276169	23.47438753	4.187082405	5.523385301	16.34743875	15.32293987	5.879732739	7.305122494	5.70155902	5.256124722	15.72383073
s__acnes	2.271714922	2.672605791	25.077951	8.775055679	19.91091314	6.280623608	5.79064588	22.40534521	3.741648107	4.409799555	16.16926503	14.38752784	5.70155902	6.414253898	5.61247216	5.256124722	14.61024499
s__granulosum	0.445434298	0	1.870824053	0.311804009	2.89532294	0.579064588	0.13363029	1.069042316	0.445434298	1.113585746	0.178173719	0.935412027	0.178173719	0.890868597	0.08908686	0	1.113585746
g__Tessaracoccus	0	0	0	0.08908686	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0.08908686	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0.04454343
f__Pseudonocardiaceae	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0
g__Actinomycetospora	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Pseudonocardia	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
f__Sporichthyaceae	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
g__Sporichthya	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
f__Streptomycetaceae	0.04454343	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kitasatospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Streptomyces	0.04454343	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0
s__lanatus	0	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mashuensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__scabrisporus	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Streptosporangiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nonomuraea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__roseoviolacea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphaerisporangium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermomonosporaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinomadura	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__vinacea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Tsukamurellaceae	0	0	0.356347439	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0.222717149
g__Tsukamurella	0	0	0.356347439	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0.222717149
unclassified	0	0	0.356347439	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0.222717149
o__Micrococcales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Coriobacteriia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Coriobacteriales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Coriobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Adlercreutzia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Atopobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__rimae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Collinsella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aerofaciens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Slackia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__MB-A2-108	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__0319-7L14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__OPB41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Rubrobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rubrobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Rubrobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rubrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Thermoleophilia	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0
o__Gaiellales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Gaiellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Solirubrobacterales	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0
f__Conexibacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Conexibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Patulibacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Solirubrobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Solirubrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0
p__Armatimonadetes	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Armatimonadia	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Armatimonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Armatimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__CL0-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__FW68	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Chthonomonadetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Chthonomonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Chthonomonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Fimbriimonadia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Fimbriimonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Fimbriimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Fimbriimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__OPB50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__BRC1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__PRR-11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Bacteroidetes	0.08908686	0	2.271714922	0	0	0.08908686	0.668151448	0.08908686	0.13363029	0.13363029	0.04454343	3.518930958	0.178173719	0.08908686	0.13363029	0	0.534521158
c__Bacteroidia	0.08908686	0	0.445434298	0	0	0	0.08908686	0.04454343	0.04454343	0.04454343	0	0.668151448	0.08908686	0	0	0	0.356347439
o__Bacteroidales	0.08908686	0	0.445434298	0	0	0	0.08908686	0.04454343	0.04454343	0.04454343	0	0.668151448	0.08908686	0	0	0	0.356347439
f__Bacteroidaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bacteroides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__caccae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ovatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__uniformis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Paraprevotellaceae	0	0	0.267260579	0	0	0	0	0	0	0.04454343	0	0.489977728	0.08908686	0	0	0	0.222717149
g__Prevotella	0	0	0.13363029	0	0	0	0	0	0	0	0	0.489977728	0.08908686	0	0	0	0.178173719
unclassified	0	0	0.13363029	0	0	0	0	0	0	0	0	0.489977728	0.08908686	0	0	0	0.178173719
g__YRC22	0	0	0.13363029	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343
unclassified	0	0	0.13363029	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343
f__Porphyromonadaceae	0	0	0	0	0	0	0.04454343	0	0	0	0	0.08908686	0	0	0	0	0.04454343
g__Porphyromonas	0	0	0	0	0	0	0.04454343	0	0	0	0	0.08908686	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0.08908686	0	0	0	0	0.04454343
g__Tannerella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Prevotellaceae	0.08908686	0	0.178173719	0	0	0	0.04454343	0.04454343	0.04454343	0	0	0.08908686	0	0	0	0	0.08908686
g__Prevotella	0.08908686	0	0.178173719	0	0	0	0.04454343	0.04454343	0.04454343	0	0	0.08908686	0	0	0	0	0.08908686
s__copri	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__melaninogenica	0	0	0.178173719	0	0	0	0.04454343	0	0.04454343	0	0	0.04454343	0	0	0	0	0.08908686
s__nanceiensis	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__ruminicola	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__stercorea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
f__Rikenellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Blvii28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__S24-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Cytophagia	0	0	0.04454343	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0
o__Cytophagales	0	0	0.04454343	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0
f__Cytophagaceae	0	0	0.04454343	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0
g__Adhaeribacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dyadobacter	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
g__Hymenobacter	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Rhodocytophaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Flavobacteriia	0	0	1.781737194	0	0	0.08908686	0.534521158	0	0	0.04454343	0	2.85077951	0.04454343	0.08908686	0.13363029	0	0.08908686
o__Flavobacteriales	0	0	1.781737194	0	0	0.08908686	0.534521158	0	0	0.04454343	0	2.85077951	0.04454343	0.08908686	0.13363029	0	0.08908686
f__Cryomorphaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Fluviicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Flavobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Algibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__lectus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Capnocytophaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ochracea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Flavobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__succinicans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Myroides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__odoratimimus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Weeksellaceae	0	0	1.781737194	0	0	0.08908686	0.534521158	0	0	0.04454343	0	2.85077951	0.04454343	0.08908686	0.13363029	0	0.08908686
g__Chryseobacterium	0	0	1.781737194	0	0	0.08908686	0.534521158	0	0	0.04454343	0	2.85077951	0.04454343	0.08908686	0.13363029	0	0.08908686
unclassified	0	0	1.781737194	0	0	0.08908686	0.534521158	0	0	0.04454343	0	2.85077951	0.04454343	0.08908686	0.13363029	0	0.08908686
g__Cloacibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Elizabethkingia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__meningoseptica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ornithobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Riemerella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Wautersiella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Weeksella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Saprospirae	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0.04454343	0	0	0	0	0	0.08908686
o__Saprospirales	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0.04454343	0	0	0	0	0	0.08908686
f__Chitinophagaceae	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0.04454343	0	0	0	0	0	0.08908686
g__Chitinophaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__arvensicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Flavihumibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Flavisolibacter	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0.08908686
unclassified	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0.08908686
g__Niabella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Niastella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sediminibacterium	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
g__Segetibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Terrimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Sphingobacteriia	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0
o__Sphingobacteriales	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0
f__Sphingobacteriaceae	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0
g__Olivibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pedobacter	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
s__cryoconitis	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphingobacterium	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__faecium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

s__mizutaii	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__multivorum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Chloroflexi	0	0	0	0	0	0	0	0	0	0	0	0	0.267260579	0	0	0	0
c__Anaerolineae	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0
o__Caldilineales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Caldilineaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SBR1031	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0
f__A4b	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0
o__SJA-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__C0119	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0
c__Chloroflexi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__AKIW781	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Chloroflexales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__FFCH7168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Roseiflexales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Roseiflexaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseiflexus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Ktedonobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__B12-WMSP1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Thermogemmatisporales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermogemmatisporaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__SHA-26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__TK10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__B07_WMSP1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__FFCH4570	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Thermomicrobia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__JG30-KF-CM45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Cyanobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__4C0d-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__MLE1-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Chloroplast	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Stramenopiles	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Streptophyta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__FBP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Firmicutes	14.12026726	91.40311804	30.46770601	81.51447661	24.81069042	34.20935412	64.85523385	44.18708241	39.77728285	65.74610245	36.34743875	24.54342984	16.48106904	40.22271715	14.96659243	8.418708241	45.077951
c__Bacilli	13.36302895	91.00222717	24.45434298	81.24721604	22.31625835	31.40311804	63.51893096	35.27839644	36.83741648	61.95991091	25.61247216	17.32739421	15.59020045	39.42093541	3.118040089	8.195991091	38.26280624
o__Bacillales	3.162583519	67.26057906	21.24721604	77.10467706	19.77728285	14.43207127	62.13808463	34.87750557	30.51224944	58.88641425	7.438752784	10.77951002	13.18485523	38.70824053	3.073496659	7.884187082	32.60579065
f__Alicyclobacillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Alicyclobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bacillaceae	0	0	0	0.04454343	0.04454343	0	0.04454343	0.04454343	0.04454343	0.08908686	0.04454343	0.13363029	0.04454343	0	0	0	0
g__Alkalibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Anoxybacillus	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
s__kestanbolensis	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
g__Bacillus	0	0	0	0.04454343	0	0	0.04454343	0.04454343	0.04454343	0	0.04454343	0.13363029	0.04454343	0	0	0	0
s__acidicola	0	0	0	0	0	0	0	0	0	0	0.04454343	0.13363029	0	0	0	0	0
s__flexus	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0
s__foraminis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__horikoshii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__muralis	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
s__trypoxylicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0
g__Geobacillus	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
s__vulcani	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Marinibacillus	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Marinococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Exiguobacteraceae	0.04454343	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Exiguobacterium	0.04454343	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Paenibacillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ammoniphilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__oxalaticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Paenibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__amylolyticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__edaphicus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__stellifer	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Planococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lysinibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__boronitolerans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Planomicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sporosarcina	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Sporolactobacillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sporolactobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Staphylococcaceae	3.118040089	67.21603563	21.24721604	77.0155902	19.73273942	14.43207127	62.0935412	34.83296214	30.46770601	58.79732739	7.394209354	10.64587973	13.1403118	38.70824053	3.073496659	7.884187082	32.60579065
g__Jeotgalicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__psychrophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Salinicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Staphylococcus	3.118040089	67.21603563	21.24721604	77.0155902	19.73273942	14.43207127	62.0935412	34.83296214	30.46770601	58.79732739	7.394209354	10.64587973	13.1403118	38.70824053	3.073496659	7.884187082	32.60579065
s__aureus	0	61.3363029	0.579064588	59.68819599	0	7.216035635	0.311804009	0	0.08908686	9.487750557	0	0	0	0	0	0	0
s__epidermidis	3.118040089	3.385300668	20.53452116	16.92650334	19.59910913	7.126948775	61.42538976	34.43207127	30.33407572	49.17594655	7.171492205	10.24498886	12.51670379	38.70824053	2.9844098	7.438752784	31.80400891
s__equorum	0	0.08908686	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0.08908686	0.04454343
s__haemolyticus	0	0.267260579	0.13363029	0.400890869	0.08908686	0	0.311804009	0.400890869	0.04454343	0.04454343	0.222717149	0.400890869	0.579064588	0	0.04454343	0.311804009	0.534521158
s__lugdunensis	0	2.138084633	0	0	0	0.08908686	0	0	0	0.08908686	0	0	0	0	0.04454343	0.04454343	0.222717149
s__pettenkoferi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__sciuri	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermoactinomycetaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Planifilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Gemellales	0	1.024498886	0.445434298	0.356347439	0	0	0	0	0.13363029	0.13363029	0	1.336302895	0	0.08908686	0	0	0.712694878
f__Gemellaceae	0	1.024498886	0.445434298	0.356347439	0	0	0	0	0.13363029	0.13363029	0	1.336302895	0	0.08908686	0	0	0.712694878
g__Gemella	0	1.024498886	0.445434298	0.356347439	0	0	0	0	0.13363029	0.13363029	0	1.336302895	0	0.08908686	0	0	0.712694878
unclassified	0	1.024498886	0.445434298	0.356347439	0	0	0	0	0.13363029	0.13363029	0	1.336302895	0	0.08908686	0	0	0.712694878
o__Lactobacillales	10.20044543	22.71714922	2.76169265	3.786191537	2.538975501	16.97104677	1.380846325	0.400890869	6.191536748	2.93986637	18.17371938	5.211581292	2.405345212	0.623608018	0.04454343	0.311804009	4.944320713
f__Aerococcaceae	10.11135857	18.93095768	0.04454343	0	2.449888641	5.924276169	0.222717149	0	6.057906459	1.069042316	18.12917595	0.04454343	1.692650334	0.534521158	0	0.13363029	0.04454343
g__Abiotrophia	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0.04454343
g__Aerococcus	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0
g__Alloiococcus	10.11135857	18.93095768	0.04454343	0	2.316258352	5.924276169	0	0	6.057906459	1.069042316	18.12917595	0	1.692650334	0.534521158	0	0	0
s__otitis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	10.11135857	18.93095768	0.04454343	0	2.316258352	5.924276169	0	0	6.057906459	1.069042316	18.12917595	0	1.692650334	0.534521158	0	0	0
g__Facklamia	0	0	0	0	0.13363029	0	0.13363029	0	0	0	0	0	0	0	0	0.13363029	0
unclassified	0	0	0	0	0.13363029	0	0.13363029	0	0	0	0	0	0	0	0	0.13363029	0
f__Carnobacteriaceae	0	0.13363029	0	0.04454343	0	0.13363029	0.04454343	0.04454343	0	0.267260579	0	1.069042316	0.222717149	0	0	0	1.024498886

g__Carnobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
s__viridans	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
g__Desemzia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Granulicatella	0	0.13363029	0	0.04454343	0	0.13363029	0.04454343	0.04454343	0	0.267260579	0	1.069042316	0.13363029	0	0	0	1.024498886
unclassified	0	0.13363029	0	0.04454343	0	0.13363029	0.04454343	0.04454343	0	0.267260579	0	1.069042316	0.13363029	0	0	0	1.024498886
f__Enterococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0.04454343	0
g__Enterococcus	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0.04454343	0
s__casseliflavus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__cecorum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0.04454343	0
f__Lactobacillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lactobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__delbrueckii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__helveticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__manihotivorans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__salivarius	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Leuconostocaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Leuconostoc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Streptococcaceae	0.08908686	3.652561247	2.71714922	3.741648107	0.08908686	10.91314031	1.113585746	0.356347439	0.13363029	1.603563474	0.04454343	4.097995546	0.445434298	0.08908686	0.04454343	0.13363029	3.875278396
g__Lactococcus	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343
g__Streptococcus	0.08908686	3.652561247	2.71714922	3.741648107	0.08908686	10.91314031	1.113585746	0.356347439	0.08908686	1.603563474	0.04454343	4.097995546	0.445434298	0.08908686	0.04454343	0.13363029	3.830734967
s__agalactiae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__anginosus	0	0	0.13363029	0	0	0	0.04454343	0	0	0	0	0	0.08908686	0	0	0	0
s__equi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__infantis	0.08908686	3.385300668	1.559020045	3.652561247	0.08908686	10.91314031	0.801781737	0.356347439	0.08908686	1.336302895	0	3.919821826	0.311804009	0.08908686	0.04454343	0.13363029	3.474387528
unclassified	0	0.267260579	1.024498886	0.08908686	0	0	0.267260579	0	0	0.267260579	0.04454343	0.178173719	0.04454343	0	0	0	0.356347439
o__Turicibacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Turicibacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Turicibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Clostridia	0.757238307	0.400890869	6.013363029	0.267260579	2.494432071	2.80623608	1.336302895	8.908685969	2.93986637	3.786191537	10.73496659	7.216035635	0.890868597	0.801781737	11.84855234	0.222717149	6.815144766
o__Clostridiales	0.757238307	0.400890869	6.013363029	0.267260579	2.494432071	2.80623608	1.336302895	8.908685969	2.93986637	3.786191537	10.73496659	7.216035635	0.890868597	0.801781737	11.84855234	0.222717149	6.815144766
f__Christensenellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Clostridiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
g__02d06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Caloramator	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
g__Clostridium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oxobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Dehalobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dehalobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Eubacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Anaerofustis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Lachnospiraceae	0	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0.08908686	0	0	0	0	0
g__Blautia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__obeum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__producta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Coprococcus	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
s__catus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__eutactus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Dorea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__formicigenerans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lachnobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Moryella	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0
s__indoligenes	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseburia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__faecis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ruminococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__gnavus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__torques	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Shuttleworthia	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
f__Mogibacteriaceae	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
g__Mogibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
f__Peptococcaceae	0	0	0.08908686	0	0	0	0	0	0.08908686	0	0	0.04454343	0	0	0	0	0
g__Peptococcus	0	0	0.04454343	0	0	0	0	0	0.08908686	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0.08908686	0	0	0.04454343	0	0	0	0	0
g__ WCHB1-84	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Peptostreptococcaceae	0	0	0.04454343	0.04454343	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0
g__Filifactor	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Peptostreptococcus	0	0	0	0.04454343	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0
s__anaerobius	0	0	0	0.04454343	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Ruminococcaceae	0	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Faecalibacterium	0	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0	0	0
s__prausnitzii	0	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Oscillospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ruminococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__bromii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__callidus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Symbiobacteriaceae	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
g__Symbiobacterium	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
s__thermophilum	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Tissierellaceae	0.579064588	0.222717149	5.523385301	0.222717149	2.449888641	2.7171492	1.158129176	8.819599109	2.672605791	3.474387528	10.73496659	6.191536748	0.757238307	0.801781737	11.84855234	0.222717149	6.414253898
g__1-68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Anaerococcus	0.489977728	0.178173719	2.138084633	0.08908686	0	2.494432071	1.113585746	6.503340757	0.801781737	1.202672606	6.013363029	4.810690423	0.712694878	0.04454343	3.563474388	0	3.296213808
unclassified	0.489977728	0.178173719	2.138084633	0.08908686	0	2.494432071	1.113585746	6.503340757	0.801781737	1.202672606	6.013363029	4.810690423	0.712694878	0.04454343	3.563474388	0	3.296213808
g__Finegoldia	0.04454343	0	2.004454343	0	0.623608018	0.04454343	0.04454343	0	0.267260579	0.579064588	1.113585746	0.445434298	0.04454343	0.222717149	1.959910913	0	0.979955457
unclassified	0.04454343	0	2.004454343	0	0.623608018	0.04454343	0.04454343	0	0.267260579	0.579064588	1.113585746	0.445434298	0.04454343	0.222717149	1.959910913	0	0.979955457
g__GW-34	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Gallicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Parvimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Peptoniphilus	0.04454343	0.04454343	1.336302895	0.08908686	1.826280624	0.178173719	0	2.316258352	1.603563474	1.692650334	3.608017817	0.935412027	0	0.534521158	6.325167038	0.222717149	2.138084633
unclassified	0.04454343	0.04454343	1.336302895	0.08908686	1.826280624	0.178173719	0	2.316258352	1.603563474	1.692650334	3.608017817	0.935412027	0	0.534521158	6.325167038	0.222717149	2.138084633
g__WAL_1855D	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__ph2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Veillonellaceae	0.178173719	0.178173719	0.356347439	0	0.04454343	0	0.13363029	0.08908686	0.04454343	0.267260579	0	0.846325167	0.04454343	0	0	0	0.400890869
g__Dialister	0.178173719	0	0.13363029	0	0	0	0	0.04454343	0	0.13363029	0	0	0	0	0	0	0
unclassified	0.178173719	0	0.13363029	0	0	0	0	0.04454343	0	0.13363029	0	0	0	0	0	0	0
g__Megasphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pelosinus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Propionispora	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
g__Selenomonas	0	0	0.04454343	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0.04454343
s__noxia	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343
g__Succiniclasticum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Veillonella	0	0.178173719	0.178173719	0	0	0	0.13363029	0.04454343	0	0.08908686	0	0.846325167	0.04454343	0	0	0	0.356347439
s__dispar	0	0.04454343	0.178173719	0	0	0	0.13363029	0	0	0	0	0.846325167	0	0	0	0	0.356347439
s__parvula	0	0.13363029	0	0	0	0	0	0.04454343	0	0.08908686	0	0	0.04454343	0	0	0	0
c__Erysipelotrichi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Erysipelotrichales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Erysipelotrichaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bulleidia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__moorei	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Eubacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__biforme	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Fusobacteria	0	0	0.400890869	0	0	0	0	0	0.356347439	0.08908686	0	1.380846325	0	0	0	0	0.712694878
c__Fusobacteriia	0	0	0.400890869	0	0	0	0	0	0.356347439	0.08908686	0	1.380846325	0	0	0	0	0.712694878
o__Fusobacteriales	0	0	0.400890869	0	0	0	0	0	0.356347439	0.08908686	0	1.380846325	0	0	0	0	0.712694878
f__Fusobacteriaceae	0	0	0.400890869	0	0	0	0	0	0.356347439	0.04454343	0	0.801781737	0	0	0	0	0.534521158
g__Fusobacterium	0	0	0.400890869	0	0	0	0	0	0.356347439	0.04454343	0	0.801781737	0	0	0	0	0.534521158
unclassified	0	0	0.400890869	0	0	0	0	0	0.356347439	0.04454343	0	0.801781737	0	0	0	0	0.534521158
f__Leptotrichiaceae	0	0	0	0	0	0	0	0	0	0.04454343	0	0.579064588	0	0	0	0	0.178173719
g__Leptotrichia	0	0	0	0	0	0	0	0	0	0.04454343	0	0.445434298	0	0	0	0	0.178173719
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0.445434298	0	0	0	0	0.178173719
g__Streptobacillus	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0
s__moniliformis	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0
p__Gemmatimonadetes	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
c__Gemm-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Gemmatimonadetes	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
o__Ellin5290	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
o__Gemmatimonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Ellin5301	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__KD8-87	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__N1423WL	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__MVP-21	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
p__Nitrospirae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Nitrospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Nitrospirales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nitrospiraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nitrospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermodesulfovibrionaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Candidatus_Magnetoovum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__OD1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__ZB2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__OP3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__koll11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__GIF10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__kpj58rc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Planctomycetes	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
c__Phycisphaerae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__WD2101	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Planctomycetia	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
o__Gemmatales	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
f__Gemmataceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Gemmata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Isosphaeraceae	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
p__Proteobacteria	0.311804009	3.563474388	3.652561247	5.122494432	2.85077951	2.004454343	5.478841871	1.915367483	0.178173719	0.712694878	0.579064588	2.093541203	7.928730512	0.668151448	0.445434298	1.781737194	4.053452116
c__Alphaproteobacteria	0.08908686	0	0	0	0.178173719	0.311804009	0.13363029	0.13363029	0.04454343	0	0	0.04454343	0.178173719	0.08908686	0	0	0.04454343
o__Caulobacterales	0.08908686	0	0	0	0	0.311804009	0	0	0	0	0	0	0	0.08908686	0	0	0
f__Caulobacteraceae	0.08908686	0	0	0	0	0.311804009	0	0	0	0	0	0	0	0.08908686	0	0	0
g__Brevundimonas	0.08908686	0	0	0	0	0.311804009	0	0	0	0	0	0	0	0.08908686	0	0	0
s__diminuta	0.08908686	0	0	0	0	0.311804009	0	0	0	0	0	0	0	0.08908686	0	0	0
g__Phenylobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Ellin329	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rhizobiales	0	0	0	0	0	0	0.13363029	0	0	0	0	0.04454343	0.04454343	0	0	0	0
f__Aurantimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bartonellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bartonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Beijerinckiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Methylocella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bradyrhizobiaceae	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Balneimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bosea	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__genosp.	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
f__Hyphomicrobiaceae	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0	0
g__Hyphomicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__sulfonivorans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodoplanes	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0	0
f__Methylobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Methylobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__komagatae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Phyllobacteriaceae	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0
g__Mesorhizobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__huakuii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nitratireductor	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0
f__Xanthobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Blastochloris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rhodobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
f__Rhodobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Rubellimicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
o__Rhodospirillales	0	0	0	0	0.178173719	0	0	0	0	0	0	0	0.08908686	0	0	0	0
f__Acetobacteraceae	0	0	0	0	0.178173719	0	0	0	0	0	0	0	0.08908686	0	0	0	0
g__Acetobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Acidisphaera	0	0	0	0	0.178173719	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.178173719	0	0	0	0	0	0	0	0	0	0	0	0
g__Acidocella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseococcus	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
g__Roseomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mucosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Swaminathania	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Rhodospirillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oleomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Sphingomonadales	0	0	0	0	0	0	0	0.13363029	0.04454343	0	0	0	0	0	0	0	0.04454343
f__Sphingomonadaceae	0	0	0	0	0	0	0	0.13363029	0.04454343	0	0	0	0	0	0	0	0.04454343
g__Kaistobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Novosphingobium	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
s__resinovorum	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
g__Sphingobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__yanoikuyae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphingomonas	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0	0	0	0.04454343
s__azotifigens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__echinoides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__wittichii	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0	0	0	0
s__yabuuchiae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
c__Betaproteobacteria	0.08908686	2.89532294	0.757238307	1.024498886	1.069042316	0.846325167	1.737193764	0.356347439	0.04454343	0.311804009	0	1.559020045	4.677060134	0.489977728	0	0.222717149	1.514476615
o__A21b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__EB1003	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Burkholderiales	0.08908686	0.13363029	0.489977728	0.445434298	0.579064588	0.178173719	0.534521158	0.311804009	0.04454343	0.222717149	0	0.356347439	0.623608018	0.13363029	0	0.222717149	0.400890869
f__Alcaligenaceae	0	0	0	0.13363029	0.04454343	0.08908686	0	0	0	0	0	0	0	0	0	0	0
g__Achromobacter	0	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Denitrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oligella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Tetrathiobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__kashmirensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0.08908686	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.04454343	0.08908686	0	0	0	0	0	0	0	0	0	0	0

f__Burkholderiaceae	0	0.04454343	0.400890869	0.13363029	0.267260579	0	0.222717149	0.08908686	0	0.13363029	0	0	0.222717149	0	0	0.04454343	0.311804009	
g__Burkholderia	0	0.04454343	0.356347439	0.04454343	0.267260579	0	0.222717149	0.08908686	0	0.04454343	0	0	0.222717149	0	0	0.04454343	0.222717149	
s__andropogonis	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
s__bryophila	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__graminis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__tuberum	0	0.04454343	0.178173719	0.04454343	0.04454343	0	0.04454343	0.08908686	0	0	0	0	0.04454343	0	0	0	0.13363029	
unclassified	0	0	0.178173719	0	0.222717149	0	0.178173719	0	0	0.04454343	0	0	0.13363029	0	0	0.04454343	0.08908686	
g__Lautropia	0	0	0.04454343	0.08908686	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0.08908686	
unclassified	0	0	0.04454343	0.08908686	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0.08908686	
g__Salinispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__tropica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Comamonadaceae	0.04454343	0.08908686	0.04454343	0	0	0.08908686	0.04454343	0.178173719	0.04454343	0.08908686	0	0.356347439	0.222717149	0	0	0.04454343	0.04454343	
g__Acidovorax	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0.311804009	0	0	0	0	0	
s__delafieldii	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0.311804009	0	0	0	0	0	
g__Alicycliphilus	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
g__Aquabacterium	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	
g__Azohydromonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Comamonas	0.04454343	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	
s__terrigena	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	
unclassified	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Delftia	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0.04454343	
unclassified	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0.04454343	
g__Diaphorobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Giesbergeria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Hylemonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Leptothrix	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Methylbium	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0.08908686	0	0	0	0	
s__petroleiphilum	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	
g__Paucibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Pelomonas	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__puraquae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Ramlibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	
g__Rubrivivax	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__gelatinosus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Schlegelella	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0	0	0	0	
g__Tepidimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Variovorax	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	
s__paradoxus	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	
f__Oxalobacteraceae	0.04454343	0	0.04454343	0.178173719	0.267260579	0	0.267260579	0.04454343	0	0	0	0	0.178173719	0.13363029	0	0.13363029	0.04454343	
g__Collimonas	0.04454343	0	0	0.08908686	0.04454343	0	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0	
unclassified	0.04454343	0	0	0.08908686	0.04454343	0	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0	
g__Cupriavidus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__gilardii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Herbaspirillum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Herminiimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Janthinobacterium	0	0	0	0	0.13363029	0	0.08908686	0	0	0	0	0	0	0.04454343	0	0	0	
s__lividum	0	0	0	0	0.13363029	0	0.08908686	0	0	0	0	0	0	0.04454343	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Oxalobacter	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__formigenes	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Polynucleobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__cosmopolitanus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0.08908686	0.08908686	0	0.178173719	0	0	0	0	0	0.178173719	0.04454343	0	0.13363029	0.04454343	
unclassified	0	0	0	0.08908686	0.08908686	0	0.178173719	0	0	0	0	0	0.178173719	0.04454343	0	0.13363029	0.04454343	
o__Ellin6067	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__MND1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__Neisseriales	0	2.76169265	0.222717149	0.489977728	0.489977728	0.668151448	1.202672606	0	0	0.08908686	0	1.202672606	4.008908686	0.356347439	0	0	1.113585746	
f__Neisseriaceae	0	2.76169265	0.222717149	0.489977728	0.489977728	0.668151448	1.202672606	0	0	0.08908686	0	1.202672606	4.008908686	0.356347439	0	0	1.113585746	
g__Aquitalea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__magnusonii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Eikenella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Kingella	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343	
unclassified	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343	
g__Microvirgula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__aerodenitrificans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Neisseria	0	2.76169265	0.04454343	0.489977728	0.489977728	0.08908686	0.445434298	0	0	0.04454343	0	1.202672606	0	0	0	0	0.13363029	
s__cinerea	0	0.04454343	0	0.13363029	0.489977728	0	0	0	0	0	0	0.222717149	0	0	0	0	0	
s__subflava	0	2.71714922	0	0.08908686	0	0	0.445434298	0	0	0.04454343	0	0.534521158	0	0	0	0	0.13363029	
unclassified	0	0	0.04454343	0.267260579	0	0.08908686	0	0	0	0	0	0.445434298	0	0	0	0	0	
g__Vitreoscilla	0	0	0.13363029	0	0	0.579064588	0.757238307	0	0	0	0	0	4.008908686	0.356347439	0	0	0.935412027	
unclassified	0	0	0.13363029	0	0	0.579064588	0.757238307	0	0	0	0	0	4.008908686	0.356347439	0	0	0.935412027	
o__Rhodocyclales	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	
f__Rhodocyclaceae	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	
g__Azospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Dok59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Methyloversatilis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Propionivibrio	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Zoogloea	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	
o__SBla14	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__SC-I-84	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
c__Deltaproteobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__Desulfovibrionales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Desulfovibrionaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Desulfovibrio	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__cavernae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__FAC87	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__MI246	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__Myxococcales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Cystobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Cystobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Haliangiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Haliangium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Myxococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Anaeromyxobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__SAR324	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__Syntrophobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Syntrophobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Syntrophobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
c__Epsilonproteobacteria	0.04454343	0	0.08908686	0	0	0	0	0	0.04454343	0.04454343	0	0.04454343	0.04454343	0	0	0	0	
o__Campylobacterales	0.04454343	0	0.08908686	0	0	0	0	0	0	0.04454343	0	0.04454343	0.04454343	0	0	0	0	
f__Campylobacteraceae	0.04454343	0	0.08908686	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	
g__Campylobacter	0.04454343	0	0.08908686	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	
s__rectus	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__ureolyticus	0.04454343	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Helicobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
g__Helicobacter	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
s__pylori	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
o__Nautiliales	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	
f__Nautiliaceae	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	
g__Nautilia	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	
c__Gammaproteobacteria	0.08908686	0.668151448	2.80623608	4.097995546	1.603563474	0.846325167	3.608017817	1.425389755	0.04454343	0.356347439	0.579064588	0.445434298	3.028953229	0.08908686	0.445434298	1.559020045	2.494432071	
o__Alteromonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Shewanellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Shewanella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__pacifica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__Enterobacteriales	0	0	0.08908686	0	0.04454343	0	0	0	0	0.04454343	0.13363029	0	0.04454343	0	0.04454343	0	0	
f__Enterobacteriaceae	0	0	0.08908686	0	0.04454343	0	0	0	0	0.04454343	0.13363029	0	0.04454343	0	0.04454343	0	0	
g__Citrobacter	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	

unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Enterobacter	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
s__cowanii	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Erwinia	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__dispersa	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Klebsiella	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0.13363029	0	0	0	0.04454343	0	0
s__oxytoca	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0
unclassified	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0.13363029	0	0	0	0	0	0
g__Salmonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__enterica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Legionellales	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0
f__Coxiellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Legionellaceae	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0
g__Legionella	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0
o__Oceanospirillales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Halomonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Halomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Oceanospirillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Marinomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__primoryensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Pasteurellales	0	0	0.08908686	0.08908686	0	0	0	0	0	0.178173719	0	0.04454343	0.356347439	0	0	0	0
f__Pasteurellaceae	0	0	0.08908686	0.08908686	0	0	0	0	0	0.178173719	0	0.04454343	0.356347439	0	0	0	0
g__Actinobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__parahaemolyticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Haemophilus	0	0	0.08908686	0.08908686	0	0	0	0	0	0.178173719	0	0.04454343	0.356347439	0	0	0	0
s__influenzae	0	0	0.04454343	0.04454343	0	0	0	0	0	0.178173719	0	0	0.311804009	0	0	0	0
s__parainfluenzae	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0
o__Pseudomonadales	0	0.04454343	0.534521158	0.08908686	0.08908686	0.222717149	0.08908686	0	0	0.04454343	0	0.08908686	0.04454343	0	0.04454343	0.04454343	1.692650334
f__Moraxellaceae	0	0	0.356347439	0	0.08908686	0.222717149	0.04454343	0	0	0	0	0.08908686	0.04454343	0	0	0	1.692650334
g__Acinetobacter	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0.04454343	0	0	0	0
s__guillouiae	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__lwoffii	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
s__rhizosphaerae	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__schindleri	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__venetianus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Alkanindiges	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Enhydrobacter	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Moraxella	0	0	0.356347439	0	0.08908686	0.222717149	0	0	0	0	0	0	0	0	0	0	1.692650334
s__ovis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.356347439	0	0.08908686	0.222717149	0	0	0	0	0	0	0	0	0	0	1.692650334
f__Pseudomonadaceae	0	0.04454343	0.178173719	0.08908686	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0.04454343	0.04454343	0
g__Pseudomonas	0	0.04454343	0.178173719	0.08908686	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0.04454343	0.04454343	0
s__alcaligenes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__fragi	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0
s__umsongensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__veronii	0	0	0	0.08908686	0	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343	0
s__viridiflava	0	0	0.178173719	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Xanthomonadales	0.08908686	0.623608018	2.093541203	3.919821826	1.380846325	0.623608018	3.518930958	1.425389755	0.04454343	0.08908686	0.445434298	0.311804009	2.583518931	0.08908686	0.356347439	1.514476615	0.801781737
f__Sinobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Hydrocarboniphaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__effusa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Xanthomonadaceae	0.08908686	0.623608018	2.093541203	3.919821826	1.380846325	0.623608018	3.518930958	1.425389755	0.04454343	0.08908686	0.445434298	0.311804009	2.583518931	0.08908686	0.356347439	1.514476615	0.801781737
g__Dokdonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dyella	0	0.13363029	0.356347439	0.400890869	0.489977728	0.04454343	0.489977728	0.178173719	0	0	0	0	0.267260579	0	0	0.178173719	0.08908686
s__ginsengisoli	0	0.13363029	0.356347439	0.400890869	0.489977728	0.04454343	0.489977728	0.178173719	0	0	0	0	0.267260579	0	0	0.178173719	0.08908686
g__Luteimonas	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0.222717149	0	0	0	0
unclassified	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0.222717149	0	0	0	0
g__Lysobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pseudoxanthomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mexicana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodanobacter	0.08908686	0.489977728	1.737193764	3.518930958	0.846325167	0.222717149	3.028953229	1.113585746	0.04454343	0.08908686	0.445434298	0.311804009	2.048997773	0.08908686	0.356347439	1.247216036	0.712694878
s__lindaniclasticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.08908686	0.489977728	1.737193764	3.518930958	0.846325167	0.222717149	3.028953229	1.113585746	0.04454343	0.08908686	0.445434298	0.311804009	2.048997773	0.08908686	0.356347439	1.247216036	0.712694878
g__Stenotrophomonas	0	0	0	0	0	0.356347439	0	0.04454343	0	0	0	0	0.04454343	0	0	0.08908686	0
s__acidaminiphila	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__geniculata	0	0	0	0	0	0.356347439	0	0.04454343	0	0	0	0	0.04454343	0	0	0.08908686	0
s__retroflexus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermomonas	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__fusca	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Xanthomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Spirochaetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Spirochaetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Borreliales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Borreliaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Spironema	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Spirochaetales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Spirochaetaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Treponema	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Synergistetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Synergistia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Synergistales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Dethiosulfovibrionaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pyramidobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__piscolens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermovirgaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermovirga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__TM7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__TM7-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__TM7-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__EW055	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Tenericutes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Mollicutes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__RF39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Thermi	0	0	0	0.13363029	0	0	0.178173719	0.178173719	0	0	0	0	0	0.04454343	0	0	0
c__Deinococci	0	0	0	0.13363029	0	0	0.178173719	0.178173719	0	0	0	0	0	0.04454343	0	0	0
o__Deinococcales	0	0	0	0.04454343	0	0	0.178173719	0.178173719	0	0	0	0	0	0.04454343	0	0	0
f__Deinococcaceae	0	0	0	0.04454343	0	0	0.178173719	0.178173719	0	0	0	0	0	0.04454343	0	0	0
g__Deinococcus	0	0	0	0.04454343	0	0	0.178173719	0.178173719	0	0	0	0	0	0.04454343	0	0	0
s__alpinitundrae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aquatilis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__geothermalis	0	0	0	0.04454343	0	0	0.13363029	0	0	0	0	0	0	0.04454343	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0.178173719	0	0	0	0	0	0	0	0	0
o__Thermales	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermaceae	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermus	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Verrucomicrobia	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Pedosphaerae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Pedosphaerales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Pedosphaeraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pedosphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Spartobacteria	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Chthoniobacterales	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Chthoniobacteraceae	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ellin506	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
p__WPS-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Total Number of Reads	18155	9498	6560	4186	7055	36273	4111	9461	24311	21500	7949	23081	7401	18537	11844	4289	3373

Sample ID	5937R	5938R	5941R	5942R	5943R	5954R	5962R	5974R	5981R	5982R	5992R	5997R	1674A	1715A	1716A	1717A	1742A	1749A
Sample Location	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**	**Nose**	**Abscess**	**Abscess**	**Abscess**	**Abscess**	**Abscess**	**Abscess**
SSTI/*S. aureus* colonization status	**NoSA Non-SSTI**	**NoSA Non-SSTI**	**NoSA Non-SSTI**	**NoSA Non-SSTI**	**NoSA Non-SSTI**	**NoSA Non-SSTI**	**NoSA Non-SSTI**	**NoSA Non-SSTI**	**NoSA Non-SSTI**	**NoSA Non-SSTI**	**NoSA Non-SSTI**	**NoSA Non-SSTI**	**MRSA**	**MRSA**	**MRSA**	**MRSA**	**MRSA**	**MRSA**
Taxon																		
p__Acidobacteria	0	0	0	0	0	0	0	0	0.04454343	0.08908686	0.13363029	0	0	0	0	0	0	0
c__Acidobacteria-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Acidobacteria-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__iii1-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Acidobacteriia	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0
o__Acidobacteriales	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0
f__Acidobacteriaceae	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Edaphobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__modestum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Terriglobus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
f__Koribacteraceae	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Candidatus_Koribacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
c__Chloracidobacteria	0	0	0	0	0	0	0	0	0	0.04454343	0.08908686	0	0	0	0	0	0	0
o__DS-100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__PK29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__RB41	0	0	0	0	0	0	0	0	0	0.04454343	0.08908686	0	0	0	0	0	0	0
f__Ellin6075	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
c__DA052	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Ellin6513	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__RB25	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
c__Solibacteres	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Solibacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__MVS-65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__PK34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Sva0725	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Sva0725	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__iii1-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__DS-18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Actinobacteria	40.31180401	91.22494432	56.39198218	69.08685969	5.523385301	59.42093541	24.85523385	6.369710468	73.1403118	52.65033408	60.75723831	56.30289532	0.13363029	36.08017817	0.178173719	0	0.04454343	0.801781737
c__Acidimicrobiia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Acidimicrobiales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__C111	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__EB1017	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Actinobacteria	40.31180401	91.22494432	56.39198218	69.08685969	5.523385301	59.37639198	24.81069042	6.369710468	73.1403118	52.65033408	60.53452116	56.25835189	0.13363029	36.08017817	0.178173719	0	0.04454343	0.801781737
o__Actinomycetales	40.31180401	91.22494432	56.39198218	69.08685969	5.523385301	59.37639198	24.81069042	6.369710468	73.1403118	52.65033408	60.53452116	56.25835189	0.13363029	36.08017817	0.178173719	0	0.04454343	0.801781737
f__Actinomycetaceae	0	0	0.13363029	0	0	0	0	0	0	0	0	0.04454343	0	0.489977728	0	0	0	0
g__Actinobaculum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinomyces	0	0	0.08908686	0	0	0	0	0	0	0	0	0.04454343	0	0.489977728	0	0	0	0
s__europaeus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__hyovaginalis	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0.489977728	0	0	0	0
g__Mobiluncus	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Varibaculum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Actinosynnemataceae	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
g__Actinoalloteichus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kutzneria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lentzea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__violacea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Saccharothrix	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
f__Beutenbergiaceae	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
f__Bogoriellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Georgenia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Brevibacteriaceae	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0.04454343	0	0	0	0
g__Brevibacterium	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0.04454343	0	0	0	0
s__aureum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__casei	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0
s__paucivorans	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
f__Cellulomonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinotalea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Cellulomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__uda	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Corynebacteriaceae	29.844098	86.14699332	46.36971047	63.74164811	4.855233853	52.20489978	10.37861915	3.385300668	48.5077951	47.03786192	57.86191537	48.86414254	0.08908686	13.05122494	0.178173719	0	0.04454343	0.311804009
g__Corynebacterium	29.844098	86.14699332	46.36971047	63.74164811	4.855233853	52.20489978	10.37861915	3.385300668	48.5077951	47.03786192	57.86191537	48.86414254	0.08908686	13.05122494	0.178173719	0	0.04454343	0.311804009
s__durum	0	0	0.178173719	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
s__kroppenstedtii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__lubricantis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mastitidis	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__pilosum	0	0.400890869	0	0.222717149	0.04454343	0.178173719	0	2.227171492	0.267260579	0	0.04454343	0.08908686	0	0.13363029	0.08908686	0	0	0
s__renale	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__simulans	0	0	0.13363029	0	0	0.04454343	0.846325167	0	0	0	0.08908686	0	0	0.04454343	0	0	0	0
s__stationis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	29.79955457	85.74610245	46.05790646	63.51893096	4.810690423	51.98218263	9.532293987	1.158129176	48.24053452	47.03786192	57.72828508	48.77505568	0.08908686	12.8285078	0.08908686	0	0.04454343	0.311804009
f__Dermabacteraceae	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
g__Brachybacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__conglomeratum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dermabacter	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
f__Dermacoccaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dermacoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Dermatophilaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dermatophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Dietziaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dietzia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Frankiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Frankia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Geodermatophilaceae	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Blastococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aggregatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Geodermatophilus	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
s__obscurus	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Modestobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Gordoniaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Gordonia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Intrasporangiaceae	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0
g__Knoellia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__subterranea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

g__Phycicoccus	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0
g__Serinicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Kineosporiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kineococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kineosporia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Microbacteriaceae	0	0	0.08908686	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Agrococcus	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__jenensis	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Clavibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__michiganensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Cryocola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Curtobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Frigoribacterium	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Leucobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Microbacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__chocolatum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__maritypicum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Mycetocola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pseudoclavibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__bifida	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Yonghaparkia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Micrococcaceae	0.04454343	0	0	0.13363029	0.04454343	0	0.08908686	0.13363029	0.04454343	0	0.13363029	0	0	0.04454343	0	0	0	0.356347439	
g__Arthrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__crystallopoietes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__psychrolactophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Citricoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__alkalitolerans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kocuria	0	0	0	0.08908686	0	0	0.08908686	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0
s__palustris	0	0	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0
s__rhizophila	0	0	0	0.08908686	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0
g__Microbispora	0.04454343	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0
s__rosea	0.04454343	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0
g__Micrococcus	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0.311804009	
s__luteus	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0.311804009	
g__Nesterenkonia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	
g__Renibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Rothia	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
s__aeria	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	
s__mucilaginosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Zhihengliuella	0	0	0	0.04454343	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	
f__Micromonosporaceae	0.623608018	0.08908686	0	0.13363029	0	2.71714922	0	0	0	0	0	0.178173719	0	0.04454343	0	0	0	0	
g__Actinocatenispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Catellatospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Couchioplanes	0.623608018	0.08908686	0	0.13363029	0	2.71714922	0	0	0	0	0	0.178173719	0	0.04454343	0	0	0	0	
s__caeruleus	0.623608018	0.08908686	0	0.13363029	0	2.71714922	0	0	0	0	0	0.178173719	0	0.04454343	0	0	0	0	
g__Solwaraspora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Verrucosispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__glhornensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Mycobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Mycobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__celatum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__gordonae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__vaccae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Nakamurellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Nocardiaceae	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	
g__Nocardia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Rhodococcus	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	
s__fascians	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__globerulus	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	
f__Nocardioidaceae	0	0.08908686	0.267260579	0	0	0	0.04454343	0.04454343	0	0.400890858	0.08908686	0.133630289	0	0.534521158	0	0	0	0	
g__Actinopolymorpha	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Aeromicrobium	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	
g__Friedmanniella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Nocardioides	0	0	0	0	0	0	0	0	0	0.08908686	0.04454343	0.04454343	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0.08908686	0.04454343	0.04454343	0	0	0	0	0	0	
g__Pimelobacter	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0.04454343	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	
g__Propionicimonas	0	0.04454343	0.267260579	0	0	0	0	0.04454343	0	0.267260579	0	0.08908686	0	0.534521158	0	0	0	0	
unclassified	0	0.04454343	0.267260579	0	0	0	0	0.04454343	0	0.267260579	0	0.08908686	0	0.534521158	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	
f__Nocardiopsaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Nocardiopsis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__composta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Promicromonosporaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Cellulosimicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Promicromonospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Propionibacteriaceae	9.799554566	4.899777283	9.443207127	5.077951002	0.534521158	4.454342984	14.25389755	2.71714922	24.54342984	5.122494432	2.227171492	6.993318486	0.04454343	21.87082405	0	0	0	0.13363029	
g__Luteococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Microlunatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Propionibacterium	9.799554566	4.899777283	9.443207127	5.077951002	0.534521158	4.454342984	14.25389755	2.71714922	24.54342984	5.122494432	2.227171492	6.993318486	0.04454343	21.87082405	0	0	0	0.13363029	
s__acnes	9.487750557	4.766146993	8.5077951	4.365256125	0.356347439	3.518930958	13.67483296	2.449888641	24.45434298	4.944320713	1.291759465	5.567928731	0.04454343	21.06904232	0	0	0	0.13363029	
s__granulosum	0.311804009	0.13363029	0.935412027	0.712694878	0.178173719	0.935412027	0.579064588	0.267260579	0.08908686	0.178173719	0.935412027	1.425389755	0	0.801781737	0	0	0	0	
g__Tessaracoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Pseudonocardiaceae	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	
g__Actinomycetospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Pseudonocardia	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	
f__Sporichthyaceae	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	
g__Sporichthya	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Streptomycetaceae	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Kitasatospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Streptomyces	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__lanatus	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__mashuensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__scabrisporus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Streptosporangiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Nonomuraea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__roseoviolacea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Sphaerisporangium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Thermomonosporaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Actinomadura	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__vinacea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Tsukamurellaceae	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Tsukamurella	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__Micrococcales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
c__Coriobacteriia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__Coriobacteriales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Coriobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Adlercreutzia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Atopobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__rimae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Collinsella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__aerofaciens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Slackia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
c__MB-A2-108	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__0319-7L14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
c__OPB41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Rubrobacteria	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
o__Rubrobacterales	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
f__Rubrobacteraceae	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Rubrobacter	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
c__Thermoleophilia	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0.178173719	0.04454343	0	0	0	0	0	0
o__Gaiellales	0	0	0	0	0	0	0	0	0	0	0.08908686	0.04454343	0	0	0	0	0	0
f__Gaiellaceae	0	0	0	0	0	0	0	0	0	0	0.08908686	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.08908686	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.08908686	0.04454343	0	0	0	0	0	0
o__Solirubrobacterales	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0.08908686	0	0	0	0	0	0	0
f__Conexibacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Conexibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Patulibacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Solirubrobacteraceae	0	0	0	0	0	0	0.04454343	0	0	0	0.08908686	0	0	0	0	0	0	0
g__Solirubrobacter	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
p__Armatimonadetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Armatimonadia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Armatimonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Armatimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__CL0-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__FW68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Chthonomonadetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Chthonomonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Chthonomonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Fimbriimonadia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Fimbriimonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Fimbriimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Fimbriimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__OPB50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__BRC1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__PRR-11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Bacteroidetes	0.08908686	0.04454343	0.579064588	0	0.13363029	0.04454343	0.13363029	0.08908686	0	0.08908686	0.222717149	0.08908686	0.04454343	0.13363029	0.04454343	0	0.04454343	0
c__Bacteroidia	0.04454343	0.04454343	0.400890869	0	0	0	0	0.08908686	0	0	0.04454343	0.04454343	0.04454343	0.13363029	0.04454343	0	0.04454343	0
o__Bacteroidales	0.04454343	0.04454343	0.400890869	0	0	0	0	0.08908686	0	0	0.04454343	0.04454343	0.04454343	0.13363029	0.04454343	0	0.04454343	0
f__Bacteroidaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bacteroides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__caccae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ovatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__uniformis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Paraprevotellaceae	0.04454343	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
g__Prevotella	0.04454343	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
unclassified	0.04454343	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0
g__YRC22	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Porphyromonadaceae	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0
g__Porphyromonas	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0
g__Tannerella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Prevotellaceae	0	0.04454343	0.222717149	0	0	0	0	0.04454343	0	0	0	0.04454343	0.04454343	0.04454343	0.04454343	0	0.04454343	0
g__Prevotella	0	0.04454343	0.222717149	0	0	0	0	0.04454343	0	0	0	0.04454343	0.04454343	0.04454343	0.04454343	0	0.04454343	0
s__copri	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	0.04454343	0.04454343	0	0.04454343	0
s__melaninogenica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__nanceiensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ruminicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__stercorea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0.222717149	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
f__Rikenellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Blvii28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__S24-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Cytophagia	0	0	0.08908686	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
o__Cytophagales	0	0	0.08908686	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
f__Cytophagaceae	0	0	0.08908686	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
g__Adhaeribacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dyadobacter	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Hymenobacter	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
g__Rhodocytophaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Flavobacteriia	0.04454343	0	0	0	0.08908686	0.04454343	0	0	0	0.04454343	0.08908686	0.04454343	0	0	0	0	0	0
o__Flavobacteriales	0.04454343	0	0	0	0.08908686	0.04454343	0	0	0	0.04454343	0.08908686	0.04454343	0	0	0	0	0	0
f__Cryomorphaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Fluviicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Flavobacteriaceae	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
g__Algibacter	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
s__lectus	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0
g__Capnocytophaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ochracea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Flavobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__succinicans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Myroides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__odoratimimus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Weeksellaceae	0.04454343	0	0	0	0.08908686	0	0	0	0	0.04454343	0.08908686	0.04454343	0	0	0	0	0	0
g__Chryseobacterium	0.04454343	0	0	0	0.08908686	0	0	0	0	0.04454343	0.08908686	0.04454343	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0.08908686	0	0	0	0	0.04454343	0.08908686	0.04454343	0	0	0	0	0	0
g__Cloacibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Elizabethkingia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__meningoseptica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ornithobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Riemerella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Wautersiella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Weeksella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Saprospirae	0	0	0.04454343	0	0.04454343	0	0.08908686	0	0	0.04454343	0.08908686	0	0	0	0	0	0	0
o__Saprospirales	0	0	0.04454343	0	0.04454343	0	0.08908686	0	0	0.04454343	0.08908686	0	0	0	0	0	0	0
f__Chitinophagaceae	0	0	0.04454343	0	0.04454343	0	0.08908686	0	0	0.04454343	0.08908686	0	0	0	0	0	0	0
g__Chitinophaga	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
s__arvensicola	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Flavihumibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Flavisolibacter	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Niabella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Niastella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sediminibacterium	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
g__Segetibacter	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Terrimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
c__Sphingobacteriia	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Sphingobacteriales	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Sphingobacteriaceae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Olivibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pedobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__cryoconitis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphingobacterium	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__faecium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

s__mizutaii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__multivorum	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Chloroflexi	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
c__Anaerolineae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Caldilineales	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Caldilineaceae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SBR1031	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__A4b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SJA-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__C0119	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
c__Chloroflexi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__AKIW781	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Chloroflexales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__FFCH7168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Roseiflexales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Roseiflexaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseiflexus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Ktedonobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__B12-WMSP1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Thermogemmatisporales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermogemmatisporaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__SHA-26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__TK10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__B07_WMSP1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__FFCH4570	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Thermomicrobia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__JG30-KF-CM45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Cyanobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__4C0d-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__MLE1-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Chloroplast	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Stramenopiles	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Streptophyta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__FBP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Firmicutes	27.92873051	7.216035635	38.21826281	22.40534521	93.71937639	38.6636971	58.70824053	91.4922049	23.29621381	46.05790646	36.61469933	42.89532294	99.64365256	60.26726058	99.24276169	99.91091314	98.30734967	90.73496659
c__Bacilli	22.89532294	4.988864143	31.62583519	20.17817372	92.87305122	36.88195991	57.55011136	91.22494432	16.52561247	44.98886414	36.30289532	39.5545657	99.5545657	59.37639198	99.24276169	99.91091314	98.30734967	90.73496659
o__Bacillales	22.67260579	4.944320713	26.90423163	16.08017817	53.71937639	34.4766147	54.38752784	91.13585746	15.59020045	38.44097996	20	26.36971047	99.5545657	56.83741648	99.19821826	99.86636971	98.30734967	90.69042316
f__Alicyclobacillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Alicyclobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bacillaceae	0	0	0.04454343	0	0.13363029	0	0.04454343	0	0.04454343	0	0	0.04454343	0	0.04454343	0	0	0	0
g__Alkalibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Anoxybacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__kestanbolensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bacillus	0	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0.04454343	0	0.04454343	0	0	0	0
s__acidicola	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
s__flexus	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
s__foraminis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__horikoshii	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__muralis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__trypoxylicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Geobacillus	0	0	0	0	0.13363029	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
s__vulcani	0	0	0	0	0.13363029	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Marinibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Marinococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Exiguobacteraceae	0	0.04454343	0	0	0	0	0	0	0.08908686	0.712694878	0.08908686	0	0	0	0	0	0	0
g__Exiguobacterium	0	0.04454343	0	0	0	0	0	0	0.08908686	0.712694878	0.08908686	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0.08908686	0.712694878	0.08908686	0	0	0	0	0	0	0
f__Paenibacillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ammoniphilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__oxalaticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Paenibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__amylolyticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__edaphicus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__stellifer	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Planococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Lysinibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__boronitolerans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Planomicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Sporosarcina	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Sporolactobacillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sporolactobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Staphylococcaceae	22.67260579	4.899777283	26.77060134	16.08017817	53.5857461	34.4766147	54.34298441	91.13585746	15.45657016	37.72828508	19.91091314	26.32516704	99.5545657	56.79287305	99.19821826	99.86636971	98.30734967	90.64587973
g__Jeotgalicoccus	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__psychrophilus	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Salinicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Staphylococcus	22.62806236	4.899777283	26.77060134	16.08017817	53.5857461	34.4766147	54.34298441	91.13585746	15.45657016	37.72828508	19.91091314	26.32516704	99.5545657	56.79287305	99.19821826	99.86636971	98.30734967	90.64587973
s__aureus	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	98.88641425	11.26948775	97.14922049	99.5545657	98.30734967	54.0311804
s__epidermidis	22.13808463	4.766146993	26.14699332	15.90200445	53.45211581	34.29844098	54.0311804	91.00222717	15.14476615	37.72828508	19.82182628	26.14699332	0.623608018	45.12249443	0.04454343	0.311804009	0	36.34743875
s__equorum	0.04454343	0	0.04454343	0.04454343	0	0	0	0	0.13363029	0	0	0	0	0.04454343	0.04454343	0	0	0
s__haemolyticus	0.445434298	0.08908686	0.579064588	0.04454343	0.08908686	0	0.311804009	0.04454343	0.178173719	0	0.08908686	0.178173719	0	0.356347439	1.959910913	0	0	0.13363029
s__lugdunensis	0	0	0	0.04454343	0.04454343	0.13363029	0	0.08908686	0	0	0	0	0.04454343	0	0	0	0	0.13363029
s__pettenkoferi	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__sciuri	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermoactinomycetaceae	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Planifilum	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Gemellales	0.04454343	0	0.13363029	0.04454343	0.04454343	0	0.08908686	0.04454343	0	0	0.04454343	0	0	0.267260579	0	0	0	0
f__Gemellaceae	0.04454343	0	0.13363029	0.04454343	0.04454343	0	0.08908686	0.04454343	0	0	0.04454343	0	0	0.267260579	0	0	0	0
g__Gemella	0.04454343	0	0.13363029	0.04454343	0.04454343	0	0.08908686	0.04454343	0	0	0.04454343	0	0	0.267260579	0	0	0	0
unclassified	0.04454343	0	0.13363029	0.04454343	0.04454343	0	0.08908686	0.04454343	0	0	0.04454343	0	0	0.267260579	0	0	0	0
o__Lactobacillales	0.178173719	0.04454343	4.587973274	4.053452116	39.1091314	2.405345212	3.073496659	0.04454343	0.935412027	6.547884187	16.25835189	13.18485523	0	2.271714922	0.04454343	0.04454343	0	0.04454343
f__Aerococcaceae	0	0	0.890868597	3.964365256	39.02004454	2.360801782	2.271714922	0	0.712694878	6.369710468	16.1247216	13.05122494	0	0	0.04454343	0	0	0
g__Abiotrophia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Aerococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Alloiococcus	0	0	0.846325167	3.964365256	39.02004454	2.360801782	2.271714922	0	0.712694878	6.369710468	16.08017817	13.05122494	0	0	0	0	0	0
s__otitis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.846325167	3.964365256	39.02004454	2.360801782	2.271714922	0	0.712694878	6.369710468	16.08017817	13.05122494	0	0	0	0	0	0
g__Facklamia	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	0	0	0
f__Carnobacteriaceae	0	0	0.267260579	0.04454343	0	0	0	0.04454343	0	0	0.04454343	0	0	0.178173719	0	0	0	0.04454343

g__Carnobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
s__viridans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Desemzia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Granulicatella	0	0	0.267260579	0.04454343	0	0	0	0.04454343	0	0	0.04454343	0	0	0.178173719	0	0	0	0	0
unclassified	0	0	0.267260579	0.04454343	0	0	0	0.04454343	0	0	0.04454343	0	0	0.178173719	0	0	0	0	0
f__Enterococcaceae	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0
g__Enterococcus	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	0
s__casseliflavus	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
s__cecorum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0
f__Lactobacillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lactobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__delbrueckii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__helveticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__manihotivorans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__salivarius	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Leuconostocaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Leuconostoc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Streptococcaceae	0.178173719	0.04454343	3.429844098	0.04454343	0.08908686	0.04454343	0.801781737	0	0.178173719	0.178173719	0.08908686	0.13363029	0	2.093541203	0	0	0	0	0
g__Lactococcus	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
g__Streptococcus	0.178173719	0.04454343	3.429844098	0.04454343	0.08908686	0.04454343	0.801781737	0	0.178173719	0.13363029	0.08908686	0.13363029	0	2.093541203	0	0	0	0	0
s__agalactiae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__anginosus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__equi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__infantis	0.178173719	0.04454343	3.028953229	0.04454343	0.08908686	0.04454343	0.712694878	0	0.08908686	0.04454343	0.08908686	0.13363029	0	1.826280624	0	0	0	0	0
unclassified	0	0	0.400890869	0	0	0	0.08908686	0	0.08908686	0.08908686	0	0	0	0.267260579	0	0	0	0	0
o__Turicibacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Turicibacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Turicibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Clostridia	5.033407572	2.227171492	6.592427617	2.227171492	0.846325167	1.781737194	1.158129176	0.267260579	6.770601336	1.069042316	0.311804009	3.340757238	0.08908686	0.846325167	0	0	0	0	0
o__Clostridiales	5.033407572	2.227171492	6.592427617	2.227171492	0.846325167	1.781737194	1.158129176	0.267260579	6.770601336	1.069042316	0.311804009	3.340757238	0.08908686	0.846325167	0	0	0	0	0
f__Christensenellaceae	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Clostridiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__02d06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Caloramator	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Clostridium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oxobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Dehalobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dehalobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Eubacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Anaerofustis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Lachnospiraceae	0.08908686	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0
g__Blautia	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
s__obeum	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0
s__producta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Coprococcus	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__catus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__eutactus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Dorea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__formicigenerans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lachnobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Moryella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__indoligenes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseburia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__faecis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ruminococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__gnavus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__torques	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Shuttleworthia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Mogibacteriaceae	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
g__Mogibacterium	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Peptococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Peptococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__WCHB1-84	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Peptostreptococcaceae	0	0	0.04454343	0	0	0	0.08908686	0	0	0	0	0	0	0.08908686	0	0	0	0	0
g__Filifactor	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Peptostreptococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__anaerobius	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0.04454343	0	0	0	0	0
f__Ruminococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0
g__Faecalibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
s__prausnitzii	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
g__Oscillospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ruminococcus	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
s__bromii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__callidus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Symbiobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Symbiobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__thermophilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Tissierellaceae	4.67706034	2.227171492	6.458797327	2.182628062	0.757238307	1.781737194	1.069042316	0.267260579	6.770601336	1.069042316	0.267260579	3.296213808	0	0.311804009	0	0	0	0	0
g__1-68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Anaerococcus	1.692650334	1.069042316	3.741648107	2.182628062	0.356347439	1.781737194	0.579064588	0.222717149	6.770601336	0.489977728	0.178173719	2.182628062	0	0.08908686	0	0	0	0	0
unclassified	1.692650334	1.069042316	3.741648107	2.182628062	0.356347439	1.781737194	0.579064588	0.222717149	6.770601336	0.489977728	0.178173719	2.182628062	0	0.08908686	0	0	0	0	0
g__Finegoldia	1.158129176	0.178173719	1.069042316	0	0	0	0.311804009	0	0	0.222717149	0.04454343	0.267260579	0	0.08908686	0	0	0	0	0
unclassified	1.158129176	0.178173719	1.069042316	0	0	0	0.311804009	0	0	0.222717149	0.04454343	0.267260579	0	0.08908686	0	0	0	0	0
g__GW-34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Gallicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Parvimonas	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0
g__Peptoniphilus	1.826280624	0.979955457	1.514476615	0	0.400890869	0	0.08908686	0.04454343	0	0.356347439	0.04454343	0.846325167	0	0.13363029	0	0	0	0	0
unclassified	1.826280624	0.979955457	1.514476615	0	0.400890869	0	0.08908686	0.04454343	0	0.356347439	0.04454343	0.846325167	0	0.13363029	0	0	0	0	0
g__WAL_1855D	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__ph2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Veillonellaceae	0.222717149	0	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0.311804009	0	0	0	0	0
g__Dialister	0.222717149	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0.222717149	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Megasphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pelosinus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Propionispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Selenomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__noxia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Succiniclasticum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Veillonella	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.311804009	0	0	0	0	0
s__dispar	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.267260579	0	0	0	0	0
s__parvula	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
c__Erysipelotrichi	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
o__Erysipelotrichales	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
f__Erysipelotrichaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Bulleidia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__moorei	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Eubacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__biforme	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
p__Fusobacteria	0	0.04454343	0.08908686	0	0.08908686	0	0	0	0	0	0	0	0	0.222717149	0	0	0	0	0
c__Fusobacteriia	0	0.04454343	0.08908686	0	0.08908686	0	0	0	0	0	0	0	0	0.222717149	0	0	0	0	0
o__Fusobacteriales	0	0.04454343	0.08908686	0	0.08908686	0	0	0	0	0	0	0	0	0.222717149	0	0	0	0	0
f__Fusobacteriaceae	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0.222717149	0	0	0	0	0
g__Fusobacterium	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0.222717149	0	0	0	0	0
unclassified	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0.222717149	0	0	0	0	0
f__Leptotrichiaceae	0	0.04454343	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Leptotrichia	0	0.04454343	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Streptobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__moniliformis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Gemmatimonadetes	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
c__Gemm-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Gemmatimonadetes	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
o__Ellin5290	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Gemmatimonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Ellin5301	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__KD8-87	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__N1423WL	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
p__MVP-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Nitrospirae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Nitrospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Nitrospirales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nitrospiraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nitrospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermodesulfovibrionaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Candidatus_Magnetoovum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__OD1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__ZB2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__OP3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__koll11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__GIF10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__kpj58rc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Planctomycetes	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0	0
c__Phycisphaerae	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
o__WD2101	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
c__Planctomycetia	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0
o__Gemmatales	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0
f__Gemmataceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Gemmata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Isosphaeraceae	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0
p__Proteobacteria	31.67037862	1.469933185	4.677060134	8.46325167	0.534521158	1.870824053	16.30289532	2.048997773	3.518930958	1.113585746	1.870824053	0.712694878	0.178173719	3.296213808	0.534521158	0.08908686	1.603563474	8.46325167
c__Alphaproteobacteria	0	0	0.13363029	0	0	0	0.04454343	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0.04454343
o__Caulobacterales	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Caulobacteraceae	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Brevundimonas	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__diminuta	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Phenylobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Ellin329	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rhizobiales	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
f__Aurantimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bartonellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bartonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Beijerinckiaceae	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
g__Methylocella	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bradyrhizobiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Balneimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bosea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__genosp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Hyphomicrobiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Hyphomicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__sulfonivorans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodoplanes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Methylobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Methylobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__komagatae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Phyllobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Mesorhizobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__huakuii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nitratireductor	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Xanthobacteraceae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Blastochloris	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rhodobacterales	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
f__Rhodobacteraceae	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
g__Rubellimicrobium	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
o__Rhodospirillales	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
f__Acetobacteraceae	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Acetobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Acidisphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Acidocella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseococcus	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Roseomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mucosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Swaminathania	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Rhodospirillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oleomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Sphingomonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
f__Sphingomonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Kaistobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Novosphingobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__resinovorum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphingobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__yanoikuyae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphingomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
s__azotifigens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__echinoides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__wittichii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__yabuuchiae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
c__Betaproteobacteria	1.202672606	0.08908686	2.449888641	0.08908686	0.267260579	1.380846325	15.05567929	1.781737194	0.579064588	0.04454343	0.311804009	0.04454343	0.04454343	2.227171492	0.08908686	0	0.222717149	0.222717149
o__A21b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__EB1003	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Burkholderiales	0.579064588	0.04454343	0.222717149	0.08908686	0.13363029	0.13363029	0.356347439	0.13363029	0.534521158	0.04454343	0.311804009	0	0.04454343	0.222717149	0.08908686	0	0.222717149	0.222717149
f__Alcaligenaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0
g__Achromobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0
g__Denitrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oligella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Tetrathiobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__kashmirensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

f__Burkholderiaceae	0.400890869	0.04454343	0.08908686	0.04454343	0.13363029	0.08908686	0.13363029	0	0.489977728	0.04454343	0	0	0.04454343	0.08908686	0.08908686	0	0.08908686	0.08908686		
g__Burkholderia	0.400890869	0.04454343	0.04454343	0.04454343	0.13363029	0.08908686	0.13363029	0	0.356347439	0.04454343	0	0	0.04454343	0	0.08908686	0	0.04454343	0.08908686		
s__andropogonis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
s__bryophila	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
s__graminis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
s__tuberum	0.13363029	0	0	0.04454343	0.04454343	0	0.08908686	0	0.178173719	0.04454343	0	0	0	0	0	0.04454343	0	0		
unclassified	0.267260579	0.04454343	0.04454343	0	0.08908686	0.08908686	0.04454343	0	0.178173719	0	0	0	0.04454343	0	0.04454343	0	0.04454343	0.08908686		
g__Lautropia	0	0	0.04454343	0	0	0	0	0	0.13363029	0	0	0	0	0.08908686	0	0	0	0		
unclassified	0	0	0.04454343	0	0	0	0	0	0.13363029	0	0	0	0	0.08908686	0	0	0	0		
g__Salinispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0		
s__tropica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0		
f__Comamonadaceae	0.08908686	0	0.13363029	0	0	0.04454343	0.08908686	0	0	0	0.04454343	0	0	0	0	0	0	0		
g__Acidovorax	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0		
s__delafieldii	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0		
g__Alicycliphilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Aquabacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Azohydromonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Comamonas	0	0	0.13363029	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0		
s__terrigena	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0		
g__Delftia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Diaphorobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Giesbergeria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Hylemonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Leptothrix	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Methylbium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
s__petroleiphilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Paucibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Pelomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
s__puraquae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Ramlibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Rubrivivax	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0		
s__gelatinosus	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0		
g__Schlegelella	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Tepidimonas	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0		
g__Variovorax	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
s__paradoxus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
f__Oxalobacteraceae	0.08908686	0	0	0.04454343	0	0	0.13363029	0.13363029	0.04454343	0	0.267260579	0	0	0	0.13363029	0	0	0.04454343	0.13363029	
g__Collimonas	0	0	0	0.04454343	0	0	0.13363029	0	0	0	0.178173719	0	0	0	0	0	0	0	0.04454343	
unclassified	0	0	0	0.04454343	0	0	0.13363029	0	0	0	0.178173719	0	0	0	0	0	0	0	0.04454343	
g__Cupriavidus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__gilardii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Herbaspirillum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Herminiimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	
g__Janthinobacterium	0	0	0	0	0	0	0	0.13363029	0	0	0.08908686	0	0	0	0	0	0	0	0	
s__lividum	0	0	0	0	0	0	0	0.13363029	0	0	0.08908686	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Oxalobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__formigenes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Polynucleobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__cosmopolitanus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0.08908686	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0.04454343	0.08908686	
unclassified	0.08908686	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343	0	0	0.04454343	0.08908686	
o__Ellin6067	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__MND1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__Neisseriales	0.623608018	0.04454343	2.227171492	0	0.13363029	1.247216036	14.69933185	1.648106904	0.04454343	0	0	0.04454343	0	2.004454343	0	0	0	0	0	
f__Neisseriaceae	0.623608018	0.04454343	2.227171492	0	0.13363029	1.247216036	14.69933185	1.648106904	0.04454343	0	0	0.04454343	0	2.004454343	0	0	0	0	0	
g__Aquitalea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__magnusonii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Eikenella	0	0	0.13363029	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0.13363029	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	
g__Kingella	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.178173719	0	0	0	0	0	
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.178173719	0	0	0	0	0	
g__Microvirgula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__aerodenitrificans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Neisseria	0	0	2.004454343	0	0.13363029	1.247216036	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0	
s__cinerea	0	0	0	0	0.08908686	1.247216036	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__subflava	0	0	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0	
unclassified	0	0	1.959910913	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Vitreoscilla	0.623608018	0.04454343	0.04454343	0	0	0	14.69933185	1.648106904	0	0	0	0.04454343	0	1.692650334	0	0	0	0	0	
unclassified	0.623608018	0.04454343	0.04454343	0	0	0	14.69933185	1.648106904	0	0	0	0.04454343	0	1.692650334	0	0	0	0	0	
o__Rhodocyclales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Rhodocyclaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Azospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Dok59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Methyloversatilis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Propionivibrio	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Zoogloea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__SBla14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__SC-I-84	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
c__Deltaproteobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__Desulfovibrionales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Desulfovibrionaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Desulfovibrio	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__cavernae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__FAC87	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__MI246	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__Myxococcales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Cystobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Cystobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Haliangiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Haliangium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Myxococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Anaeromyxobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__SAR324	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
o__Syntrophobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Syntrophobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Syntrophobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
c__Epsilonproteobacteria	0.178173719	0.08908686	0	0	0.04454343	0	0.04454343	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	
o__Campylobacterales	0.178173719	0.08908686	0	0	0.04454343	0	0.04454343	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	
f__Campylobacteraceae	0.178173719	0.08908686	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	
g__Campylobacter	0.178173719	0.08908686	0	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0	0	0	
s__rectus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
s__ureolyticus	0.178173719	0.08908686	0	0	0.04454343	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	
f__Helicobacteraceae	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	
g__Helicobacter	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	
s__pylori	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	
o__Nautiliales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
f__Nautiliaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Nautilia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
c__Gammaproteobacteria	30.28953229	1.291759465	2.093541203	8.374164811	0.222717149	0.489977728	1.158129176	0.267260579	2.93986637	1.024498886	1.514476615	0.623608018	0.13363029	1.024498886	0.445434298	0.08908686	1.380846325	8.195991091		
o__Alteromonadales	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
f__Shewanellaceae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Shewanella	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
s__pacifica	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
o__Enterobacteriales	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0.04454343	0		
f__Enterobacteriaceae	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0.04454343	0		
g__Citrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		

unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Enterobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__cowanii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Erwinia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__dispersa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Klebsiella	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0
s__oxytoca	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Salmonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__enterica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Legionellales	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
f__Coxiellaceae	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
f__Legionellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Legionella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Oceanospirillales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Halomonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Halomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Oceanospirillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Marinomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__primoryensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Pasteurellales	12.42761693	0	0.04454343	7.483296214	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Pasteurellaceae	12.42761693	0	0.04454343	7.483296214	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__parahaemolyticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Haemophilus	12.42761693	0	0.04454343	7.483296214	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__influenzae	12.42761693	0	0	7.483296214	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__parainfluenzae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Pseudomonadales	0.04454343	0.04454343	0	0.08908686	0	0	0.08908686	0	0	0.579064588	1.158129176	0.04454343	0.04454343	0	0	0	0	0
f__Moraxellaceae	0	0.04454343	0	0.04454343	0	0	0	0	0	0.579064588	1.158129176	0.04454343	0.04454343	0	0	0	0	0
g__Acinetobacter	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__guillouiae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__lwoffii	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__rhizosphaerae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__schindleri	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__venetianus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Alkanindiges	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Enhydrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Moraxella	0	0	0	0.04454343	0	0	0	0	0	0.579064588	1.158129176	0.04454343	0	0	0	0	0	0
s__ovis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0.579064588	1.158129176	0.04454343	0	0	0	0	0	0
f__Pseudomonadaceae	0.04454343	0	0	0.04454343	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0
g__Pseudomonas	0.04454343	0	0	0.04454343	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0
s__alcaligenes	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
s__fragi	0.04454343	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
s__umsongensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__veronii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__viridiflava	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Xanthomonadales	17.81737194	1.247216036	2.004454343	0.801781737	0.222717149	0.489977728	1.069042316	0.267260579	2.85077951	0.445434298	0.311804009	0.579064588	0.08908686	1.024498886	0.445434298	0.08908686	1.336302895	8.195991091
f__Sinobacteraceae	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0
g__Hydrocarboniphaga	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
s__effusa	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0
f__Xanthomonadaceae	17.81737194	1.247216036	2.004454343	0.801781737	0.222717149	0.489977728	1.069042316	0.222717149	2.80623608	0.445434298	0.311804009	0.579064588	0.08908686	1.024498886	0.445434298	0.08908686	1.336302895	8.195991091
g__Dokdonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dyella	13.94209354	1.024498886	0.08908686	0.08908686	0.04454343	0.400890869	0.178173719	0	0.489977728	0	0.08908686	0.489977728	0	0.178173719	0	0	1.113585746	6.503340757
s__ginsengisoli	13.94209354	1.024498886	0.08908686	0.08908686	0.04454343	0.400890869	0.178173719	0	0.489977728	0	0.08908686	0.489977728	0	0.178173719	0	0	1.113585746	6.503340757
g__Luteimonas	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lysobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pseudoxanthomonas	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mexicana	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodanobacter	3.741648107	0.222717149	1.781737194	0.668151448	0.178173719	0.08908686	0.846325167	0.222717149	2.316258352	0.445434298	0.222717149	0.08908686	0.08908686	0.846325167	0.445434298	0.08908686	0.222717149	1.648106904
s__lindaniclasticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	3.741648107	0.222717149	1.781737194	0.668151448	0.178173719	0.08908686	0.846325167	0.222717149	2.316258352	0.445434298	0.222717149	0.08908686	0.08908686	0.846325167	0.445434298	0.08908686	0.222717149	1.648106904
g__Stenotrophomonas	0.04454343	0	0.13363029	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.04454343
s__acidaminiphila	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__geniculata	0.04454343	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.04454343
s__retroflexus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__fusca	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Xanthomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Spirochaetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Spirochaetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Borreliales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Borreliaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Spironema	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Spirochaetales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Spirochaetaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Treponema	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Synergistetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Synergistia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Synergistales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Dethiosulfovibrionaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pyramidobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__piscolens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermovirgaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermovirga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__TM7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__TM7-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__TM7-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__EW055	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Tenericutes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Mollicutes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__RF39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Thermi	0	0	0	0.04454343	0	0	0	0	0	0	0.178173719	0	0	0	0	0	0	0
c__Deinococci	0	0	0	0.04454343	0	0	0	0	0	0	0.178173719	0	0	0	0	0	0	0
o__Deinococcales	0	0	0	0	0	0	0	0	0	0	0.178173719	0	0	0	0	0	0	0
f__Deinococcaceae	0	0	0	0	0	0	0	0	0	0	0.178173719	0	0	0	0	0	0	0
g__Deinococcus	0	0	0	0	0	0	0	0	0	0	0.178173719	0	0	0	0	0	0	0
s__alpinitundrae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aquatilis	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
s__geothermalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0	0	0	0
o__Thermales	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermaceae	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermus	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Verrucomicrobia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Pedosphaerae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Pedosphaerales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Pedosphaeraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pedosphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Spartobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Chthoniobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Chthoniobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ellin506	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__WPS-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Total Number of Reads	4505	6336	4115	6854	6726	11545	11108	18143	3451	23300	20076	37266	16328	7925	11848	8672	14515	10026

Sample ID	1751A	1766A	1767A	1858A	1863A	1867A	1978A	1990A	2012A	2123A	1683A	1737A	1781A	1790A	1859A	1920A	1933A	1977A	1993A
Sample Location	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess
SSTI/*S. aureus* colonization status	MRSA	MRSA	MRSA	MRSA	MRSA	MRSA	MRSA	MRSA	MRSA	MRSA	MSSA	MSSA	MSSA	MSSA	MSSA	MSSA	MSSA	MSSA	MSSA
Taxon																			
p__Acidobacteria	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Acidobacteria-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Acidobacteria-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__iii1-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Acidobacteriia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Acidobacteriales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Acidobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Edaphobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__modestum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Terriglobus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Koribacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Candidatus_Koribacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Chloracidobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__DS-100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__PK29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__RB41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Ellin6075	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__DA052	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Ellin6513	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__RB25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Solibacteres	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Solibacterales	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__MVS-65	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__PK34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Sva0725	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Sva0725	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__iii1-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__DS-18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Actinobacteria	2.271714922	0	0.935412027	0.178173719	0.04454343	0.04454343	0.178173719	0.13363029	0	0.04454343	0	0.489977728	4.810690423	0.08908686	6.191536748	0.712694878	0	0.178173719	0.04454343
c__Acidimicrobiia	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Acidimicrobiales	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__C111	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__EB1017	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Actinobacteria	2.182628062	0	0.935412027	0.178173719	0.04454343	0.04454343	0.178173719	0.13363029	0	0.04454343	0	0.489977728	4.810690423	0.08908686	6.146993318	0.712694878	0	0.178173719	0.04454343
o__Actinomycetales	2.182628062	0	0.935412027	0.178173719	0.04454343	0.04454343	0.178173719	0.13363029	0	0.04454343	0	0.489977728	4.810690423	0.08908686	6.146993318	0.712694878	0	0.178173719	0.04454343
f__Actinomycetaceae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinobaculum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinomyces	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__europaeus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__hyovaginalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Mobiluncus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Varibaculum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Actinosynnemataceae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinoalloteichus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kutzneria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lentzea	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__violacea	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Saccharothrix	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Beutenbergiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bogoriellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Georgenia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Brevibacteriaceae	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Brevibacterium	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aureum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__casei	0	0	0.04454343	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
s__paucivorans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Cellulomonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinotalea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Cellulomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__uda	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Corynebacteriaceae	1.514476615	0	0.400890869	0.178173719	0.04454343	0	0.04454343	0.04454343	0	0.04454343	0	0	4.231625835	0.04454343	5.968819599	0.668151448	0	0.13363029	0
g__Corynebacterium	1.514476615	0	0.400890869	0.178173719	0.04454343	0	0.04454343	0.04454343	0	0.04454343	0	0	4.231625835	0.04454343	5.968819599	0.668151448	0	0.13363029	0
s__durum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__kroppenstedtii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__lubricantis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mastitidis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__pilosum	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0
s__renale	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__simulans	0	0	0	0	0	0	0	0	0	0	0	0	3.786191537	0	1.158129176	0	0	0.04454343	0
s__stationis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	1.514476615	0	0.400890869	0.178173719	0	0	0.04454343	0.04454343	0	0.04454343	0	0	0.445434298	0.04454343	4.810690423	0.623608018	0	0.04454343	0
f__Dermabacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0
g__Brachybacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__conglomeratum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dermabacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0
f__Dermacoccaceae	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0
g__Dermacoccus	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0
f__Dermatophilaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dermatophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Dietziaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dietzia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Frankiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Frankia	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Geodermatophilaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Blastococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aggregatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Geodermatophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__obscurus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Modestobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Gordoniaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Gordonia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Intrasporangiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Knoellia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__subterranea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

g__Phycicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Serinicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Kineosporiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kineococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kineosporia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Microbacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Agrococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__jenensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Clavibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__michiganensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Cryocola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Curtobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Frigoribacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Leucobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Microbacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__chocolatum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__maritypicum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Mycetocola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pseudoclavibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__bifida	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Yonghaparkia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Micrococcaceae	0.311804009	0	0.356347439	0	0	0	0.04454343	0	0	0	0	0	0.178173719	0	0	0.04454343	0	0.04454343	0.04454343	0
g__Arthrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__crystallopoietes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__psychrolactophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Citricoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__alkalitolerans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kocuria	0.04454343	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
s__palustris	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__rhizophila	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Microbispora	0	0	0	0	0	0	0	0	0	0	0	0	0.178173719	0	0	0	0	0	0	0
s__rosea	0	0	0	0	0	0	0	0	0	0	0	0	0.178173719	0	0	0	0	0	0	0
g__Micrococcus	0.267260579	0	0.356347439	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0.04454343	0
s__luteus	0.267260579	0	0.356347439	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.04454343	0.04454343	0
g__Nesterenkonia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Renibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rothia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aeria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mucilaginosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Zhihengliuella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Micromonosporaceae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinocatenispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Catellatospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Couchioplanes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__caeruleus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Solwaraspora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Verrucosispora	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__glhomensis	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Mycobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Mycobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__celatum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__gordonae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__vaccae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nakamurellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nocardiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nocardia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__fascians	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__globerulus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nocardioidaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinopolymorpha	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Aeromicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Friedmanniella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nocardioides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pimelobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Propionicimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nocardiopsaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nocardiopsis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__composta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Promicromonosporaceae	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Cellulosimicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Promicromonospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Propionibacteriaceae	0.267260579	0	0	0	0	0	0.08908686	0.08908686	0	0	0	0.489977728	0.267260579	0	0.04454343	0	0	0	0	0
g__Luteococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Microlunatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Propionibacterium	0.267260579	0	0	0	0	0	0.08908686	0.08908686	0	0	0	0.489977728	0.267260579	0	0	0	0	0	0	0
s__acnes	0.267260579	0	0	0	0	0	0.08908686	0.08908686	0	0	0	0.489977728	0.267260579	0	0	0	0	0	0	0
s__granulosum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Tessaracoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
f__Pseudonocardiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinomycetospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pseudonocardia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Sporichthyaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sporichthya	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Streptomycetaceae	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kitasatospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Streptomyces	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__lanatus	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mashuensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__scabrisporus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Streptosporangiaceae	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nonomuraea	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__roseoviolacea	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphaerisporangium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermomonosporaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinomadura	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__vinacea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Tsukamurellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Tsukamurella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Micrococcales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Coriobacteriia	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
o__Coriobacteriales	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
f__Coriobacteriaceae	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Adlercreutzia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Atopobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__rimae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Collinsella	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aerofaciens	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Slackia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__MB-A2-108	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__0319-7L14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__OPB41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Rubrobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rubrobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Rubrobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rubrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Thermoleophilia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Gaiellales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Gaiellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Solirubrobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Conexibacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Conexibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Patulibacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Solirubrobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Solirubrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Armatimonadetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Armatimonadia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Armatimonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Armatimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__CL0-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__FW68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Chthonomonadetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Chthonomonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Chthonomonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Fimbriimonadia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Fimbriimonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Fimbriimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Fimbriimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__OPB50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__BRC1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__PRR-11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Bacteroidetes	0	0	0.267260579	0	0.04454343	0.13363029	0	0	0	0	0.08908686	0.04454343	0.400890869	0	0	0.04454343	0	0	0.13363029
c__Bacteroidia	0	0	0.178173719	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343
o__Bacteroidales	0	0	0.178173719	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0.04454343
f__Bacteroidaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bacteroides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__caccae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ovatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__uniformis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Paraprevotellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Prevotella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__YRC22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Porphyromonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Porphyromonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Tannerella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Prevotellaceae	0	0	0.178173719	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
g__Prevotella	0	0	0.178173719	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
s__copri	0	0	0.178173719	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0
s__melaninogenica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__nanceiensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ruminicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__stercorea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Rikenellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Blvii28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
f__S24-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Cytophagia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
o__Cytophagales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
f__Cytophagaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Adhaeribacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dyadobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Hymenobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodocytophaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Flavobacteriia	0	0	0.08908686	0	0.04454343	0.13363029	0	0	0	0	0.04454343	0	0.356347439	0	0	0.04454343	0	0	0
o__Flavobacteriales	0	0	0.08908686	0	0.04454343	0.13363029	0	0	0	0	0.04454343	0	0.356347439	0	0	0.04454343	0	0	0
f__Cryomorphaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Fluviicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Flavobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
g__Algibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__lectus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Capnocytophaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ochracea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Flavobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__succinicans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Myroides	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
s__odoratimimus	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
f__Weeksellaceae	0	0	0.08908686	0	0.04454343	0.13363029	0	0	0	0	0.04454343	0	0.311804009	0	0	0.04454343	0	0	0
g__Chryseobacterium	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0.178173719	0	0	0.04454343	0	0	0
unclassified	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0.178173719	0	0	0.04454343	0	0	0
g__Cloacibacterium	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.08908686	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.08908686	0	0	0	0	0	0
g__Elizabethkingia	0	0	0	0	0.04454343	0.13363029	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
s__meningoseptica	0	0	0	0	0.04454343	0.13363029	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
g__Ornithobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Riemerella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Wautersiella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Weeksella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Saprospirae	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343
o__Saprospirales	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343
f__Chitinophagaceae	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0.04454343
g__Chitinophaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__arvensicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Flavihumibacter	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
g__Flavisolibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Niabella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Niastella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sediminibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Segetibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Terrimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Sphingobacteriia	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
o__Sphingobacteriales	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
f__Sphingobacteriaceae	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
g__Olivibacter	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0
g__Pedobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__cryoconitis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphingobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__faecium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

s__mizutaii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__multivorum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Chloroflexi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Anaerolineae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Caldilineales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Caldilineaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SBR1031	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__A4b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SJA-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__C0119	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Chloroflexi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__AKIW781	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Chloroflexales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__FFCH7168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Roseiflexales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Roseiflexaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseiflexus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Ktedonobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__B12-WMSP1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Thermogemmatisporales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermogemmatisporaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__SHA-26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__TK10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__B07_WMSP1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__FFCH4570	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Thermomicrobia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__JG30-KF-CM45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Cyanobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__4C0d-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__MLE1-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Chloroplast	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Stramenopiles	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Streptophyta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__FBP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Firmicutes	94.65478842	99.86636971	76.5701559	99.82182628	99.91091314	99.68819599	98.12917595	99.73273942	99.68819599	99.82182628	99.5545657	98.97550111	90.91314031	99.86636971	93.67483296	98.97550111	99.95545657	99.77728285	99.82182628
c__Bacilli	94.65478842	99.86636971	76.30289532	98.57461024	99.91091314	99.68819599	97.99554566	99.73273942	99.68819599	99.82182628	99.5545657	98.97550111	90.91314031	99.86636971	93.40757238	98.97550111	99.95545657	99.77728285	99.77728285
o__Bacillales	94.38752784	99.86636971	76.16926503	98.48552339	99.91091314	99.59910913	97.95100223	99.73273942	99.64365256	99.82182628	99.5545657	98.97550111	90.86859688	99.86636971	59.86636971	98.97550111	99.95545657	99.77728285	99.77728285
f__Alicyclobacillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Alicyclobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bacillaceae	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Alkalibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Anoxybacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__kestanbolensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bacillus	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__acidicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__flexus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__foraminis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__horikoshii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__muralis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__trypoxylicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Geobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__vulcani	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Marinibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Marinococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Exiguobacteraceae	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0
g__Exiguobacterium	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0.04454343	0	0	0	0
f__Paenibacillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ammoniphilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__oxalaticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Paenibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__amylolyticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__edaphicus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__stellifer	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Planococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lysinibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__boronitolerans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Planomicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sporosarcina	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Sporolactobacillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sporolactobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Staphylococcaceae	94.38752784	99.86636971	76.16926503	98.48552339	99.91091314	99.51002227	97.95100223	99.73273942	99.64365256	99.82182628	99.5545657	98.97550111	90.86859688	99.82182628	59.82182628	98.97550111	99.95545657	99.73273942	99.77728285
g__Jeotgalicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__psychrophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Salinicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Staphylococcus	94.38752784	99.86636971	76.16926503	98.48552339	99.91091314	99.51002227	97.95100223	99.73273942	99.64365256	99.82182628	99.5545657	98.97550111	90.86859688	99.82182628	59.82182628	98.97550111	99.95545657	99.73273942	99.77728285
s__aureus	91.9376392	99.86636971	74.65478842	98.48552339	99.91091314	99.15367483	97.81737194	99.73273942	99.59910913	99.82182628	99.51002227	98.79732739	84.67706013	99.51002227	55.81291759	98.12917595	99.46547884	99.33184855	99.73273942
s__epidermidis	0.04454343	0	0	0	0	0.04454343	0.04454343	0	0	0	0	0.13363029	5.567928731	0.04454343	0.04454343	0	0.445434298	0.356347439	0
s__equorum	0.04454343	0	0.178173719	0	0	0	0	0	0	0	0.04454343	0.04454343	0.178173719	0	0	0	0	0.04454343	0
s__haemolyticus	2.227171492	0	1.336302895	0	0	0.311804009	0.08908686	0	0.04454343	0	0	0	0.400890869	0.267260579	3.830734967	0.801781737	0	0	0.04454343
s__lugdunensis	0.13363029	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0.13363029	0.04454343	0.04454343	0	0
s__pettenkoferi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__sciuri	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermoactinomycetaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Planifilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Gemellales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Gemellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Gemella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Lactobacillales	0.267260579	0	0.13363029	0.08908686	0	0.08908686	0.04454343	0	0.04454343	0	0	0	0.04454343	0	33.54120267	0	0	0	0
f__Aerococcaceae	0.178173719	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Abiotrophia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Aerococcus	0.178173719	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.178173719	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Alloiococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__otitis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Facklamia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Carnobacteriaceae	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0

g__Carnobacterium	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
s__viridans	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0
g__Desemzia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Granulicatella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Enterococcaceae	0	0	0.08908686	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
g__Enterococcus	0	0	0.08908686	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
s__casseliflavus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__cecorum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.08908686	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0	0	0
f__Lactobacillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lactobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__delbrueckii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__helveticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__manihotivorans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__salivarius	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Leuconostocaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Leuconostoc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Streptococcaceae	0.04454343	0	0.04454343	0.08908686	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	33.54120267	0	0	0	0
g__Lactococcus	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Streptococcus	0	0	0.04454343	0.08908686	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	33.54120267	0	0	0	0
s__agalactiae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	30.77951002	0	0	0	0
s__anginosus	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__equi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.76169265	0	0	0	0
s__infantis	0	0	0.04454343	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Turicibacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Turicibacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Turicibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Clostridia	0	0	0.267260579	1.247216036	0	0	0.13363029	0	0	0	0	0	0	0	0	0.267260579	0	0	0	0.04454343
o__Clostridiales	0	0	0.267260579	1.247216036	0	0	0.13363029	0	0	0	0	0	0	0	0	0.267260579	0	0	0	0.04454343
f__Christensenellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Clostridiaceae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__02d06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Caloramator	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Clostridium	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oxobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Dehalobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dehalobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Eubacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Anaerofustis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Lachnospiraceae	0	0	0.04454343	0.222717149	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Blautia	0	0	0.04454343	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__obeum	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__producta	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Coprococcus	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__catus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__eutactus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dorea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__formicigenerans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lachnobacterium	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Moryella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__indoligenes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseburia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__faecis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ruminococcus	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__gnavus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__torques	0	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Shuttleworthia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Mogibacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Mogibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Peptococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Peptococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__WCHB1-84	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Peptostreptococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Filifactor	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Peptostreptococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__anaerobius	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Ruminococcaceae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Faecalibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__prausnitzii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oscillospira	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ruminococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
s__bromii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__callidus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Symbiobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Symbiobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__thermophilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Tissierellaceae	0	0	0.08908686	1.024498886	0	0	0.13363029	0	0	0	0	0	0	0	0	0.267260579	0	0	0	0
g__1-68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Anaerococcus	0	0	0.04454343	0.534521158	0	0	0.08908686	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0
unclassified	0	0	0.04454343	0.534521158	0	0	0.08908686	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0
g__Finegoldia	0	0	0.04454343	0.267260579	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0
unclassified	0	0	0.04454343	0.267260579	0	0	0	0	0	0	0	0	0	0	0	0.13363029	0	0	0	0
g__GW-34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Gallicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Parvimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Peptoniphilus	0	0	0	0.222717149	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.222717149	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0
g__WAL_1855D	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__ph2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Veillonellaceae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dialister	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Megasphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pelosinus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Propionispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Selenomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__noxia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Succiniclasticum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Veillonella	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__dispar	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__parvula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Erysipelotrichi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Erysipelotrichales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Erysipelotrichaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bulleidia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__moorei	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Eubacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__biforme	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Fusobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Fusobacteriia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Fusobacteriales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Fusobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Fusobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Leptotrichiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Leptotrichia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Streptobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__moniliformis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Gemmatimonadetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Gemm-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Gemmatimonadetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Ellin5290	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Gemmatimonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Ellin5301	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__KD8-87	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__N1423WL	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__MVP-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Nitrospirae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Nitrospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Nitrospirales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nitrospiraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nitrospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermodesulfovibrionaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Candidatus_Magnetoovum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__OD1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__ZB2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__OP3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__koll11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__GIF10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__kpj58rc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Planctomycetes	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Phycisphaerae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__WD2101	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Planctomycetia	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Gemmatales	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Gemmataceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Gemmata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Isosphaeraceae	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Proteobacteria	2.9844098	0.08908686	22.22717149	0	0	0.13363029	1.692650334	0.13363029	0.311804009	0.13363029	0.356347439	0.489977728	3.875278396	0.04454343	0.13363029	0.267260579	0.04454343	0.04454343	0
c__Alphaproteobacteria	0.04454343	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Caulobacterales	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Caulobacteraceae	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Brevundimonas	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__diminuta	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Phenylobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Ellin329	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rhizobiales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Aurantimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bartonellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bartonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Beijerinckiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Methylocella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bradyrhizobiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Balneimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bosea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__genosp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Hyphomicrobiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Hyphomicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__sulfonivorans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodoplanes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Methylobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Methylobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__komagatae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Phyllobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Mesorhizobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__huakuii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nitratireductor	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Xanthobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Blastochloris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rhodobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Rhodobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rubellimicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rhodospirillales	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Acetobacteraceae	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Acetobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Acidisphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Acidocella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mucosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Swaminathania	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Rhodospirillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oleomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Sphingomonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Sphingomonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kaistobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Novosphingobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__resinovorum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphingobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__yanoikuyae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphingomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__azotifigens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__echinoides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__wittichii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__yabuuchiae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Betaproteobacteria	0	0	0.534521158	0	0	0.04454343	0.356347439	0	0	0.04454343	0.08908686	0.04454343	0.489977728	0.04454343	0.08908686	0.08908686	0.04454343	0	0
o__A21b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__EB1003	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Burkholderiales	0	0	0.534521158	0	0	0.04454343	0.356347439	0	0	0.04454343	0.08908686	0.04454343	0.400890869	0.04454343	0.08908686	0.08908686	0.04454343	0	0
f__Alcaligenaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Achromobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Denitrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oligella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Tetrathiobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__kashmirensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

f__Burkholderiaceae	0	0	0.311804009	0	0	0	0.267260579	0	0	0	0	0.04454343	0.267260579	0	0	0.08908686	0	0	0
g__Burkholderia	0	0	0.311804009	0	0	0	0.267260579	0	0	0	0	0.04454343	0.267260579	0	0	0.08908686	0	0	0
s__andropogonis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__bryophila	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__graminis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__tuberum	0	0	0.04454343	0	0	0	0.08908686	0	0	0	0	0	0.08908686	0	0	0.04454343	0	0	0
unclassified	0	0	0.267260579	0	0	0	0.178173719	0	0	0	0	0.04454343	0.178173719	0	0	0.04454343	0	0	0
g__Lautropia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Salinispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__tropica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Comamonadaceae	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0
g__Acidovorax	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__delafieldii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Alicycliphilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Aquabacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Azohydromonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Comamonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__terrigena	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Delftia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Diaphorobacter	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0	0	0
g__Giesbergeria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Hylemonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Leptothrix	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Methylibium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__petroleiphilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Paucibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pelomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__puraquae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ramlibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rubrivivax	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__gelatinosus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Schlegelella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Tepidimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Variovorax	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__paradoxus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Oxalobacteraceae	0	0	0.222717149	0	0	0.04454343	0.08908686	0	0	0.04454343	0	0	0.13363029	0.04454343	0.04454343	0	0.04454343	0	0
g__Collimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Cupriavidus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__gilardii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Herbaspirillum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Herminiimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Janthinobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__lividum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oxalobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__formigenes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Polynucleobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__cosmopolitanus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.222717149	0	0	0.04454343	0.08908686	0	0	0.04454343	0	0	0.13363029	0.04454343	0.04454343	0	0.04454343	0	0
unclassified	0	0	0.222717149	0	0	0.04454343	0.08908686	0	0	0.04454343	0	0	0.13363029	0.04454343	0.04454343	0	0.04454343	0	0
o__Ellin6067	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__MND1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Neisseriales	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0
f__Neisseriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0
g__Aquitalea	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0
s__magnusonii	0	0	0	0	0	0	0	0	0	0	0	0	0.08908686	0	0	0	0	0	0
g__Eikenella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kingella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Microvirgula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aerodenitrificans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Neisseria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__cinerea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__subflava	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Vitreoscilla	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rhodocyclales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Rhodocyclaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Azospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dok59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Methyloversatilis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Propionivibrio	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Zoogloea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SBla14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SC-I-84	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Deltaproteobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Desulfovibrionales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Desulfovibrionaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Desulfovibrio	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__cavernae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__FAC87	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__MI246	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Myxococcales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Cystobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Cystobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Haliangiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Haliangium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Myxococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Anaeromyxobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SAR324	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Syntrophobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Syntrophobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Syntrophobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Epsilonproteobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Campylobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Campylobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Campylobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__rectus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ureolyticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Helicobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Helicobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__pylori	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Nautiliales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nautiliaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nautilia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Gammaproteobacteria	2.93986637	0.08908686	21.6481069	0	0	0.08908686	1.336302895	0.13363029	0.311804009	0.08908686	0.267260579	0.445434298	3.385300668	0	0.04454343	0.178173719	0	0.04454343	0
o__Alteromonadales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Shewanellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Shewanella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__pacifica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Enterobacteriales	0.04454343	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
f__Enterobacteriaceae	0.04454343	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Citrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Enterobacter	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__cowanii	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Erwinia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__dispersa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Klebsiella	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__oxytoca	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Salmonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__enterica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Legionellales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Coxiellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Legionellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Legionella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Oceanospirillales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Halomonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Halomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Oceanospirillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Marinomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__primoryensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Pasteurellales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Pasteurellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__parahaemolyticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Haemophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__influenzae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__parainfluenzae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Pseudomonadales	0.08908686	0.04454343	0.267260579	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0
f__Moraxellaceae	0.08908686	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Acinetobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__guillouiae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__lwoffii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__rhizosphaerae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__schindleri	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__venetianus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Alkanindiges	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Enhydrobacter	0.08908686	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.08908686	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Moraxella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ovis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Pseudomonadaceae	0	0.04454343	0.222717149	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Pseudomonas	0	0.04454343	0.222717149	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0
s__alcaligenes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__fragi	0	0.04454343	0.13363029	0	0	0	0.04454343	0	0	0	0	0	0	0	0.04454343	0	0	0	0
s__umsongensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__veronii	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__viridiflava	0	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Xanthomonadales	2.80623608	0.04454343	21.29175947	0	0	0.08908686	1.291759465	0.13363029	0.311804009	0.08908686	0.267260579	0.445434298	3.385300668	0	0	0.178173719	0	0	0
f__Sinobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Hydrocarboniphaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__effusa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Xanthomonadaceae	2.80623608	0.04454343	21.29175947	0	0	0.08908686	1.291759465	0.13363029	0.311804009	0.08908686	0.267260579	0.445434298	3.385300668	0	0	0.178173719	0	0	0
g__Dokdonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Dyella	2.182628062	0	17.59465479	0	0	0	0.222717149	0	0.13363029	0	0	0.08908686	0.178173719	0	0	0.08908686	0	0	0
s__ginsengisoli	2.182628062	0	17.59465479	0	0	0	0.222717149	0	0.13363029	0	0	0.08908686	0.178173719	0	0	0.08908686	0	0	0
g__Luteimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lysobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pseudoxanthomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mexicana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodanobacter	0.534521158	0.04454343	3.608017817	0	0	0	1.069042316	0.13363029	0.178173719	0.08908686	0.267260579	0.356347439	3.207126949	0	0	0.08908686	0	0	0
s__lindaniclasticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.534521158	0.04454343	3.608017817	0	0	0	1.069042316	0.13363029	0.178173719	0.08908686	0.267260579	0.356347439	3.207126949	0	0	0.08908686	0	0	0
g__Stenotrophomonas	0.04454343	0	0.08908686	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0
s__acidaminiphila	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__geniculata	0.04454343	0	0.08908686	0	0	0.08908686	0	0	0	0	0	0	0	0	0	0	0	0	0
s__retroflexus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__fusca	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Xanthomonas	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Spirochaetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Spirochaetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Borreliales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Borreliaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Spironema	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Spirochaetales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Spirochaetaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Treponema	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Synergistetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Synergistia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Synergistales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Dethiosulfovibrionaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pyramidobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__piscolens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermovirgaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermovirga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__TM7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__TM7-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__TM7-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__EW055	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Tenericutes	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Mollicutes	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__RF39	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Thermi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Deinococci	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Deinococcales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Deinococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Deinococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__alpinitundrae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aquatilis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__geothermalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Thermales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Verrucomicrobia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Pedosphaerae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Pedosphaerales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Pedosphaeraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pedosphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Spartobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Chthoniobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Chthoniobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ellin506	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__WPS-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Total Number of Reads	24890	21972	8847	32387	27661	8707	8896	36376	19077	28597	31913	13605	6795	28996	11818	16476	23438	36975	22811

Sample ID	2046A	2050A	2051A	2139A	2168A	1712A	1761A	1852A	1899A	2000A	2010A	2171A
Sample Location	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess
SSTI/*S. aureus* colonization status	MSSA	MSSA	MSSA	MSSA	MSSA	NoSA	NoSA	NoSA	NoSA	NoSA	NoSA	NoSA
Taxon												
p__Acidobacteria	0	0	0	0	0	0	0	0	0	0	0.08908686	0
c__Acidobacteria-5	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Acidobacteria-6	0	0	0	0	0	0	0	0	0	0	0	0
o__iii1-15	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Acidobacteriia	0	0	0	0	0	0	0	0	0	0	0	0
o__Acidobacteriales	0	0	0	0	0	0	0	0	0	0	0	0
f__Acidobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Edaphobacter	0	0	0	0	0	0	0	0	0	0	0	0
s__modestum	0	0	0	0	0	0	0	0	0	0	0	0
g__Terriglobus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Koribacteraceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Candidatus_Koribacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Chloracidobacteria	0	0	0	0	0	0	0	0	0	0	0.08908686	0
o__DS-100	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__PK29	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__RB41	0	0	0	0	0	0	0	0	0	0	0.08908686	0
f__Ellin6075	0	0	0	0	0	0	0	0	0	0	0.08908686	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.08908686	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.08908686	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__DA052	0	0	0	0	0	0	0	0	0	0	0	0
o__Ellin6513	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__RB25	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Solibacteres	0	0	0	0	0	0	0	0	0	0	0	0
o__Solibacterales	0	0	0	0	0	0	0	0	0	0	0	0
f__MVS-65	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__PK34	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Sva0725	0	0	0	0	0	0	0	0	0	0	0	0
o__Sva0725	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__iii1-8	0	0	0	0	0	0	0	0	0	0	0	0
o__DS-18	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
p__Actinobacteria	0.267260579	91.44766147	0	2.316258352	0	1.380846325	0.400890869	0.668151448	17.68374165	0	56.65924276	86.32516704
c__Acidimicrobiia	0	0	0	0	0	0	0	0	0	0	0	0
o__Acidimicrobiales	0	0	0	0	0	0	0	0	0	0	0	0
f__C111	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__EB1017	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Actinobacteria	0.267260579	91.44766147	0	2.316258352	0	1.202672606	0.400890869	0.668151448	17.68374165	0	56.65924276	86.23608018
o__Actinomycetales	0.267260579	91.44766147	0	2.316258352	0	1.202672606	0.400890869	0.668151448	17.68374165	0	56.65924276	86.23608018
f__Actinomycetaceae	0	0	0	0	0	0.579064588	0.04454343	0	0.04454343	0	0.08908686	0
g__Actinobaculum	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinomyces	0	0	0	0	0	0.579064588	0.04454343	0	0	0	0.08908686	0
s__europaeus	0	0	0	0	0	0	0	0	0	0	0	0
s__hyovaginalis	0	0	0	0	0	0.44543429	8	0	0	0	0	0
unclassified	0	0	0	0	0	0.13363029	0.04454343	0	0	0	0.08908686	0
g__Mobiluncus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Varibaculum	0	0	0	0	0	0	0	0	0.04454343	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0
f__Actinosynnemataceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinoalloteichus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Kutzneria	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Lentzea	0	0	0	0	0	0	0	0	0	0	0	0
s__violacea	0	0	0	0	0	0	0	0	0	0	0	0
g__Saccharothrix	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Beutenbergiaceae	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Bogoriellaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Georgenia	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Brevibacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Brevibacterium	0	0	0	0	0	0	0	0	0	0	0	0
s__aureum	0	0	0	0	0	0	0	0	0	0	0	0
s__casei	0	0	0	0	0	0	0	0	0	0	0	0
s__paucivorans	0	0	0	0	0	0	0	0	0	0	0	0
f__Cellulomonadaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinotalea	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Cellulomonas	0	0	0	0	0	0	0	0	0	0	0	0
s__uda	0	0	0	0	0	0	0	0	0	0	0	0
f__Corynebacteriaceae	0.222717149	90.73496659	0	0	0	0.623608018	0.222717149	0.623608018	17.50556793	0	0.712694878	27.52783964
g__Corynebacterium	0.222717149	90.73496659	0	0	0	0.623608018	0.222717149	0.623608018	17.50556793	0	0.712694878	27.52783964
s__durum	0	0	0	0	0	0	0	0	0	0	0	0.04454343
s__kroppenstedtii	0	0	0	0	0	0	0	0	0	0	0	0
s__lubricantis	0	0	0	0	0	0	0	0	0	0	0	0
s__mastitidis	0	0	0	0	0	0	0	0	0	0	0	0
s__pilosum	0	0.13363029	0	0	0	0	0	0	0	0	0	0.04454343
s__renale	0	0	0	0	0	0	0	0	0	0	0	0
s__simulans	0.04454343	0	0	0	0	0.08908686	0	0.489977728	0.400890869	0	0	0
s__stationis	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.178173719	90.60133631	0	0	0	0.534521158	0.222717149	0.13363029	17.10467706	0	0.712694878	27.43875278
f__Dermabacteraceae	0	0	0	0	0	0	0	0	0.08908686	0	0	0
g__Brachybacterium	0	0	0	0	0	0	0	0	0	0	0	0
s__conglomeratum	0	0	0	0	0	0	0	0	0	0	0	0
g__Dermabacter	0	0	0	0	0	0	0	0	0.08908686	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.08908686	0	0	0
f__Dermacoccaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Dermacoccus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Dermatophilaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Dermatophilus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Dietziaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Dietzia	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Frankiaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Frankia	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Geodermatophilaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Blastococcus	0	0	0	0	0	0	0	0	0	0	0	0
s__aggregatus	0	0	0	0	0	0	0	0	0	0	0	0
g__Geodermatophilus	0	0	0	0	0	0	0	0	0	0	0	0
s__obscurus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Modestobacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Gordoniaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Gordonia	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Intrasporangiaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Knoellia	0	0	0	0	0	0	0	0	0	0	0	0
s__subterranea	0	0	0	0	0	0	0	0	0	0	0	0

g__Phycicoccus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Serinicoccus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Kineosporiaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Kineococcus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Kineosporia	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Microbacteriaceae	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Agrococcus	0	0	0	0	0	0	0	0	0	0	0	0
s__jenensis	0	0	0	0	0	0	0	0	0	0	0	0
g__Clavibacter	0	0	0	0	0	0	0	0	0	0	0	0
s__michiganensis	0	0	0	0	0	0	0	0	0	0	0	0
g__Cryocola	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Curtobacterium	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Frigoribacterium	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Leucobacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Microbacterium	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__chocolatum	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__maritypicum	0	0	0	0	0	0	0	0	0	0	0	0
g__Mycetocola	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Pseudoclavibacter	0	0	0	0	0	0	0	0	0	0	0	0
s__bifida	0	0	0	0	0	0	0	0	0	0	0	0
g__Yonghaparkia	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Micrococcaceae	0.04454343	0	0	0	0	0	0.04454343	0.04454343	0	0	0.04454343	0.267260579
g__Arthrobacter	0	0	0	0	0	0	0	0.04454343	0	0	0	0
s__crystallopoietes	0	0	0	0	0	0	0	0.04454343	0	0	0	0
s__psychrolactophilus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Citricoccus	0	0	0	0	0	0	0	0	0	0	0	0
s__alkalitolerans	0	0	0	0	0	0	0	0	0	0	0	0
g__Kocuria	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__palustris	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__rhizophila	0	0	0	0	0	0	0	0	0	0	0	0
g__Microbispora	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__rosea	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Micrococcus	0.04454343	0	0	0	0	0	0	0	0	0	0	0.267260579
s__luteus	0.04454343	0	0	0	0	0	0	0	0	0	0	0.267260579
g__Nesterenkonia	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Renibacterium	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Rothia	0	0	0	0	0	0	0	0	0	0	0	0
s__aeria	0	0	0	0	0	0	0	0	0	0	0	0
s__mucilaginosa	0	0	0	0	0	0	0	0	0	0	0	0
g__Zhihengliuella	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Micromonosporaceae	0	0	0	0.04454343	0	0	0	0	0	0	0	0
g__Actinocatenispora	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Catellatospora	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Couchioplanes	0	0	0	0.04454343	0	0	0	0	0	0	0	0
s__caeruleus	0	0	0	0.04454343	0	0	0	0	0	0	0	0
g__Solwaraspora	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Verrucosispora	0	0	0	0	0	0	0	0	0	0	0	0
s__glhornensis	0	0	0	0	0	0	0	0	0	0	0	0
f__Mycobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Mycobacterium	0	0	0	0	0	0	0	0	0	0	0	0
s__celatum	0	0	0	0	0	0	0	0	0	0	0	0
s__gordonae	0	0	0	0	0	0	0	0	0	0	0	0
s__vaccae	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Nakamurellaceae	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0
f__Nocardiaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Nocardia	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodococcus	0	0	0	0	0	0	0	0	0	0	0	0
s__fascians	0	0	0	0	0	0	0	0	0	0	0	0
s__globerulus	0	0	0	0	0	0	0	0	0	0	0	0
f__Nocardioidaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinopolymorpha	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Aeromicrobium	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Friedmanniella	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Nocardioides	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Pimelobacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Propionicimonas	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Nocardiopsaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Nocardiopsis	0	0	0	0	0	0	0	0	0	0	0	0
s__composta	0	0	0	0	0	0	0	0	0	0	0	0
f__Promicromonosporaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Cellulosimicrobium	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Promicromonospora	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Propionibacteriaceae	0	0.712694878	0	2.271714922	0	0	0.08908686	0	0.04454343	0	55.72383073	58.39643653
g__Luteococcus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Microlunatus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Propionibacterium	0	0.712694878	0	2.271714922	0	0	0.08908686	0	0.04454343	0	55.72383073	58.39643653
s__acnes	0	0.668151448	0	2.271714922	0	0	0.08908686	0	0.04454343	0	55.67928731	57.14922049
s__granulosum	0	0.04454343	0	0	0	0	0	0	0	0	0.04454343	1.247216036
g__Tessaracoccus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Pseudonocardiaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinomycetospora	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Pseudonocardia	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Sporichthyaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Sporichthya	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Streptomycetaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Kitasatospora	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Streptomyces	0	0	0	0	0	0	0	0	0	0	0	0
s__lanatus	0	0	0	0	0	0	0	0	0	0	0	0
s__mashuensis	0	0	0	0	0	0	0	0	0	0	0	0
s__scabrisporus	0	0	0	0	0	0	0	0	0	0	0	0
f__Streptosporangiaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Nonomuraea	0	0	0	0	0	0	0	0	0	0	0	0
s__roseoviolacea	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphaerisporangium	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermomonosporaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinomadura	0	0	0	0	0	0	0	0	0	0	0	0
s__vinacea	0	0	0	0	0	0	0	0	0	0	0	0
f__Tsukamurellaceae	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Tsukamurella	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343
o__Micrococcales	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Coriobacteriia	0	0	0	0	0	0.04454343	0	0	0	0	0	0
o__Coriobacteriales	0	0	0	0	0	0.04454343	0	0	0	0	0	0
f__Coriobacteriaceae	0	0	0	0	0	0.04454343	0	0	0	0	0	0
g__Adlercreutzia	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Atopobium	0	0	0	0	0	0	0	0	0	0	0	0
s__rimae	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Collinsella	0	0	0	0	0	0	0	0	0	0	0	0
s__aerofaciens	0	0	0	0	0	0	0	0	0	0	0	0
g__Slackia	0	0	0	0	0	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0
c__MB-A2-108	0	0	0	0	0	0	0	0	0	0	0	0.04454343
o__0319-7L14	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343
c__OPB41	0	0	0	0	0	0.13363029	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.13363029	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.13363029	0	0	0	0	0	0

unclassified	0	0	0	0	0	0.13363029	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.13363029	0	0	0	0	0	0
c__Rubrobacteria	0	0	0	0	0	0	0	0	0	0	0	0
o__Rubrobacterales	0	0	0	0	0	0	0	0	0	0	0	0
f__Rubrobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Rubrobacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Thermoleophilia	0	0	0	0	0	0	0	0	0	0	0	0.04454343
o__Gaiellales	0	0	0	0	0	0	0	0	0	0	0	0
f__Gaiellaceae	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__Solirubrobacterales	0	0	0	0	0	0	0	0	0	0	0	0.04454343
f__Conexibacteraceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Conexibacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Patulibacteraceae	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Solirubrobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Solirubrobacter	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
p__Armatimonadetes	0	0	0	0	0	0	0	0	0	0	0	0
c__Armatimonadia	0	0	0	0	0	0	0	0	0	0	0	0
o__Armatimonadales	0	0	0	0	0	0	0	0	0	0	0	0
f__Armatimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__C10-1	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__FW68	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Chthonomonadetes	0	0	0	0	0	0	0	0	0	0	0	0
o__Chthonomonadales	0	0	0	0	0	0	0	0	0	0	0	0
f__Chthonomonadaceae	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Fimbriimonadia	0	0	0	0	0	0	0	0	0	0	0	0
o__Fimbriimonadales	0	0	0	0	0	0	0	0	0	0	0	0
f__Fimbriimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Fimbriimonas	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__OP8S0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
p__BRC1	0	0	0	0	0	0	0	0	0	0	0	0
c__PRR-11	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
p__Bacteroidetes	0	0	0	0	0	15.18930958	0.13363029	0.712694878	0.846325167	0	0.489977728	0.178173719
c__Bacteroidia	0	0	0	0	0	15.18930958	0.04454343	0.712694878	0.801781737	0	0.356347439	0.04454343
o__Bacteroidales	0	0	0	0	0	15.18930958	0.04454343	0.712694878	0.801781737	0	0.356347439	0.04454343
f__Bacteroidaceae	0	0	0	0	0	3.251670379	0	0.222717149	0.311804009	0	0.13363029	0
g__Bacteroides	0	0	0	0	0	3.251670379	0	0.222717149	0.311804009	0	0.13363029	0
s__caccae	0	0	0	0	0	0	0	0.04454343	0	0	0	0
s__ovatus	0	0	0	0	0	3.251670379	0	0.08908686	0.267260579	0	0	0
s__uniformis	0	0	0	0	0	0	0	0.08908686	0.04454343	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.08908686	0
f__Paraprevotellaceae	0	0	0	0	0	0	0	0	0	0	0.08908686	0
g__Prevotella	0	0	0	0	0	0	0	0	0	0	0.08908686	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.08908686	0
g__YRC22	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Porphyromonadaceae	0	0	0	0	0	9.086859688	0	0	0.489977728	0	0.08908686	0.04454343
g__Porphyromonas	0	0	0	0	0	9.086859688	0	0	0.489977728	0	0	0.04454343
unclassified	0	0	0	0	0	9.086859688	0	0	0.489977728	0	0	0.04454343
g__Tannerella	0	0	0	0	0	0	0	0	0	0	0.08908686	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.08908686	0
f__Prevotellaceae	0	0	0	0	0	2.85077951	0.04454343	0.222717149	0	0	0.04454343	0
g__Prevotella	0	0	0	0	0	2.85077951	0.04454343	0.222717149	0	0	0.04454343	0
s__copri	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__melaninogenica	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__nanceiensis	0	0	0	0	0	0	0	0	0	0	0	0
s__ruminicola	0	0	0	0	0	0	0	0	0	0	0	0
s__stercorea	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	2.85077951	0	0.222717149	0	0	0	0
f__Rikenellaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Bivi28	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__S24-7	0	0	0	0	0	0	0	0.267260579	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.267260579	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.267260579	0	0	0	0
c__Cytophagia	0	0	0	0	0	0	0	0	0	0	0	0
o__Cytophagales	0	0	0	0	0	0	0	0	0	0	0	0
f__Cytophagaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Adhaeribacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Dyadobacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Hymenobacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodocytophaga	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Flavobacteriia	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0.08908686
o__Flavobacteriales	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0.08908686
f__Cryomorphaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Fluviicola	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Flavobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Algibacter	0	0	0	0	0	0	0	0	0	0	0	0
s__lectus	0	0	0	0	0	0	0	0	0	0	0	0
g__Capnocytophaga	0	0	0	0	0	0	0	0	0	0	0	0
s__ochracea	0	0	0	0	0	0	0	0	0	0	0	0
g__Flavobacterium	0	0	0	0	0	0	0	0	0	0	0	0
s__succinicans	0	0	0	0	0	0	0	0	0	0	0	0
g__Myroides	0	0	0	0	0	0	0	0	0	0	0	0
s__odoratimimus	0	0	0	0	0	0	0	0	0	0	0	0
f__Weeksellaceae	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0.08908686
g__Chryseobacterium	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0.04454343	0	0	0
g__Cloacibacterium	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Elizabethkingia	0	0	0	0	0	0	0	0	0	0	0	0
s__meningoseptica	0	0	0	0	0	0	0	0	0	0	0	0
g__Ornithobacterium	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Riemerella	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Wautersiella	0	0	0	0	0	0	0	0	0	0	0	0.08908686
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.08908686
g__Weeksella	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Saprospirae	0	0	0	0	0	0	0	0	0	0	0.13363029	0.04454343
o__Saprospirales	0	0	0	0	0	0	0	0	0	0	0.13363029	0.04454343
f__Chitinophagaceae	0	0	0	0	0	0	0	0	0	0	0.13363029	0.04454343
g__Chitinophaga	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__arvensicola	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Flavihumibacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Flavisolibacter	0	0	0	0	0	0	0	0	0	0	0.08908686	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.08908686	0
g__Niabella	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Niastella	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Sediminibacterium	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Segetibacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Terrimonas	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343
c__Sphingobacteriia	0	0	0	0	0	0	0.04454343	0	0	0	0	0
o__Sphingobacteriales	0	0	0	0	0	0	0.04454343	0	0	0	0	0
f__Sphingobacteriaceae	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Olivibacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Pedobacter	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__cryoconitis	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Sphingobacterium	0	0	0	0	0	0	0	0	0	0	0	0
s__faecium	0	0	0	0	0	0	0	0	0	0	0	0

s__mizutaii	0	0	0	0	0	0	0	0	0	0	0	0
s__multivorum	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
p__Chloroflexi	0	0	0	0	0	0	0.04454343	0	0	0	0	0
c__Anaerolineae	0	0	0	0	0	0	0	0	0	0	0	0
o__Caldilineales	0	0	0	0	0	0	0	0	0	0	0	0
f__Caldilineaceae	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__SBR1031	0	0	0	0	0	0	0	0	0	0	0	0
f__A4b	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__SJA-15	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__C0119	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Chloroflexi	0	0	0	0	0	0	0	0	0	0	0	0
o__AKIW781	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__Chloroflexales	0	0	0	0	0	0	0	0	0	0	0	0
f__FFCH7168	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__Roseiflexales	0	0	0	0	0	0	0	0	0	0	0	0
f__Roseiflexaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseiflexus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Ktedonobacteria	0	0	0	0	0	0	0	0	0	0	0	0
o__B12-WMSP1	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__Thermogemmatisporales	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermogemmatisporaceae	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__SHA-26	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__TK10	0	0	0	0	0	0	0	0	0	0	0	0
o__B07_WMSP1	0	0	0	0	0	0	0	0	0	0	0	0
f__FFCH4570	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Thermomicrobia	0	0	0	0	0	0	0.04454343	0	0	0	0	0
o__JG30-KF-CM45	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0
p__Cyanobacteria	0	0	0	0	0	0	0	0	0	0	0	0
c__4C0d-2	0	0	0	0	0	0	0	0	0	0	0	0
o__MLE1-12	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Chloroplast	0	0	0	0	0	0	0	0	0	0	0	0
o__Stramenopiles	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__Streptophyta	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
p__FBP	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0
p__Firmicutes	98.97550111	8.46325167	100	97.68374165	100	12.60579065	92.69487751	98.53006682	81.38084633	100	41.02449889	11.80400891
c__Bacilli	98.88641425	8.106904232	100	97.68374165	100	0.979955457	92.47216036	95.18930958	51.18040089	100	39.91091314	5.968819599
o__Bacillales	98.88641425	5.211581292	100	97.68374165	27.88418708	0.979955457	92.3830735	0.04454343	51.13585746	100	39.28730512	5.65701559
f__Alicyclobacillaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Alicyclobacillus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Bacillaceae	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0.04454343	0
g__Alkalibacillus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Anoxybacillus	0	0	0	0	0	0	0	0	0	0	0	0
s__kestanbolensis	0	0	0	0	0	0	0	0	0	0	0	0
g__Bacillus	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0.04454343	0
s__acidicola	0	0	0	0	0	0	0	0	0	0	0	0
s__flexus	0	0	0	0	0	0	0	0	0	0	0	0
s__foraminis	0	0	0	0	0	0	0	0	0	0	0	0
s__horikoshii	0	0	0	0	0	0	0	0	0	0	0	0
s__muralis	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__trypoxylicola	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.04454343	0	0	0	0	0.04454343	0	0	0
g__Geobacillus	0	0	0	0	0	0	0	0	0	0	0	0
s__vulcani	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Marinibacillus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Marinococcus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Exiguobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Exiguobacterium	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Paenibacillaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Ammoniphilus	0	0	0	0	0	0	0	0	0	0	0	0
s__oxalaticus	0	0	0	0	0	0	0	0	0	0	0	0
g__Paenibacillus	0	0	0	0	0	0	0	0	0	0	0	0
s__amylolyticus	0	0	0	0	0	0	0	0	0	0	0	0
s__edaphicus	0	0	0	0	0	0	0	0	0	0	0	0
s__stellifer	0	0	0	0	0	0	0	0	0	0	0	0
f__Planococcaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Lysinibacillus	0	0	0	0	0	0	0	0	0	0	0	0
s__boronitolerans	0	0	0	0	0	0	0	0	0	0	0	0
g__Planomicrobium	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Sporosarcina	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Sporolactobacillaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Sporolactobacillus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Staphylococcaceae	98.88641425	5.211581292	100	97.63919822	27.88418708	0.979955457	92.3830735	0.04454343	51.09131403	100	39.24276169	5.65701559
g__Jeotgalicoccus	0	0	0	0	0	0	0	0	0	0	0	0.08908686
s__psychrophilus	0	0	0	0	0	0	0	0	0	0	0	0.08908686
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Salinicoccus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Staphylococcus	98.88641425	5.211581292	100	97.63919822	27.88418708	0.979955457	92.3830735	0.04454343	51.09131403	100	39.24276169	5.567928731
s__aureus	97.9064588	0	100	97.28285078	27.79510022	0	0.08908686	0	49.08685969	100	0.04454343	0.04454343
s__epidermidis	0.757238307	5.167037862	0	0.178173719	0	0.757238307	0.08908686	0.04454343	0.04454343	0	38.6636971	5.211581292
s__equorum	0.04454343	0	0	0.13363029	0.04454343	0	0.445434298	0	0	0	0.04454343	0
s__haemolyticus	0.178173719	0.04454343	0	0.04454343	0.04454343	0.222717149	91.75946548	0	1.959910913	0	0.489977728	0.08908686
s__lugdunensis	0	0	0	0	0	0	0	0	0	0	0	0.222717149
s__pettenkoferi	0	0	0	0	0	0	0	0	0	0	0	0
s__sciuri	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermoactinomycetaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Planifilum	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__Gemellales	0	0	0	0	0	0	0	0	0	0	0.04454343	0.08908686
f__Gemellaceae	0	0	0	0	0	0	0	0	0	0	0.04454343	0.08908686
g__Gemella	0	0	0	0	0	0	0	0	0	0	0.04454343	0.08908686
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0.08908686
o__Lactobacillales	0	2.89532294	0	0	72.11581292	0	0.08908686	95.14476615	0.04454343	0	0.579064588	0.222717149
f__Aerococcaceae	0	2.89532294	0	0	0	0	0	0	0.04454343	0	0.04454343	0
g__Abiotrophia	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Aerococcus	0	0	0	0	0	0	0	0	0.04454343	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0
g__Alloiococcus	0	2.89532294	0	0	0	0	0	0	0	0	0.04454343	0
s__otitis	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	2.89532294	0	0	0	0	0	0	0	0	0.04454343	0
g__Facklamia	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Carnobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0.04454343

g__Carnobacterium	0	0	0	0	0	0	0	0	0	0	0	0
s__viridans	0	0	0	0	0	0	0	0	0	0	0	0
g__Desemzia	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Granulicatella	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343
f__Enterococcaceae	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Enterococcus	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__casseliflavus	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__cecorum	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Lactobacillaceae	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Lactobacillus	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__delbrueckii	0	0	0	0	0	0	0	0	0	0	0	0
s__helveticus	0	0	0	0	0	0	0	0	0	0	0	0
s__manihotivorans	0	0	0	0	0	0	0	0	0	0	0	0
s__salivarius	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0
f__Leuconostocaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Leuconostoc	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Streptococcaceae	0	0	0	0	72.11581292	0	0	95.14476615	0	0	0.534521158	0.178173719
g__Lactococcus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Streptococcus	0	0	0	0	72.11581292	0	0	95.14476615	0	0	0.534521158	0.178173719
s__agalactiae	0	0	0	0	72.11581292	0	0	0.04454343	0	0	0	0
s__anginosus	0	0	0	0	0	0	0	95.10022272	0	0	0	0
s__equi	0	0	0	0	0	0	0	0	0	0	0	0
s__infantis	0	0	0	0	0	0	0	0	0	0	0.356347439	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.178173719	0.178173719
o__Turicibacterales	0	0	0	0	0	0	0	0	0	0	0	0
f__Turicibacteraceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Turicibacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Clostridia	0.08908686	0.356347439	0	0	0	11.62583519	0.222717149	3.251670379	30.11135857	0	1.069042316	5.83518931
o__Clostridiales	0.08908686	0.356347439	0	0	0	11.62583519	0.222717149	3.251670379	30.11135857	0	1.069042316	5.83518931
f__Christensenellaceae	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Clostridiaceae	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__02d06	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Caloramator	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Clostridium	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Oxobacter	0	0	0	0	0	0	0.04454343	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0
f__Dehalobacteriaceae	0	0	0	0	0	0	0	0.04454343	0	0	0	0
g__Dehalobacterium	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0
f__Eubacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Anaerofustis	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Lachnospiraceae	0.04454343	0	0	0	0	0	0.08908686	1.559020045	0.489977728	0	0.356347439	0
g__Blautia	0	0	0	0	0	0	0	0.178173719	0.08908686	0	0	0
s__obeum	0	0	0	0	0	0	0	0.178173719	0.08908686	0	0	0
s__producta	0	0	0	0	0	0	0	0	0	0	0	0
g__Coprococcus	0.04454343	0	0	0	0	0	0	0.489977728	0.04454343	0	0.08908686	0
s__catus	0	0	0	0	0	0	0	0.04454343	0	0	0.08908686	0
s__eutactus	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0.04454343	0	0	0	0	0	0	0.400890869	0.04454343	0	0	0
g__Dorea	0	0	0	0	0	0	0	0.08908686	0	0	0	0
s__formicigenerans	0	0	0	0	0	0	0	0.08908686	0	0	0	0
g__Lachnobacterium	0	0	0	0	0	0	0.04454343	0.222717149	0.08908686	0	0.08908686	0
unclassified	0	0	0	0	0	0	0.04454343	0.222717149	0.08908686	0	0.08908686	0
g__Moryella	0	0	0	0	0	0	0.04454343	0.13363029	0	0	0	0
s__indoligenes	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0.13363029	0	0	0	0
g__Roseburia	0	0	0	0	0	0	0	0.08908686	0	0	0.08908686	0
s__faecis	0	0	0	0	0	0	0	0.08908686	0	0	0.08908686	0
g__Ruminococcus	0	0	0	0	0	0	0	0.311804009	0.267260579	0	0.08908686	0
s__gnavus	0	0	0	0	0	0	0	0.08908686	0.13363029	0	0.08908686	0
s__torques	0	0	0	0	0	0	0	0.222717149	0.13363029	0	0	0
g__Shuttleworthia	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.04454343	0	0	0	0
f__Mogibacteriaceae	0	0	0	0	0	0.178173719	0	0.08908686	0.178173719	0	0	0
g__Mogibacterium	0	0	0	0	0	0.13363029	0	0.04454343	0.13363029	0	0	0
unclassified	0	0	0	0	0	0.13363029	0	0.04454343	0.13363029	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0.04454343	0.04454343	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0.04454343	0.04454343	0	0	0
f__Peptococcaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Peptococcus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__WCHB1-84	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Peptostreptococcaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Filifactor	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Peptostreptococcus	0	0	0	0	0	0	0	0	0	0	0	0
s__anaerobius	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Ruminococcaceae	0	0	0	0	0	0	0.08908686	1.425389755	0.267260579	0	0.400890869	0
g__Faecalibacterium	0	0	0	0	0	0	0	0.712694878	0.08908686	0	0.04454343	0
s__prausnitzii	0	0	0	0	0	0	0	0.712694878	0.08908686	0	0.04454343	0
g__Oscillospira	0	0	0	0	0	0	0	0.222717149	0.04454343	0	0	0
unclassified	0	0	0	0	0	0	0	0.222717149	0.04454343	0	0	0
g__Ruminococcus	0	0	0	0	0	0	0.08908686	0.356347439	0.13363029	0	0.178173719	0
s__bromii	0	0	0	0	0	0	0	0.222717149	0	0	0.04454343	0
s__callidus	0	0	0	0	0	0	0	0.04454343	0	0	0	0
unclassified	0	0	0	0	0	0	0.08908686	0.08908686	0.13363029	0	0.13363029	0
unclassified	0	0	0	0	0	0	0	0.13363029	0	0	0.178173719	0
unclassified	0	0	0	0	0	0	0	0.13363029	0	0	0.178173719	0
f__Symbiobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Symbiobacterium	0	0	0	0	0	0	0	0	0	0	0	0
s__thermophilum	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Tissierellaceae	0.04454343	0.356347439	0	0	0	9.042316258	0	0.13363029	29.08685969	0	0.08908686	5.70155902
g__1-68	0	0	0	0	0	0.222717149	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.222717149	0	0	0	0	0	0
g__Anaerococcus	0	0.13363029	0	0	0	5.300668151	0	0.08908686	18.08463252	0	0	3.652561247
unclassified	0	0.13363029	0	0	0	5.300668151	0	0.08908686	18.08463252	0	0	3.652561247
g__Finegoldia	0	0.04454343	0	0	0	0.311804009	0	0	5.300668151	0	0	0.267260579
unclassified	0	0.04454343	0	0	0	0.311804009	0	0	5.300668151	0	0	0.267260579
g__GW-34	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Gallicola	0	0	0	0	0	0	0	0	0.356347439	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.356347439	0	0	0
g__Parvimonas	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Peptoniphilus	0	0.178173719	0	0	0	2.9844098	0	0.04454343	4.231625835	0	0.08908686	1.781737194
unclassified	0	0.178173719	0	0	0	2.9844098	0	0.04454343	4.231625835	0	0.08908686	1.781737194
g__WAL_1855D	0.04454343	0	0	0	0	0.178173719	0	0	1.113585746	0	0	0
unclassified	0.04454343	0	0	0	0	0.178173719	0	0	1.113585746	0	0	0
g__ph2	0	0	0	0	0	0.04454343	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.04454343	0	0	0	0	0	0
f__Veillonellaceae	0	0	0	0	0	2.405345212	0	0	0.08908686	0	0.222717149	0.13363029
g__Dialister	0	0	0	0	0	2.405345212	0	0	0.08908686	0	0	0.13363029
unclassified	0	0	0	0	0	2.405345212	0	0	0.08908686	0	0	0.13363029
g__Megasphaera	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Pelosinus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Propionispora	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Selenomonas	0	0	0	0	0	0	0	0	0	0	0	0
s__noxia	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Succiniclasticum	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Veillonella	0	0	0	0	0	0	0	0	0	0	0.222717149	0
s__dispar	0	0	0	0	0	0	0	0	0	0	0.222717149	0
s__parvula	0	0	0	0	0	0	0	0	0	0	0	0
c__Erysipelotrichi	0	0	0	0	0	0	0	0	0.08908686	0.08908686	0.04454343	0
o__Erysipelotrichales	0	0	0	0	0	0	0	0	0.08908686	0.08908686	0.04454343	0
f__Erysipelotrichaceae	0	0	0	0	0	0	0	0	0.08908686	0.08908686	0.04454343	0
g__Bulleidia	0	0	0	0	0	0	0	0	0	0	0	0
s__moorei	0	0	0	0	0	0	0	0	0	0	0	0
g__Eubacterium	0	0	0	0	0	0	0	0	0.08908686	0.08908686	0.04454343	0
s__biforme	0	0	0	0	0	0	0	0	0.08908686	0.08908686	0.04454343	0
p__Fusobacteria	0	0	0	0	0	0	70.77951002	0	0	0	0	0
c__Fusobacteriia	0	0	0	0	0	0	70.77951002	0	0	0	0	0
o__Fusobacteriales	0	0	0	0	0	0	70.77951002	0	0	0	0	0
f__Fusobacteriaceae	0	0	0	0	0	0	70.77951002	0	0	0	0	0
g__Fusobacterium	0	0	0	0	0	0	70.77951002	0	0	0	0	0
unclassified	0	0	0	0	0	0	70.77951002	0	0	0	0	0
f__Leptotrichiaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Leptotrichia	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Streptobacillus	0	0	0	0	0	0	0	0	0	0	0	0
s__moniliformis	0	0	0	0	0	0	0	0	0	0	0	0
p__Gemmatimonadetes	0	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343
c__Gemm-1	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0

unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Gemmatimonadetes	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	
o__Ellin5290	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
o__Gemmatimonadales	0	0	0	0	0	0	0	0	0	0.04454343	0.04454343	
f__Ellin5301	0	0	0	0	0	0	0	0	0	0	0.04454343	
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	
unclassified	0	0	0	0	0	0	0	0	0	0.04454343	0	
o__KD8-87	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
o__N1423WL	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
p__MVP-21	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
p__Nitrospirae	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	
c__Nitrospira	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	
o__Nitrospirales	0	0.04454343	0	0	0	0	0	0	0.04454343	0	0	
f__Nitrospiraceae	0	0.04454343	0	0	0	0	0	0	0	0	0	
g__Nitrospira	0	0.04454343	0	0	0	0	0	0	0	0	0	
unclassified	0	0.04454343	0	0	0	0	0	0	0	0	0	
f__Thermodesulfovibrionaceae	0	0	0	0	0	0	0	0	0.04454343	0	0	
g__Candidatus_Magnetoovum	0	0	0	0	0	0	0	0	0.04454343	0	0	
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	
p__OD1	0	0	0	0	0	0	0	0	0	0	0	
c__ZB2	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
p__OP3	0	0	0	0	0	0	0	0	0	0	0	
c__koll11	0	0	0	0	0	0	0	0	0	0	0	
o__GIF10	0	0	0	0	0	0	0	0	0	0	0	
f__kpj58rc	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
p__Planctomycetes	0	0	0	0	0	0	0	0	0	0	0	
c__Phycisphaerae	0	0	0	0	0	0	0	0	0	0	0	
o__WD2101	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
c__Planctomycetia	0	0	0	0	0	0	0	0	0	0	0	
o__Gemmatales	0	0	0	0	0	0	0	0	0	0	0	
f__Gemmataceae	0	0	0	0	0	0	0	0	0	0	0	
g__Gemmata	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
f__Isosphaeraceae	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
p__Proteobacteria	0.757238307	0.04454343	0	0	0	0.04454343	6.726057906	0	0.04454343	0	1.603563474	1.648106904
c__Alphaproteobacteria	0	0	0	0	0	0	0.04454343	0	0	0	0	0.08908686
o__Caulobacterales	0	0	0	0	0	0	0	0	0	0	0	0.04454343
f__Caulobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Brevundimonas	0	0	0	0	0	0	0	0	0	0	0	0.04454343
s__diminuta	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Phenylobacterium	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
o__Ellin329	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
o__Rhizobiales	0	0	0	0	0	0	0	0	0	0	0	
f__Aurantimonadaceae	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
f__Bartonellaceae	0	0	0	0	0	0	0	0	0	0	0	
g__Bartonella	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
f__Beijerinckiaceae	0	0	0	0	0	0	0	0	0	0	0	
g__Methylocella	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
f__Bradyrhizobiaceae	0	0	0	0	0	0	0	0	0	0	0	
g__Balneimonas	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
g__Bosea	0	0	0	0	0	0	0	0	0	0	0	
s__genosp.	0	0	0	0	0	0	0	0	0	0	0	
f__Hyphomicrobiaceae	0	0	0	0	0	0	0	0	0	0	0	
g__Hyphomicrobium	0	0	0	0	0	0	0	0	0	0	0	
s__sulfonivorans	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
g__Rhodoplanes	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
f__Methylobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	
g__Methylobacterium	0	0	0	0	0	0	0	0	0	0	0	
s__komagatae	0	0	0	0	0	0	0	0	0	0	0	
f__Phyllobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	
g__Mesorhizobium	0	0	0	0	0	0	0	0	0	0	0	
s__huakuii	0	0	0	0	0	0	0	0	0	0	0	
g__Nitratireductor	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
f__Xanthobacteraceae	0	0	0	0	0	0	0	0	0	0	0	
g__Blastochloris	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
o__Rhodobacterales	0	0	0	0	0	0	0	0	0	0	0	
f__Rhodobacteraceae	0	0	0	0	0	0	0	0	0	0	0	
g__Rubellimicrobium	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
o__Rhodospirillales	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	
f__Acetobacteraceae	0	0	0	0	0	0	0.04454343	0	0	0	0.04454343	
g__Acetobacter	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
g__Acidisphaera	0	0	0	0	0	0	0	0	0	0	0.04454343	
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	
g__Acidocella	0	0	0	0	0	0	0.04454343	0	0	0	0	
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	
g__Roseococcus	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
g__Roseomonas	0	0	0	0	0	0	0	0	0	0	0	
s__mucosa	0	0	0	0	0	0	0	0	0	0	0	
g__Swaminathania	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
f__Rhodospirillaceae	0	0	0	0	0	0	0	0	0	0	0	
g__Oleomonas	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
o__Sphingomonadales	0	0	0	0	0	0	0	0	0	0	0	
f__Sphingomonadaceae	0	0	0	0	0	0	0	0	0	0	0	
g__Kaistobacter	0	0	0	0	0	0	0	0	0	0	0	
unclassified	0	0	0	0	0	0	0	0	0	0	0	
g__Novosphingobium	0	0	0	0	0	0	0	0	0	0	0	
s__resinovorum	0	0	0	0	0	0	0	0	0	0	0	
g__Sphingobium	0	0	0	0	0	0	0	0	0	0	0	
s__yanoikuyae	0	0	0	0	0	0	0	0	0	0	0	
g__Sphingomonas	0	0	0	0	0	0	0	0	0	0	0	
s__azotifigens	0	0	0	0	0	0	0	0	0	0	0	
s__echinoides	0	0	0	0	0	0	0	0	0	0	0	
s__wittichii	0	0	0	0	0	0	0	0	0	0	0	
s__yabuuchiae	0	0	0	0	0	0	0	0	0	0	0	
c__Betaproteobacteria	0.178173719	0	0	0	0	0	0.712694878	0	0.04454343	0	0.08908686	1.113585746
o__A21b	0	0	0	0	0	0	0	0	0	0	0	0
f__EB1003	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__Burkholderiales	0.178173719	0	0	0	0	0	0.712694878	0	0.04454343	0	0.04454343	0.178173719
f__Alcaligenaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Achromobacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Denitrobacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Oligella	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Tetrathiobacter	0	0	0	0	0	0	0	0	0	0	0	0
s__kashmirensis	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0

f__Burkholderiaceae	0.08908686	0	0	0	0	0	0.13363029	0	0	0	0.04454343	0
g__Burkholderia	0.08908686	0	0	0	0	0	0.13363029	0	0	0	0	0
s__andropogonis	0	0	0	0	0	0	0	0	0	0	0	0
s__bryophila	0	0	0	0	0	0	0	0	0	0	0	0
s__graminis	0	0	0	0	0	0	0	0	0	0	0	0
s__tuberum	0.08908686	0	0	0	0	0	0.08908686	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Lautropia	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Salinispora	0	0	0	0	0	0	0	0	0	0	0	0
s__tropica	0	0	0	0	0	0	0	0	0	0	0	0
f__Comamonadaceae	0	0	0	0	0	0	0	0	0.04454343	0	0	0.04454343
g__Acidovorax	0	0	0	0	0	0	0	0	0	0	0	0
s__delafieldii	0	0	0	0	0	0	0	0	0	0	0	0
g__Alicycliphilus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Aquabacterium	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Azohydromonas	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Comamonas	0	0	0	0	0	0	0	0	0	0	0	0.04454343
s__terrigena	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Delftia	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Diaphorobacter	0	0	0	0	0	0	0	0	0.04454343	0	0	0
unclassified	0	0	0	0	0	0	0	0	0.04454343	0	0	0
g__Giesbergeria	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Hylemonella	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Leptothrix	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Methylibium	0	0	0	0	0	0	0	0	0	0	0	0
s__petroleiphilum	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Paucibacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Pelomonas	0	0	0	0	0	0	0	0	0	0	0	0
s__puraquae	0	0	0	0	0	0	0	0	0	0	0	0
g__Ramlibacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Rubrivivax	0	0	0	0	0	0	0	0	0	0	0	0
s__gelatinosus	0	0	0	0	0	0	0	0	0	0	0	0
g__Schlegelella	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Tepidimonas	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Variovorax	0	0	0	0	0	0	0	0	0	0	0	0
s__paradoxus	0	0	0	0	0	0	0	0	0	0	0	0
f__Oxalobacteraceae	0.08908686	0	0	0	0	0	0.579064588	0	0	0	0	0.13363029
g__Collimonas	0	0	0	0	0	0	0	0	0	0	0	0.13363029
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.13363029
g__Cupriavidus	0	0	0	0	0	0	0	0	0	0	0	0
s__gilardii	0	0	0	0	0	0	0	0	0	0	0	0
g__Herbaspirillum	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Herminiimonas	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Janthinobacterium	0	0	0	0	0	0	0	0	0	0	0	0
s__lividum	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Oxalobacter	0	0	0	0	0	0	0	0	0	0	0	0
s__formigenes	0	0	0	0	0	0	0	0	0	0	0	0
g__Polynucleobacter	0	0	0	0	0	0	0	0	0	0	0	0
s__cosmopolitanus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.08908686	0	0	0	0	0	0.579064588	0	0	0	0	0
unclassified	0.08908686	0	0	0	0	0	0.579064588	0	0	0	0	0
o__Ellin6067	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__MND1	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__Neisseriales	0	0	0	0	0	0	0	0	0	0	0.04454343	0.935412027
f__Neisseriaceae	0	0	0	0	0	0	0	0	0	0	0.04454343	0.935412027
g__Aquitalea	0	0	0	0	0	0	0	0	0	0	0	0
s__magnusonii	0	0	0	0	0	0	0	0	0	0	0	0
g__Eikenella	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Kingella	0	0	0	0	0	0	0	0	0	0	0	0.04454343
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04454343
g__Microvirgula	0	0	0	0	0	0	0	0	0	0	0	0
s__aerodenitrificans	0	0	0	0	0	0	0	0	0	0	0	0
g__Neisseria	0	0	0	0	0	0	0	0	0	0	0.04454343	0.579064588
s__cinerea	0	0	0	0	0	0	0	0	0	0	0	0
s__subflava	0	0	0	0	0	0	0	0	0	0	0.04454343	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.579064588
g__Vitreoscilla	0	0	0	0	0	0	0	0	0	0	0	0.311804009
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.311804009
o__Rhodocyclales	0	0	0	0	0	0	0	0	0	0	0	0
f__Rhodocyclaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Azospira	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Dok59	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Methyloversatilis	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Propionivibrio	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Zoogloea	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__SBla14	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__SC-I-84	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Deltaproteobacteria	0	0	0	0	0	0	0	0	0	0	0	0
o__Desulfovibrionales	0	0	0	0	0	0	0	0	0	0	0	0
f__Desulfovibrionaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Desulfovibrio	0	0	0	0	0	0	0	0	0	0	0	0
s__cavernae	0	0	0	0	0	0	0	0	0	0	0	0
o__FAC87	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__Mil246	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__Myxococcales	0	0	0	0	0	0	0	0	0	0	0	0
f__Cystobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Cystobacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Haliangiaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Haliangium	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Myxococcaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Anaeromyxobacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__SAR324	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__Syntrophobacterales	0	0	0	0	0	0	0	0	0	0	0	0
f__Syntrophobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Syntrophobacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Epsilonproteobacteria	0	0	0	0	0	0	0.04454343	0	0	0	0	0
o__Campylobacterales	0	0	0	0	0	0	0.04454343	0	0	0	0	0
f__Campylobacteraceae	0	0	0	0	0	0	0.04454343	0	0	0	0	0
g__Campylobacter	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__rectus	0	0	0	0	0	0	0	0	0	0	0	0
s__ureolyticus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0.04454343	0	0	0	0	0
f__Helicobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Helicobacter	0	0	0	0	0	0	0	0	0	0	0	0
s__pylori	0	0	0	0	0	0	0	0	0	0	0	0
o__Nautiliales	0	0	0	0	0	0	0	0	0	0	0	0
f__Nautiliaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Nautilia	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Gammaproteobacteria	0.579064588	0.04454343	0	0	0	0	5.968819599	0	0	0	1.514476615	0.445434298
o__Alteromonadales	0	0	0	0	0	0	0	0	0	0	0	0
f__Shewanellaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Shewanella	0	0	0	0	0	0	0	0	0	0	0	0
s__pacifica	0	0	0	0	0	0	0	0	0	0	0	0
o__Enterobacteriales	0	0	0	0	0	0	0.08908686	0	0	0	0	0
f__Enterobacteriaceae	0	0	0	0	0	0	0.08908686	0	0	0	0	0
g__Citrobacter	0	0	0	0	0	0	0	0	0	0	0	0

unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Enterobacter	0	0	0	0	0	0	0	0	0	0	0	0
s__cowanii	0	0	0	0	0	0	0	0	0	0	0	0
g__Erwinia	0	0	0	0	0	0	0	0	0	0	0	0
s__dispersa	0	0	0	0	0	0	0	0	0	0	0	0
g__Klebsiella	0	0	0	0	0	0	0.08908686	0	0	0	0	0
s__oxytoca	0	0	0	0	0	0	0.08908686	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Salmonella	0	0	0	0	0	0	0	0	0	0	0	0
s__enterica	0	0	0	0	0	0	0	0	0	0	0	0
o__Legionellales	0	0	0	0	0	0	0	0	0	0	0	0
f__Coxiellaceae	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Legionellaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Legionella	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__Oceanospirillales	0	0	0	0	0	0	0	0	0	0	0	0
f__Halomonadaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Halomonas	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Oceanospirillaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Marinomonas	0	0	0	0	0	0	0	0	0	0	0	0
s__primoryensis	0	0	0	0	0	0	0	0	0	0	0	0
o__Pasteurellales	0	0	0	0	0	0	0	0	0	0	0	0
f__Pasteurellaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinobacillus	0	0	0	0	0	0	0	0	0	0	0	0
s__parahaemolyticus	0	0	0	0	0	0	0	0	0	0	0	0
g__Haemophilus	0	0	0	0	0	0	0	0	0	0	0	0
s__influenzae	0	0	0	0	0	0	0	0	0	0	0	0
s__parainfluenzae	0	0	0	0	0	0	0	0	0	0	0	0
o__Pseudomonadales	0	0	0	0	0	0	0.13363029	0	0	0	0.04454343	0
f__Moraxellaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Acinetobacter	0	0	0	0	0	0	0	0	0	0	0	0
s__guillouiae	0	0	0	0	0	0	0	0	0	0	0	0
s__lwoffii	0	0	0	0	0	0	0	0	0	0	0	0
s__rhizosphaerae	0	0	0	0	0	0	0	0	0	0	0	0
s__schindleri	0	0	0	0	0	0	0	0	0	0	0	0
s__venetianus	0	0	0	0	0	0	0	0	0	0	0	0
g__Alkanindiges	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Enhydrobacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Moraxella	0	0	0	0	0	0	0	0	0	0	0	0
s__ovis	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Pseudomonadaceae	0	0	0	0	0	0	0.13363029	0	0	0	0.04454343	0
g__Pseudomonas	0	0	0	0	0	0	0.13363029	0	0	0	0.04454343	0
s__alcaligenes	0	0	0	0	0	0	0	0	0	0	0	0
s__fragi	0	0	0	0	0	0	0.08908686	0	0	0	0	0
s__umsongensis	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__veronii	0	0	0	0	0	0	0.04454343	0	0	0	0	0
s__viridiflava	0	0	0	0	0	0	0	0	0	0	0	0
o__Xanthomonadales	0.579064588	0.04454343	0	0	0	0	5.74610245	0	0	0	1.469933185	0.445434298
f__Sinobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Hydrocarboniphaga	0	0	0	0	0	0	0	0	0	0	0	0
s__effusa	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
f__Xanthomonadaceae	0.579064588	0.04454343	0	0	0	0	5.74610245	0	0	0	1.469933185	0.445434298
g__Dokdonella	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Dyella	0.08908686	0	0	0	0	0	0.979955457	0	0	0	0.222717149	0
s__ginsengisoli	0.08908686	0	0	0	0	0	0.979955457	0	0	0	0.222717149	0
g__Luteimonas	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Lysobacter	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Pseudoxanthomonas	0	0	0	0	0	0	0	0	0	0	0	0
s__mexicana	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodanobacter	0.489977728	0.04454343	0	0	0	0	4.766146993	0	0	0	1.202672606	0.445434298
s__lindaniclasticus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.489977728	0.04454343	0	0	0	0	4.766146993	0	0	0	1.202672606	0.445434298
g__Stenotrophomonas	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__acidaminiphila	0	0	0	0	0	0	0	0	0	0	0	0
s__geniculata	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__retroflexus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermomonas	0	0	0	0	0	0	0	0	0	0	0	0
s__fusca	0	0	0	0	0	0	0	0	0	0	0	0
g__Xanthomonas	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
p__Spirochaetes	0	0	0	0	0	0	0	0.08908686	0	0	0	0
c__Spirochaetes	0	0	0	0	0	0	0	0.08908686	0	0	0	0
o__Borreliales	0	0	0	0	0	0	0	0.08908686	0	0	0	0
f__Borreliaceae	0	0	0	0	0	0	0	0.08908686	0	0	0	0
g__Spironema	0	0	0	0	0	0	0	0.08908686	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.08908686	0	0	0	0
o__Spirochaetales	0	0	0	0	0	0	0	0	0	0	0	0
f__Spirochaetaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Treponema	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
p__Synergistetes	0	0	0	0	0	0	0	0	0	0	0	0
c__Synergistia	0	0	0	0	0	0	0	0	0	0	0	0
o__Synergistales	0	0	0	0	0	0	0	0	0	0	0	0
f__Dethiosulfovibrionaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Pyramidobacter	0	0	0	0	0	0	0	0	0	0	0	0
s__piscolens	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermovirgaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermovirga	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
p__TM7	0	0	0	0	0	0	0	0	0	0	0	0
c__TM7-1	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__TM7-3	0	0	0	0	0	0	0	0	0	0	0	0
o__EW055	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
p__Tenericutes	0	0	0	0	0	0	0	0	0	0	0	0
c__Mollicutes	0	0	0	0	0	0	0	0	0	0	0	0
o__RF39	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
p__Thermi	0	0	0	0	0	0	0	0	0	0	0.04454343	0
c__Deinococci	0	0	0	0	0	0	0	0	0	0	0.04454343	0
o__Deinococcales	0	0	0	0	0	0	0	0	0	0	0.04454343	0
f__Deinococcaceae	0	0	0	0	0	0	0	0	0	0	0.04454343	0
g__Deinococcus	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__alpinitundrae	0	0	0	0	0	0	0	0	0	0	0.04454343	0
s__aquatilis	0	0	0	0	0	0	0	0	0	0	0	0
s__geothermalis	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
o__Thermales	0	0	0	0	0	0	0	0	0	0	0	0
f__Thermaceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermus	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
p__Verrucomicrobia	0	0	0	0	0	0	0	0	0	0	0	0
c__Pedosphaerae	0	0	0	0	0	0	0	0	0	0	0	0
o__Pedosphaerales	0	0	0	0	0	0	0	0	0	0	0	0
f__Pedosphaeraceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Pedosphaera	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
c__Spartobacteria	0	0	0	0	0	0	0	0	0	0	0	0
o__Chthoniobacterales	0	0	0	0	0	0	0	0	0	0	0	0
f__Chthoniobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0
g__Ellin506	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
p__WPS-2	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0
Total Number of Reads	16626	40512	44189	30195	43401	29072	3002	17015	23635	24943	3685	14156

CHAPTER THREE: Bacterial Etiology and Risk Factors Associated with Cellulitis and Purulent Skin Abscesses in Military Trainees

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The work presented in this chapter is the sole work of R.C. Johnson with the following exceptions: abscess/cellulitis cultures were processed by Martin Army Community Hospital microbiology laboratory; study oversight at Fort Benning provided M.W. Ellis, E.V. Millar, and C.D. Schlett; sample acquisition provided by J.B. Lanier; risk factor assessment performed by C.D. Schlett, E.V. Millar, D. Mor; pulsed-field gel electrophoresis and antibiotic susceptibility testing performed by E. Elassal; ASO and DNase B titers performed by D.K. Bishop; full-length 16S rRNA sequencing performed by P.T. LaBreck; 454 sequencing performed by C.L. Redden and K.A. Bishop-Lilly.

ABSTRACT

Skin and soft-tissue infections (SSTIs) remain one of the most predominant bacterial infections seen in the hospital today. Certain populations, such as military personnel, are disproportionately affected by SSTIs. A recent investigation in our laboratory revealed that while purulent SSTIs in military infantry were primarily dominated by the Gram-positive pathogen *Staphylococcus aureus*, there were also a large

number of polymicrobial infections. Although *S. aureus* is associated with purulent SSTI, it is unclear to what degree this pathogen causes cellulitis. Furthermore, while broad risk factors associated with SSTI have been established, specific risk factors associated with either purulent (abscesses) or non-purulent (cellulitis) infections have not been thoroughly elucidated. To address these knowledge gaps, we enrolled 200 military trainees at Fort Benning who developed either cutaneous abscesses or cellulitis and assessed exposure to known SSTI risk factors. This analysis revealed that while most risk factors were not significantly different between the disease types, nasal colonization with MRSA was associated with abscess formation, while cellulitis development was statistically linked to prior blister formation and ethnicity. To investigate differences in microbial composition between the two SSTIs, we collected 18 swabs and 22 leading edge aspirates from individuals suffering from cutaneous abscess and cellulitis, respectively. Genomic DNA was extracted from all samples and the V1 to V3 region of the 16S rRNA gene was PCR amplified and sequenced using 454 high-throughput sequencing technology. Additionally, we collected relevant clinical information from the military trainees including anti-streptolysin O (ASO) and anti-DNase B titers. In agreement with our previous study, we found that while most of the purulent abscesses were primarily composed of *S. aureus*, mixed infections were common. Interestingly, the bacterial compositions of the cellulitis microbiomes were dramatically different from the purulent abscesses; bacteria from the Proteobacteria phylum predominated. These data emphasize important epidemiological and microbial differences between purulent and non-purulent SSTIs that should be considered when treating these complicated infections.

INTRODUCTION

Skin and soft-tissue infections (SSTIs) are among the most frequently observed infections in the ambulatory and hospital settings (72; 127; 226). In 2005 alone, approximately 14.2 million SSTI cases were reported in the United States; a 65% increase from 1997 (127). While severe SSTIs such as necrotizing fasciitis are routinely reported, the bulk of disease manifests as abscesses and cellulitis. In fact, cutaneous abscesses and cellulitis accounted for 95% of the observed SSTI increase from 1997 to 2005 (127). While numerous SSTI risk factors have been established in response to this increased prevalence, whether certain risk factors are specifically associated with either cutaneous abscess or cellulitis formation have yet to be determined.

Although SSTIs afflict millions of individuals world-wide, certain congregate populations, such as military service members, are at increased risk (36; 342). Indeed, there were roughly 62,000 ambulatory visits and 1,500 hospitalizations attributed to SSTIs in the military in 2010 (4). The alarming increase in SSTI prevalence in the military and general public is largely attributed to the emergence of community-associated methicillin-resistant *Staphylococcus aureus* (CA-MRSA) (148). In an era of drug resistant bacterial pathogens, such as CA-MRSA, bacterial culture and antibiotic susceptibility testing is imperative for proper treatment of SSTI. While CA-MRSA has been identified as the leading cause of most purulent SSTIs (203; 283), to what extent this pathogen causes cellulitis infections remains unknown.

Without a site to culture, bacterial etiology for non-purulent cellulitis has been historically unsuccessful. However, dogma suggests that cellulitis is caused by both *S.*

aureus and beta-hemolytic streptococci (BHS); the actual degree each pathogen contributes in unclear (117; 251; 295). Additionally, despite diverse sample collection methods (punch biopsy, needle aspirate and blood sample), a pathogen is isolated less than 30% of the time (71; 216; 235; 286). In other words, microbial diagnosis is undefined in more than 70% of all cellulitis cases. To further complicate matters, recent studies have shown that SSTIs, particularly purulent abscesses, can by polymicrobial in nature (144). The changing epidemiology and uncertainty of microbial etiology have exposed important SSTI knowledge gaps. Herein we report our findings from an epidemiological analysis to discern SSTI-specific risk factors as well as detailed characterization of the microbiomes of both purulent and non-purulent SSTI using a high-throughput sequencing strategy. Together, our data indicate that while abscess and cellulitis are both considered SSTIs, they represent clinically unique infections that may require individualized treatments.

MATERIALS AND METHODS

Study design and participants

We enrolled a total of 240 U.S. Army infantry trainees stationed at Fort Benning, GA; 40 were part of the microbiome portion of the study and 200 were utilized for SSTI risk factor assessment. The study population was all male, ages 17-39, and in good physical condition. Patient demographics for the 40 microbiome study participants are shown in Table 6 and Table 7. All military trainees enrolled were part of an ongoing research study aimed at elucidation of the epidemiology, etiology, immunology, and

economic burden of SSTIs in military trainees. The study was approved by the Uniformed Services University Infectious Disease Institutional Review Board.

Enrollment and data collection

Military trainees that presented to the Troop Medical Clinic (TMC) with an SSTI were enrolled in the study and placed into one of two groups contingent on infection type: cutaneous abscess or cellulitis group. While the cutaneous abscess group presented with an infection that required incision and drainage, the cellulitis group presented with diffuse inflammation of the skin with no purulent exudate. All participants were assessed for nasal colonization by *S. aureus* as previously described (144). Exclusion criteria included prior antibiotic administration within two weeks before initial presentation, infection on the face or associated with a surgical site, animal or human bite wound cellulitis, evidence or suspected bacteremia/sepsis/deep soft tissue infection, or any underlying condition such as neutropenia, vascular insufficiency or diabetes.

For the 18 microbiome participants with cutaneous abscess, the skin at the site of infection was sterilized with chlorhexidine prior to incision. Two swabs were then obtained from within the abscess cavity: one was sent for microbiological culture, and the other was used for microbiome analysis. For the 22 cellulitis infections, we obtained samples via needle aspiration using a 22-gauge needle attached to a 10 ml plastic syringe loaded with sterile phosphate buffered saline (PBS). The needle was inserted into the subcutaneous tissue of the leading edge of inflammation and 1.5 ml of PBS was slowly injected and then immediately aspirated. One half of the recovered PBS (approximately

Table 6. Purulent abscess patient information

Patient ID	Age / Race	Site of Infection	Abscess Culture	Area Erythema (initial/days 2-3/days 21-28)[a]	Body Site Colonization			
					Nose	Oropharynx	Perianal	Inguinal
1782	22/White	Hand	ND	ND	CNS	CNS	CNS	MSSA
1868	17/White	Elbow	MSSA	ND	MSSA	CNS	MSSA	CNS
1871	21/White	Elbow	Other[b]	ND	MRSA	NG	CNS	CNS
1876	18/White	Buttock	MRSA	8.5/-/0	CNS	CNS	MRSA	ND
1914	18/White	Foot	ND	ND	CNS	CNS	NC	CNS
1955	17/White	Lower Leg	MRSA	ND	CNS	NC	NC	NC
1957	17/Asian	Forearm	MRSA	ND	MSSA	MSSA	NC	NC
1983	18/White	Chest	ND	ND	CNS	CNS	NC	NC
2018	18/White	Foot	MRSA	ND	MSSA	MSSA	CNS	CNS
2058	26/White	Axilla	ND	ND	MSSA	CNS	NC	CNS
2067	22/White	Lower Leg	ND	42.5/-/0	MSSA	MSSA	CNS	CNS
2086	19/Asian	Forearm	ND	ND	CNS	CNS	NC	NC
2094	24/White	Knee	ND	ND	CNS	MSSA	NC	MSSA
2120	19/White	Axilla	ND	ND	MSSA	MSSA	NC	CNS
2152	19/Other	Axilla	ND	ND	MSSA	ND	NC	NC
2157	19/White	Hand	Other[b]	ND	NC	MSSA	NC	NC
2160	18/White	Foot	Other[b]	ND	MSSA	CNS	NC	NC
2202	18/White	Axilla	MRSA	ND	CNS	CNS	NC	CNS

Abbreviations and symbols: ND, not determined; NG, no growth; CNS, Coagulase-negative *Staphylococcus*; NC, not consented; MSSA, methicillin-sensitive *S. aureus*; MRSA, methicillin-resistant *S. aureus*

[a] Area measured in centimeters. A dash indicates no measurement taken.

[b] Indicates non-*S. aureus* bacterial growth.

Table 7. Cellulitis patient information

Patient ID	Age / Race	Site of Infection	ASO Titers[a] (Acute/Conv)	Anti-DNase B Titers[a] (Acute/Conv)	Aspirate Culture	Area Erythema (initial/days 2-3/days 21-28)[b]	Body Site Colonization				Subsequent abscess formation
							Nose	Oropharynx	Perianal	Inguinal	
1680	19/White	Foot	ND	ND	ND	203/144/0	MSSA	MSSA	NC	CNS	N
1739	17/White	Lower Leg	9/7	<95 /<95	NG	216/212.5/0	CNS	CNS	CNS	MSSA	N
1773	21/White	Forearm	**499**/**483**	<95/<95	NG	228/205/0	CNS	NG	MSSA	CNS	N
2055	18/White	Foot	**437**/**423**	<95/102	NG	405/240/0	CNS	CNS	NC	NC	N
2080	23/White	Foot	92/**324**	<95/<95	ND	-	MSSA	CNS	MSSA	MSSA	N
2083	18/White	Foot	**448**/NA	<95/NA	CNS	48/25/-	MSSA	CNS	MSSA	CNS	ND
2124	20/White	Foot	**220**/**206**	<95/<95	NG	115/110/0	MSSA	MSSA	MSSA	MSSA	N
2128	22/White	Elbow	52/47	<95/109	NG	228/144/0	MSSA	CNS	CNS	CNS	N
2129	22/White	Forearm	100/100	109/<95	NG	225/0/0	CNS	CNS	CNS	CNS	N
2171	24/White	Thigh	**439**/129	207/124	NG	238/84/0	MSSA	CNS	MSSA	MSSA	Y
2172	19/White	Foot	119/113	<95/<95	NG	115.5/116/0	MSSA	MSSA	CNS	CNS	N
2203	21/White	Foot	41/37	97/111	NG	-	MSSA	NG	NC	MSSA	N
2213	18/White	Knee	85/87	<95/<95	NG	289/-/0	MSSA	MSSA	MSSA	CNS	N
2250	24/White	Foot	58/62	<95/<95	NG	72.25/36/0	MSSA	CNS	NC	MSSA	N
2306	22/White	Foot	25/25	<95/<95	NG	38.25/0/0	CNS	CNS	NC	CNS	N
2326	23/White	Foot	**226**/**229**	100/289	NG	135/24/0	MSSA	MSSA	CNS	CNS	N
2367	20/White	Knee	**247**/**259**	<95/<95	NG	532/49/0	MSSA	MSSA	MSSA	MSSA	N
2423	21/White	Foot	92/86	103/<95	ND	36/30/0	NC	NC	NC	NC	N
2637	24/White	Elbow	10/12	<95/<95	NG	144/0/0	MSSA	MSSA	CNS	MSSA	N
2758	24/White	Arm, Elbow	13/<6	<95/<95	ND	-	MRSA	MRSA	MRSA	MRSA	N
2867	18/White	Thigh	147/138	<95/<95	NG	100/36/0	MSSA	MSSA	NC	NC	N
2913	18/White	Thigh	19/16	<95/<95	NG	90/0/0	CNS	CNS	CNS	CNS	N

Abbreviations and symbols: ND, not determined; NG, no growth; N, no; Y, yes; CNS, Coagulase-negative *Staphylococcus*; NC, not consented; MSSA, methicillin-sensitive *S. aureus*; MRSA, methicillin-resistant *S. aureus*

[a] ASO and DNase B titers are represented as IU/ml and U/ml, respectively. Normal ranges: ASO <200 IU/ml, DNase B <301 U/ml. Titers were measured upon initial admission to the TMC (acute) and at 12-14 days post admission (conv). Elevated titer levels are depicted in bold.

[b] Area measured in centimeters. A dash indicates no measurement taken.

0.5 ml) was immediately frozen at -80°C and sent for microbiome analysis. The remaining half was promptly sent for microbiological culture. Post aspiration, the patient underwent phlebotomy to obtain serum samples for immunological surveillance (acute samples) and was monitored for 21-28 days at which time a second phlebotomy was performed (convalescent samples).

In addition to infection culture analysis, additional swabs were simultaneously taken and used to assess carriage of *S. aureus* at various body sites including the oropharynx, inguinal, and perianal regions. Anatomical site colonization samples were cultured in enriched broth as previously described (77). Follow-up assessments at days 2-3 and 21-28 for all patients were conducted to monitor SSTI resolution.

For the 200 SSTI risk factor assessment participants (103 abscess, 97 cellulitis), pertinent medical and demographic information was collected. Additionally, the patients were issued a questionnaire to assess prior exposure to SSTI risk factors. Data from the questionnaire is shown in Table 8.

Microbiological and molecular analysis

Culture analyses for both cellulitis and abscess samples were conducted according to standard procedures at the Martin Army Community Hospital microbiology laboratory (78). *S. aureus* isolates were typed using pulsed-field gel electrophoresis (PFGE) and resistance/virulence determinants were assessed using PCR as previously described (82).

Serological analysis

Acute and convalescent blood samples were allowed to clot for a minimum of 30 minutes and serum was isolated by centrifugation at 2500 rpm for 15 minutes. Anti-

Table 8. Abscess and cellulitis risk factor assessment

	SSTI Cases (n=200)		
	Abscess Only (n=103)	Cellulitis Only (n=97)	P-Value[b]
Median Age, years (Range)	19 (18-21)	20 (18-22)	0.08
Ethnicity: White	74 (71.8)	83 (85.6)	0.02
Median (Range) No. of Weeks in Training at Enrollment	5 (3-8)	4 (2-7)	0.2
Season of Enrollment			0.59
Spring	21 (20.4)	21 (21.6)	
Summer	49 (47.6)	39 (40.2)	
Fall	22 (21.4)	21 (21.6)	
Winter	11 (10.7)	16 (16.5)	
Nasal Colonization with *S. aureus*	54 (52.4)	49 (50.5)	0.79
Nasal Colonization with MRSA[c]	24 (44.4)	24 (14.3)	0.002
Risk Factor: Past Year			
Admitted to a Hospital	5 (4.9)	4 (4.1)	0.79
Worked at a Hospital	4 (3.9)	2 (2.1)	0.68
Known or Suspected SSTI/MSSA Infection	7 (6.8)	6 (6.2)	0.85
Taken an Antibiotic in Past 6 mos.	18 (17.5)	10 (10.3)	0.14
Risk Factor: 3 mos. Prior to Fort Benning			
Contact with a Person with SSTI	4 (3.9)	2 (2.1)	0.68
Risk Factor: While at Fort Benning			
History of SSTI	1 (1)	3 (3.1)	0.36
Contact with a Person with SSTI	30 (29.1)	25 (25.8)	0.57
Abrasions/Cuts	57 (55.3)	50 (51.5)	0.59
Blister	44 (42.7)	59 (60.8)	0.01
Insect Bite	29 (28.2)	29 (29.9)	0.79
Risk Factor: Trainee Survey			
Do Not Wash Hands or Use Sanitizer	0 (0)	1 (1)	0.79
Do Not Shower Daily	0 (0)	0 (0)	0.79
Share Towels and Clothing	2 (1.9)	6 (6.2)	0.16
Share or Borrow Razors	1 (1)	1 (1)	1
Do Not Wash Towels	1 (1)	4 (4.1)	0.14
Do Not Wash PT Uniform	0 (0)	2 (2.1)	0.14
Do Not Wash ACU	0 (0)	2 (2.1)	0.14
Shave Body Parts Other than Face	17 (16.5)	18 (18.6)	0.73
Bunkmate/Battle Buddy had Skin/MRSA Infection	13 (12.6)	7 (7.2)	0.2
Sexual Contact in Past 6 mos. with Someone with SSTI	2 (1.9)	0 (0)	0.5

[a] Unless specified, the numbers in parenthesis correspond to the percentage of total individuals with either abscess or cellulitis.
[b] P-values calculated with chi square test. For counts less than 5, Fisher's exact test was used. P-values for median data were generated using the Wilcoxon rank-sum test.
[c] Numbers in parenthesis correspond to the percentage of total individuals that were nasal carriers of *S. aureus*

streptococcal DNAse B, and Streptolysin O (ASO) antibody titer determinations were performed at the reference laboratory QuestDiagnostics (Chantilly, VA).

DNA extraction, amplification, and sequencing

For the purulent abscess swabs, bacterial genomic DNA extraction and PCR amplification was performed in an identical fashion as previously described (144). For the cellulitis aspirates, 0.5 mls of the recovered PBS was mixed with an equal volume of lysis solution (GenElute bacterial genomic DNA kit (Sigma-Aldrich)) containing lysozyme (45 mg/ml), mutanolysin (125 U/ml), and lysostaphin (0.16 mg/ml) and allowed to incubate for 30 min at 37°C. Proteinase K (0.95 mg/ml) and lysis solution C (1 ml) were subsequently added to the sample and incubated for 10 minutes at 55°C. The remaining column purification steps were performed to the manufacturer's specifications. Amplification of the V1-V3 region of the 16S rRNA gene from the purulent abscess and cellulitis specimens was performed as previously described (144). All 40 samples were multiplexed and sequenced in a single 454 pyrosequencing run using the Roche GS FLX Titanium 454 sequencer at the Naval Medical Research Center in Fredrick, Maryland. Raw DNA sequences were quality processed and assigned taxonomy information using Mothur (v.1.34.4) as previously described (144). To control for possible reagent contaminates, we also prepared 0.5 mls of sterile PBS for 16S amplification and sequencing using the same reagents and 454 sequencer as described above. The PBS sample was sequenced in a separate pyroseqeuncing reaction in combination with an ongoing fecal microbiome study in our laboratory and yielded 3 usable reads; all of which were assigned to the alphaproteobacteria class.

Full-length 16S rRNA gene sequencing

Total genomic DNA from four cellulitis samples were subjected to PCR amplification of the 16S rRNA gene using the 8F and 1492R primers (299). The PCRs were performed in 50 µl reactions containing nuclease-free water, 125 U FideliTaq DNA polymerase (Affymetrix), and 0.6 µM of the forward and reverse primers. PCR mixtures were incubated at 95°C for 90 seconds, 34 cycles of 95°C for 30 seconds, 50°C for 30 seconds and 68°C for 2 minutes followed by a final extension of 68°C for 5 minutes. Five technical replicates of each PCR reaction were combined and purified using the QIAquick PCR Purification Kit (Qiagen). The purified PCR products were then ligated into the pGEM-T easy vector (Promega) and transformed into *E. coli* TOP10 cells. Transformants were selected on LB agar supplemented with Ampicillin (Amp) (100 µg/ml), X-gal (40 µg/ml) and IPTG (1 µM). At least 10 white colonies per transformation were selected and grown overnight in LB-Amp broth with shaking at 200 rpm. Plasmids were isolated using the QIAprep Spin Miniprep Kit (Qiagen).

Seven sequencing reactions were performed for each sample to ensure complete coverage of both strands of the 16S rRNA gene. The insert within the pGEM-T easy vector was sequenced using the following primers: T7, SP6, 8F, 1492R, 515F, 806R, and 919F (Promega) (299; 319). PCR and sequencing were performed as previously described (80). DNA chromatograms were visualized using Chromas Lite (Technelysium). Full-length 16S sequences were manually assembled and taxonomy information was assigned after alignment to the RDP database (57).

Statistical analyses

For the risk factor assessment analysis, p-values for the "median age, years (range)" and "median (range) no. of weeks in training at enrollment" were calculated with the Wilcoxon rank-sum test. For all other comparisons, the chi square test was used to generate p-values. When variable counts were less than 5, the Fisher's exact p-value was used.

RESULTS

Cellulitis and abscess risk-factor assessment

While numerous established risk factors for SSTI development have been identified, no group has assessed the contribution of these risk factors to either abscess or cellulitis formation within the same population. Thus, we enrolled 103 military trainees that developed a purulent abscess and 97 that presented with cellulitis and assessed for known SSTI risk factors (Table 8). For the majority of the risk factors assessed, the percentages of trainees in the abscess and cellulitis groups were not significantly different. However, we found that white ethnicity and blister formation were significantly associated with cellulitis development. Conversely, for patients that were *S. aureus* carriers, MRSA nasal colonization was linked to abscess formation.

Participant infection and body site culture

Of the 18 microbiome participants that developed cutaneous abscess, 9 had bacterial growth upon abscess culture. Of these 9, 5 were positive for MRSA (55.6%), 1

for MSSA (11.1%), and 3 grew non-*S. aureus* bacteria (33.3%) (Table 5). Unlike the cutaneous abscesses, only one of the 18 cellulitis aspirates analyzed (5.6%) grew bacteria (Coagulase-negative *Staphylococcus* (CNS)) (Table 7). Body site culture analysis for all 40 microbiome participants revealed that *S. aureus* (MRSA and MSSA) was routinely found throughout the body (abscess group: nose-52.9%, oropharynx-37.5%, perianal-33.3%, inguinal-20%) (cellulitis group: nose-71.4%, oropharynx-42.9%, perianal-53.3%, inguinal-47.4%) (Tables 6 & 7). While MSSA and CNS were frequently isolated from all body sites, MRSA was only detected 6 times total: twice in the nose, once in the oropharynx, twice in the perianal region, and once at the inguinal body site. Of note, one cellulitis patient (ID# 2758) had MRSA cultured from all 4 body sites tested.

ASO and anti-DNase B titer analysis

Previous studies have linked *Streptococcus* with cellulitis etiology (129; 142; 165; 216). We therefore assessed *Streptococcus* exposure using a serological approach. Upon admission to the clinic, 7 of the 22 cellulitis patients (31.8%) had elevated ASO titers (Table 7). Of those 7 patients, 5 maintained elevated ASO titers up to 21-28 days post SSTI diagnosis. We observed one patient that presented with normal ASO levels that eventually increased to above normal levels 21-28 days later, as well as a separate patient with the opposite ASO titer profile: elevated acute ASO titers and normal convalescent ASO titers. Anti-DNase B titers were unremarkable for all cellulitis patients at both acute and convalescent time points. Of note, linear regression analysis revealed no correlation between ASO titer levels and *Streptococcus* abundance levels (data not shown).

Sequencing results

While risk factor assessment revealed minimal differences between cellulitis and purulent abscesses, we also wanted to discern any differences in bacterial composition between the two SSTIs using a high-throughput sequencing approach. In total, we sequenced 40 SSTI samples (18 purulent abscess and 22 cellulitis) in a single 454 pyrosequencing run and yielded 1,515,532 raw sequences. 953,505 (63%) reads were removed from the analysis post quality filtering and contaminate/chimera detection. Overall, our sample set contained 1,007 unique reads with an average read length of 257 (range, 230 to 283) nucleotides. On average, there were 30,744 reads associated with each purulent abscess sample (range, 6,663 to 55,430). However, we observed a dramatic reduction in associated reads for the cellulitis samples. In fact, 4 of the 22 cellulitis samples had 0 associated reads. For the remaining 18, there were on average 480 associated reads per cellulitis sample (range, 149 to 956). This initial observation suggests that the bacterial load within the cellulitis samples is dramatically reduced compared to the purulent samples. Good's coverage values suggests that the number of reads associated with each sample accurately depict the total level of biodiversity (abscess samples: >99.4%; cellulitis samples: >95.9%). Subsampling was not performed for our data set given that no diversity comparisons were utilized. The percent abundance of each observed taxon for both infection types and the negative control is included in Table 10 (S2).

Purulent abscess microbiome

Analysis of the 18 purulent abscess samples revealed that the most abundant bacterial phylum present was Firmicutes (98.2% average abundance) (Figure 12A). At the species level, the most abundant bacterium present was *Staphylococcus aureus* (92.9% average abundance) (Figure 12C). Similar to a previous study (144), we observed a significant number of mixed infections; approximately 22% of the samples (4 of 18) had no single bacterial species reach an abundance level greater than 90%. While all purulent samples were sequence positive for *S. aureus*, additional abscess cohabitants included *Staphylococcus epidermidis, Streptococcus agalactiae, Staphylococcus haemolyticus,* and *Staphylococcus lugdunensis*.

Cellulitis microbiome

We next assigned taxonomy information to the 18 needle-aspirate samples that yielded usable sequences. In contrast to the purulent abscess samples, the most abundant bacterial phylum observed was Proteobacteria (89.8% average abundance) with Firmicutes representing the next most abundant phylum (5.9% average abundance) (Figure 12B). Further taxonomic investigation revealed that the most abundant bacterial species present was the gammaproteobacterium *Rhodanobacter terrae* (66.8% average abundance). While *Rhodanobacter* dominated the vast majority of cellulitis samples, other clinically relevant genera present included *Streptococcus, Staphylococcus, Propionibacterium*, and *Burkholderia* (Figure 12D).

To confirm and extend the taxonomy observation obtained by looking at the V1-V3 portion of the 16S rRNA, we next amplified, cloned and sequenced at least 10 full-length 16S genes from four separate cellulitis samples: 2055, 2080, 2203, and 2250. In

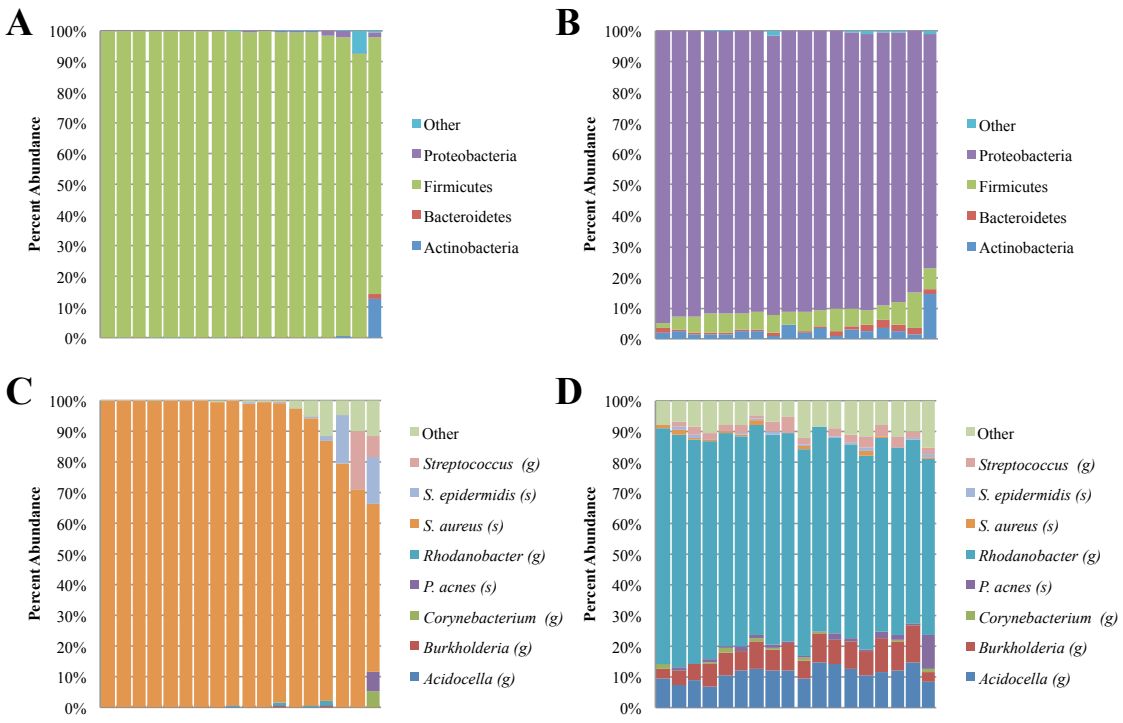

Figure 12. Microbial composition within purulent abscesses (A and C) and cellulitis (B and D) samples.

The microbiomes were characterized at the bacterial phylum level (A and B) as well as the genus (g) and species (s) levels (C and D). Each column corresponds to a single SSTI microbiome.

Table 9. Full-Length 16S rRNA taxonomy from Cellulitis Samples

	2055	2080	2203	2250
Clone 1	*Rhodanobacter terrae*; SPg; FJ405366 100%	uncultured bacterium; nbu286c01c1; KF063132 100%	uncultured bacterium; nbu286c01c1; KF063132 98.8%	uncultured bacterium; nbu286c01c1; KF063132 100%
	Rhodanobacter glycinis; MO64; EU912469 99.8%	*Dyella sp*. K4; FR874237 99.1%	*Dyella sp*. K4; FR874237 94.2%	*Dyella sp*. K4; FR874237 99.1%
	Rhodanobacter glycinis; MO64; EU912469 99.8%	*Rhodanobacter sp*. A2-60; KF441591 98.4%	*Rhodanobacter sp*. A2-60; KF441591 90.3%	*Rhodanobacter sp*. A2-60; KF441591 98.4%
Clone 2	*Rhodanobacter terrae*; SPg; FJ405366 100%	uncultured bacterium; nbu286c01c1; KF063132 99.0%	uncultured bacterium; nbu286c01c1; KF063132 99.0%	uncultured bacterium; nbu286c01c1; KF063132 99.8%
	Rhodanobacter glycinis; MO64; EU912469 99.8%	*Dyella sp*. K4; FR874237 99.0%	*Dyella sp*. K4; FR874237 0.939	*Dyella sp*. K4; FR874237 0.989
	Rhodanobacter terrae str. SPg 96.42%	*Rhodanobacter sp*. A2-60; KF441591 98.3%	*Rhodanobacter sp*. A2-60; KF441591 90.1%	*Rhodanobacter sp*. A2-60; KF441591 98.3%
Clone 3	uncultured bacterium; nbu286c01c1; KF063132 99.2%	uncultured bacterium; nbu286c01c1; KF063132 99.4%	uncultured bacterium; nbu286c01c1; KF063132 99.4%	uncultured bacterium; nbu286c01c1; KF063132 99.3%
	Dyella sp. K4; FR874237 94.2%	*Dyella sp*. K4; FR874237 94.2%	*Dyella sp*. K4; FR874237 94.3%	*Dyella sp*. K4; FR874237 94.4%
	Rhodanobacter sp. A2-60; KF441591 90.8%	*Rhodanobacter sp*. A2-60; KF441591 90.9%	*Rhodanobacter sp*. A2-60; KF441591 89.1%	*Rhodanobacter sp*. A2-60; KF441591 90.1%
Clone 4	uncultured bacterium; nbu286c01c1; KF063132 99.9%	uncultured bacterium; nbu286c01c1; KF063132 99.9%	uncultured bacterium; nbu286c01c1; KF063132 98.5%	uncultured bacterium; nbu286c01c1; KF063132 99.3%
	Dyella sp. K4; FR874237 0.943	*Dyella sp*. K4; FR874237 94.8%	*Dyella sp*. K4; FR874237 93.7%	*Dyella sp*. K4; FR874237 94.2%
	Rhodanobacter sp. A2-60; KF441591 90.6%	*Rhodanobacter sp*. A2-60; KF441591 91.1%	*Rhodanobacter sp*. A2-60; KF441591 90.0%	*Rhodanobacter sp*. A2-60; KF441591 90.1%
Clone 5	uncultured bacterium; nbu286c01c1; KF063132 99.9%	uncultured bacterium; nbu286c01c1; KF063132 99.1%	uncultured bacterium; nbu286c01c1; KF063132 99.4%	uncultured bacterium; nbu286c01c1; KF063132 99.1%
	Dyella sp. K4; FR874237 0.948	*Dyella sp*. K4; FR874237 94.2%	*Dyella sp*. K4; FR874237 94.2%	*Dyella sp*. K4; FR874237 94.0%
	Rhodanobacter sp. A2-60; KF441591 91.1%	*Rhodanobacter sp*. A2-60; KF441591 90.2%	*Rhodanobacter sp*. A2-60; KF441591 90.6%	*Rhodanobacter sp*. A2-60; KF441591 90.5%
Clone 6	uncultured bacterium; nbu286c01c1; KF063132 99.2%	uncultured bacterium; nbu286c01c1; KF063132 99.0%	bacterium BM0247; JQ680693 100%	uncultured bacterium; nbu286c01c1; KF063132 99.5%
	Dyella sp. K4; FR874237 94.1%	*Dyella sp*. K4; FR874237 0.933	*Escherichia coli*; r47; JQ661027 99.8%	*Dyella sp*. K4; FR874237 94.3%
	Rhodanobacter sp. A2-60; KF441591 90.1%	*Rhodanobacter sp*. A2-60; KF441591 89.5%	*Escherichia coli*; H16; JN129456 99.8%	*Rhodanobacter sp*. A2-60; KF441591 90.6%
Clone 7	*Rhodanobacter glycinis*; MO64; EU912469 100%	uncultured bacterium; nbu286c01c1; KF063132 99.5%	*Rhodanobacter terrae*; SPg; FJ405366 100%	uncultured bacterium; nbu286c01c1; KF063132 99.3%
	Rhodanobacter sp. B64; EU194895 100%	*Dyella sp*. K4; FR874237 94.4%	*Rhodanobacter glycinis*; MO64; EU912469 99.8%	*Dyella sp*. K4; FR874237 94.2%
	Rhodanobacter terrae; SPg; FJ405366 99.8%	*Rhodanobacter sp*. A2-60; KF441591 90.7%	*Rhodanobacter sp*. B64; EU194895 99.5%	*Rhodanobacter sp*. A2-60; KF441591 90.3%
Clone 8	*Escherichia coli*; r47; JQ661027 99.1%	uncultured bacterium; nbu286c01c1; KF063132 99.4%	uncultured bacterium; nbu286c01c1; KF063132 98.3%	Uncultured bacterium JF204832 100%
	uncultured organism; ELU0124-T310-S-NI_000496; HQ791715 99.1%	*Dyella sp*. K4; FR874237 94.2%	*Dyella sp*. K4; FR874237 93.3%	uncultured bacterium; ncd2350h08c1; JF205603 100%
	Escherichia coli; NBRC 12062; AB680228 99.1%	*Rhodanobacter sp*. A2-60; KF441591 90.6%	*Rhodanobacter sp*. A2-60; KF441591 89.9%	*Streptococcus oralis* ATCC 700233 99.6%
Clone 9	uncultured bacterium GQ096144 99.6%	uncultured bacterium; nbu286c01c1; KF063132 99.1%	uncultured bacterium; nbu286c01c1; KF063132 99.6%	uncultured bacterium; nbu286c01c1; KF063132 99.4%
	Acinetobacter parvus KJ806336 99.6%	*Dyella sp*. K4; FR874237 93.9%	*Dyella sp*. K4; FR874237 94.5%	*Dyella sp*. K4; FR874237 94.2%
	uncultured bacterium; nbw109h05c1; GQ007804 99.3%	*Rhodanobacter sp*. A2-60; KF441591 90.4%	*Rhodanobacter sp*. A2-60; KF441591 90.9%	*Rhodanobacter sp*. A2-60; KF441591 90.6%

Clone 10	*Rhodanobacter glycinis*; MO64; EU912469 98.7%	uncultured bacterium; nbu286c01c1; KF063132 99.9%	uncultured bacterium; nbu286c01c1; KF063132 99.1%	uncultured bacterium; nbu286c01c1; KF063132 98.0%
	Rhodanobacter sp. B64; EU194895 98.7%	*Dyella sp*. K4; FR874237 94.8%	*Dyella sp*. K4; FR874237 93.9%	*Dyella sp*. K4; FR874237 93.2%
	Rhodanobacter terrae; SPg; FJ405366 98.0%	*Rhodanobacter sp*. A2-60; KF441591 91.1%	*Rhodanobacter sp*. A2-60; KF441591 88.8%	*Rhodanobacter sp*. A2-60; KF441591 90.0%
Clone 11	uncultured bacterium; nbu286c01c1; KF063132 99.9%		uncultured bacterium; nbu286c01c1; KF063132 99.5%	
	Dyella sp. K4; FR874237 94.8%		*Dyella sp*. K4; FR874237 94.6%	
	Rhodanobacter sp. A2-60; KF441591 91.1%		*Rhodanobacter sp*. A2-60; KF441591 90.9%	

Taxonomy information according to the RDP database. GenBank accession listed after species name. Top three hits per clone are given. Percentages represent percent identity.

support of the 454 sequencing data, a large proportion of the full-length 16S sequences were classified as *Rhodanobacter* (Table 9). In addition, many of the sequences were assigned to the closely related *Dyella* genus. Besides *Rhodanobacter* and *Dyella*, we also detected *Acinetobacter* and *Streptococcus*. Additionally, two of the samples were identified as *E. coli.* While this may indicate infection with *E. coli*, it may also be due to purification of contaminate *E. coli* DNA from the *E. coli* TOP 10 cells that carried the cloned 16S sequences.

DISCUSSION

Given the dramatic differences in physical presentation between cutaneous abscess and cellulitis, it stands to reason that there may be specific risk factors and/or microbial profiles associated with each SSTI type. In our military specific study population, we found that the bulk of the risk factors assessed were not significantly different between cutaneous abscess and cellulitis patients. However, we did find that white ethnicity and prior blister formation were strongly associated with cellulitis while cutaneous abscess formation was linked to nasal colonization with MRSA. These apparent risk factor differences prompted a subsequent investigation into the bacterial composition of SSTIs. Our high-throughput sequencing and culture data confirmed that *S. aureus* is typically associated with cutaneous abscess. For cellulitis aspirates, however, we observed a dramatic difference in microbiota as compared to abscesses; *Rhodanobacter*/*Dyella* were identified as the predominant genera. To our knowledge, this is the first clinical investigation that utilizes an epidemiological approach in addition to

high-throughput sequencing to characterize the two most commonly diagnosed SSTIs, cellulitis and cutaneous abscess.

To date, there are numerous risk factors associated with SSTI development. These include, but are not limited to injectional drug use, diabetes, and antecedent *S. aureus* carriage (79; 251; 280). Unfortunately, most of these studies failed to differentiate between the various SSTI types. By separating military trainees with SSTI into either an "abscess only" or "cellulitis only" group, we were able to discern any SSTI-specific risk factors (Table 8) Our findings are in agreement with a UK-based prospective study of 150 patients with lower limb cellulitis and 300 healthy controls that also observed an association between cellulitis development and white ethnicity (120). Of note, that study also suggested that preceding blister formation may be a risk factor of cellulitis but the findings failed to reach statistical significance (120). With respect to abscess formation, we found that trainees colonized with MRSA were more likely to harbor an abscess rather than cellulitis. This is not entirely surprising given the high prevalence of MRSA-associated abscesses in the military and general population (89; 206; 226). Although these data suggest a clear association between MRSA and abscess formation, it may also infer that MRSA is less likely to be the cause of cellulitis infections. This is further supported by the low abundance of *Staphylococcus aureus* detected in the skin of cellulitis infection (< 2% percent abundance) (Figure 12). While the exact contribution of *S. aureus* to cellulitis infections remains unclear, our data suggests that other bacterial species may be involved.

With minor differences in associated risk factors, we also sought to determine any differences in bacterial composition between cutaneous abscess and cellulitis. Recently,

we characterized 40 abscess microbiomes in military trainees at Fort Benning (144). We found that while most abscesses were dominated by *S. aureus*, polymicrobial infections were prevalent. Given this interesting phenomenon, we enrolled an additional 18 trainees suffering from cutaneous abscess and found remarkably similar microbial compositions; while *S. aureus* dominated most abscesses, there were 4 mixed infections. Given that polymicrobial SSTIs are typically associated with severe disease such as necrotizing fasciitis (76; 194), it would perhaps be interesting in future studies to document the progression of a polymicrobial abscess as opposed to a monomicrobial infection.

Unlike purulent abscesses, we observed cellulitis microbiomes rich in Proteobacteria, particularly from the *Rhodanobacter*/*Dyella* genera. Of note, there are no prior reports that suggest that *Rhodanobacter* or *Dyella* infect humans or carry virulence factors. Thus, given the study population of military trainees, perhaps *Rhodanobacter* gains entry into the skin via minor cuts and abrasions and subsequent contact with the soil. These findings further add to the ongoing debate regarding the bacterial etiology of cellulitis. In a pediatric study that utilized needle aspirates, 3 of the 20 patients cultured (15%) yielded a pathogen, all of which were MRSA (231). A separate study in adults found that only 5 of 50 (10%) cellulitis aspirates were culture positive (129). Given the limited success of aspirate culture, more sensitive detection methods such as PCR and DNA sequencing are being considered. Similar to our study, a recent investigation also subjected needle aspirates to high-throughput sequencing (63). Interestingly, they found a wide array of atypical bacteria that were not observed in our study such as *Acidovorax,* *Enterococcus,* and *Lactococcus*. There are numerous reasons that could explain this discrepancy; these include differences in study populations, site of needle aspiration

(center versus leading edge), or sequencing data analysis pipelines. Despite these differences, both studies suggest a potential role of atypical bacterial in cellulitis infections. We can hypothesize that cellulitis pathology may be an immune response to the presence of the atypical bacterium (*i.e. Rhodanobacter)*. This idea is supported by previous reports that suggest an inflammatory component to cellulitis infections (65) and the observation that cellulitis is often resolved by the use of NSAIDS and steroids (23; 65). Thus, cellulitis may be a nonspecific immune response to atypical bacteria rather than an actual infection.

Despite conflicting results exploring cellulitis etiology, culture-based techniques favor *S. aureus* as the principal cause over beta-hemolytic streptococci (BHS) (49). While only one aspirate in our study yielded CNS, 8 of the cellulitis patients had elevated ASO titers at the acute and/or convalescent time points: a 36.4% seroconversion rate indicative of BHS exposure. In an investigation assessing serologic conversion, 73% of non-purulent cellulitis was suggested to be caused by BHS and 27% was not identifiable (142). Another study yielded a similar percent serconversion rate (74%) for cellulitis and erysipelas (171). Together these reports suggest the bulk of non-purulent cellulitis may be caused by BHS. While the ASO seroconversion rate in our study was lower than previous reports, it still represents a significant proportion of our total population. While our pyrosequencing data did detect *Streptococcus* within cellulitis infections (Figure 12D), it represented a minor fraction of the total number of reads (approximately 2-5% average abundance) and was greatly outnumbered by the atypical bacteria discussed above.

As with most clinical studies, there are limitations to our study. For our protocol, needle aspiration was performed on cellulitis patients and not healthy controls; a

limitation set forth by the Institutional Review Board. It should be noted that a few studies have begun to characterize the "healthy subcutaneous tissue microbiome," and have detected bacteria such as *Propionibacterium acnes, Staphylococcus epidermidis,* and *Pseudomonas spp.* in both the reticular and dermal adipose layers (213). Interestingly, all three of these organisms were also detected in our cellulitis aspirates (Table 10 (S2)). While it is premature to speculate on the role of these subcutaneous bacteria in cellulitis, our data will be of use in the future as researchers continue to investigate cellulitis etiology. Secondly, for the risk factor analysis, self-reporting can be error prone if the patient either cannot accurately recall specific events in their medical history or chose to withhold information. However, given our military study population, we expect minimal error due to self-reporting. We also note that while elevated ASO titers suggest BHS exposure, it is difficult to determine if they are associated with cellulitis or prior exposure to BHS (ex. strep throat). It is also possible given the low abundance of bacteria observed in cellulitis infections that ASO titers may not yet be detectable (false-negative). Additionally, our study population is composed entirely of young, healthy males stationed at Fort Benning and may not accurately represent SSTIs in the general public or in non-healthy/immunocompromised patients. Lastly, we acknowledge that participation was suboptimal for the body site colonization data, particularly for the inguinal and perianal locations. However, this data will be valuable in the future as we continue to sample military trainees at Fort Benning as part of additional ongoing research projects.

In conclusion, our results emphasize that cutaneous abscess and cellulitis represent two distinct diseases. While purulent abscesses are rich in *S. aureus* and

associated with MRSA nasal colonization, non-purulent cellulitis is composed of atypical bacteria such as *Rhodanobacter/Dyella* and linked to white ethnicity and prior blister formation. Thus, while both infections are considered SSTIs, they are dramatically different than one another and treatment should be uniquely tailored to either cutaneous abscess or cellulitis.

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Table 10 (S2). Percent abundance of each taxon per sample according to the GreenGenes database.

Each column represents one sample and is labeled with sample ID, infection group (abscess or cellulitis), and total number of reads associated with each sample. The results for the PBS negative control are included.

Sample ID	1782A	1868A	1871A	1876A	1914A	1955A	1957A	1983A	2018A	2058A	2067A	2086A	2094A	2120A	2152A	2157A	2160A	2202A	1680Z	1739Z	1773Z
Infection Group	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Abscess	Cellulitis	Cellulitis	Cellulitis
Total Number of Reads	24790	34340	43378	44406	12870	8829	28913	6663	55430	20582	24886	49846	40747	19458	42355	34994	7977	52922	638	346	825
Taxon																					
p__Acidobacteria	0	0	0	0	0.03885004	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0.31347962	0	0
c__Acidobacteria	0	0	0	0	0.01554002	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Acidobacteriales	0	0	0	0	0.01554002	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Acidobacteriaceae	0	0	0	0	0.01554002	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.01554002	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.01554002	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Solibacteres	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Solibacterales	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__MVS-65	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__[Chloracidobacteria]	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0.31347962	0	0
o__RB41	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0.31347962	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0.31347962	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0.31347962	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0.31347962	0	0
p__Actinobacteria	0.16538927	0.03494467	0.02535848	0.00225195	12.8982129	0.73621022	0.02075191	0.06003302	0.00902039	0.1020309	0.02009162	0.00601854	0.03435836	0.01541782	0.11096683	0.03143396	0.06268021	0.00377915	14.7335423	1.15606936	3.15151515
c__Actinobacteria	0.16538927	0.03494467	0.02535848	0.00225195	12.8904429	0.72488391	0.02075191	0.06003302	0.00902039	0.1020309	0.02009162	0.00601854	0.03435836	0.01541782	0.11096683	0.03143396	0.06268021	0.00377915	14.7335423	1.15606936	3.15151515
o__Actinomycetales	0.16538927	0.03494467	0.02535848	0.00225195	12.8904429	0.72488391	0.02075191	0.06003302	0.00902039	0.1020309	0.02009162	0.00601854	0.03435836	0.01541782	0.11096683	0.03143396	0.06268021	0.00377915	14.7335423	1.15606936	3.15151515
f__Actinomycetaceae	0	0	0	0	0.14763015	0.01132631	0	0	0	0	0	0	0	0	0.002361	0.00285763	0	0	0.62695925	0	0.36363636
g__Actinobaculum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
g__Actinomyces	0	0	0	0	0.14763015	0.01132631	0	0	0	0	0	0	0	0	0	0.00285763	0	0	0.47021944	0	0.36363636
unclassified	0	0	0	0	0.14763015	0.01132631	0	0	0	0	0	0	0	0	0	0.00285763	0	0	0.47021944	0	0.36363636
g__Varibaculum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
f__Actinosynnemataceae	0	0	0.00230532	0	0	0	0.00345865	0	0	0	0	0	0	0	0	0	0	0	0.31347962	0	0
g__Lechevalieria	0	0	0.00230532	0	0	0	0.00345865	0	0	0	0	0	0	0	0	0	0	0	0.31347962	0	0
s__aerocolonigenes	0	0	0.00230532	0	0	0	0.00345865	0	0	0	0	0	0	0	0	0	0	0	0.31347962	0	0
f__Bogoriellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00285763	0	0	0	0	0
g__Georgenia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00285763	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00285763	0	0	0	0	0
f__Brevibacteriaceae	0	0	0	0	0.09324009	0	0	0.03001651	0	0	0.00803665	0.00200618	0	0	0	0	0	0	0	0	0
g__Brevibacterium	0	0	0	0	0.09324009	0	0	0.03001651	0	0	0.00803665	0.00200618	0	0	0	0	0	0	0	0	0
s__casei	0	0	0	0	0.08547009	0	0	0	0	0	0.00803665	0	0	0	0	0	0	0	0	0	0
s__paucivorans	0	0	0	0	0.00777001	0	0	0.03001651	0	0	0	0.00200618	0	0	0	0	0	0	0	0	0
f__Corynebacteriaceae	0.13715208	0	0.00922126	0	5.5011655	0.37376826	0	0.01500825	0.00180408	0.07773783	0	0.00200618	0.00490834	0	0.09443985	0.02286106	0.03760812	0	1.41065831	0	1.33333333
g__Corynebacterium	0.13715208	0	0.00922126	0	5.5011655	0.37376826	0	0.01500825	0.00180408	0.07773783	0	0.00200618	0.00490834	0	0.09443985	0.02286106	0.03760812	0	1.41065831	0	1.33333333
s__durum	0	0	0	0	0.26418026	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__kroppenstedtii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__lubricantis	0	0	0	0	0	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__pilosum	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__simulans	0	0	0.00461063	0	0.06216006	0	0	0	0	0.01943446	0	0	0	0	0	0.00571527	0	0	0	0	0
unclassified	0.13715208	0	0.00461063	0	5.16705517	0.36244195	0	0.01500825	0.00180408	0.05830337	0	0.00200618	0.00490834	0	0.09443985	0.0171458	0.03760812	0	1.41065831	0	1.33333333
f__Dermabacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Brachybacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__conglomeratum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Frankiaceae	0	0	0	0	0	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Geodermatophilaceae	0	0	0	0	0	0.02265262	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Blastococcus	0	0	0	0	0	0.02265262	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aggregatus	0	0	0	0	0	0.02265262	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Gordoniaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0.24242424
g__Gordonia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0.24242424
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0.24242424
f__Intrasporangiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lapillicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__jejuensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Microbacteriaceae	0	0	0	0	0.02331002	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0.31347962	1.15606936	0
g__Curtobacterium	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Frigoribacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.15606936	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.15606936	0
g__Leucobacter	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
g__Microbacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.31347962	0	0
s__chocolatum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.31347962	0	0
s__maritypicum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Mycetocola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Micrococcaceae	0	0.01456028	0.01152658	0.00225195	0.2020202	0.15856835	0.00345865	0	0	0.00971723	0	0	0.00736251	0	0.00472199	0	0	0	0.78369906	0	0.36363636
g__Arthrobacter	0	0.00291206	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__psychrolactophilus	0	0.00291206	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kocuria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.62695925	0	0
s__rhizophila	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.62695925	0	0
g__Microbispora	0	0.00291206	0.01152658	0	0	0	0.00345865	0	0	0.00485861	0	0	0.00736251	0	0	0	0	0	0	0	0
s__rosea	0	0.00291206	0.01152658	0	0	0	0.00345865	0	0	0.00485861	0	0	0.00736251	0	0	0	0	0	0	0	0
g__Micrococcus	0	0	0	0.00225195	0.11655012	0.14724204	0	0	0	0	0	0	0	0	0.00472199	0	0	0	0.15673981	0	0
s__luteus	0	0	0	0.00225195	0.11655012	0.14724204	0	0	0	0	0	0	0	0	0.00472199	0	0	0	0.15673981	0	0
g__Nesterenkonia	0	0.00582411	0	0	0	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.12121212
unclassified	0	0.00582411	0	0	0	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.12121212
g__Renibacterium	0	0.00291206	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.00291206	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rothia	0	0	0	0	0.08547009	0	0	0	0	0.00485861	0	0	0	0	0	0	0	0	0	0	0.24242424
s__aeria	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__dentocariosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mucilaginosa	0	0	0	0	0.07770008	0	0	0	0	0.00485861	0	0	0	0	0	0	0	0	0	0	0.24242424
f__Micromonosporaceae	0.01210165	0	0	0	0.04662005	0.04530524	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Micromonospora	0.01210165	0	0	0	0.04662005	0.03397893	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__narathiwatensis	0.01210165	0	0	0	0.04662005	0.03397893	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Solwaraspora	0	0	0	0	0	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nocardioidaceae	0	0	0	0	0.10878011	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
g__Aeromicrobium	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Friedmanniella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nocardioides	0	0	0	0	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
s__dokdonensis	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__furvisabuli	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__panacihumi	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__terrigena	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
g__Propionicimonas	0	0	0	0	0.07770008	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.07770008	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Promicromonosporaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Xylanimicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__pachnodae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Propionibacteriaceae	0.01613554	0.02038439	0.00230532	0	6.61227661	0.1019368	0.01383461	0.01500825	0.00721631	0.01457584	0.01205497	0.00200618	0.02208752	0.01541782	0.00708299	0.00285763	0.02507208	0.00377915	10.9717868	0	0.84848485
g__Propionibacterium	0.01613554	0.02038439	0.00230532	0	6.61227661	0.1019368	0.01383461	0.01500825	0.00721631	0.01457584	0.01205497	0.00200618	0.02208752	0.01541782	0.00708299	0.00285763	0.02507208	0.00377915	10.9717868	0	0.84848485
s__acnes	0.01613554	0.02038439	0.00230532	0	6.14607615	0.1019368	0.01383461	0.01500825	0.00721631	0.01457584	0.01205497	0.00200618	0.02208752	0.01541782	0.002361	0.00285763	0.02507208	0.00377915	10.9717868	0	0.84848485
s__granulosum	0	0	0	0	0.46620047	0	0	0	0	0	0	0	0	0	0.00472199	0	0	0	0	0	0
f__Tsukamurellaceae	0	0	0	0	0.15540016	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Tsukamurella	0	0	0	0	0.15540016	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.15540016	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Yaniellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Yaniella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Thermoleophilia	0	0	0	0	0.00777001	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Solirubrobacterales	0	0	0	0	0.00777001	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Conexibacteraceae	0	0	0	0	0.00777001	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Conexibacter	0	0	0	0	0	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Patulibacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Bacteroidetes	0	0.00582411	0	0.00225195	1.51515152	0	0.00345865	0.07504127	0.00360815	0.02915169	0	0	0	0	0.03305395	0.00285763	0.05014416	0	1.56739812	0.57803468	0.84848485
c__Bacteroidia	0	0.00291206	0	0.00225195	0.77700078	0	0.00345865	0	0	0.00971723	0	0	0	0	0.02833196	0	0	0	0.78369906	0.57803468	0.12121212
o__Bacteroidales	0	0.00291206	0	0.00225195	0.77700078	0	0.00345865	0	0	0.00971723	0	0	0	0	0.02833196	0	0	0	0.78369906	0.57803468	0.12121212
f__Porphyromonadaceae	0	0	0	0	0.17094017	0	0	0	0	0	0	0	0	0	0.01416598	0	0	0	0.31347962	0	0
g__Paludibacter	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Porphyromonas	0	0	0	0	0.16317016	0	0	0	0	0	0	0	0	0	0.01416598	0	0	0	0.31347962	0	0
s__endodontalis	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.15540016	0	0	0	0	0	0	0	0	0	0.01416598	0	0	0	0.31347962	0	0
f__Prevotellaceae	0	0.00291206	0	0.00225195	0.04662005	0	0	0	0	0	0	0	0	0	0.01180498	0	0	0	0.15673981	0.28901734	0.12121212
g__Prevotella	0	0.00291206	0	0.00225195	0.04662005	0	0	0	0	0	0	0	0	0	0.01180498	0	0	0	0.15673981	0.28901734	0.12121212
s__copri	0	0.00291206	0	0.00225195	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__melaninogenica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0.28901734	0.12121212
s__nanceiensis	0	0	0	0	0.03108003	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__pallens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__stercorea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
unclassified	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0.00944399	0	0	0	0	0	0
f__Rikenellaceae	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Blvii28	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__S24-7	0	0	0	0	0	0	0	0	0	0.00971723	0	0	0	0	0	0	0	0	0.31347962	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.00971723	0	0	0	0	0	0	0	0	0.31347962	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.00971723	0	0	0	0	0	0	0	0	0.31347962	0	0
f__[Paraprevotellaceae]	0	0	0	0	0.54390054	0	0.00345865	0	0	0	0	0	0	0	0.002361	0	0	0	0	0.28901734	0
g__YRC22	0	0	0	0	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__[Prevotella]	0	0	0	0	0.52059052	0	0.00345865	0	0	0	0	0	0	0	0.002361	0	0	0	0	0.28901734	0
unclassified	0	0	0	0	0.52059052	0	0.00345865	0	0	0	0	0	0	0	0.002361	0	0	0	0	0.28901734	0
c__Cytophagia	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Cytophagales	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Cytophagaceae	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Hymenobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sporocytophaga	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Flavobacteriia	0	0.00291206	0	0	0.72261072	0	0	0.07504127	0.00360815	0.01943446	0	0	0	0	0.00472199	0.00285763	0.05014416	0	0.62695925	0	0.72727273
o__Flavobacteriales	0	0.00291206	0	0	0.72261072	0	0	0.07504127	0.00360815	0.01943446	0	0	0	0	0.00472199	0.00285763	0.05014416	0	0.62695925	0	0.72727273
f__Flavobacteriaceae	0	0	0	0	0.02331002	0	0	0.03001651	0.00360815	0.00485861	0	0	0	0	0	0	0.01253604	0	0	0	0.12121212
g__Capnocytophaga	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ochracea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Flavobacterium	0	0	0	0	0	0	0	0.03001651	0.00180408	0.00485861	0	0	0	0	0	0	0	0	0	0	0
s__gelidilacus	0	0	0	0	0	0	0	0	0	0.00485861	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.03001651	0.00180408	0	0	0	0	0	0	0	0	0	0	0	0
g__Lutaonella	0	0	0	0	0	0	0	0	0.00180408	0	0	0	0	0	0	0	0	0	0	0	0
s__thermophilus	0	0	0	0	0	0	0	0	0.00180408	0	0	0	0	0	0	0	0	0	0	0	0
g__Myroides	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0.01253604	0	0	0	0.12121212
s__odoratimimus	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0.01253604	0	0	0	0.12121212
g__Sediminicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__luteus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__[Weeksellaceae]	0	0.00291206	0	0	0.6993007	0	0	0.04502476	0	0.01457584	0	0	0	0	0.00472199	0.00285763	0.03760812	0	0.62695925	0	0.60606061
g__Bergeyella	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__zoohelcum	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Chryseobacterium	0	0	0	0	0.18648019	0	0	0.01500825	0	0.00971723	0	0	0	0	0	0	0.02507208	0	0.47021944	0	0.60606061
unclassified	0	0	0	0	0.18648019	0	0	0.01500825	0	0.00971723	0	0	0	0	0	0	0.02507208	0	0.47021944	0	0.60606061
g__Cloacibacterium	0	0	0	0	0.00777001	0	0	0.01500825	0	0	0	0	0	0	0	0	0.01253604	0	0.15673981	0	0
unclassified	0	0	0	0	0.00777001	0	0	0.01500825	0	0	0	0	0	0	0	0	0.01253604	0	0.15673981	0	0
g__Elizabethkingia	0	0.00291206	0	0	0.03108003	0	0	0.01500825	0	0	0	0	0	0	0.00472199	0.00285763	0	0	0	0	0
s__meningoseptica	0	0.00291206	0	0	0.03108003	0	0	0.01500825	0	0	0	0	0	0	0.00472199	0.00285763	0	0	0	0	0
g__Riemerella	0	0	0	0	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Wautersiella	0	0	0	0	0	0	0	0	0	0.00485861	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.00485861	0	0	0	0	0	0	0	0	0	0	0
g__Weeksella	0	0	0	0	0.44289044	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__virosa	0	0	0	0	0.44289044	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Sphingobacteriia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Sphingobacteriales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Sphingobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphingobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__multivorum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__[Saprospirae]	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
o__[Saprospirales]	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
f__Chitinophagaceae	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
g__Flavisolibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
g__Segetibacter	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Chloroflexi	0	0	0	0	0.02331002	0	0	0.04502476	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Anaerolineae	0	0	0	0	0	0	0	0.04502476	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Caldilineales	0	0	0	0	0	0	0	0.03001651	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Caldilineaceae	0	0	0	0	0	0	0	0.03001651	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.03001651	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.03001651	0	0	0	0	0	0	0	0	0	0	0	0	0
o__SBR1031	0	0	0	0	0	0	0	0.01500825	0	0	0	0	0	0	0	0	0	0	0	0	0
f__SJA-101	0	0	0	0	0	0	0	0.01500825	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.01500825	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.01500825	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Ellin6529	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Gitt-GS-136	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Cyanobacteria	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__ML635J-21	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Firmicutes	99.6450182	99.7146185	99.7602471	99.9054182	83.6363636	97.2024012	99.6575935	99.5497524	99.9494858	99.4509766	99.8312304	99.8776231	99.7913957	99.3216158	92.3668988	99.7628165	98.2700263	99.9300858	6.73981191	5.78034682	5.93939394
c__Bacilli	99.6329165	99.7087944	99.7464152	99.9054182	81.7404817	97.2024012	99.6541348	99.5047276	99.9494858	99.4266835	99.8272121	99.8716045	99.7913957	99.3216158	89.8642427	99.7599589	98.2449542	99.9300858	5.64263323	4.33526012	5.93939394
o__Bacillales	99.6208148	99.7000582	99.7394993	99.8986623	71.3908314	96.9985276	99.612631	99.4897193	99.9458777	99.3926732	99.8191754	99.8595675	99.7913957	99.3010587	71.1439027	99.7142367	97.9315532	99.9281962	2.6645768	1.73410405	1.81818182
f__Alicyclobacillaceae	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Alicyclobacillus	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bacillaceae	0	0.00291206	0	0	0.00777001	0.03397893	0	0.01500825	0	0	0.00401832	0	0	0.01027855	0.00472199	0.00285763	0	0.00188957	0	0	0
g__Bacillus	0	0.00291206	0	0	0.00777001	0.03397893	0	0.01500825	0	0	0.00401832	0	0	0.01027855	0.00472199	0.00285763	0	0.00188957	0	0	0
s__cereus	0	0.00291206	0	0	0	0.02265262	0	0.01500825	0	0	0.00401832	0	0	0	0.002361	0	0	0.00188957	0	0	0
s__flexus	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01027855	0	0	0	0	0	0	0
s__fumarioli	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__safensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
s__trypoxylicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00285763	0	0	0	0	0
unclassified	0	0	0	0	0	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Geobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Listeriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01027855	0	0	0	0	0	0	0
g__Listeria	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01027855	0	0	0	0	0	0	0
s__monocytogenes	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01027855	0	0	0	0	0	0	0
f__Paenibacillaceae	0	0	0.01844253	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Brevibacillus	0	0	0.01844253	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__invocatus	0	0	0.01844253	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Paenibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__amylolyticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Planococcaceae	0	0.00291206	0	0.00225195	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0.47021944	0	0
g__Rummeliibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.47021944	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.47021944	0	0
g__Staphylococcus	0	0.00291206	0	0.00225195	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__saprophyticus	0	0.00291206	0	0.00225195	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Staphylococcaceae	99.6208148	99.6942341	99.7210568	99.8964104	71.3519814	96.9645486	99.612631	99.4747111	99.9458777	99.382956	99.8151571	99.8595675	99.7913957	99.2805016	71.1391807	99.7113791	97.9315532	99.9263066	2.19435737	1.73410405	1.81818182
g__Jeotgalicoccus	0	0.00291206	0	0	0.01554002	0	0	0	0	0.00971723	0	0	0	0	0.00472199	0	0	0	0	0	0
s__psychrophilus	0	0.00291206	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0.00472199	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.00971723	0	0	0	0	0	0	0	0	0	0	0
g__Macrococcus	0	0	0	0	0	0.02265262	0	0	0	0	0	0	0	0	0	0.00285763	0	0	0	0	0
s__brunensis	0	0	0	0	0	0.02265262	0	0	0	0	0	0	0	0	0	0.00285763	0	0	0	0	0
g__Staphylococcus	99.6208148	99.6913221	99.7210568	99.8964104	71.3364413	96.941896	99.612631	99.4747111	99.9458777	99.3732388	99.8151571	99.8595675	99.7913957	99.2805016	71.1344587	99.7085215	97.9315532	99.9263066	2.19435737	1.73410405	1.81818182
s__aureus	99.056071	99.6534653	99.6980036	99.090213	54.6930847	84.414996	99.5918791	99.2495873	97.0900235	93.8538529	99.7990838	99.8354933	99.7742165	99.2342481	71.0518239	79.4336172	97.6432243	99.9206379	0.47021944	0.57803468	0.36363636
s__epidermidis	0.09681323	0.03785673	0.01152658	0.55397919	15.4234654	1.46109412	0.00345865	0	0.02525708	0.51987173	0.00803665	0.01604943	0.00245417	0.01027855	0.00472199	15.4940847	0.01253604	0.00377915	1.09717868	0.86705202	0
s__equorum	0	0	0.00461063	0.00900779	0.02331002	0.01132631	0.01037596	0.09004953	0	0.02915169	0.00803665	0.00401236	0.00736251	0.0205571	0.00944399	0.00571527	0.08775229	0	0	0	0
s__haemolyticus	0.46793062	0	0.00691595	0.00225195	1.1965812	11.0318269	0.0069173	0.13507429	0	0.01943446	0	0.00401236	0	0.01027855	0.06846889	0.00571527	0.18804062	0.00188957	0.62695925	0.28901734	0
s__lugdunensis	0	0	0	0.24095843	0	0.02265262	0	0	2.83059715	4.950928	0	0	0.00490834	0.00513927	0	4.76938904	0	0	0	0	1.45454545
s__succinus	0	0	0	0	0	0	0	0	0	0	0	0	0.00245417	0	0	0	0	0	0	0	0
f__Thermoactinomycetaceae	0	0	0	0	0	0	0	0	0	0.00971723	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.00971723	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.00971723	0	0	0	0	0	0	0	0	0	0	0
f__[Exiguobacteraceae]	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Exiguobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Gemellales	0	0	0	0	1.67832168	0	0	0	0	0	0	0	0	0	0.0613859	0.00571527	0.03760812	0	0	0	0.24242424
f__Gemellaceae	0	0	0	0	1.67832168	0	0	0	0	0	0	0	0	0	0.0613859	0.00571527	0.03760812	0	0	0	0.24242424
g__Gemella	0	0	0	0	1.67832168	0	0	0	0	0	0	0	0	0	0.0613859	0.00571527	0.03760812	0	0	0	0.24242424
unclassified	0	0	0	0	1.67832168	0	0	0	0	0	0	0	0	0	0.0613859	0.00571527	0.03760812	0	0	0	0.24242424
o__Lactobacillales	0.01210165	0.00873617	0.00691595	0.00675584	8.67132867	0.2038736	0.04150382	0.01500825	0.00360815	0.0340103	0.00803665	0.01203707	0	0.0205571	18.6589541	0.04000686	0.2757929	0.00188957	2.97805643	2.60115607	3.87878788
f__Aerococcaceae	0.00403388	0	0	0.00225195	0.02331002	0.11326311	0	0	0	0.00485861	0.00401832	0	0	0	0	0	0	0	0	0	0
g__Aerococcus	0	0	0	0.00225195	0.01554002	0.11326311	0	0	0	0.00485861	0.00401832	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.00225195	0.01554002	0.11326311	0	0	0	0.00485861	0.00401832	0	0	0	0	0	0	0	0	0	0
g__Alloiococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

g__Facklamia	0.00403388	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.00403388	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Carnobacteriaceae	0	0	0	0	1.75602176	0.01132631	0.00345865	0	0.00180408	0.00485861	0	0.00200618	0	0	0.00472199	0.00285763	0.08775229	0	0.47021944	0	0
g__Carnobacterium	0	0	0	0	0.00777001	0.01132631	0	0	0.00180408	0	0	0	0	0	0.002361	0.00285763	0.03760812	0	0	0	0
s__viridans	0	0	0	0	0.00777001	0.01132631	0	0	0.00180408	0	0	0	0	0	0.002361	0.00285763	0.03760812	0	0	0	0
g__Granulicatella	0	0	0	0	1.74825175	0	0.00345865	0	0	0.00485861	0	0.00200618	0	0	0.002361	0	0.05014416	0	0.47021944	0	0
unclassified	0	0	0	0	1.74825175	0	0.00345865	0	0	0.00485861	0	0.00200618	0	0	0.002361	0	0.05014416	0	0.47021944	0	0
f__Enterococcaceae	0	0.00582411	0	0	0.00777001	0.06795787	0.00345865	0.01500825	0	0	0	0.00200618	0	0	0	0.00285763	0	0	0	0	0
g__Enterococcus	0	0.00582411	0	0	0.00777001	0.06795787	0.00345865	0.01500825	0	0	0	0.00200618	0	0	0	0.00285763	0	0	0	0	0
s__casseliflavus	0	0.00291206	0	0	0	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.00291206	0	0	0.00777001	0.05663156	0.00345865	0.01500825	0	0	0	0.00200618	0	0	0	0.00285763	0	0	0	0	0
f__Lactobacillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lactobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__helveticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Streptococcaceae	0.00806777	0.00291206	0.00691595	0.0045039	6.88422688	0.01132631	0.03458652	0	0.00180408	0.02429307	0.00401832	0.00802472	0	0.0205571	18.6542321	0.03429159	0.18804062	0.00188957	2.50783699	2.60115607	3.87878788
g__Lactococcus	0.00403388	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00571527	0	0	0	0	1.45454545
unclassified	0.00403388	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00571527	0	0	0	0	1.45454545
g__Streptococcus	0.00403388	0.00291206	0.00691595	0.0045039	6.88422688	0.01132631	0.03458652	0	0.00180408	0.02429307	0.00401832	0.00802472	0	0.0205571	18.6542321	0.02857633	0.18804062	0.00188957	2.50783699	2.60115607	2.42424242
s__agalactiae	0	0	0	0	1.04895105	0	0	0	0	0	0	0	0	0	18.5432653	0	0	0	0	0	0
s__anginosus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00472199	0	0	0	0	0	0
s__infantis	0.00403388	0	0.00691595	0.00225195	5.60994561	0	0.01729326	0	0	0.01943446	0.00401832	0.00601854	0	0.0205571	0.10152284	0.02286106	0.18804062	0	2.35109718	2.31213873	1.33333333
s__minor	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
unclassified	0	0.00291206	0	0.00225195	0.22533023	0.01132631	0.01729326	0	0.00180408	0.00485861	0	0.00200618	0	0	0.002361	0.00571527	0	0.00188957	0.15673981	0.28901734	1.09090909
c__Clostridia	0.01210165	0.00582411	0.01152658	0	1.8958819	0	0.00345865	0.04502476	0	0.02429307	0.00401832	0.00601854	0	0	2.50265612	0.00285763	0.02507208	0	1.09717868	1.44508671	0
o__Clostridiales	0.01210165	0.00582411	0.01152658	0	1.8958819	0	0.00345865	0.04502476	0	0.02429307	0.00401832	0.00601854	0	0	2.50265612	0.00285763	0.02507208	0	1.09717868	1.44508671	0
f__Clostridiaceae	0	0	0.00461063	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	1.15606936	0
g__02d06	0	0	0.00230532	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.00230532	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Clostridium	0	0	0.00230532	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	1.15606936	0
s__kluyveri	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0.28901734	0
s__sartagoforme	0	0	0.00230532	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.86705202	0
s__septicum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Lachnospiraceae	0	0.00291206	0.00461063	0	0.03885004	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Blautia	0	0.00291206	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__producta	0	0.00291206	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Catonella	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Clostridium	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__celerecrescens	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__clostridioforme	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oribacterium	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pseudobutyrivibrio	0	0	0.00230532	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.00230532	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseburia	0	0	0.00230532	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__faecis	0	0	0.00230532	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Peptococcaceae	0	0	0	0	0.00777001	0	0	0.04502476	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Desulfosporosinus	0	0	0	0	0.00777001	0	0	0.04502476	0	0	0	0	0	0	0	0	0	0	0	0	0
s__meridiei	0	0	0	0	0.00777001	0	0	0.04502476	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Peptostreptococcaceae	0	0	0	0	0.01554002	0	0	0	0	0	0	0.00200618	0	0	2.27600047	0	0	0	0	0	0
g__Filifactor	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Peptostreptococcus	0	0	0	0	0.00777001	0	0	0	0	0	0	0.00200618	0	0	2.27363948	0	0	0	0	0	0
s__anaerobius	0	0	0	0	0.00777001	0	0	0	0	0	0	0.00200618	0	0	2.27363948	0	0	0	0	0	0
g__[Clostridium]	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
s__difficile	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Ruminococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00472199	0	0	0	0	0	0
g__Ruminococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00472199	0	0	0	0	0	0
s__bromii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00472199	0	0	0	0	0	0
f__Symbiobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Symbiobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__thermophilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Veillonellaceae	0	0.00291206	0.00230532	0	0.5982906	0	0	0	0	0	0	0.00401236	0	0	0.00708299	0	0	0	0.47021944	0	0
g__Dialister	0	0.00291206	0.00230532	0	0.00777001	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
unclassified	0	0.00291206	0.00230532	0	0.00777001	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
g__Megasphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
g__Selenomonas	0	0	0	0	0.03108003	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__noxia	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Veillonella	0	0	0	0	0.55944056	0	0	0	0	0	0	0.00401236	0	0	0.00472199	0	0	0	0.31347962	0	0
s__dispar	0	0	0	0	0.15540016	0	0	0	0	0	0	0.00401236	0	0	0.00472199	0	0	0	0.31347962	0	0
s__parvula	0	0	0	0	0.4040404	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__[Mogibacteriaceae]	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0.00472199	0	0	0	0	0	0
g__Mogibacterium	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
f__[Tissierellaceae]	0.01210165	0	0	0	1.21989122	0	0.00345865	0	0	0.02429307	0.00401832	0	0	0	0.21012867	0.00285763	0.02507208	0	0.47021944	0.28901734	0
g__1-68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Anaerococcus	0.00403388	0	0	0	0.71484071	0	0	0	0	0.02429307	0	0	0	0	0.02124897	0.00285763	0.01253604	0	0.31347962	0	0
unclassified	0.00403388	0	0	0	0.71484071	0	0	0	0	0.02429307	0	0	0	0	0.02124897	0.00285763	0.01253604	0	0.31347962	0	0
g__Finegoldia	0	0	0	0	0.25641026	0	0.00345865	0	0	0	0.00401832	0	0	0	0.10388384	0	0	0	0.15673981	0.28901734	0
unclassified	0	0	0	0	0.25641026	0	0.00345865	0	0	0	0.00401832	0	0	0	0.10388384	0	0	0	0.15673981	0.28901734	0
g__Parvimonas	0.00806777	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0.08499587	0	0	0	0	0	0
unclassified	0.00806777	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0.08499587	0	0	0	0	0	0
g__Peptoniphilus	0	0	0	0	0.24087024	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.24087024	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__ph2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01253604	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01253604	0	0	0	0
c__Erysipelotrichi	0	0	0.00230532	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Erysipelotrichales	0	0	0.00230532	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Erysipelotrichaceae	0	0	0.00230532	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__[Eubacterium]	0	0	0.00230532	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__biforme	0	0	0.00230532	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Fusobacteria	0	0.00291206	0	0	0.58275058	0	0	0	0	0.00485861	0	0	0	0	7.46074844	0	0	0	0.47021944	0	0.48484848
c__Fusobacteriia	0	0.00291206	0	0	0.58275058	0	0	0	0	0.00485861	0	0	0	0	7.46074844	0	0	0	0.47021944	0	0.48484848
o__Fusobacteriales	0	0.00291206	0	0	0.58275058	0	0	0	0	0.00485861	0	0	0	0	7.46074844	0	0	0	0.47021944	0	0.48484848
f__Fusobacteriaceae	0	0	0	0	0.41958042	0	0	0	0	0.00485861	0	0	0	0	7.46074844	0	0	0	0.47021944	0	0.48484848
g__Fusobacterium	0	0	0	0	0.41958042	0	0	0	0	0.00485861	0	0	0	0	7.46074844	0	0	0	0.47021944	0	0.48484848
unclassified	0	0	0	0	0.41958042	0	0	0	0	0.00485861	0	0	0	0	7.46074844	0	0	0	0.47021944	0	0.48484848
f__Leptotrichiaceae	0	0.00291206	0	0	0.16317016	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Leptotrichia	0	0.00291206	0	0	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.00291206	0	0	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Streptobacillus	0	0	0	0	0.13986014	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__moniliformis	0	0	0	0	0.13986014	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Gemmatimonadetes	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Gemm-1	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Planctomycetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
c__Planctomycetia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
o__Gemmatales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
f__Isosphaeraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
p__Proteobacteria	0.18959258	0.24170064	0.21439439	0.09007792	1.18881119	2.03873598	0.31819597	0.27014858	0.03788562	0.41298222	0.14867797	0.11635838	0.17424596	0.65782711	0.02833196	0.20289192	1.6171493	0.06613507	75.7053292	91.0404624	89.5757576
c__Alphaproteobacteria	0.02823719	0.02329645	0.02535848	0.01351169	0.11655012	0.22652622	0.06571438	0.04502476	0.00721631	0.05344476	0.01607329	0.0100309	0.02945002	0.09764621	0.00472199	0.02571869	0.23818478	0.00566872	10.9717868	10.1156069	11.2727273
o__Caulobacterales	0	0	0	0	0.04662005	0	0	0	0	0.00971723	0	0	0	0	0	0	0	0.00188957	0	0	0
f__Caulobacteraceae	0	0	0	0	0.04662005	0	0	0	0	0.00971723	0	0	0	0	0	0	0	0.00188957	0	0	0
g__Brevundimonas	0	0	0	0	0	0	0	0	0	0.00971723	0	0	0	0	0	0	0	0.00188957	0	0	0
s__diminuta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00188957	0	0	0
s__staleyi	0	0	0	0	0	0	0	0	0	0.00971723	0	0	0	0	0	0	0	0	0	0	0
g__Caulobacter	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__vibrioides	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Phenylobacterium	0	0	0	0	0.03108003	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.03108003	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rhizobiales	0.00403388	0	0.00461063	0.00225195	0.03108003	0.01132631	0	0	0.00180408	0.00971723	0	0	0	0	0.00472199	0	0	0.00188957	0.15673981	0.86705202	0.36363636
f__Aurantimonadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Bradyrhizobiaceae	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
g__Balneimonas	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bosea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
s__genosp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
f__Brucellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00188957	0	0	0
g__Pseudochrobactrum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00188957	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00188957	0	0	0
f__Hyphomicrobiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0.57803468	0
g__Devosia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
g__Rhodomicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.57803468	0
s__vannielii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.57803468	0
f__Methylobacteriaceae	0	0	0.00461063	0	0.00777001	0	0	0	0	0.00485861	0	0	0	0	0.002361	0	0	0	0	0	0.36363636
g__Methylobacterium	0	0	0.00461063	0	0.00777001	0	0	0	0	0.00485861	0	0	0	0	0.002361	0	0	0	0	0	0.36363636
s__adhaesivum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.12121212
s__hispanicum	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__komagatae	0	0	0.00461063	0	0	0	0	0	0	0.00485861	0	0	0	0	0	0	0	0	0	0	0.24242424
s__organophilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0

f__Phyllobacteriaceae	0.00403388	0	0	0	0	0	0	0	0	0.00485861	0	0	0	0	0	0	0	0	0	0.28901734	0
g__Aminobacter	0.00403388	0	0	0	0	0	0	0	0	0.00485861	0	0	0	0	0	0	0	0	0	0.28901734	0
unclassified	0.00403388	0	0	0	0	0	0	0	0	0.00485861	0	0	0	0	0	0	0	0	0	0.28901734	0
f__Rhizobiaceae	0	0	0	0.00225195	0.00777001	0.01132631	0	0	0.00180408	0	0	0	0	0	0	0	0	0	0	0	0
g__Agrobacterium	0	0	0	0.00225195	0.00777001	0.01132631	0	0	0.00180408	0	0	0	0	0	0	0	0	0	0	0	0
s__sullae	0	0	0	0.00225195	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.01132631	0	0	0.00180408	0	0	0	0	0	0	0	0	0	0	0	0
o__Rhodobacterales	0	0	0	0	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Rhodobacteraceae	0	0	0	0	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Paracoccus	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s_aminovorans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__marcusii	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rubellimicrobium	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rhodospirillales	0.01613554	0.02329645	0.02074784	0.01125974	0	0.21519991	0.06225573	0.01500825	0.00541223	0.02915169	0.01607329	0.00802472	0.02699585	0.09250694	0	0.02571869	0.22564874	0.00188957	8.77742947	8.95953757	10.5454545
f__Acetobacteraceae	0.01613554	0.02329645	0.02074784	0.01125974	0	0.21519991	0.06225573	0	0.00541223	0.02429307	0.01607329	0.00802472	0.02699585	0.09250694	0	0.02571869	0.22564874	0.00188957	8.77742947	8.95953757	10.5454545
g__Acidocella	0.01613554	0.02329645	0.02074784	0.01125974	0	0.21519991	0.06225573	0	0.00541223	0.02429307	0.01607329	0.00802472	0.02699585	0.09250694	0	0.02571869	0.22564874	0.00188957	8.62068966	8.95953757	10.5454545
unclassified	0.01613554	0.02329645	0.02074784	0.01125974	0	0.21519991	0.06225573	0	0.00541223	0.02429307	0.01607329	0.00802472	0.02699585	0.09250694	0	0.02571869	0.22564874	0.00188957	8.62068966	8.95953757	10.5454545
g__Roseococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
f__Rhodospirillaceae	0	0	0	0	0	0	0	0.01500825	0	0.00485861	0	0	0	0	0	0	0	0	0	0	0
g__Defluviicoccus	0	0	0	0	0	0	0	0.01500825	0	0	0	0	0	0	0	0	0	0	0	0	0
s__vanus	0	0	0	0	0	0	0	0.01500825	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oleomonas	0	0	0	0	0	0	0	0	0	0.00485861	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0.00485861	0	0	0	0	0	0	0	0	0	0	0
o__Sphingomonadales	0.00806777	0	0	0	0.01554002	0	0.00345865	0.03001651	0	0.00485861	0	0.00200618	0.00245417	0.00513927	0	0	0.01253604	0	2.03761755	0.28901734	0.36363636
f__Erythrobacteraceae	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lutibacterium	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Sphingomonadaceae	0.00806777	0	0	0	0.00777001	0	0.00345865	0.03001651	0	0.00485861	0	0.00200618	0.00245417	0.00513927	0	0	0.01253604	0	2.03761755	0.28901734	0.36363636
g__Kaistobacter	0	0	0	0	0	0	0	0.03001651	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.03001651	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Sphingobium	0.00403388	0	0	0	0	0	0.00345865	0	0	0	0	0	0.00245417	0.00513927	0	0	0.01253604	0	1.09717868	0.28901734	0.12121212
s__yanoikuyae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01253604	0	0	0.28901734	0
unclassified	0.00403388	0	0	0	0	0	0.00345865	0	0	0	0	0	0.00245417	0.00513927	0	0	0	0	1.09717868	0	0.12121212
g__Sphingomonas	0.00403388	0	0	0	0	0	0	0	0	0.00485861	0	0.00200618	0	0	0	0	0	0	0.94043887	0	0.24242424
s__azotifigens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
s__echinoides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__suberifaciens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__yabuuchiae	0.00403388	0	0	0	0	0	0	0	0	0.00485861	0	0.00200618	0	0	0	0	0	0	0.78369906	0	0.24242424
g__Sphingopyxis	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__alaskensis	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Betaproteobacteria	0.03227108	0.04368084	0.04380101	0.0045039	0.90909091	0.26050515	0.02421056	0.18009905	0.00541223	0.09717229	0.02410994	0.01805561	0.02454168	0.06681057	0.01416598	0.04000686	0.2757929	0.00944787	6.73981191	6.3583815	8
o__Burkholderiales	0.03227108	0.04076878	0.04380101	0.0045039	0.14763015	0.26050515	0.02421056	0.15008255	0.00541223	0.09231367	0.02410994	0.01604943	0.02454168	0.06681057	0.00944399	0.04000686	0.2757929	0.00944787	6.42633229	6.3583815	8
f__Burkholderiaceae	0.02420331	0.0262085	0.02766379	0.00225195	0.05439005	0.15856835	0.02075191	0.03001651	0.00360815	0.04858614	0.02009162	0.01404325	0.01227084	0.04625347	0	0.02857633	0.17550458	0.00755829	2.82131661	5.20231214	7.63636364
g__Burkholderia	0.02420331	0.0262085	0.02766379	0.00225195	0.01554002	0.15856835	0.02075191	0.03001651	0.00360815	0.04858614	0.02009162	0.01404325	0.01227084	0.04625347	0	0.02857633	0.17550458	0.00755829	2.82131661	5.20231214	7.51515152
s__bryophila	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.28901734	0
s__graminis	0	0	0	0	0	0	0	0.01500825	0	0	0	0	0	0	0	0	0	0	0	0	0
s__tuberum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.02420331	0.0262085	0.02766379	0.00225195	0.01554002	0.15856835	0.02075191	0.01500825	0.00360815	0.04858614	0.02009162	0.01404325	0.01227084	0.04625347	0	0.02857633	0.17550458	0.00755829	2.82131661	4.9132948	7.51515152
g__Lautropia	0	0	0	0	0.03885004	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.03885004	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pandoraea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.12121212
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.12121212
g__Salinispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__tropica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Comamonadaceae	0	0.01164822	0.00461063	0	0.03108003	0.01132631	0	0	0	0.01943446	0	0	0	0	0	0	0.01253604	0	2.50783699	0.28901734	0.36363636
g__Acidovorax	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0.31347962	0	0
s__citrulli	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__delafieldii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.31347962	0	0
s__facilis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Aquabacterium	0	0.00291206	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.47021944	0.28901734	0
unclassified	0	0.00291206	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.47021944	0.28901734	0
g__Comamonas	0	0	0.00461063	0	0	0.01132631	0	0	0	0	0	0	0	0	0	0	0.01253604	0	0	0	0
s__terrigena	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.00461063	0	0	0.01132631	0	0	0	0	0	0	0	0	0	0	0.01253604	0	0	0	0
g__Delftia	0	0.00291206	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.62695925	0	0.12121212
unclassified	0	0.00291206	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.62695925	0	0.12121212
g__Diaphorobacter	0	0.00582411	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
unclassified	0	0.00582411	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
g__Pelomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.31347962	0	0.24242424
s__puraquae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.31347962	0	0.24242424
g__Pseudorhodoferax	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.47021944	0	0
s__soli	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.47021944	0	0
g__Roseateles	0	0	0	0	0.00777001	0	0	0	0	0.00485861	0	0	0	0	0	0	0	0	0	0	0
s__depolymerans	0	0	0	0	0.00777001	0	0	0	0	0.00485861	0	0	0	0	0	0	0	0	0	0	0
g__Variovorax	0	0	0	0	0	0	0	0	0	0.01457584	0	0	0	0	0	0	0	0	0.15673981	0	0
s__paradoxus	0	0	0	0	0	0	0	0	0	0.01457584	0	0	0	0	0	0	0	0	0.15673981	0	0
g__Vitreoscilla	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__filiformis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Oxalobacteraceae	0.00806777	0.00291206	0.01152658	0.00225195	0.06216006	0.09061049	0.00345865	0.12006604	0.00180408	0.02429307	0.00401832	0.00200618	0.01227084	0.0205571	0.00944399	0.01143053	0.08775229	0.00188957	1.09717868	0.86705202	0
g__Cupriavidus	0	0	0	0	0.01554002	0	0	0.01500825	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
unclassified	0	0	0	0	0.01554002	0	0	0.01500825	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
g__Herbaspirillum	0	0	0.00230532	0	0	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
unclassified	0	0	0.00230532	0	0	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
g__Herminiimonas	0	0	0.00691595	0.00225195	0.03108003	0.05663156	0.00345865	0.06003302	0.00180408	0.01457584	0.00401832	0.00200618	0.00981667	0.01541782	0	0.0085729	0.03760812	0	0.47021944	0	0
s__fonticola	0	0	0.00691595	0.00225195	0.03108003	0.05663156	0.00345865	0.06003302	0.00180408	0.01457584	0.00401832	0.00200618	0.00981667	0.01541782	0	0.0085729	0.03760812	0	0.47021944	0	0
g__Janthinobacterium	0	0	0	0	0	0	0	0.01500825	0	0	0	0	0	0	0	0	0	0	0	0	0
s__lividum	0	0	0	0	0	0	0	0.01500825	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Massilia	0.00806777	0	0.00230532	0	0.00777001	0.02265262	0	0	0	0	0	0	0	0	0	0	0.02507208	0	0.31347962	0	0
s__aerilata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01253604	0	0	0	0
s__aurea	0.00806777	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__niastensis	0	0	0	0	0.00777001	0.02265262	0	0	0	0	0	0	0	0	0	0	0	0	0.31347962	0	0
s__timonae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01253604	0	0	0	0
s__varians	0	0	0.00230532	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Paucimonas	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__lemoignei	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ralstonia	0	0.00291206	0	0	0	0.01132631	0	0.03001651	0	0.00971723	0	0	0.00245417	0.00513927	0.00472199	0.00285763	0.02507208	0.00188957	0.31347962	0.86705202	0
unclassified	0	0.00291206	0	0	0	0.01132631	0	0.03001651	0	0.00971723	0	0	0.00245417	0.00513927	0.00472199	0.00285763	0.02507208	0.00188957	0.31347962	0.86705202	0
g__Telluria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mixta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__IS-44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Methylophilales	0	0	0	0	0	0	0	0.01500825	0	0.00485861	0	0.00200618	0	0	0	0	0	0	0	0	0
f__Methylophilaceae	0	0	0	0	0	0	0	0.01500825	0	0.00485861	0	0.00200618	0	0	0	0	0	0	0	0	0
g__Methylobacillus	0	0	0	0	0	0	0	0.01500825	0	0.00485861	0	0.00200618	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.01500825	0	0.00485861	0	0.00200618	0	0	0	0	0	0	0	0	0
o__Neisseriales	0	0.00291206	0	0	0.76146076	0	0	0.01500825	0	0	0	0	0	0	0.00472199	0	0	0	0.15673981	0	0
f__Neisseriaceae	0	0.00291206	0	0	0.76146076	0	0	0.01500825	0	0	0	0	0	0	0.00472199	0	0	0	0.15673981	0	0
g__Aquitalea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
s__magnusonii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
g__Kingella	0	0	0	0	0.10878011	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.10878011	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Neisseria	0	0.00291206	0	0	0.65268065	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0.15673981	0	0
s__cinerea	0	0	0	0	0.1010101	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__subflava	0	0.00291206	0	0	0.55167055	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0.15673981	0	0
g__Vogesella	0	0	0	0	0	0	0	0.01500825	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0.01500825	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rhodocyclales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
f__Rhodocyclaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
g__Azospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__KD1-23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Zoogloea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15673981	0	0
c__Deltaproteobacteria	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Myxococcales	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__0319-6G20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nannocystaceae	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Plesiocystis	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Polyangiaceae	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Polyangium	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__fumosum	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Epsilonproteobacteria	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0.62695925	0	0.12121212
o__Campylobacterales	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0.62695925	0	0.12121212
f__Campylobacteraceae	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Campylobacter	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__ureolyticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Helicobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.62695925	0	0.12121212
g__Helicobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.62695925	0	0.12121212
s__pylori	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.62695925	0	0.12121212
c__Gammaproteobacteria	0.12908431	0.17472335	0.14523491	0.07206233	0.13209013	1.55170461	0.22827102	0.04502476	0.02525708	0.26236517	0.10849474	0.08827188	0.12025425	0.49337034	0.00944399	0.13716637	1.10317162	0.05101848	57.3667712	74.566474	70.1818182
o__Enterobacteriales	0	0	0	0	0	0	0	0	0	0.02429307	0	0	0.00245417	0	0	0.00571527	0	0.00377915	0	0.57803468	0
f__Enterobacteriaceae	0	0	0	0	0	0	0	0	0	0.02429307	0	0	0.00245417	0	0	0.00571527	0	0.00377915	0	0.57803468	0
g__Enterobacter	0	0	0	0	0	0	0	0	0	0	0	0	0.00245417	0	0	0.00571527	0	0	0	0.57803468	0
s__aerogenes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__cowanii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__hormaechei	0	0	0	0	0	0	0	0	0	0	0	0	0.00245417	0	0	0.00571527	0	0	0	0.57803468	0
g__Pantoea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

s__ananatis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Salmonella	0	0	0	0	0	0	0	0	0	0.02429307	0	0	0	0	0	0	0	0.00377915	0	0	0
s__enterica	0	0	0	0	0	0	0	0	0	0.02429307	0	0	0	0	0	0	0	0.00377915	0	0	0
g__Yokenella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__regensburgei	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Pasteurellales	0	0	0	0	0.05439005	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
f__Pasteurellaceae	0	0	0	0	0.05439005	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
g__Aggregatibacter	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__segnis	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Haemophilus	0	0	0	0	0.04662005	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
s__influenzae	0	0	0	0	0.03885004	0	0	0	0	0	0	0	0	0	0.002361	0	0	0	0	0	0
s__parainfluenzae	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Pseudomonadales	0.00403388	0	0.00461063	0	0.04662005	0.05663156	0	0.04502476	0	0.01943446	0	0	0	0.03597492	0.002361	0.0085729	0.03760812	0.00188957	0	0.57803468	0.36363636
f__Moraxellaceae	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.28901734	0.12121212
g__Acinetobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.28901734	0
s__lwoffii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__rhizosphaerae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.28901734	0
g__Enhydrobacter	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Moraxella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.12121212
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.12121212
f__Pseudomonadaceae	0.00403388	0	0.00461063	0	0.03108003	0.05663156	0	0.04502476	0	0.01943446	0	0	0	0.03597492	0.002361	0.0085729	0.03760812	0.00188957	0	0.28901734	0.24242424
g__Pseudomonas	0.00403388	0	0.00461063	0	0.03108003	0.05663156	0	0.04502476	0	0.01943446	0	0	0	0.03597492	0.002361	0.0085729	0.03760812	0.00188957	0	0.28901734	0.24242424
s__umsongensis	0.00403388	0	0.00230532	0	0.01554002	0.03397893	0	0.03001651	0	0.00971723	0	0	0	0.03083565	0.002361	0.00285763	0.01253604	0	0	0.28901734	0
s__veronii	0	0	0.00230532	0	0	0.02265262	0	0	0	0.00971723	0	0	0	0.00513927	0	0.00571527	0.02507208	0	0	0	0.24242424
s__viridiflava	0	0	0	0	0.01554002	0	0	0.01500825	0	0	0	0	0	0	0	0	0	0.00188957	0	0	0
o__Thiotrichales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01253604	0	0	0	0
f__Thiotrichaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01253604	0	0	0	0
g__Beggiatoa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01253604	0	0	0	0
s__alba	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01253604	0	0	0	0
o__Xanthomonadales	0.12505042	0.17472335	0.14062428	0.07206233	0.03108003	1.49507305	0.22827102	0	0.02525708	0.21863764	0.10849474	0.08827188	0.11780008	0.45739542	0.00472199	0.12287821	1.05302745	0.04534976	57.3667712	73.4104046	69.8181818
f__Xanthomonadaceae	0.12505042	0.17472335	0.14062428	0.07206233	0.03108003	1.49507305	0.22827102	0	0.02525708	0.21863764	0.10849474	0.08827188	0.11780008	0.45739542	0.00472199	0.12287821	1.05302745	0.04534976	57.3667712	73.4104046	69.8181818
g__Dyella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.12121212
s__japonica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.12121212
g__Fulvimonas	0	0	0	0	0	0.03397893	0	0	0	0	0.00803665	0	0	0	0	0	0	0	0	0	0.36363636
s__soli	0	0	0	0	0	0.03397893	0	0	0	0	0.00803665	0	0	0	0	0	0	0	0	0	0.36363636
g__Pseudoxanthomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__kaohsiungensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodanobacter	0.12505042	0.1718113	0.14062428	0.07206233	0	1.46109412	0.22481237	0	0.02525708	0.21377903	0.10045809	0.08827188	0.11780008	0.45225614	0.00472199	0.12287821	1.01541933	0.04534976	57.0532915	73.1213873	69.2121212
s__terrae	0.12505042	0.1718113	0.14062428	0.07206233	0	1.46109412	0.22481237	0	0.02525708	0.21377903	0.10045809	0.08827188	0.11780008	0.45225614	0.00472199	0.12287821	1.01541933	0.04534976	57.0532915	73.1213873	69.2121212
g__Stenotrophomonas	0	0.00291206	0	0	0.01554002	0	0.00345865	0	0	0.00485861	0	0	0	0.00513927	0	0	0.03760812	0	0.31347962	0.28901734	0.12121212
s__geniculata	0	0	0	0	0.01554002	0	0.00345865	0	0	0.00485861	0	0	0	0.00513927	0	0	0.03760812	0	0.31347962	0.28901734	0.12121212
s__maltophilia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__rhizophila	0	0.00291206	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Xanthomonas	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__axonopodis	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Spirochaetes	0	0	0	0	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Spirochaetes	0	0	0	0	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Spirochaetales	0	0	0	0	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Spirochaetaceae	0	0	0	0	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Treponema	0	0	0	0	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__socranskii	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.01554002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__TM7	0	0	0	0	0.05439005	0	0	0	0	0	0	0	0	0	0	0	0	0	0.31347962	1.44508671	0
c__TM7-1	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.00777001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__TM7-3	0	0	0	0	0.04662005	0	0	0	0	0	0	0	0	0	0	0	0	0	0.31347962	1.44508671	0
o__EW055	0	0	0	0	0.04662005	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.44508671	0
unclassified	0	0	0	0	0.04662005	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.44508671	0
unclassified	0	0	0	0	0.04662005	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.44508671	0
unclassified	0	0	0	0	0.04662005	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.44508671	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.31347962	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.31347962	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.31347962	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.31347962	0	0
p__[Thermi]	0	0	0	0	0.02331002	0.01132631	0	0	0	0	0	0	0	0.00513927	0	0	0	0	0	0	0
c__Deinococci	0	0	0	0	0.02331002	0.01132631	0	0	0	0	0	0	0	0.00513927	0	0	0	0	0	0	0
o__Deinococcales	0	0	0	0	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Deinococcaceae	0	0	0	0	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Deinococcus	0	0	0	0	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0.02331002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Thermales	0	0	0	0	0	0.01132631	0	0	0	0	0	0	0	0.00513927	0	0	0	0	0	0	0
f__Thermaceae	0	0	0	0	0	0.01132631	0	0	0	0	0	0	0	0.00513927	0	0	0	0	0	0	0
g__Meiothermus	0	0	0	0	0	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0.01132631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermus	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00513927	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00513927	0	0	0	0	0	0	0

Sample ID	2055Z	2080Z	2083Z	2128Z	2129Z	2172Z	2203Z	2250Z	2306Z	2326Z	2367Z	2423Z	2637Z	2758Z	2867Z	PBS
Infection Group	Cellulitis	Cellulitis	Cellulitis	Cellulitis	Cellulitis	Cellulitis	Cellulitis	Cellulitis	Cellulitis	Cellulitis	Cellulitis	Cellulitis	Cellulitis	Cellulitis	Cellulitis	Control
Total Number of Reads	577	474	489	289	270	247	149	299	565	322	432	459	956	721	583	3
Taxon																
p__Acidobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Acidobacteriia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Acidobacteriales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Acidobacteriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Solibacteres	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Solibacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__MVS-65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__[Chloracidobacteria]	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__RB41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Actinobacteria	1.3864818	2.32067511	4.49897751	1.73010381	2.22222222	2.4291498	3.3557047	3.34448161	2.12389381	1.24223602	2.5462963	1.08932462	1.67364017	1.66435506	2.5728988	0
c__Actinobacteria	1.3864818	2.32067511	4.49897751	1.73010381	2.22222222	2.4291498	3.3557047	3.34448161	2.12389381	1.24223602	2.5462963	1.08932462	1.67364017	1.52565881	2.5728988	0
o__Actinomycetales	1.3864818	2.32067511	4.49897751	1.73010381	2.22222222	2.4291498	3.3557047	3.34448161	2.12389381	1.24223602	2.5462963	1.08932462	1.67364017	1.52565881	2.5728988	0
f__Actinomycetaceae	0	0	0	0.34602076	0	0	0	0	0.17699115	0.31055901	0	0	0.20920502	0	0.17152659	0
g__Actinobaculum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Actinomyces	0	0	0	0.34602076	0	0	0	0	0.17699115	0.31055901	0	0	0.20920502	0	0.17152659	0
unclassified	0	0	0	0.34602076	0	0	0	0	0.17699115	0.31055901	0	0	0.20920502	0	0.17152659	0
g__Varibaculum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Actinosynnemataceae	0.17331023	0.21097046	0	0	0	0	0	0.3344816	0	0	0.46296296	0	0	0.27739251	0	0
g__Lechevalieria	0.17331023	0.21097046	0	0	0	0	0	0.3344816	0	0	0.46296296	0	0	0.27739251	0	0
s__aerocolonigenes	0.17331023	0.21097046	0	0	0	0	0	0.3344816	0	0	0.46296296	0	0	0.27739251	0	0
f__Bogoriellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Georgenia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Brevibacteriaceae	0.17331023	0.21097046	0	0	0	0	0	0	0	0	0.23148148	0	0	0	0.34305317	0
g__Brevibacterium	0.17331023	0.21097046	0	0	0	0	0	0	0	0	0.23148148	0	0	0	0.34305317	0
s__casei	0	0.21097046	0	0	0	0	0	0	0	0	0.23148148	0	0	0	0.34305317	0
s__paucivorans	0.17331023	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Corynebacteriaceae	0.17331023	0.42194093	0	0.69204152	1.48148148	1.2145749	0	0.3344816	0.53097345	0	0.69444444	0.21786492	0.10460251	0	0.68610635	0
g__Corynebacterium	0.17331023	0.42194093	0	0.69204152	1.48148148	1.2145749	0	0.3344816	0.53097345	0	0.69444444	0.21786492	0.10460251	0	0.68610635	0
s__durum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__kroppenstedtii	0	0	0	0	0	0	0	0	0	0	0	0	0.10460251	0	0	0
s__lubricantis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__pilosum	0	0	0	0	0	1.2145749	0	0	0	0	0	0	0	0	0	0
s__simulans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.17331023	0.42194093	0	0.69204152	1.48148148	0	0	0.3344816	0.53097345	0	0.69444444	0.21786492	0	0	0.68610635	0
f__Dermabacteraceae	0	0	0.61349693	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Brachybacterium	0	0	0.61349693	0	0	0	0	0	0	0	0	0	0	0	0	0
s__conglomeratum	0	0	0.61349693	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Frankiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Geodermatophilaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Blastococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__aggregatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Gordoniaceae	0	0.63291139	0.61349693	0	0	0	0	0.66889632	0	0	0.23148148	0	0.20920502	0	0	0
g__Gordonia	0	0.63291139	0.61349693	0	0	0	0	0.66889632	0	0	0.23148148	0	0.20920502	0	0	0
unclassified	0	0.63291139	0.61349693	0	0	0	0	0.66889632	0	0	0.23148148	0	0.20920502	0	0	0
f__Intrasporangiaceae	0	0	0	0	0	0	1.34228188	0	0	0	0	0	0	0	0	0
g__Lapillicoccus	0	0	0	0	0	0	1.34228188	0	0	0	0	0	0	0	0	0
s__jejuensis	0	0	0	0	0	0	1.34228188	0	0	0	0	0	0	0	0	0
f__Microbacteriaceae	0.17331023	0.21097046	0	0.69204152	0.37037037	0	0	0	0	0	0	0	0	0	0.17152659	0
g__Curtobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Frigoribacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Leucobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Microbacterium	0.17331023	0.21097046	0	0.34602076	0.37037037	0	0	0	0	0	0	0	0	0	0.17152659	0
s__chocolatum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__maritypicum	0.17331023	0.21097046	0	0.34602076	0.37037037	0	0	0	0	0	0	0	0	0	0.17152659	0
g__Mycetocola	0	0	0	0.34602076	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0.34602076	0	0	0	0	0	0	0	0	0	0	0	0
f__Micrococcaceae	0	0.42194093	0.40899796	0	0	0	0	0	0	0	0	0	0	0.41608877	0.17152659	0
g__Arthrobacter	0	0	0.20449898	0	0	0	0	0	0	0	0	0	0	0	0	0
s__psychrolactophilus	0	0	0.20449898	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Kocuria	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27739251	0	0
s__rhizophila	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27739251	0	0
g__Microbispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__rosea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Micrococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__luteus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nesterenkonia	0	0.21097046	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.21097046	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Renibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rothia	0	0.21097046	0.20449898	0	0	0	0	0	0	0	0	0	0	0.13869626	0.17152659	0
s__aeria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__dentocariosa	0	0.21097046	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__mucilaginosa	0	0	0.20449898	0	0	0	0	0	0	0	0	0	0	0.13869626	0.17152659	0
f__Micromonosporaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Micromonospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__narathiwatensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Solwaraspora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Nocardioidaceae	0	0	0.40899796	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Aeromicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Friedmanniella	0	0	0.20449898	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0.20449898	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Nocardioides	0	0	0.20449898	0	0	0	0	0	0	0	0	0	0	0	0	0
s__dokdonensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__furvisabuli	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__panacihumi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__terrigena	0	0	0.20449898	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Propionicimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Promicromonosporaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13869626	0	0
g__Xylanimicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13869626	0	0
s__pachnodae	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13869626	0	0
f__Propionibacteriaceae	0.6932409	0.21097046	2.45398773	0	0.37037037	1.2145749	2.01342282	2.00668896	1.4159292	0.93167702	0.92592593	0.87145969	1.15062762	0.55478502	1.02915952	0
g__Propionibacterium	0.6932409	0.21097046	2.45398773	0	0.37037037	1.2145749	2.01342282	2.00668896	1.4159292	0.93167702	0.92592593	0.87145969	1.15062762	0.55478502	1.02915952	0
s__acnes	0.6932409	0.21097046	2.24948875	0	0.37037037	1.2145749	2.01342282	1.6722408	1.4159292	0.93167702	0.69444444	0.87145969	1.15062762	0.55478502	1.02915952	0
s__granulosum	0	0	0.20449898	0	0	0	0	0.3344816	0	0	0.23148148	0	0	0	0	0
f__Tsukamurellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Tsukamurella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Yaniellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13869626	0	0
g__Yaniella	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13869626	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13869626	0	0
c__Thermoleophilia	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13869626	0	0
o__Solirubrobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13869626	0	0
f__Conexibacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Conexibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Patulibacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13869626	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13869626	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13869626	0	0
p__Bacteroidetes	0.51993068	0.84388186	0	1.73010381	0.74074074	0.4048583	0.67114094	2.67558528	0.53097345	0.62111801	1.85185185	1.30718954	0.52301255	1.66435506	2.05831904	0
c__Bacteroidia	0	0.21097046	0	0	0	0.4048583	0	0	0	0	0.23148148	0	0.10460251	0	0.85763293	0
o__Bacteroidales	0	0.21097046	0	0	0	0.4048583	0	0	0	0	0.23148148	0	0.10460251	0	0.85763293	0
f__Porphyromonadaceae	0	0.21097046	0	0	0	0	0	0	0	0	0	0	0.10460251	0	0	0
g__Paludibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Porphyromonas	0	0.21097046	0	0	0	0	0	0	0	0	0	0	0.10460251	0	0	0
s__endodontalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0.21097046	0	0	0	0	0	0	0	0	0	0	0.10460251	0	0	0
f__Prevotellaceae	0	0	0	0	0	0.4048583	0	0	0	0	0.23148148	0	0	0	0.51457976	0
g__Prevotella	0	0	0	0	0	0.4048583	0	0	0	0	0.23148148	0	0	0	0.51457976	0
s__copri	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__melaninogenica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.34305317	0
s__nanceiensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__pallens	0	0	0	0	0	0.4048583	0	0	0	0	0	0	0	0	0	0
s__stercorea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.17152659	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.23148148	0	0	0	0	0
f__Rikenellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Blvii28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__S24-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__[Paraprevotellaceae]	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.34305317	0
g__YRC22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__[Prevotella]	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.34305317	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.34305317	0
c__Cytophagia	0	0.21097046	0	0	0	0	0	0	0.3344816	0	0	0	0	0	0	0	0	0
o__Cytophagales	0	0.21097046	0	0	0	0	0	0	0.3344816	0	0	0	0	0	0	0	0	0
f__Cytophagaceae	0	0.21097046	0	0	0	0	0	0	0.3344816	0	0	0	0	0	0	0	0	0
g__Hymenobacter	0	0.21097046	0	0	0	0	0	0	0.3344816	0	0	0	0	0	0	0	0	0
unclassified	0	0.21097046	0	0	0	0	0	0	0.3344816	0	0	0	0	0	0	0	0	0
g__Sporocytophaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Flavobacteriia	0.51993068	0.42194093	0	1.38408304	0.74074074	0	0.67114094	2.34113712	0.53097345	0.62111801	1.38888889	1.08932462	0.41841004	1.66435506	1.20068611	0		
o__Flavobacteriales	0.51993068	0.42194093	0	1.38408304	0.74074074	0	0.67114094	2.34113712	0.53097345	0.62111801	1.38888889	1.08932462	0.41841004	1.66435506	1.20068611	0		
f__Flavobacteriaceae	0	0.21097046	0	1.03806228	0.37037037	0	0	1.00334448	0.3539823	0	0	0.65359477	0	0.55478502	0.34305317	0		
g__Capnocytophaga	0	0	0	0	0	0	0	0.66889632	0	0	0	0	0	0	0	0		
s__ochracea	0	0	0	0	0	0	0	0.66889632	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Flavobacterium	0	0.21097046	0	0	0	0	0	0	0	0	0	0	0.43572985	0	0	0		
s__gelidilacus	0	0.21097046	0	0	0	0	0	0	0	0	0	0	0.43572985	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Lutaonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
s__thermophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Myroides	0	0	0	0	0.37037037	0	0	0.3344816	0	0	0	0	0	0.55478502	0.34305317	0		
s__odoratimimus	0	0	0	0	0.37037037	0	0	0.3344816	0	0	0	0	0	0.55478502	0.34305317	0		
g__Sediminicola	0	0	0	1.03806228	0	0	0	0	0.3539823	0	0	0.21786492	0	0	0	0		
s__luteus	0	0	0	1.03806228	0	0	0	0	0.3539823	0	0	0.21786492	0	0	0	0		
f__[Weeksellaceae]	0.51993068	0.21097046	0	0.34602076	0.37037037	0	0.67114094	1.33779264	0.17699115	0.62111801	1.38888889	0.43572985	0.41841004	1.10957004	0.85763293	0		
g__Bergeyella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
s__zoohelcum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Chryseobacterium	0.17331023	0.21097046	0	0.34602076	0.37037037	0	0.67114094	1.33779264	0.17699115	0.31055901	1.38888889	0.43572985	0.31380753	0.27739251	0.85763293	0		
unclassified	0.17331023	0.21097046	0	0.34602076	0.37037037	0	0.67114094	1.33779264	0.17699115	0.31055901	1.38888889	0.43572985	0.31380753	0.27739251	0.85763293	0		
g__Cloacibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0.83217753	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.83217753	0	0		
g__Elizabethkingia	0.34662045	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
s__meningoseptica	0.34662045	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Riemerella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Wautersiella	0	0	0	0	0	0	0	0	0	0.31055901	0	0	0.10460251	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0.31055901	0	0	0.10460251	0	0	0		
g__Weeksella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
s__virosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
c__Sphingobacteriia	0	0	0	0.34602076	0	0	0	0	0	0	0.23148148	0.21786492	0	0	0	0		
o__Sphingobacteriales	0	0	0	0.34602076	0	0	0	0	0	0	0.23148148	0.21786492	0	0	0	0		
f__Sphingobacteriaceae	0	0	0	0.34602076	0	0	0	0	0	0	0.23148148	0.21786492	0	0	0	0		
g__Sphingobacterium	0	0	0	0.34602076	0	0	0	0	0	0	0.23148148	0.21786492	0	0	0	0		
s__multivorum	0	0	0	0.34602076	0	0	0	0	0	0	0.23148148	0.21786492	0	0	0	0		
c__[Saprospirae]	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
o__[Saprospirales]	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
f__Chitinophagaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Flavisolibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Segetibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
p__Chloroflexi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
c__Anaerolineae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
o__Caldilineales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
f__Caldilineaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
o__SBR1031	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
f__SJA-101	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
c__Ellin6529	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
c__Gitt-GS-136	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
p__Cyanobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
c__ML635J-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
p__Firmicutes	6.41247834	5.48523207	4.49897751	1.73010381	4.07407407	5.66801619	5.36912752	5.01672241	6.37168142	5.59006211	7.40740741	7.62527233	5.85774059	11.9278779	4.80274443	0		
c__Bacilli	6.06585789	4.43037975	4.08997955	0.34602076	2.59259259	5.26315789	5.36912752	4.68227425	5.13274336	5.59006211	6.48148148	6.31808279	5.75313808	10.4022191	4.80274443	0		
o__Bacillales	4.50606586	1.89873418	1.02249489	0.34602076	2.59259259	4.4534413	2.01342282	0.33444816	2.30088496	0.31055901	3.47222222	3.26797386	2.30125523	6.51872399	1.02915952	0		
f__Alicyclobacillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Alicyclobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
f__Bacillaceae	0.17331023	0	0	0.34602076	0	0.8097166	0	0	0	0	0	0	0	0.83217753	0	0		
g__Bacillus	0.17331023	0	0	0	0	0.8097166	0	0	0	0	0	0	0	0.83217753	0	0		
s__cereus	0.17331023	0	0	0	0	0.8097166	0	0	0	0	0	0	0	0	0	0		
s__flexus	0	0	0	0	0	0	0	0	0	0	0	0	0	0.83217753	0	0		
s__fumarioli	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
s__safensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
s__trypoxylicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Geobacillus	0	0	0	0.34602076	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0.34602076	0	0	0	0	0	0	0	0	0	0	0	0		
f__Listeriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Listeria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
s__monocytogenes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
f__Paenibacillaceae	0	0.42194093	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Brevibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
s__invocatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Paenibacillus	0	0.42194093	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
s__amylolyticus	0	0.42194093	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
f__Planococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Rummeliibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Staphylococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
s__saprophyticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
f__Staphylococcaceae	4.15944541	1.47679325	1.02249489	0	2.59259259	3.6437247	2.01342282	0.33444816	2.12389381	0.31055901	3.47222222	3.26797386	2.30125523	5.68654646	1.02915952	0		
g__Jeotgalicoccus	0	0.21097046	0	0	0	0	0	0	0	0	0	0	0.10460251	0	0	0		
s__psychrophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0.21097046	0	0	0	0	0	0	0	0	0	0	0.10460251	0	0	0		
g__Macrococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
s__brunensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Staphylococcus	4.15944541	1.26582278	1.02249489	0	2.59259259	3.6437247	2.01342282	0.33444816	2.12389381	0.31055901	3.47222222	3.26797386	2.19665272	5.68654646	1.02915952	0		
s__aureus	1.3864818	0	0	0	0.74074074	1.2145749	0.67114094	0	0	0	1.15740741	0	0.41841004	1.80305132	0.17152659	0		
s__epidermidis	1.3864818	0.63291139	0.61349693	0	0.37037037	0.8097166	0	0.33444816	1.0619469	0	0.46296296	0.65359477	0.94142259	0.97087379	0.17152659	0		
s__equorum	0.17331023	0	0	0	1.11111111	0	0	0	0	0	0	0	0	0	0	0		
s__haemolyticus	1.21317158	0	0	0	0.37037037	1.6194332	1.34228188	0	1.0619469	0.31055901	1.62037037	0	0.83682008	2.49653259	0.68610635	0		
s__lugdunensis	0	0.63291139	0.40899796	0	0	0	0	0	0	0	0.23148148	2.61437908	0	0.41608877	0	0		
s__succinus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
f__Thermoactinomycetaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
f__[Exiguobacteraceae]	0.17331023	0	0	0	0	0	0	0	0.17699115	0	0	0	0	0	0	0		
g__Exiguobacterium	0.17331023	0	0	0	0	0	0	0	0.17699115	0	0	0	0	0	0	0		
unclassified	0.17331023	0	0	0	0	0	0	0	0.17699115	0	0	0	0	0	0	0		
o__Gemellales	0.17331023	0	0.61349693	0	0	0	0	0	0	0	0	0.43572985	0	0.13869626	0	0		
f__Gemellaceae	0.17331023	0	0.61349693	0	0	0	0	0	0	0	0	0.43572985	0	0.13869626	0	0		
g__Gemella	0.17331023	0	0.61349693	0	0	0	0	0	0	0	0	0.43572985	0	0.13869626	0	0		
unclassified	0.17331023	0	0.61349693	0	0	0	0	0	0	0	0	0.43572985	0	0.13869626	0	0		
o__Lactobacillales	1.3864818	2.53164557	2.45398773	0	0	0.8097166	3.3557047	4.34782609	2.83185841	5.27950311	3.00925926	2.61437908	3.45188285	3.74479889	3.77358491	0		
f__Aerococcaceae	0	0.21097046	0	0	0	0	0	0	0	0	0	0.21786492	0	0	0	0		
g__Aerococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Alloiococcus	0	0	0	0	0	0	0	0	0	0	0	0.21786492	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0.21786492	0	0	0	0		
g__Facklamia	0	0.21097046	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0.21097046	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
f__Carnobacteriaceae	0	0	0	0	0	0	0	1.00334448	0	0	0.92592593	0	0.52301255	0	0.34305317	0		
g__Carnobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
s__viridans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Granulicatella	0	0	0	0	0	0	0	1.00334448	0	0	0.92592593	0	0.52301255	0	0.34305317	0		
unclassified	0	0	0	0	0	0	0	1.00334448	0	0	0.92592593	0	0.52301255	0	0.34305317	0		
f__Enterococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Enterococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
s__casseliflavus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
f__Lactobacillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0.20920502	0.27739251	0	0		
g__Lactobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0.20920502	0.27739251	0	0		
s__helveticus	0	0	0	0	0	0	0	0	0	0	0	0	0.20920502	0.27739251	0	0		
f__Streptococcaceae	1.3864818	2.32067511	2.45398773	0	0	0.8097166	3.3557047	3.34448161	2.83185841	5.27950311	2.08333333	2.39651416	2.71966527	3.46740638	3.43053173	0		
g__Lactococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.02915952	0		
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.02915952	0		

g__Streptococcus	1.3864818	2.32067511	2.45398773	0	0	0.8097166	3.3557047	3.34448161	2.83185841	5.27950311	2.08333333	2.39651416	2.71966527	3.46740638	2.40137221	0
s__agalactiae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__anginosus	0	0	0	0	0	0	0	0	0.17699115	0	0	0	0	0	0	0
s__infantis	0.86655113	2.32067511	2.04498978	0	0	0.8097166	1.34228188	1.33779264	2.30088496	4.03726708	1.85185185	1.96078431	2.19665272	2.49653259	2.05831904	0
s__minor	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0.51993068	0	0.40899796	0	0	0	0.20134282	2.00668896	0.3539823	1.24223602	0.23148148	0.43572985	0.52301255	0.97087379	0.34305317	0
c__Clostridia	0.34662045	1.05485232	0.40899796	1.38408304	1.48148148	0.4048583	0	0.33444816	1.23893805	0	0.92592593	1.30718954	0.10460251	1.52565881	0	0
o__Clostridiales	0.34662045	1.05485232	0.40899796	1.38408304	1.48148148	0.4048583	0	0.33444816	1.23893805	0	0.92592593	1.30718954	0.10460251	1.52565881	0	0
f__Clostridiaceae	0	0	0.40899796	1.38408304	1.48148148	0.4048583	0	0	0	0	0	0.65359477	0	0.69348128	0	0
g__02d06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Clostridium	0	0	0.40899796	1.38408304	1.48148148	0.4048583	0	0	0	0	0	0.65359477	0	0.69348128	0	0
s__kluyveri	0	0	0	1.38408304	1.48148148	0.4048583	0	0	0	0	0	0	0	0	0	0
s__sartagoforme	0	0	0.20449898	0	0	0	0	0	0	0	0	0.65359477	0	0.13869626	0	0
s__septicum	0	0	0.20449898	0	0	0	0	0	0	0	0	0	0	0.55478502	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Lachnospiraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Blautia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__producta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Catonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Clostridium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__celerecrescens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__clostridioforme	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oribacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pseudobutyrivibrio	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Roseburia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__faecis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Peptococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Desulfosporosinus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__meridiei	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Peptostreptococcaceae	0	0	0	0	0	0	0	0	0	0	0.46296296	0	0.10460251	0	0	0
g__Filifactor	0	0	0	0	0	0	0	0	0	0	0.46296296	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.46296296	0	0	0	0	0
g__Peptostreptococcus	0	0	0	0	0	0	0	0	0	0	0	0	0.10460251	0	0	0
s__anaerobius	0	0	0	0	0	0	0	0	0	0	0	0	0.10460251	0	0	0
g__[Clostridium]	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__difficile	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Ruminococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Ruminococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__bromii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Symbiobacteriaceae	0	0	0	0	0	0	0	0	0	0	0.23148148	0	0	0	0	0
g__Symbiobacterium	0	0	0	0	0	0	0	0	0	0	0.23148148	0	0	0	0	0
s__thermophilum	0	0	0	0	0	0	0	0	0	0	0.23148148	0	0	0	0	0
f__Veillonellaceae	0	0.42194093	0	0	0	0	0	0	0.53097345	0	0	0	0	0	0	0
g__Dialister	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Megasphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Selenomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__noxia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Veillonella	0	0.42194093	0	0	0	0	0	0	0.53097345	0	0	0	0	0	0	0
s__dispar	0	0.42194093	0	0	0	0	0	0	0.53097345	0	0	0	0	0	0	0
s__parvula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__[Mogibacteriaceae]	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Mogibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__[Tissierellaceae]	0.34662045	0.63291139	0	0	0	0	0	0.33444816	0.7079646	0	0.23148148	0.65359477	0	0.83217753	0	0
g__1-68	0	0	0	0	0	0	0	0	0	0	0	0	0	0.41608877	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.41608877	0	0
g__Anaerococcus	0.17331023	0	0	0	0	0	0	0.33444816	0.53097345	0	0	0	0	0	0	0
unclassified	0.17331023	0	0	0	0	0	0	0.33444816	0.53097345	0	0	0	0	0	0	0
g__Finegoldia	0	0.63291139	0	0	0	0	0	0	0	0	0.23148148	0.43572985	0	0.13869626	0	0
unclassified	0	0.63291139	0	0	0	0	0	0	0	0	0.23148148	0.43572985	0	0.13869626	0	0
g__Parvimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Peptoniphilus	0.17331023	0	0	0	0	0	0	0	0.17699115	0	0	0.21786492	0	0.27739251	0	0
unclassified	0.17331023	0	0	0	0	0	0	0	0.17699115	0	0	0.21786492	0	0.27739251	0	0
g__ph2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Erysipelotrichi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Erysipelotrichales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Erysipelotrichaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__[Eubacterium]	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__biforme	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Fusobacteria	0.17331023	0	0	0	0	0	0	0.33444816	0	0	0.23148148	0	0	0	0.68610635	0
c__Fusobacteriia	0.17331023	0	0	0	0	0	0	0.33444816	0	0	0.23148148	0	0	0	0.68610635	0
o__Fusobacteriales	0.17331023	0	0	0	0	0	0	0.33444816	0	0	0.23148148	0	0	0	0.68610635	0
f__Fusobacteriaceae	0	0	0	0	0	0	0	0.33444816	0	0	0	0	0	0	0.68610635	0
g__Fusobacterium	0	0	0	0	0	0	0	0.33444816	0	0	0	0	0	0	0.68610635	0
unclassified	0	0	0	0	0	0	0	0.33444816	0	0	0	0	0	0	0.68610635	0
f__Leptotrichiaceae	0.17331023	0	0	0	0	0	0	0	0	0	0.23148148	0	0	0	0	0
g__Leptotrichia	0.17331023	0	0	0	0	0	0	0	0	0	0.23148148	0	0	0	0	0
unclassified	0.17331023	0	0	0	0	0	0	0	0	0	0.23148148	0	0	0	0	0
g__Streptobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__moniliformis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Gemmatimonadetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Gemm-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Planctomycetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Planctomycetia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Gemmatales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Isosphaeraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Proteobacteria	91.507799	91.350211	91.002045	94.8096886	92.962963	91.4979757	90.6040268	88.6287625	90.9734513	92.5465839	87.7314815	89.9782135	91.8410042	84.7434119	89.5368782	100
c__Alphaproteobacteria	8.31889081	15.8227848	15.7464213	14.8788927	10.7407407	13.3603239	11.409396	13.3779264	13.0973451	13.0434783	10.6481481	15.0326797	12.6569038	10.6796117	7.37564322	100
o__Caulobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	33.3333333
f__Caulobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	33.3333333
g__Brevundimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__diminuta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__staleyi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Caulobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__vibrioides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Phenylobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	33.3333333
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	33.3333333
o__Rhizobiales	0.51993068	0.21097046	0.81799591	0	1.48148148	0.4048583	0	0.33444816	0.17699115	0.31055901	0.46296296	0.21786492	0.20920502	0	0	0
f__Aurantimonadaceae	0	0	0	0	0	0	0	0	0	0	0.46296296	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.46296296	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.46296296	0	0	0	0	0
f__Bradyrhizobiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Balneimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Bosea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__genosp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Brucellaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Pseudochrobactrum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Hyphomicrobiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Devosia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rhodomicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__vanniellii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Methylobacteriaceae	0	0	0	0	0	0.4048583	0	0.33444816	0	0	0	0.21786492	0.10460251	0	0	0
g__Methylobacterium	0	0	0	0	0	0.4048583	0	0.33444816	0	0	0	0.21786492	0.10460251	0	0	0
s__adhaesivum	0	0	0	0	0	0.4048583	0	0.33444816	0	0	0	0.21786492	0	0	0	0
s__hispanicum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__komagatae	0	0	0	0	0	0	0	0	0	0	0	0	0.10460251	0	0	0
s__organophilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Phyllobacteriaceae	0.51993068	0.21097046	0.81799591	0	1.48148148	0	0	0	0.17699115	0.31055901	0	0	0.10460251	0	0	0
g__Aminobacter	0.51993068	0.21097046	0.81799591	0	1.48148148	0	0	0	0.17699115	0.31055901	0	0	0.10460251	0	0	0
unclassified	0.51993068	0.21097046	0.81799591	0	1.48148148	0	0	0	0.17699115	0.31055901	0	0	0.10460251	0	0	0
f__Rhizobiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Agrobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__sullae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rhodobacterales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.6666667
f__Rhodobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.6666667
g__Paracoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.6666667
s__aminovorans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.6666667
s__marcusii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Rubellimicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Rhodospirillales	7.62564991	14.978903	14.3149284	14.532872	9.25925926	12.5506073	11.409396	12.0401338	12.2123894	12.1118012	9.49074074	12.6361656	12.1338912	10.2635229	7.03259005	0
f__Acetobacteraceae	7.62564991	14.978903	14.3149284	14.532872	9.25925926	12.5506073	11.409396	12.0401338	12.2123894	12.1118012	9.49074074	12.6361656	12.1338912	10.2635229	7.03259005	0
g__Acidocella	7.62564991	14.978903	14.3149284	14.532872	9.25925926	12.5506073	11.409396	12.0401338	12.2123894	12.1118012	9.49074074	12.6361656	12.1338912	10.2635229	7.03259005	0

unclassified	7.62564991	14.978903	14.3149284	14.532872	9.25925926	12.5506073	11.409396	12.0401338	12.2123894	12.1118012	9.49074074	12.6361656	12.1338912	10.2635229	7.03259005	0			
g__Roseococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
f__Rhodospirillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
g__Defluviicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
s__vanus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
g__Oleomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
o__Sphingomonadales	0.17331023	0.63291139	0.61349693	0.34602076	0	0.4048583	0	1.00334448	0.7079646	0.62111801	0.69444444	2.17864924	0.31380753	0.41608877	0.34305317	0			
f__Erythrobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
g__Lutibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
f__Sphingomonadaceae	0.17331023	0.63291139	0.61349693	0.34602076	0	0.4048583	0	1.00334448	0.7079646	0.62111801	0.69444444	2.17864924	0.31380753	0.41608877	0.34305317	0			
g__Kaistobacter	0	0	0	0	0	0	0	1.00334448	0	0	0	0	0	0	0	0			
unclassified	0	0	0	0	0	0	0	1.00334448	0	0	0	0	0	0	0	0			
g__Sphingobium	0	0	0	0	0	0.4048583	0	0	0	0.62111801	0.46296296	0.43572985	0	0.27739251	0	0			
s__yanoikuyae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
unclassified	0	0	0	0	0	0.4048583	0	0	0	0.62111801	0.46296296	0.43572985	0	0.27739251	0	0			
g__Sphingomonas	0.17331023	0.63291139	0.61349693	0.34602076	0	0	0	0	0.7079646	0	0.23148148	1.74291939	0.31380753	0.13869626	0.34305317	0			
s__azotifigens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
s__echinoides	0.17331023	0.63291139	0	0.34602076	0	0	0	0	0	0	0	0	1.30718954	0.20920502	0.13869626	0.17152659	0		
s__suberifaciens	0	0	0	0	0	0	0	0	0	0	0	0.21786492	0	0	0	0			
s__yabuuchiae	0	0	0.61349693	0	0	0	0	0	0.7079646	0	0.23148148	0.21786492	0.10460251	0	0.17152659	0			
g__Sphingopyxis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
s__alaskensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
c__Betaproteobacteria	6.23916811	13.0801688	10.6339468	12.1107266	4.07407407	9.71659919	15.4362416	13.3779264	8.84955752	9.62732919	8.10185185	11.1111111	8.57740586	10.2635229	8.74785592	0			
o__Burkholderiales	6.23916811	13.0801688	10.2249489	12.1107266	4.07407407	9.71659919	15.4362416	13.3779264	8.67256637	9.31677019	8.10185185	10.8932462	8.15899582	10.1248266	8.40480274	0			
f__Burkholderiaceae	4.50606586	11.6033755	8.58895706	9.68858131	3.33333333	8.90688259	12.0805369	9.69899666	7.07964602	8.69565217	6.01851852	8.93246187	6.38075314	8.32177531	7.20411664	0			
g__Burkholderia	4.50606586	11.6033755	7.77096115	9.68858131	3.33333333	8.90688259	11.409396	9.69899666	6.54867257	8.69565217	6.01851852	8.93246187	6.38075314	8.18307906	7.20411664	0			
s__bryophila	0	0	0	0	0	0	0	0.66889632	0	0	0	0	0	0	0	0			
s__graminis	0	0	0	0	0	0	0	0	0	0.17699115	0	0	0	0	0	0			
s__tuberum	0.17331023	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
unclassified	4.33275563	11.6033755	7.77096115	9.68858131	3.33333333	8.90688259	11.409396	9.03010033	6.37168142	8.69565217	6.01851852	8.93246187	6.38075314	8.18307906	7.20411664	0			
g__Lautropia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
g__Pandoraea	0	0	0.20449898	0	0	0	0	0	0	0.17699115	0	0	0	0	0.13869626	0			
unclassified	0	0	0.20449898	0	0	0	0	0	0	0.17699115	0	0	0	0	0.13869626	0			
g__Salinispora	0	0	0.61349693	0	0	0	0.67114094	0	0.3539823	0	0	0	0	0	0	0			
s__tropica	0	0	0.61349693	0	0	0	0.67114094	0	0.3539823	0	0	0	0	0	0	0			
f__Comamonadaceae	0.34662045	0.21097046	1.02249489	0	0.37037037	0.8097166	1.34228188	1.00334448	0.3539823	0	0.46296296	0.21786492	0.94142259	0.41608877	0.85763293	0			
g__Acidovorax	0.17331023	0.21097046	0.40899796	0	0	0	0	0	0	0	0.23148148	0	0.31380753	0	0	0			
s__citrulli	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
s__delafieldii	0	0.21097046	0.40899796	0	0	0	0	0	0	0	0.23148148	0	0.31380753	0	0	0			
s__facilis	0.17331023	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
g__Aquabacterium	0	0	0	0	0	0	0	0.66889632	0	0	0	0	0	0	0	0			
unclassified	0	0	0	0	0	0	0	0.66889632	0	0	0	0	0	0	0	0			
g__Comamonas	0	0	0	0	0	0	0	0	0	0	0.23148148	0	0	0.41608877	0	0			
s__terrigena	0	0	0	0	0	0	0	0	0	0	0.23148148	0	0	0	0	0			
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.41608877	0	0			
g__Delftia	0	0	0	0	0	0.8097166	0.67114094	0.33444816	0	0	0	0	0.31380753	0	0.34305317	0			
unclassified	0	0	0	0	0	0.8097166	0.67114094	0.33444816	0	0	0	0	0.31380753	0	0.34305317	0			
g__Diaphorobacter	0	0	0.40899796	0	0	0	0	0	0	0	0	0	0	0	0	0			
unclassified	0	0	0.40899796	0	0	0	0	0	0	0	0	0	0	0	0	0			
g__Pelomonas	0	0	0	0	0	0	0.67114094	0	0	0	0	0.21786492	0	0	0	0			
s__puraquae	0	0	0	0	0	0	0.67114094	0	0	0	0	0.21786492	0	0	0	0			
g__Pseudorhodoferax	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
s__soli	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
g__Roseateles	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
s__depolymerans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
g__Variovorax	0.17331023	0	0.20449898	0	0.37037037	0	0	0	0.3539823	0	0	0	0.20920502	0	0.51457976	0			
s__paradoxus	0.17331023	0	0.20449898	0	0.37037037	0	0	0	0.3539823	0	0	0	0.20920502	0	0.51457976	0			
g__Vitreoscilla	0	0	0	0	0	0	0	0	0	0	0	0	0.10460251	0	0	0			
s__filiformis	0	0	0	0	0	0	0	0	0	0	0	0	0.10460251	0	0	0			
f__Oxalobacteraceae	1.3864818	1.26582278	0.61349693	2.42214533	0.37037037	0	2.01342282	2.67558528	1.23893805	0.62111801	1.62037037	1.74291939	0.83682008	1.38696255	0.34305317	0			
g__Cupriavidus	0	0	0	0	0.37037037	0	0	0	0	0	0	0	0	0	0	0			
unclassified	0	0	0	0	0.37037037	0	0	0	0	0	0	0	0	0	0	0			
g__Herbaspirillum	0	0	0	0.34602076	0	0	0	0	0.3539823	0	0	0	0	0	0	0			
unclassified	0	0	0	0.34602076	0	0	0	0	0.3539823	0	0	0	0	0	0	0			
g__Herminiimonas	0.17331023	0	0.20449898	0.34602076	0	0	0	0	0	0	0	0.21786492	0.10460251	1.2482663	0	0			
s__fonticola	0.17331023	0	0.20449898	0.34602076	0	0	0	0	0	0	0	0.21786492	0.10460251	1.2482663	0	0			
g__Janthinobacterium	0	0.42194093	0	0	0	0	0	0	0	0	0.46296296	0.21786492	0	0	0	0			
s__lividum	0	0.42194093	0	0	0	0	0	0	0	0	0.46296296	0.21786492	0	0	0	0			
g__Massilia	0	0	0.20449898	0	0	0	0	1.6722408	0	0	0	0.43572985	0	0	0	0			
s__aerilata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
s__aurea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
s__niastensis	0	0	0.20449898	0	0	0	0	1.6722408	0	0	0	0	0	0	0	0			
s__timonae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
s__varians	0	0	0	0	0	0	0	0	0	0	0	0.43572985	0	0	0	0			
g__Paucimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
s__lemoignei	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
g__Ralstonia	1.21317158	0.84388186	0.20449898	1.38408304	0	0	2.01342282	1.00334448	0.88495575	0.62111801	1.15740741	0.87145969	0.73221757	0.13869626	0.34305317	0			
unclassified	1.21317158	0.84388186	0.20449898	1.38408304	0	0	2.01342282	1.00334448	0.88495575	0.62111801	1.15740741	0.87145969	0.73221757	0.13869626	0.34305317	0			
g__Telluria	0	0	0	0.34602076	0	0	0	0	0	0	0	0	0	0	0	0			
s__mixta	0	0	0	0.34602076	0	0	0	0	0	0	0	0	0	0	0	0			
o__IS-44	0	0	0.40899796	0	0	0	0	0	0	0	0	0	0	0	0	0			
unclassified	0	0	0.40899796	0	0	0	0	0	0	0	0	0	0	0	0	0			
unclassified	0	0	0.40899796	0	0	0	0	0	0	0	0	0	0	0	0	0			
unclassified	0	0	0.40899796	0	0	0	0	0	0	0	0	0	0	0	0	0			
o__Methylophilales	0	0	0	0	0	0	0	0	0.17699115	0	0	0	0.20920502	0	0	0			
f__Methylophilaceae	0	0	0	0	0	0	0	0	0.17699115	0	0	0	0.20920502	0	0	0			
g__Methylobacillus	0	0	0	0	0	0	0	0	0.17699115	0	0	0	0.20920502	0	0	0			
unclassified	0	0	0	0	0	0	0	0	0.17699115	0	0	0	0.20920502	0	0	0			
o__Neisseriales	0	0	0	0	0	0	0	0	0	0	0	0.21786492	0	0.13869626	0.34305317	0			
f__Neisseriaceae	0	0	0	0	0	0	0	0	0	0	0	0.21786492	0	0.13869626	0.34305317	0			
g__Aquitalea	0	0	0	0	0	0	0	0	0	0	0	0.21786492	0	0.13869626	0.17152659	0			
s__magnusonii	0	0	0	0	0	0	0	0	0	0	0	0.21786492	0	0.13869626	0.17152659	0			
g__Kingella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
g__Neisseria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.17152659	0			
s__cinerea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
s__subflava	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.17152659	0			
g__Vogesella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
o__Rhodocyclales	0	0	0	0	0	0	0	0	0	0.31055901	0	0	0.20920502	0	0	0			
f__Rhodocyclaceae	0	0	0	0	0	0	0	0	0	0.31055901	0	0	0.20920502	0	0	0			
g__Azospira	0	0	0	0	0	0	0	0	0	0	0	0	0.20920502	0	0	0			
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.20920502	0	0	0			
g__KD1-23	0	0	0	0	0	0	0	0	0	0.31055901	0	0	0	0	0	0			
unclassified	0	0	0	0	0	0	0	0	0	0.31055901	0	0	0	0	0	0			
g__Zoogloea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
c__Deltaproteobacteria	0	0	0	0.69204152	0	0	0	0	0	0	0	0	0	0	0	0			
o__Myxococcales	0	0	0	0.69204152	0	0	0	0	0	0	0	0	0	0	0	0			
f__0319-6G20	0	0	0	0.69204152	0	0	0	0	0	0	0	0	0	0	0	0			
unclassified	0	0	0	0.69204152	0	0	0	0	0	0	0	0	0	0	0	0			
unclassified	0	0	0	0.69204152	0	0	0	0	0	0	0	0	0	0	0	0			
f__Nannocystaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
g__Plesiocystis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
f__Polyangiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
g__Polyangium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
s__fumosum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
c__Epsilonproteobacteria	0	0	0	0	0	0	0	0	0.3539823	0	0	0	0	0.13869626	0	0			
o__Campylobacterales	0	0	0	0	0	0	0	0	0.3539823	0	0	0	0	0.13869626	0	0			
f__Campylobacteraceae	0	0	0	0	0	0	0	0	0.3539823	0	0	0	0	0.13869626	0	0			
g__Campylobacter	0	0	0	0	0	0	0	0	0.3539823	0	0	0	0	0.13869626	0	0			
s__ureolyticus	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13869626	0	0			
unclassified	0	0	0	0	0	0	0	0	0.3539823	0	0	0	0	0	0	0			
f__Helicobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
g__Helicobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
s__pylori	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
c__Gammaproteobacteria	76.94974	62.4472574	64.6216769	67.1280277	78.1481481	68.4210526	63.7583893	61.8729097	68.6725664	69.8757764	68.9814815	63.8344227	70.6066946	63.6615811	73.4133791	0			
o__Enterobacteriales	0.34662045	0.84388186	0.61349693	0.34602076	0.74074074	0	0	0.33444816	0.3539823	0	0	0	0.41841004	0	1.20068611	0			
f__Enterobacteriaceae	0.34662045	0.84388186	0.61349693	0.34602076	0.74074074	0	0	0.33444816	0.3539823	0	0	0	0.41841004	0	1.20068611	0			
g__Enterobacter	0.34662045	0.84388186	0.40899796	0.34602076	0.37037037	0	0	0	0.3539823	0	0	0	0.41841004	0	0.85763293	0			
s__aerogenes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.17152659	0			
s__cowanii	0	0.42194093	0	0.34602076	0.37037037	0	0	0	0	0	0	0	0	0	0.34305317	0			
s__hormaechei	0.34662045	0.42194093	0.40899796	0	0	0	0	0	0.3539823	0	0	0	0.41841004	0	0.34305317	0			
g__Pantoea	0	0	0	0	0.37037037	0	0	0.33444816	0	0	0	0	0	0	0.34305317	0			
s__ananatis	0	0	0	0	0.37037037	0	0	0.33444816	0	0	0	0	0	0	0.34305317	0			
g__Salmonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
s__enterica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
g__Yokenella	0	0	0.20449898	0	0	0	0	0	0	0	0	0	0	0	0	0			
s__regensburgei	0	0	0.20449898	0	0	0	0	0	0	0	0	0	0	0	0	0			
o__Pasteurellales	0	0	0	0	0	0	0	0	0	0.31055901	0	0	0	0.13869626	0	0			
f__Pasteurellaceae	0	0	0	0	0	0	0	0	0	0.31055901	0	0	0	0.13869626	0	0			
g__Aggregatibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
s__segnis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
g__Haemophilus	0	0	0	0	0	0	0	0	0	0.31055901	0	0	0	0.13869626	0	0			
s__influenzae	0	0	0	0	0	0	0	0	0	0.31055901	0	0	0	0	0	0			
s__parainfluenzae	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13869626	0	0			
o__Pseudomonadales	0.6932409	0	0.61349693	0.34602076	0.37037037	0	0	0.33444816	0	0.93167702	0.92592593	0.21786492	0.83682008	0	0.17152659	0			
f__Moraxellaceae	0.17331023	0	0	0	0	0	0	0	0	0	0	0	0	0	0.17152659	0			
g__Acinetobacter	0.17331023	0	0	0	0	0	0	0	0	0	0	0	0	0	0.17152659	0			
s__lwoffii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.17152659	0			
s__rhizosphaerae	0.17331023	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			

g__Enhydrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Moraxella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Pseudomonadaceae	0.51993068	0	0.61349693	0.34602076	0.37037037	0	0	0.33444816	0	0.93167702	0.92592593	0.21786492	0.83682008	0	0	0
g__Pseudomonas	0.51993068	0	0.61349693	0.34602076	0.37037037	0	0	0.33444816	0	0.93167702	0.92592593	0.21786492	0.83682008	0	0	0
s__umsongensis	0.17331023	0	0	0.34602076	0.37037037	0	0	0	0	0	0.92592593	0	0.62761506	0	0	0
s__veronii	0.34662045	0	0.61349693	0	0	0	0	0.33444816	0	0.93167702	0	0.21786492	0.10460251	0	0	0
s__viridiflava	0	0	0	0	0	0	0	0	0	0	0	0	0.10460251	0	0	0
o__Thiotrichales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.17152659	0
f__Thiotrichaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.17152659	0
g__Beggiatoa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.17152659	0
s__alba	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.17152659	0
o__Xanthomonadales	75.9098787	61.6033755	63.394683	66.4359862	77.037037	68.4210526	63.7583893	61.2040134	68.3185841	68.6335404	68.0555556	63.6165577	69.3514644	63.5228849	71.8696398	0
f__Xanthomonadaceae	75.9098787	61.6033755	63.394683	66.4359862	77.037037	68.4210526	63.7583893	61.2040134	68.3185841	68.6335404	68.0555556	63.6165577	69.3514644	63.5228849	71.8696398	0
g__Dyella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__japonica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Fulvimonas	0	0	0	0	0	0	0	0	0	0	0	0	0.31380753	0.13869626	0	0
s__soli	0	0	0	0	0	0	0	0	0	0	0	0	0.31380753	0.13869626	0	0
g__Pseudoxanthomonas	0	0	0	0	0	0	0	0	0	0	0	0	0.20920502	0	0	0
s__kaohsiungensis	0	0	0	0	0	0	0	0	0	0	0	0	0.20920502	0	0	0
g__Rhodanobacter	75.9098787	59.9156118	63.394683	66.4359862	76.6666667	68.4210526	63.0872483	60.8695652	68.3185841	67.7018634	67.3611111	63.1808279	68.5146444	63.1067961	71.0120069	0
s__terrae	75.9098787	59.9156118	63.394683	66.4359862	76.6666667	68.4210526	63.0872483	60.8695652	68.3185841	67.7018634	67.3611111	63.1808279	68.5146444	63.1067961	71.0120069	0
g__Stenotrophomonas	0	1.68776371	0	0	0.37037037	0	0.67114094	0.33444816	0	0.93167702	0.69444444	0.43572985	0.31380753	0.27739251	0.85763293	0
s__geniculata	0	1.68776371	0	0	0.37037037	0	0	0.33444816	0	0.62111801	0.46296296	0.21786492	0	0.13869626	0.85763293	0
s__maltophilia	0	0	0	0	0	0	0.67114094	0	0	0	0	0	0	0	0	0
s__rhizophila	0	0	0	0	0	0	0	0	0	0.31055901	0.23148148	0.21786492	0.31380753	0.13869626	0	0
g__Xanthomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__axonopodis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Spirochaetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__Spirochaetes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Spirochaetales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Spirochaetaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Treponema	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
s__socranskii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__TM7	0	0	0	0	0	0	0	0	0	0	0.23148148	0	0	0	0.34305317	0
c__TM7-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
c__TM7-3	0	0	0	0	0	0	0	0	0	0	0.23148148	0	0	0	0.34305317	0
o__EW055	0	0	0	0	0	0	0	0	0	0	0.23148148	0	0	0	0.34305317	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.23148148	0	0	0	0.34305317	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.23148148	0	0	0	0.34305317	0
unclassified	0	0	0	0	0	0	0	0	0	0	0.23148148	0	0	0	0.34305317	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p__[Thermi]	0	0	0	0	0	0	0	0	0	0	0	0	0.10460251	0	0	0
c__Deinococci	0	0	0	0	0	0	0	0	0	0	0	0	0.10460251	0	0	0
o__Deinococcales	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
f__Deinococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Deinococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
o__Thermales	0	0	0	0	0	0	0	0	0	0	0	0	0.10460251	0	0	0
f__Thermaceae	0	0	0	0	0	0	0	0	0	0	0	0	0.10460251	0	0	0
g__Meiothermus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Thermus	0	0	0	0	0	0	0	0	0	0	0	0	0.10460251	0	0	0
unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.10460251	0	0	0

CHAPTER FOUR: Recurrent Methicillin-Resistant *Staphylococcus aureus* Cutaneous Abscesses and the Selection of Reduced Chlorhexidine Susceptibility During Chlorhexidine Use

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The work presented in this chapter is the sole work of R.C. Johnson with the following exceptions: K. Crawford performed pulsed field gel electrophoresis and PCR for toxin/resistance genes; study oversight at Fort Benning provided by C.D. Schlett and M.W. Ellis; strain isolation performed by J.B. Lanier.

ABSTRACT

We describe the selection of reduced chlorhexidine susceptibility during chlorhexidine use in a patient with two episodes of cutaneous USA300 methicillin-resistant *Staphylococcus aureus* (MRSA) abscess. The second clinical isolate harbors a novel plasmid that encodes the QacA efflux pump. Greater use of chlorhexidine for disease prevention warrants surveillance for resistance.

CASE REPORT

An 18 year-old man undergoing Infantry basic training at Fort Benning, Georgia, presented to the outpatient clinic in July complaining of a painful skin lesion on his left knee. On physical examination, the patient was afebrile (37° C) and examination was remarkable only for a pre-patellar nodule that was erythematous, warm, indurated, tender, and fluctuant. The patient had no other skin lesions and no lymphadenopathy. The remainder of his exam was normal and the patient did not report a history of cutaneous abscesses. The patient was diagnosed with a cutaneous abscess without joint involvement and underwent incision and drainage. The purulent material underwent standard wound culture and yielded methicillin-resistant *Staphylococcus aureus* (MRSA) using the BD Phoenix automated microbiology system (Becton Dickinson, Sparks, MD). The isolate was resistant to oxacillin and erythromycin and had inducible clindamycin resistance as determined by double-disk diffusion (95), but was susceptible to trimethoprim-sulfamethoxazole (TMP-SMX), doxycycline, levofloxacin, linezolid, daptomycin, and vancomycin (Table 11). With no known medication allergies, the patient was treated with a ten day course of twice-daily Double Strength (DS) TMP-SMX and underwent serial follow-up examinations and wound care with complete resolution of his abscess within 14 days.

Nine weeks after his initial presentation, the patient returned to the clinic. This time he complained of a similar painful lesion on his left foot. On physical examination, the patient was again afebrile (37° C) and examination was remarkable only for an inflamed and fluctuant nodule on the dorsum of his left foot. The patient was again

Table 11. Molecular characteristics and antimicrobial susceptibilities of clinical MRSA isolates

Characteristic	**Clinical Isolate 1 (C01)**	**Clinical Isolate 2 (C02)**
Sequence type	ST8	ST8
Pulsed-field type	USA300	USA300
Oxacillin	Resistant	Resistant
Erythromycin	Resistant	Resistant
Clindamycin	Inducible resistance	Inducible resistance
TMP-SMX	Susceptible	Susceptible
Doxycycline	Susceptible	Susceptible
Daptomycin	Susceptible	Susceptible
Vancomycin	Susceptible	Susceptible
Levofloxacin	Susceptible	Resistant
qacA gene	Negative	Positive
mecA	Positive	Positive
SCCmec Type	IV	IV
PVL	Positive	Positive
mupA	Negative	Negative
norA	Positive	Positive
Chlorhexidine MIC	0.3 μg/mL	0.8 μg/mL

diagnosed with a cutaneous abscess and underwent incision and drainage with standard wound cultures yielding MRSA. This second clinical isolate shared the same antibiotic susceptibility pattern as the first MRSA isolate; however, it was resistant to levofloxacin (Table 11). The patient was treated in a similar fashion as the first episode and recovered without additional recurrences.

The patient was a soldier participating in a prospective cluster-randomized trial aimed at preventing skin and soft-tissue infections, which are common in this population (83). The patient was in a study group that received chlorhexidine for weekly showering (4% chlorhexidine gluconate, Hibiclens®, Mölnlycke Heath Care, Norcross, Georgia). As part of the protocol, the patient completed a questionnaire at the time of his second episode that queried his chlorhexidine use; he reported using the agent every other week throughout his training. In terms of chlorhexidine use, the patient would have used the agent 1-2 times before his first episode, and 4-5 times prior to the second episode.

The two MRSA isolates underwent molecular analysis including typing with pulsed-field gel electrophoresis (PFGE) (193), multilocus sequence typing (MLST) (84), and polymerase chain reaction (PCR) to assess for toxin (98) and resistance genes (45; 189). PFGE findings were resolved and analyzed using BioNumerics (Applied Math, Austin, TX). Both MRSA isolates were sequence type 8 (ST8), USA300, staphylococcal cassette chromosome *mec* type IV (SCCIIV), positive for Panton-Valentine leukocidin (*lukS-PV*) and negative for high level mupirocin resistance (*mupA*). The first clinical isolate (C01) was negative for the chlorhexidine resistance genes (*qacA/B*), but the second clinical isolate (C02) was positive for *qacA/B*. As part of the research protocol

(2), anterior nares sampling at the second episode revealed that the patient was colonized with a separate, unrelated methicillin-susceptible *S. aureus* strain (sequence type 30).

Both clinical isolates underwent chlorhexidine susceptibility testing. Briefly, about $4x10^4$ colony forming units (CFUs) from an overnight culture were inoculated into 1 mL of Cation Adjusted Mueller Hinton II Broth (BD BBL) containing purified chlorhexidine (Sigma) that ranged in concentration from 0 to 1 μg/mL. The cultures were grown overnight with shaking (220 rpm). Upon visual analysis (Figure 13), the minimum inhibitory concentration (MIC) of chlorhexidine for the C01 isolate was 0.3 μg/mL while the C02 isolate had a MIC of 0.8 μg/mL: approximate 2.7 fold increase over C01.

Previous reports have found that mutations in the promoter of the *norA* efflux pump can lead to increases in *norA* transcription, which result in increased resistance to antiseptic agents such as chlorhexidine (99; 220). The promoter region of *norA* was PCR amplified and sequenced using the 5'-GTCTTGGTCATCTGCAAAGGTTG-3' and 5'-GACTGGTATTACTAAACCGATACC-3' primers. Additionally, the 5'-GGTGGTATGAGTGCTGGTATGG-3' and 5'-GCATACGATGTGAAACTTCTGCC-3' primers were used to assess *norA* transcription via RT-PCR. Total RNA was extracted from the C01 and C02 isolates using the Qiagen EasyRNA kit. Prior to RNA extraction, *S. aureus* was lysed by incubation in lysis buffer containing buffer TE, lysostaphin (20 μg/mL), and proteinase K (200 μg/mL) for 1 hour. cDNA was synthesized from total RNA using the QuantiTect Reverse Transcription kit (Qiagen). All PCR and sequencing reactions were performed as previously described (80). RT-PCR was performed in 10 μL reactions containing 1X SYBR Green (Qiagen) and 1.5 μM of each primer. Reaction mixtures were incubated for 5 minutes at 95°C followed by 35 cycles of 95°C for 10 s

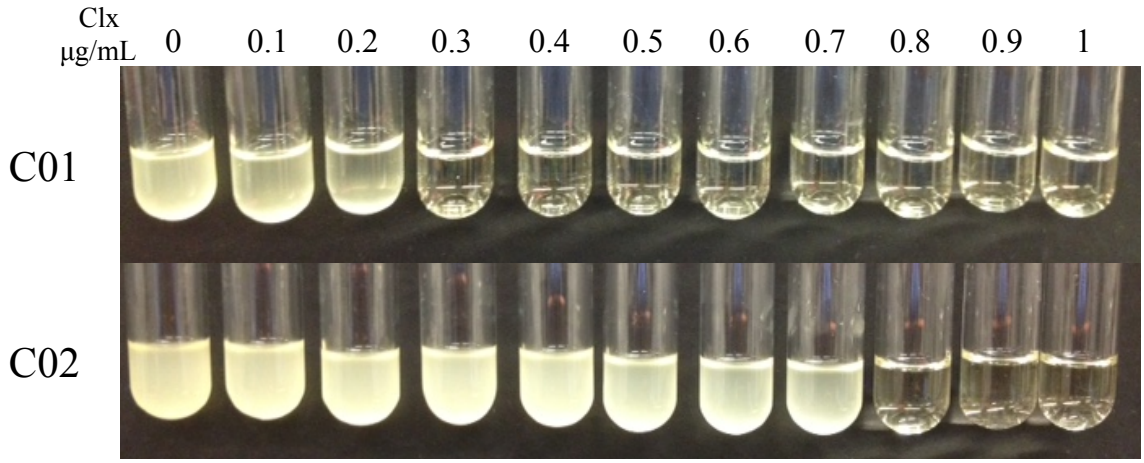

Figure 13. Minimum inhibitory concentration (MIC) of chlorhexidine (Clx) for the two *Staphylococcus aureus* abscess isolates (C01 and C02).
The concentration of Clx tested ranged from 0 to 1 µg/mL. All cultures were inoculated with approximately 4 x 10^4 colony forming units (CFUs) and grown overnight at 37°C with shaking at 220 rpm. The MIC for the C01 strain was determined to be 0.3 µg/mL while the C02 isolate had a MIC of 0.8 µg/mL.

then 50°C for 10 s. Fluorescence readings were acquired at the end of each cycle using the Qiagen Rotor-Gene Q RT-PCR Machine. Sequencing data analysis revealed that the C01 and C02 *norA* promoters were identical in nucleotide composition. Not surprisingly, *norA* expression in the C02 isolate was indistinguishable from C01.

Plasmid extraction using the Qiagen Plasmid Purification kit and subsequent PCR amplification (5'-GCTGCATTTATGACAATGTTTG-3' and 5'-AATCCCACCTACTAAAGCAG-3') (304) and visualization on a 1% agarose gel revealed that the *qacA* gene was only detectable in the C02 isolate. Given the high level of nucleotide similarity between the *qacA* and *qacB* genes, we sequenced and then compared the DNA sequence of *qacA* from the C02 plasmid to the canonical *qacA* (accession number: GU565967.1) and *qacB* (accession number: AF053772.1) sequences. Of the seven amino acid differences described by Paulsen *et al*. that distinguish *qacA* from *qacB,* 6 of the *qacA* residues were observed in the *qacA* gene from C02; this includes a key aspartic acid residue carried at amino acid position 323 (232). The one amino acid residue that differed from the *qacA* consensus occurred at the first position, where an alternative lysine start codon was found. In total, the data suggest that C02 harbors the *qacA* gene. Finally, to ensure that the C02 isolate was the only strain that expressed the *qacA* efflux pump, we utilized cDNA as a template for *qacA* PCR amplification using the same *qacA* detection/sequencing primers as mentioned beforehand. Amplicon detection on a 1% agarose gel confirmed that the C02 isolate actively expressed the *qacA* gene while the C01 isolate did not.

Previous reports have found that *qacA* is typically encoded on the pSK1 family of plasmids (188; 218). We therefore sequenced approximately 550 base pairs upstream of

the *qacA* gene using the 5'-CTCCAATCCTTATAGACCGTGC-3' primer; we found a high level of nucleotide similarity to the pSK1 DNA sequence (Genbank accession number NC_014369) (>99% nucleotide similarity). To determine if the plasmid was indeed pSK1, we next used the pSK1 plasmid sequence to design a series of 10 PCR primer pairs that span the entire plasmid (Table 12). We found that only the primer pair that encompassed the *qacA* gene (primer pair 9) yielded a PCR amplicon of the correct size in the CO2 isolate. This led us to conclude that the *qacA* gene found in the C02 isolate may be encoded on a pSK1-like plasmid, but not on pSK1 itself.

To assess clonality between the two isolates, total DNA was prepared from both isolates via phenol-chloroform extraction and was subjected to Pacific Biosciences RS II SMRT whole-genome sequencing (University of Maryland, School of Medicine, Institute for Genome Sciences). A single closed circular chromosome and plasmid were obtained for each isolate. A comprehensive list of chromosome and plasmid characteristics is included (Table 13). Genome analysis revealed that the C01 isolate contained 2,770 chromosomal open reading frames (ORFs) and was approximately 2.92 megabase pairs in length. Conversely, the C02 isolate had a reduced chromosome of 2.86 megabase pairs encoding 2,704 ORFs. In addition to whole gene changes, we observed over 140 single nucleotide polymorphisms (SNPs) between the two chromosomes, which suggests that the two isolates are genetically distinct. Of note, two nonsynonymous SNPs in the C02 *gyrA* and *grlA* genes (C251T and T239A, respectively) were detected. These SNPs result in a S84L amino acid mutation in GyrA and a F80Y mutation in GrlA that have previously been shown to contribute to quinolone resistance (271; 290; 317) and therefore likely explain the levofloxacin resistance of the C02 isolate.

Table 12. pSK1-like plasmid PCR primer panel

Primer Pair	Forward Primer (5'-3')	Reverse Primer (5'-3')
1	ggagcactagtagcaactttcatc	ccagagccgatgctacgc
2	gccttaaaattccaggcgc	gctgaaagttatagagcggc
3	gaagcacttgcatacgatagtg	gctcacgctataccgacattc
4	ctaacgtgcgatcagatgcttg	gcaccctcagaagccattc
5	cgcagttggagcaagtgag	ctttatcttcgactctatcacgaac
6	catcatagcaccagtcatcag	gtgtgcgatcatcgcgtctattc
7	caattaccttggcacttaccaaatg	ggttggaagaacgcacatatg
8	cttagatagtagccaacggctac	catcgtatcgatcttgttgtcc
9	cgatcgcacggtctataagg	gctttgaatctcttcgcttttcag
10	cgaagacgcctttcaatataccg	cctagagcttgccatgtatatg

Table 13. Genome and plasmid statisitics

Chromosome	Plasmid	Size (bp)	%GC	# of ORFs	Average Gene Length (bp)	% Coding
C01	-	2,918,599	32.8	2,770	879	84.5
C02	-	2,864,998	32.8	2,704	882	84.4
-	pC01	27,044	30.6	32	592	70.1
-	pC02	61,537	29.5	71	677	78.2

The pC01 and pC02 plasmid sequences were analyzed using the Basic Local Alignment Software Tool (BLAST, NCBI). While the pC01 sequence shared near perfect identity to known *S. aureus* plasmids such as SAP046A (GenBank accession no. NC_013294.1), the pC02 plasmid was significantly larger and less than 40% of the plasmid contained regions of similarity to other sequences in the NCBI database. Annotation of the pC02 plasmid revealed the presence of numerous proteins that range in cellular processes including DNA replication (Ssb, TopB), transcriptional regulation (QacR) and substrate translocation (CadC). The fully annotated pC02 map is depicted in Figure 14 (59). The *qacA*-containing pC02 plasmid appears to be novel and may represent an additional class of antimicrobial resistance plasmids in *S. aureus*. The C01 and C02 genomes and plasmids were submitted to NCBI and given the following accession numbers: CP012118, CP012119, CP012120, and CP012121.

DISCUSSION

Chlorhexidine is a broad-spectrum topical biguanide cationic antiseptic agent with activity against *Staphylococcus aureus* (192; 200). Although it has been used for decades in various roles, ranging from hand washing to preoperative skin preparation, chlorhexidine has been increasingly employed for the prevention of both nosocomial (46; 52; 87; 133) and community-associated infections (83; 103; 198; 325). Evidence from large randomized-control trials points to the importance of chlorhexidine in prevention of the spread of drug-resistant organisms and hospital acquired infections (52; 133; 199).

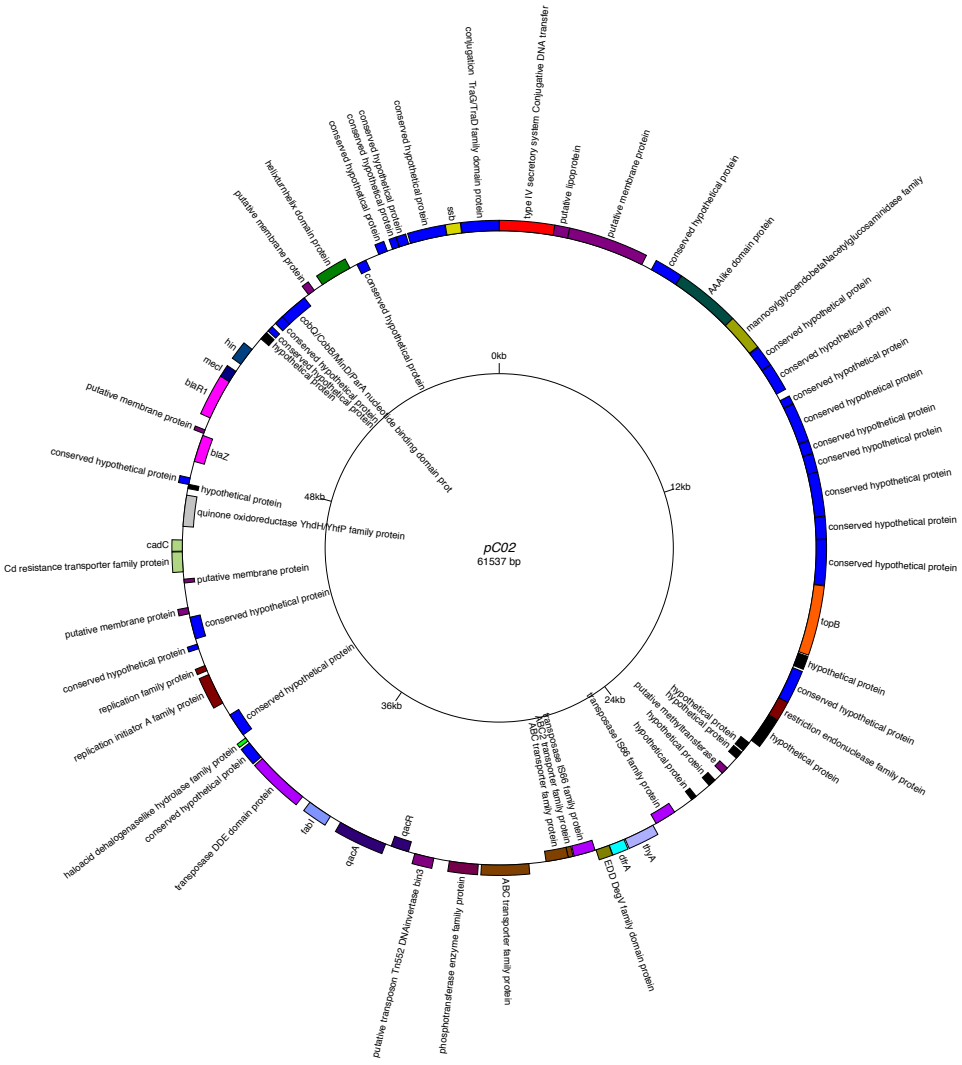

Figure 14. Annotated map of the pC02 plasmid.
Sequencing and annotation was performed at the University of Maryland Institute for Genome Sciences and was visualized using GenomeVX.

Indeed, chlorhexidine has also been an integral component of strategies aimed at prevention of recurrent MRSA SSTI in individuals and households (104; 198).

Despite its widespread use, the prevalence of chlorhexidine resistance in the U.S. is low (approximately 1%) (103; 190; 268); this is in contrast to observations in other countries (304; 314). When used in large trials, both in community and hospital settings, chlorhexidine resistance has been only rarely reported (52; 133; 268; 325). Nevertheless, with the widespread and increasing use of this agent, experience has shown that there is appropriate concern for the potential emergence of chlorhexidine resistance (314). Additional studies that investigate the frequency of chlorhexidine use and selection of chlorhexidine resistant strains must be conducted to ensure proper chlorhexidine stewardship.

The plasmid-borne *qacA* gene in particular encodes an efflux pump that has been shown in numerous reports to confer resistance to numerous hydrophobic compounds, including cationic biocides, such as chlorhexidine (131; 169; 192). While there are no established breakpoints for chlorhexidine resistance, the presence of these genes has been associated both with increased MIC and with untoward clinical outcomes (20; 61; 168; 225). Interestingly, multiple reports have identified chlorhexidine resistant *S. aureus* isolates with MICs of ≥ 4 μg/mL (61; 190; 268). The isolate described in this report, however, showed a reduced MIC (≤ 0.8 μg/mL). While the reason for the lower MIC is not clear, this may be due to reduced translation efficiency due to the alternate start codon found in the C02 *qacA* gene (221). The presence of *qacA/B* and increased MIC are sometimes poorly correlated (190); however, in our isolates, an increase in MIC was clearly observed for the *qacA*-positive C02 strain. We cannot determine the overall

clinical impact of this reduced chlorhexidine susceptibility in our patient other than to note that he developed a second USA300 MRSA abscess.

Chlorhexidine has residual antibacterial activity, which may be beneficial in reducing bacterial burden or preventing the spread of resistant organisms (238); however, this residual activity may also contribute to an environment that ultimately fosters resistance (304). Since our patient utilized chlorhexidine every other week, this may have played a part in the selection of reduced chlorhexidine susceptibility in the patient. Evidence suggests that the *qacA* gene may be able to be horizontally transferred across various staphylococcal species (131; 219). This typically is plasmid mediated since numerous reports have shown that the *qacA* gene is often encoded on a plasmid from the pSK1-family of vectors (159; 169). Although we do not know its original source, *qacA* in our identified clinical MRSA isolate was carried on a large, uncharacterized plasmid, which shows limited similarity to pSK1. This finding suggests that transmission of *qacA* is not limited to the pSK1-like vectors. Furthermore, the identification of this novel *qacA*-containing plasmid combined with the now ubiquitous use of chlorhexidine, highlights the need for increased surveillance programs that would seek to understand the evolution of *qacA* transmission across MRSA isolates and potentially across other staphylococcal species.

In summary, to our knowledge, this is the first report of the selection for increased chlorhexidine MICs while using chlorhexidine in a community-based patient with recurrent USA300 MRSA SSTI. In light of recent clinical trials that show the benefit of chlorhexidine in prevention of drug-resistant infections, the medical community should anticipate greater use of this agent, and consequently increased resistance. Further study

and surveillance for the emergence of chlorhexidine resistance should be considered in healthcare and community settings that use chlorhexidine for disease prevention.

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CHAPTER FIVE: Discussion

Despite the advances in medicine, the incidence rate of SSTIs among the human population continues to rise. Furthermore, SSTI prevention measures and treatments are repeatedly unsuccessful; a clear indication that our understanding of SSTIs is profoundly limited. While there are numerous factors that contribute to the complexity of SSTIs, two overarching unknowns include SSTI etiology and associated risk factors. As such, the primary goal of this dissertation was to investigate these two variables at the molecular and microbiome levels. Specifically, the studies described herein concentrate on the contribution of *Staphylococcus aureus* to SSTI formation and susceptibility.

In Chapter 2, we utilized high-throughput sequencing to characterize the nasal microbiomes of military trainees that either did or did not harbor a purulent abscess. We determined that bacteria from the Proteobacterial phylum were more abundant in the nares of individuals that did not have an SSTI. Additionally, we detected differences in microbial diversity between the SSTI and healthy nasal microbiomes that were independent of *S. aureus* colonization status. After looking at the nasal microbiome, we also determined the bacterial composition of purulent abscesses; while most purulent abscesses were dominated by *S. aureus,* polymicrobial infections were frequently observed. Finally, we demonstrated that the presence or absence of *S. aureus* in the nose and abscess had a profound impact on microbiome composition. Together, these data emphasize the complexity of the nasal and abscess microbiomes and provide a novel correlation between SSTI development and nasal microbiome composition.

The bacterial etiology of SSTIs is a debated topic in medicine. Specifically, the microbial species responsible for the often uncultivable cellulitis infections remains unclear. In Chapter 3, we sought to characterize the microbiome of both purulent and non-purulent (cellulitis) infections using a high-throughput sequencing strategy. We showed that the bacterial composition between the two SSTIs was remarkably different. We also employed a epidemiological analysis to assess risk factors associated with either purulent or non-purulent SSTIs. These results demonstrate the variability between SSTI disease types and emphasize the need for bacterial culture when treating SSTIs.

Finally, in Chapter 4, we employed molecular techniques in conjunction with whole-genome sequencing to characterize two strains of *S. aureus* that caused sequential SSTIs in a single military trainee. Interestingly, the patient was an active participant of a chlorhexidine soap hygiene trial. We found that the second isolate of *S. aureus* exhibited decreased susceptibility to chlorhexidine potentially due to the acquisition of the QacA efflux pump. Of epidemiological interest, the *qacA* gene was encoded on a large, previously uncharacterized plasmid. This clinical study demonstrates that in an era of increased chlorhexidine use, resistant strains are present in the population and are capable of causing SSTIs.

THE FUTURE OF HUMAN MICROBIOME RESEARCH

The study of the human microbiome has undoubtedly altered our perception of human health. Given the enormous numbers of colonizing bacteria, viruses, fungi, and protozoans, humans are now considered to be multi-organismal and should be treated as such. Research in the human microbiome field, while still in its infancy, is progressing at

a rapid rate, and there are elevated expectations of novel therapeutics and disease cures. Similar to the human microbiome project, the human genome project was initially created with high expectations; by merely analyzing an individual's DNA, scientists would be able to predict future disease susceptibilities and fine-tune personalized treatments. After more than 10 years since the first draft human genome was published, there have been numerous breakthroughs that have linked specific DNA signatures to human disease (114; 161). Interestingly, studies indicate that the variability between any two human genomes (~0.5%) is dwarfed by the variation between human microbiomes (173). Furthermore, this variability in microbiota can dramatically fluctuate over time (97), which sets the stage for hypothesis driven research projects that attempt to elucidate the mechanisms behind this microbial dysbiosis. Additionally, therapeutics that alter microbiome composition should prove easier, both technically and ethically, than genome manipulation. However, as with the human genome project, researchers and clinicians will likely need to be patient when it comes to microbiome therapies; while our current understanding of the human microbiome has exploded over the last decade, this growth in knowledge should not be misconstrued as a complete understanding of the interactions of humans with their bacterial inhabitants. The human microbiome is still an emerging science with major advances yet to come. As such, it is our hope that this thesis will serve as an important building block that will help researchers start to understand how the human microbiome influences our health. Furthermore, by studying the human microbiome and its association with SSTI formation, we provide the foundation required for future microbiome related therapies aimed at SSTI prevention.

CAN WE IDENTIFY A "MARKER" MICROBIOME?

One of the most exciting aspects of microbiome research is the potential for utilizing microbial composition as a predictor of disease susceptibilities. From a public health perspective, the ability to identify specific microbiome perturbations or signatures that can be exploited as a simple diagnostic would be ideal. While numerous studies have investigated how specific diseases alter microbial composition (50; 113; 204; 242), significantly fewer studies have performed longitudinal analyses that determine if a particular microbiome signature makes an individual more or less susceptible to future disease development. Indeed, the data from our microbiome related studies are limited to a single time point. Consequently, whether a reduction of Proteobacteria in the nares (Chapter 2) or presence of *Rhodanobacter* in the skin (Chapter 3) is a marker for future SSTI formation cannot be determined without assessing bacterial abundance levels prior to SSTI. Unfortunately, longitudinal analyses aimed at measuring changes in microbiome composition before and after disease formation are confounded by the uncertainty that a sufficient number of individuals will develop the disease being studied. Thus, the study of many diseases is hampered by the sample size required to obtain meaningful results. This can partially be overcome by looking within "at risk" populations. For example, given the high rates of SSTIs among military trainees at Fort Benning (3; 82), this population may be ideal for identification of a marker microbiome associated with future SSTI development. To this end, our laboratory is currently in the midst of a 14-week longitudinal analysis in which samples from trainees will be collected at 5 time points beginning upon initial admission to Fort Benning. In addition to the anterior nares, samples will be collected from other common *S. aureus*-associated body sites such as

oropharynx, inguinal, and perianal region. By enrolling a large number of trainees (~600), it is predicted that a substantial number of participants will develop a SSTI. Thus, it is our hope that we can build upon the data in this dissertation in order to identify a "marker" microbiome that may be used to identify those trainees that are at highest risk for SSTI development.

Given the difficulty associated with the identification of disease-predicting microbiomes, a growing body of research has instead concentrated on using the microbiome to diagnose diseases that, if not detected early, can have severe manifestations. For instance, it is estimated that nearly half of the individuals with Type 2 diabetes are undiagnosed, and may go undetected for up to a decade (123; 124). Recent evidence suggests that early detection of Type 2 diabetes can vastly improve disease outcome and quality of life (126). Indeed, microbiome analysis was successfully used to identify approximately 60,000 microbial markers for Type 2 diabetes (246). In particular, it was shown that key butyrate-producing bacteria were less abundant and opportunistic pathogens were enriched in the gut of diabetics compared to healthy controls (246). Similar approaches have been implemented to identify microbial biomarkers associated with the early diagnosis of colorectal, oral, and esophageal cancers (182; 184; 339). Furthermore, for patients currently suffering from diseases such as HIV and idiopathic pulmonary fibrosis, specific fluctuation in the microbiome may indicate future disease progression (121; 312). While SSTI formation has been the main clinical outcome assessed in this dissertation, it may be valuable to assess microbiome alterations for any individuals that progress to more severe disease such as necrotizing fasciitis or bacteremia. Furthermore, as shown in Chapter 2 and 3, many of the purulent abscesses

analyzed were comprised of mixed infections. While it remains unclear whether polymicrobial SSTIs impact disease prognosis, this is an obvious microbiome signature that warrants further investigation. Together, the identification of specific marker microbiomes is of great interest to the medical community and will likely influence how clinicians diagnosis and treat patients in the future.

THE INTERACTIONS BETWEEN HUMANS AND AN EVOLVING PATHOGEN: *STAPHYLOCOCCUS AUREUS*

In 1880, a Scottish surgeon by the name of Alexander Ogston became interested in a bacterium isolated from wound infections that appeared as "a bunch of grapes" under the microscope (217). 135 years later, *S. aureus* is still considered an important bacterial pathogen associated with human infections. Despite advances in hygiene practices and antibiotic therapy, *S. aureus* continues to evolve in order to efficiently colonize and infect humans. Of the most notable *S. aureus* evolutions, the acquisition of methicillin resistance has resulted in an ongoing epidemic of methicillin resistant *S. aureus* (MRSA)-associated infections in both the community and hospital settings. Interestingly, while antibiotic resistance acquisition often results in diminished bacterial fitness (157; 186; 197), MRSA, particularly community-associated MRSA, appears to efficiently compensate for any possible fitness defect (58; 135). In fact, numerous reports suggest that antibiotic resistant strains of *S. aureus* exhibit enhanced virulence and pathogenesis (66; 176; 316). This is particularly worrisome given the small window between antibiotic introduction and corresponding detection of resistant *S. aureus* strains: less than 4 years for penicillin and 2 years for methicillin (43; 229). In Chapter 2, all study participants were co-enrolled in a hygiene trial where they were instructed to use a chlorhexidine

body wash weekly (82). Interestingly, as described in Chapter 4, one of the study participants developed a SSTI that contained a strain of *S. aureus* that harbored a large (>60kb), novel plasmid that encoded the QacA efflux pump. This pump has been shown to confer resistance to quaternary ammonium compounds (QACs) and cationic agents such as chlorhexidine (131; 169; 192). Whether this plasmid-containing strain of *S. aureus* exhibits altered fitness or virulence has yet to be determined. Interestingly, in *Listeria monocytogenes*, exposure to sublethal levels of QACs increased expression of virulence genes (146). Conversely, growth in subinhibitory concentrations of chlorhexidine leads to decreased exotoxin synthesis in *Streptococcus agalactiae* (107). Although we do not currently know how widespread this novel *qacA*-containing plasmid is among *S. aureus* isolates, reports have shown that the prevalence of chlorhexidine resistant isolates is low (~1-2%) (268). Nevertheless, this vector may present a potential threat to human health and should be closely monitored.

Colonization with *S. aureus* is a complicated matter. From a clinical and epidemiological standpoint, individuals fall into one of three groups: persistent carriers, non-carriers, and those that are intermittently colonized (nonpersistent carriers) (306). Interestingly, these three groups appear to harbor unique microbial and immunological signatures. For example, in the anterior nares, a decrease in bacterial diversity was observed in nonpersistent carriers as compared to carriers and non-carriers (334). Furthermore, non-carriers appear to have the unique ability to resist experimental colonization by *S. aureus* (34). Although the mechanism behind this "*S.aureus*-colonization resistance" is still unknown, there is likely an immune system component. Surprisingly, some research also suggests that *S. aureus* carriers are not at a complete

health disadvantage. While persistent carriers are at increased risk for numerous *S. aureus* related infections, *S. aureus* bacteremia is remarkably more frequently fatal in non-carriers (323). Thus, colonization with *S. aureus* may actually "prime" the immune system so that it is better prepared to combat *S. aureus* bacteremia. Together, these data emphasize key health differences among the three *S. aureus* colonization groups. Unfortunately, as mentioned above, our studies are limited to a single time point which makes discerning between *S. aureus* carriers, non-carriers, and nonpersistent carriers impossible. Although we show that the nasal microbiota can differ dramatically depending on the presence or absence of *S. aureus* (Chapter 2), how the nasal microbiota varies in response to SSTIs among the various *S. aureus* colonization groups has yet to be determined. To address this question, culture data from the aforementioned longitudinal study will be used to assign military trainees into the various *S. aureus* colonization groups. By controlling for *S. aureus* colonization status, subsequent analysis of body site microbiomes should prove more accurate and may reveal key microbiome signatures that would otherwise be masked by the variability associated with the dynamic nature of *S. aureus* colonization.

While *S. aureus* preferentially colonizes the anterior nares, it is capable of colonizing many additional anatomical locations: inguinal, perianal, oropharynx, etc. (74; 336). The impact of *S. aureus* colonization on the microbiome at these various body sites, as well as alterations due to SSTI formation, are currently under investigation in our laboratory. Preliminary data suggest that if *S. aureus* is found at one anatomical location, it is typically found throughout the body (J. Singh, R.C. Johnson, C.D. Schlett, J.B. Lanier, E.R. Hall, N. Teneza-Mora M.W. Ellis, D.S. Merrell, unpublished data). These

data indicate that *S. aureus* is an incredibly robust organism that is ubiquitous not only at the interpersonal level, but the intrapersonal level as well.

SSTI INTERVENTIONS FOR THE MILITARY: FORT BENNING RESEARCH SITE

Poor hygiene, crowded living conditions, and frequent skin abrasions make up the perfect epidemiological recipe for future SSTI formation. Unfortunately, all of these conditions apply to members of the military, especially those undergoing basic training. As such, our study population concentrated exclusively on military trainees stationed at Fort Benning, one of the nations largest military training facilities. While the research described herein has direct implications for Fort Benning military trainees, how accurately these data represent SSTIs in the general population is unclear. With nationwide representation, it can be argued that Fort Benning is a geographically diverse training facility and thus may represent SSTI infections throughout the United States. However, with respect to patient demographics, our study population was composed predominately of young, white/Caucasian males in good physical condition. Studies have shown that SSTIs may present differently in other populations such as the elderly and immunocompromised (70). Therefore, it would be interesting to assess any differences in body site and SSTI microbiome composition among these alternative populations. Furthermore, while some studies have suggested a potential difference between various male and female microbiomes (115; 340), it is unknown if the results described in this thesis would also apply to women. Nonetheless, given the extremely high prevalence of SSTIs within the military, further characterization of trainee specific SSTIs should prove valuable.

SSTI INTERVENTIONS FOR THE MILITARY: TRAINEES AT HIGH RISK FOR SSTI

There have been numerous studies aimed at SSTI prevention in the military. One Fort Benning study investigated the effect of enhanced hygiene education and chlorhexidine body wash on combating SSTI development (82). Although SSTI rates remained the same among the various hygiene groups, a similar study in military trainees at a separate training facility observed a significant reduction in SSTI rates with the use of chlorhexidine body wash (205). Although the SSTI interventions described in these two studies were largely similar, there did exist minor procedural variations that may explain the differences in body wash efficacy such as frequency of use as well as when the body wash was administered (82; 205). Nevertheless, the discordance between these two studies emphasizes our limited understanding of SSTI development and may also suggest that novel prevention measures are needed.

In order to reduce SSTI rates in the military, it could be beneficial to group trainees into a "high risk" or "low risk" category. However, categorization would require initial screening upon basic training admission. Ideally, screening tools should be cheap, quick, and accurate. The detection of *S. aureus* in the nares via nasal swab and plating on selective media would be a beneficial first line screening tool to identify "high risk" individuals (79). However, given that *S. aureus* non-carriers also routinely develop SSTI, additional screening stools should be utilized in conjunction with *S. aureus* detection. For example, the nasal microbiota may provide additional microbial cues that may be indicators of future SSTI development. In Chapter 2, we show that Proteobacteria were significantly more abundant in the nares of trainees that did not harbor a SSTI as

compared to those that did have a SSTI (Chapter 2). This data may suggest that SSTI-predictive microbial signatures may reside within the Proteobacterial phylum. Thus, the rapid identification and quantification of non-*S. aureus* SSTI risk factors in the nares is of great interest to the military.

Previous research suggests that approximately 80% of the time, the infecting strain of *S. aureus* is identical to the colonizing strain in the nares (67; 153; 322). In theory, eradication of *S. aureus* from the nares could prevent endogenous infections and therefore reduce SSTI rates. To this end, numerous groups have explored methods to convert *S. aureus* carriers (high risk) to non-carriers (low risk) (53; 274). Indeed, it is recommended in the UK that individuals colonized with MRSA receive nasal mupirocin (56). Although mupirocin is a potent decolonizing agent, patients routinely become recolonized or harbor a mupirocin resistant strain of *S. aureus* (141; 236; 313). To overcome the transient effect of mupirocin, additional research has concentrated on using competing bacterial species that will not only reduce *S. aureus* levels, but will also confer long lasting protection from recolonization (179; 302; 334). Of particular interest, artificial inoculation of various *Corynebacterium* species has been shown to clear *S. aureus* from the nasal cavity (302). Nasal isolates of *Corynebacterium* have also been shown to inhibit the growth of *S. aureus in vitro* (334) (B. Hardy, D.S. Merrell, unpublished data). As shown in Chapter 2, this inverse correlation between *S. aureus* and *Corynebacterium* in the nares was also observed among trainees at Fort Benning. The effect of *Corynebacterium* implantation in the nares of trainees upon admission to basic training on subsequent SSTI rates merits further investigation. Furthermore, elucidation

of the mechanisms behind this bacterial antagonism could provide novel insight into *S. aureus* physiology and pathogenesis.

In addition to screening for *S. aureus* carriers, further characterization of the colonizing strain may prove useful. Strains of *S. aureus* are incredibly diverse and not all express the same virulence factors (208). For instance, a trainee colonized with PVL-positive CA-MRSA may be placed in the "high risk" group compared to a MSSA or coagulase-negative *S. aureus* carrier. Strain characterization can also be used to monitor the spread of specific strains within the military setting. This is especially relevant given the novel *S. aureus qacA*-containing plasmid described in Chapter 4 that confers decreased chlorhexidine susceptibility. In depth surveillance of resistance determinants will not only provide important information for disease prevention, but will also serve as the basis for hypothesis-driven research aimed at molecular interventions to combat spread of resistant pathogens.

While it is important to identify individuals at "high risk" and "low risk" for future SSTI development, we must acknowledge the fact that the term "SSTI" represents a wide array of skin infections, with some being significantly more common than others. For example, abscesses and cellulitis infections are by far the two most prevalent SSTIs in the military (3). Given the differences in bacterial etiology, physical presentation, and treatment options between abscesses and cellulitis, the identification of specific "SSTI type" risk factors would be very useful to the military. As shown in Chapter 3, nasal colonization with MRSA may be associated specifically with abscess formation while white ethnicity and antecedent blister formation were potential risk factors for cellulitis. However, our study was limited in that there were relatively few participants (200)

compared to other risk factor assessment studies (81). Additionally, as mentioned above, these risk factors may only apply to our male-dominated military population. Thus, a larger, more demographically diverse study is needed. Despite these limitations, these data can be used in conjunction with other established SSTI risk factors to identify and monitor those trainees that are highly susceptible to future abscess and/or cellulitis infections.

SSTI INTERVENTIONS FOR THE MILITARY: IMPORTANCE OF SSTI RESEARCH

Unfortunately, SSTIs represent just one disease that is rampant in members of the U.S. military. While SSTI remains the most common infectious cause of hospital admission within the first two year of military service (5), trainees are routinely admitted for other conditions such as mental disorders, traumatic brain injury, alcohol and drug abuse, and sexually transmitted diseases (5; 331; 332). Why then should the military continue to concentrate on SSTI prevention? From a financial standpoint, it is estimated that the average cost of hospitalization for *S. aureus*-associated SSTIs in the US in 2009 was approximately $11,622 (284). By factoring in the number of hospitalization in 2008 due to bacterial skin infection in the U.S. Armed Forces (~1,500), SSTIs alone cost the military over $17 million per year (4). This is likely a conservative approximation given that not all SSTIs are caused by *S. aureus*. Thus, SSTIs represent a significant financial burden to the military. While not all SSTIs require admission to the hospital, a much larger proportion of trainees with SSTI are placed on limited duty. In a recent SSTI-prevention clinical trial at Fort Benning, of the 1,377 trainees that developed SSTI, 67% of them were given work/duty limitations for an average length of 6.9 days (82).

Combined with the nearly 20,000 new trainees per year at Fort Benning and predicted SSTI incidence rate of 1 in 10, this translates to over 9,000 combined days of limited service per year (3). Therefore, further research aimed at SSTI prevention in the military is necessary to help alleviate the financial and medical hardships imposed by SSTIs.

LOOKING FORWARD: THE FUTURE OF SSTI RESEARCH AND TREATMENT

Despite the seemingly dire state of SSTIs in the military and throughout the world, our understanding of SSTI causes/pathogenesis/etiology is rapidly progressing. This is in part a reflection of new and improved research technologies such as high-throughput sequencing. The ability to characterize SSTI and body site microbiomes, as well as the ability to sequence the human genome, has nearly limitless applications when addressing important research questions. Consequently, the generation of enormous amounts of data requires development of analytical tools that can manipulate DNA sequences on a large scale while differentiating between quality DNA reads and potential contaminates. Although a few of these tools have been created (38; 270), they will require continual modification in order to keep up with the rapid advancement of new sequencing technologies. Thus, while it is important to study the microbiological and epidemiological aspects of SSTIs, it is equally important that new molecular and computational tools be developed in order to advance SSTI research.

Despite the findings described in this dissertation, there are still numerous unanswered questions. Not surprisingly, the vast majority of these questions are derived from the ever-increasing complexity associated with SSTI etiology. What exactly is the cause of cellulitis? Is cellulitis even caused by a bacterium or several bacteria? How do

polymicrobial infections differ from monomicrobial infections? With the aid of high-throughput sequencing and careful study design, the answers to these conundrums are within reach.

In addition to SSTI etiology, there are other microbiological, epidemiological, and clinical questions that continue to elude researchers and physicians. How does reduced susceptibility to antibiotics/antimicrobials affect SSTI pathogenesis? What is the prevalence of antibiotic resistance markers among SSTI *S. aureus* isolates? Can we potentially treat or prevent SSTIs with strains of bacteria that have anti-*S. aureus* properties? With such a large number of unresolved questions, this makes SSTI research a very important but equally exciting field to investigate in the future.

CONCLUSION

Skin and soft-tissue infections are inherently difficult to study given the wide range in clinical presentation and the heterogeneous nature of *S. aureus*. This is further complicated by the fact that not all SSTIs are caused by *S. aureus*. Despite our increased understanding of SSTI causes and pathogenesis, the incidence rates continue to rise, especially in the military (4). In order to combat the surging SSTI rates, numerous groups have attempted to develop vaccines that effectively prevent individuals from becoming carriers of *S. aureus,* particularly in the nares (62; 267). Unfortunately, the various tested vaccines have been largely unsuccessful. Thus, there is an increased pressure to develop other means to prevent future SSTI formation. As highlighted in this dissertation, significant consideration should be given to the human microbiome. In particular, how can the microbiota at various body sites, as well as at the site of infection, be exploited to

assess SSTI susceptibility and disease progression? The answer to these questions holds the potential to dramatically influence how we treat and prevent SSTIs in the future.

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APPENDIX A: Dynamic HypA Zinc site is Essential for Acid Viability and Proper Urease Maturation in *Helicobacter pylori*

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The work presented in this chapter is the sole work of R.C. Johnson with the following exceptions: H.Q. Hu created the constructs for the site-directed mutagenesis of *hypA* Zn-binding site and performed the urease activity assays.

ABSTRACT

Helicobacter pylori requires urease activity in order to survive in the acid environment of the human stomach. Urease is regulated in part by nickelation, a process that requires the HypA protein, which is a putative nickel metallochaperone that is generally associated with hydrogenase maturation. However, in *H. pylori,* HypA plays a dual role. In addition to an N-terminal nickel binding site, HypA proteins also contain a structural zinc site that is coordinated by two rigorously conserved CXXC sequences, which in *H. pylori* are flanked by His residues. These structural Zn sites are known to be dynamic, converting from $Zn(Cys)_4$ centers at pH = 7.2 to $Zn(Cys)_2(His)_2$ centers at pH = 6.3 in the presence of Ni(II) ions. In this study, mutant strains of *H. pylori* that express zinc site variants of the HypA protein are used to show that the structural changes in the zinc site are important for the acid viability of the bacterium, and that a reduction in acid

viability in these variants can be traced in large measure to deficient urease activity. This in turn leads to a model that connects the $Zn(Cys)_4$ coordination to urease maturation.

INTRODUCTION

Helicobacter pylori (H. pylori) is a Gram negative bacterium that colonizes the human gastric mucosa (15). Infection causes chronic inflammation and is a major risk factor for development of peptic ulcers and cancer (19; 20; 23). *H. pylori* is a prevalent pathogen that colonizes approximately one-third to one-half of the worldwide adult population (10). Successful colonization of the acidic environment of the stomach requires the activity of urease (7-9), a nickel-dependent enzyme that catalyzes the hydrolysis of urea to ammonia and carbon dioxide (5; 27). Urease is highly expressed in *H. pylori*, representing up to 10% of the total protein (2). However, the enzyme remains inactive without maturation through nickel insertion into the active site (5; 27).

H. pylori urease maturation is dependent on accessory proteins UreIEFGH (5; 27). Additionally, HypA and HypB, accessory proteins normally involved in the maturation of NiFe-hydrogenases, also aid in urease maturation; deletion of *hypA* or *hypB* results in urease deficiency in *H. pylori* despite the presence of the full *ureIEFGH* cascade (4; 17; 18). Urease deficient phenotypes in *hypAB* deletion mutants can be compensated for by addition of Ni to the media, implicating the role of HypA and HypB in nickel delivery to the urease maturation pathway (4; 18). The traditionally hydrogenase-specific nickel metallochaperone, HypA, has been shown to interact directly with a urease-specific nickel metallochaperone, UreE, *in vitro*, providing a possible link

for the role of HypA in urease maturation (4). Several studies have interrogated the interaction between HypA and UreE. Biophysical characterizations show that HypA can outcompete UreG for interaction with UreE (3). Additionally, nickel transfer from HypA to UreE has been shown to involve the interaction of the HypA nickel-binding domain and the UreE nickel-binding C-terminus (26).

As shown in Figure 15, the overall protein structure of HypA has been shown by nuclear magnetic resonance (NMR) to have a distinct nickel-binding domain and structural zinc-binding domain [PDB: 2KDX] (24). In addition to the two conserved CXXC motifs in the HypA structural zinc site, the *H. pylori* zinc binding motifs also have His residues closely flanking the conserved motifs. The structural zinc site has also been extensively characterized by X-ray absorption spectroscopy (XAS), demonstrating that the WT HypA protein structural zinc site is dynamic (11; 14). The average Zn coordination at pH 7.2 is $Zn(Cys)_4$, which changes to $Zn(Cys)_2(His)_2$ at pH 6.3 (the estimated internal pH of *H. pylori* under acid shock conditions) with nickel bound in the nickel site (11; 14). The dynamic nature of the HypA zinc site is lost when any one of the four cysteine residues in the CXXC motif is mutated to alanine or aspartate, and results in locking of the zinc coordination in the $Zn\text{-}Cys_2His_2$ structure (acidic conformation) (11). The dynamic nature of the HypA zinc site is also lost when either of the histidine residues flanking the CXXC motifs are mutated to alanine; this change results in locking of the zinc coordination in the $Zn\text{-}Cys_4$ structure (neutral conformation) (11). These structure-locking mutants of HypA are ideal for interrogation of the role of the HypA zinc site and corresponding protein conformations in urease maturation and acid resistance in *H. pylori*, and are the focus of this study. Herein we create a series of isogenic *H. pylori*

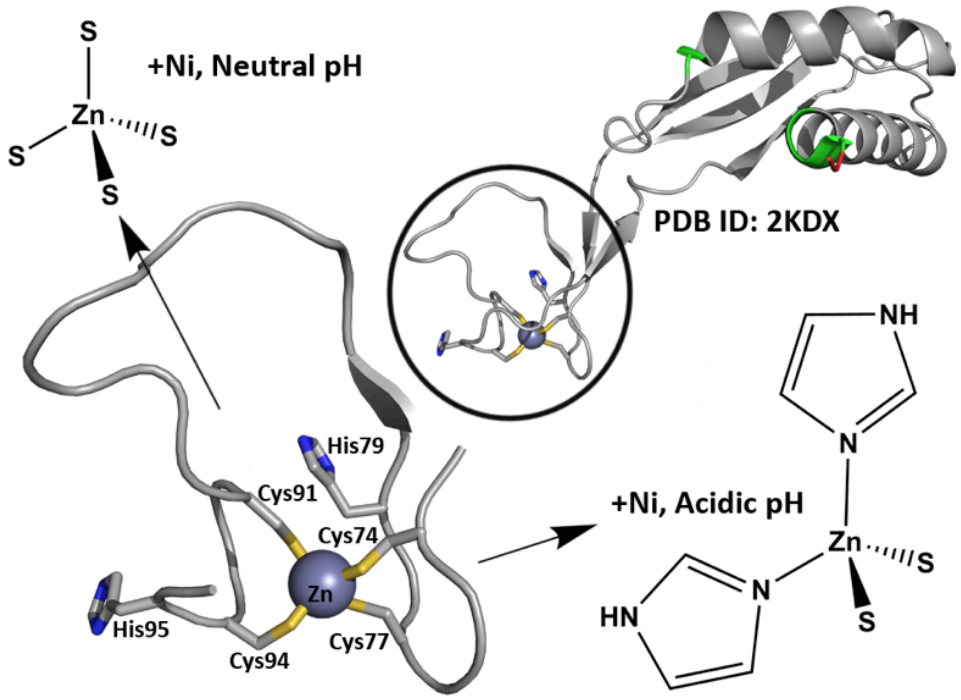

Figure 15. The structure and dynamics of the HypA Zn site has been characterized. The NMR structure of HypA (24) (PDB ID: 2KDX) shows distinct Ni- and Zn-binding domains, where known Ni-binding residues are colored in green (non-native residues leftover from affinity-tag processing shown in red). Close-up look of the Zn site reveals two CXXC motifs with flanking His residues (Zn shown as gray sphere). The Zn site has also been shown to alter its average structure depending on pH and Ni-binding; at acidic conditions with Ni-bound, two His amidazoles replace two of the sulfurs from the Cys residues.

strains that each express zinc site mutant *hypA* variants under the control of the endogenous promoter, and then utilize these mutants to define the contribution of the conserved HypA motifs to *H. pylori* acid viability and urease activity. These studies connect the point mutations in the structural zinc site of a nickel metallochaperone, HypA, to changes in acid viability and urease maturation *in vivo*.

MATERIALS AND METHODS

Bacterial growth conditions

All *H. pylori* strains were maintained at -80°C in brain heart infusion broth (Becton Dickinson) supplemented with 10% fetal bovine serum (FBS) and 20% glycerol and were cultivated on horse blood agar (HBA) medium containing 4% columbia agar base (Neogen Corp), 5% defibrinated horse blood (HemoStat Laboratories, Dixon, CA), 0.2% β-cyclodextrin (Sigma), 10 μg/mL of vancomycin (Amresco), 2.5 U/mL of polymyxin B (Sigma), 5 μg/mL of trimethoprim (Sigma), and 5 μg/mL of amphotericin B (Amresco). Where required, 5% sucrose was added to HBA for selection of sucrose sensitive strains. Liquid growth of *H. pylori* was performed in brucella broth (Neogen Corp) with 10% FBS and 10μg/mL of vancomycin. All *H. pylori* cultures were grown under microaerobic conditions (5% O_2, 10% CO_2, and 85% N_2) at 37°C with 100rpm shaking for liquid cultures. *H. pylori* strain G27 was used for all experiments (1). *Escherichia coli* Top10 cells were either grown on LB agar or in LB liquid medium with shaking at 225rpm. Kanamycin (25μg/mL) and ampicillin (100μg/mL) were used for bacterial selection.

***hypA* mutant construction**

H. pylori G27 genomic DNA was used as the template for mutant construct development. A *hypA* mutant strain containing a *kan-sacB* cassette insertion was constructed as follows. The HypA_Up_F and HypA_Up_R primers (Table 14) were used to amplify a 556 base pair segment of DNA that spanned 398 base pairs upstream of *hypA* (HPG27_832) and 158 base pairs into the *hypA* coding region. Additionally, the HypA_Dn_F and HypA_Dn_R primers (Table 14) were used to amplify a 532 base pair region that began at nucleotide position 160 of *hypA* and spanned 337 base pairs downstream of the *hypA* stop codon. The HypA_Up_R and HypA_Dn_F primers were designed to contain identical flanking sequences, which harbored XhoI and XbaI restriction enzyme sites. Thus, the upstream and downstream amplicons were next fused together utilizing splicing by overlap extension (SOE) PCR (12). The resulting spliced product was cloned into the pGEM-T easy vector (Promega) and transformed into *E. coli* Top10 cells. The *kan-sacB* cassette (6), which confers resistance to kanamycin and sensitivity to sucrose, was amplified from pKSF-II (6) using primers Kan_SacB_F and Kan_SacB_R, which were designed to incorporate a XhoI and XbaI restriction site, respectively. The resulting fragment was digested with XhoI and XbaI and was then inserted between the spliced *hypA* fragments that had been similarly digested. The resulting construct was then transformed into *H. pylori* G27 and transformants were selected on HBA plates containing kanamycin. Successful insertion of the *kan-sacB* cassette into the *hypA* gene was confirmed by PCR and sequencing using the

Table 14. Strain, plasmids, and primers used in this study

Strains	**Description**	**Reference**
DSM1	G27 WT	(1)
DSM43	G27 Δ*ureB* Kan^R	(13), This study
DSM1283	G27 *hypA*::*kan-sacB* Kan^R Suc^S	This study
DSM1295	G27 *hypA* restorant	This study
DSM1296	G27 *hypA* C74A	This study
DSM1297	G27 *hypA* C94D	This study
DSM1298	G27 *hypA* C91A	This study
DSM1299	G27 *hypA* C91D	This study
DSM1300	G27 *hypA* H95A	This study
DSM1301	G27 *hypA* C74D	This study
DSM1363	G27 *hypA* C77A	This study
DSM1364	G27 *hypA* C77D	This study
DSM1365	G27 *hypA* H79A	This study
DSM1366	G27 *hypA* C94A	This study

Plasmids	**Description**	**Reference**
pDSM3	pKSF-II	(6)
pDSM32	pEJ22	(13)
pJI110	pET22b(+) vector with *hypA* WT coding sequence	(11; 14), This study
pET22b-HypA(C74A)	pET22b(+) vector with *hypA* C74A coding sequence	This study
pET22b-HypA(C74D)	pET22b(+) vector with *hypA* C74D coding sequence	This study
pET22b-HypA(C77A)	pET22b(+) vector with *hypA* C77A coding sequence	This study
pET22b-HypA(C77D)	pET22b(+) vector with *hypA* C77D coding sequence	This study
pET22b-HypA(H79A)	pET22b(+) vector with *hypA* H95A coding sequence	This study
pET22b-HypA(C91A)	pET22b(+) vector with *hypA* C91A coding sequence	This study
pET22b-HypA(C91D)	pET22b(+) vector with *hypA* C91D coding sequence	This study
pET22b-HypA(C94A)	pET22b(+) vector with *hypA* C94A coding sequence	This study
pET22b-HypA(C94D)	pET22b(+) vector with *hypA* C94D coding sequence	This study
pET22b-HypA(H95A)	pET22b(+) vector with *hypA* H95A coding sequence	This study

Primers	**Sequence (5'-3')**	**Reference**
HypA_Up_F	CCGCTTTGATTCAGATGGGGTG	This study
HypA_Up_R*	*TCTAGA*AGCTTGCGATCGCTCGAGACTCTAAAAGTCTCAAACGCGCTC	This study
HypA_Dn_F*	*CTCGAG*CGATCGCAAGCTTCTAGAGAATCTTTGGTGTGTAAAGACGC	This study
HypA_Dn_R	GCAAAACGCTGCGGTATTGC	This study
Kan_SacB_F*	GTGGG*CTCGAG*CCCGGGCGAACCATTTGAGGTGA	This study
Kan_SacB_R*	GCGCG*TCTAGA*TATAAGCCCATTTTCATGC	This study
HypA_Confirm_F	GGCTAACGAGCGTGGATAAG	This study
HypA_Confirm_R	GCACTCACTAAAATCGTGGGC	This study
HypA_seq_F	CTAAAGCGGTAACCACATCCG	This study
HypA_seq_R	GACTTGCTTCAATTCCAAACGG	This study
HypA_C74A_F	GGTTGAATTAGAAGCCAAGGATTGTTCGCATGTTTTTAAGCCTAACGCG	(11)
HypA_C74A_R	CGCGTTAGGCTTAAAAACATGCGAACAATCCTTGGCTTCTAATTCAACC	(11)
HypA_C74D_F	GGTTGAATTAGAAGACAAGGATTGTTCGCATGTTTTTAAGCCTAACGCG	(11)
HypA_C74D_R	CGCGTTAGGCTTAAAAACATGCGAACAATCCTTGTCTTCTAATTCAACC	(11)
HypA_C77A_F	GAATTAGAATGCAAGGATGCTTCGCATGTTTTTAAGCCTAACGCGC	(11)
HypA_C77A_R	GCGCGTTAGGCTTAAAAACATGCGAAGCATCCTTGCATTCTAATT	(11)
HypA_C77D_F	GAATTAGAATGCAAGGATGATTCGCATGTTTTTAAGCCTAACGCGC	(11)
HypA_C77D_R	GCGCGTAGGCTTAAAAACATGCGAATCATCCTTGCATTCTAATTC	(11)
HypA_H79A_F	GCAAGGATTGTTCGGCTGTTTTTAAGCCTAACGCGCTAG	(11)
HypA_H79A_R	GTTAGGCTTAAAAACAGCCGAACAC	(11), This study
HypA_C91A_F	GCGCTAGATTATGGGGTGGCTGAGAAATGCCACAGC	(11)
HypA_C91A_R	GCTGTGGCATTTCTCAGCCACCCCATAATCTAGCGC	(11)
HypA_C91D_F	CGCCGTAGATTATGGGGTGGATGAGAAATGCCACAGC	(11)
HypA_C91D_R	GCTGTGGCACTTTCTCATCCACCCCATAATCTAGCGCG	(11)
HypA_C94A_F	GGTGTGTGAGAAAGCCCACAGCAAG	(11)
HypA_C94A_R	AACATTCTTGCTGTGGGCTTTCTCAC	(11)
HypA_C94D_F	GGGGTGTGTGAGAAAGACCACAGCAAGAATGTTATTATCAC	(11), This study
HypA_C94D_R	GTGATAATAACATTCTTGCTGTGGTCTTTCTCACACACCCC	(11), This study
HypA_H95A_F	GTGTGTGAGAAATGCGCCAGCAAGAATGTTATTATC	(11), This study
HypA_H95A_R	GATAATAACATTCTTGCTGGGCGCATTTCTCACACAC	(11), This study

*Restriction enzyme sites are italicized (XhoI or XbaI); Underline denotes nucleotide changes made to the pJI110 (wild type *hypA*) plasmid

HypA_Confirm_F/R and HypA_seq_F/R primers, respectively. The resulting mutant strain was named DSM1283.

Site-directed mutagenesis of *hypA* Zn-binding site

Mutations of the cysteines in the HypA CXXC motifs (Cys71, Cys74, Cys91 and Cys94) to alanine or aspartatic acid and the flanking histidines (His79 and His95) to alanine were constructed by polymerase chain reaction (PCR) using the wild type *hypA* sequence carried on a plasmid (pET-22b(+)) as a template (11). The plasmid carrying the wild type *hypA* was transformed into NovaBlue (Novagen) competent cells and then reisolated using the Axyprep Plasmid MiniPrep Kit (Axygen) and used as the DNA template in all subsequent PCR reactions. PCR primers were designed to incorporate the desired mutations and are listed in Table 14. Reactions were carried out in 50μL volumes using 1ng of template DNA and 2.5ng or 2μM of each primer per reaction. Successful PCR amplifications were confirmed by 0.8% agarose gel electrophoresis. Products were then cloned into the pET-22b(+) vector, and transformed into NovaBlue competent cells. Single colonies were selected and grown to saturation in 5mL liquid cultures of LB-Miller (Fisher Scientific) media supplemented with ampicillin at 37°C. Cells were pelleted by centrifugation at 6,000 g for 5 minutes and plasmids were isolated using the Axyprep Plasmid MiniPrep Kit. Successful mutations were confirmed by plasmid sequencing (GENEWIZ, Inc.).

We utilized the wild-type or mutant HypA pET-22b(+) plasmids, which each contained the entire HypA coding region, to move the mutant constructs of interest into the *H. pylori* chromosome. Each of the constructs were individually transformed into

DSM1283, and double crossover events in which the *kan-sacB* cassette was replaced by the mutagenized *hypA* gene carried on the pET-22b(+) vector were selected for based on sucrose resistance. Sucrose resistant transformants were screened for kanamycin sensitivity and proper integration of the *hypA* construct was confirmed by PCR and sequencing using the HypA_Confirm_F/R and HypA_seq_F/R primers, respectively. In total, *H. pylori* mutant strains were made that contained the following *hypA* mutations: C74A (DSM1296), C74D (DSM1301), C77A (DSM1363), C77D (DSM1364), H79A (DSM1365), C91A (DSM1298), C91D (DSM1299), C94A (DSM1366), C94D (DSM1297), and H95A (DSM1300). In addition, a *hypA*-restorant (*hypA*-R; DSM1295) in which the *kan-sacB* cassette was replaced by the wild type *hypA* gene was also created in order to control for any defects that may have resulted due to genetic manipulation.

Acid resistance testing

Each of the ten *hypA* Zn-site *H. pylori* mutants were tested for acid resistance. Additionally, the wild type *H. pylori* strain, the *hypA::kan-sacB* mutant, and the *hypA* restorant were included as controls. Furthermore, a urease-deficient mutant of *H. pylori* (DSM43) in which the kanamycin resistance cassette replaced the *ureB* subunit was used as a positive control for acid sensitivity; DSM43 was created by transforming wild type *H. pylori* with vector pEJ22 as previously described (13). Assays were conducted as follows: 20mL liquid cultures of *H. pylori* were inoculated to an optical density (600nm) of 0.05 from overnight liquid grown bacterial cells and then allowed to grow for approximately 19 hours. 1mL aliquots were removed from the culture and pelleted by centrifugation. The supernatants were removed and the bacterial pellet was resuspended

in 1mL of phosphate buffered saline (PBS) at pH 6 or 2.3, with or without supplementation with 5mM urea. Immediately after the bacterial pellets were resuspended, an aliquot was removed, serially diluted in brucella broth and plated on HBA plates to determine colony forming units (CFU) per milliliter. The cultures were then incubated in 1.5mL capped tubes for 1 hour at 37°C. At this point, a second aliquot was removed from the cultures, immediately serially diluted, and plated to determine CFU/mL as described above. Percent survival after 1 hour incubation in the various PBS solutions was determined for each bacterial strain. At least three biological replicates were performed for each strain.

Urease activity assay

Urease activities were determined for each of the ten *hypA* Zn-site variants, the wild type *H. pylori* strain, the *hypA::kan-sacB* mutant, and the *hypA* restorant strain. For each strain, 8mL liquid cultures of *H. pylori* were inoculated to an optical density (600nm) of 0.05 from overnight liquid grown bacterial cells and then allowed to grow for approximately 22 hours. At that point, 1mL aliquots were removed from the culture and pelleted by centrifugation (~10^8 cells). The supernatants were removed and the bacterial pellets were stored at -20°C until ready for urease assays. The frozen cells were thawed and then resuspended in 750μL of ice cold HEPES buffer (pH 7.0), 1mM phenylmethanesulfonyl fluoride (PMSF) (MP Biomedicals, LLC), and 1X protease inhibitor cocktail (Sigma-Aldrich) and then lysed by sonication at 70% power for 6 pulses (2-second each) on ice. Lysate was centrifuged at 15,000-g for 10 minutes to remove insoluble fractions from soluble whole cell extracts. Soluble whole cell extracts

were kept at 4°C for up to one month and insoluble fractions were stored at -20°C. Total protein concentration in soluble whole cell extract was assessed by Bradford Assay using the Coomassie Protein Assay Kit (Thermo Scientific).

Urease activities for each strain were determined using a modified phenol-hypochlorite method to assay the amount of ammonia released in the soluble whole cell extract of *H. pylori* lysate in the presence of urea (16; 22). For each strain, 5µL of whole cell extract was added to 245µL of urease reaction buffer (50mM HEPES, 25mM Urea, pH 7.0), and incubated at 37°C for 20 minutes to allow for ammonia production. The reaction was quenched with the sequential addition of 375µL of phenol-hypochlorite buffer A (100mM phenol, 167.8µM sodium nitroprusside) and then the addition of 375µL of phenol-hypochlorite buffer B (125mM NaOH, 0.044% NaClO); samples were mixed with quick vortexing after the addition of each buffer. The assay mixture was incubated at 37°C for 30 minutes to allow for color development (the conversion of ammonia to indophenol) and the absorbance was evaluated at 625nm. Assays were performed alongside a standard curve created using known amounts of ammonium chloride (0.24 – 500nmol) in place of whole cell extract. The urease activity of *ΔureB* strain was set as background and subtracted from the activity of all other strains. Urease activity for the various mutants was normalized to the *hypA*-restorant (*hypA*-R; DSM1295) *H. pylori* as 100%. All experiments were performed in triplicate with two independently grown cultures.

RESULTS

HypA Zn-binding sites are important for acid survival

To determine whether changes in the zinc binding sites of HypA affected acid resistance of *H. pylori*, we created strains of *H. pylori* in which the Cys residues found in the two CXXC motifs associated with zinc binding (Cys74, Cys77, Cys91 and Cys94) and the two His residues (His79 and His95) that flank these two CXXC motifs were mutated. Cys residues were changed to Asp and Ala, while His residues were changed to Ala. We then utilized these 10 HypA mutant strains in combination with the wild type strain, a *hypA* mutant (*hypA::kan-sacB*), a *hypA*-restorant (*hypA*-R) and the *ureB* mutant (*ΔureB*) control strains to assess acid resistance. All 14 of these *H. pylori* strains showed similar robust survival profiles when exposed to pH 6 in the presence or absence of 5mM urea (Figure 16A, B). Conversely, when exposed to pH 2.3, all of the *H. pylori* strains, including the wild type, showed a dramatic decrease in viability; less than 0.01% of the inoculum survived at pH 2.3 in the absence of urea (Figure 16C). However, when urea was supplemented to the pH 2.3 buffer, we began to detect differences in acid resistance across the various strains (Figure 16D). As expected, the wild type *H. pylori* strain and the *hypA*-restorant were able to efficiently utilize the supplemented urea as a substrate for the urease system and survive the acidic challenge. Also as expected, the urease deficient *ΔureB* strain was incredibly acid sensitive; no surviving bacteria were detected (limit of detection 500 CFU/mL equating to 0.0001% survival). The *ΔhypA* strain that carried an insertion in the *hypA* coding sequence was also deficient in its ability to resist acidic stress (< 3% survival). This result confirmed previous studies that indicated that HypA is necessary for efficient urease activity (4; 17; 18). For the various Zn-binding site mutants, mutation of Cys77, His79, and His95 of HypA resulted in no changes in acid

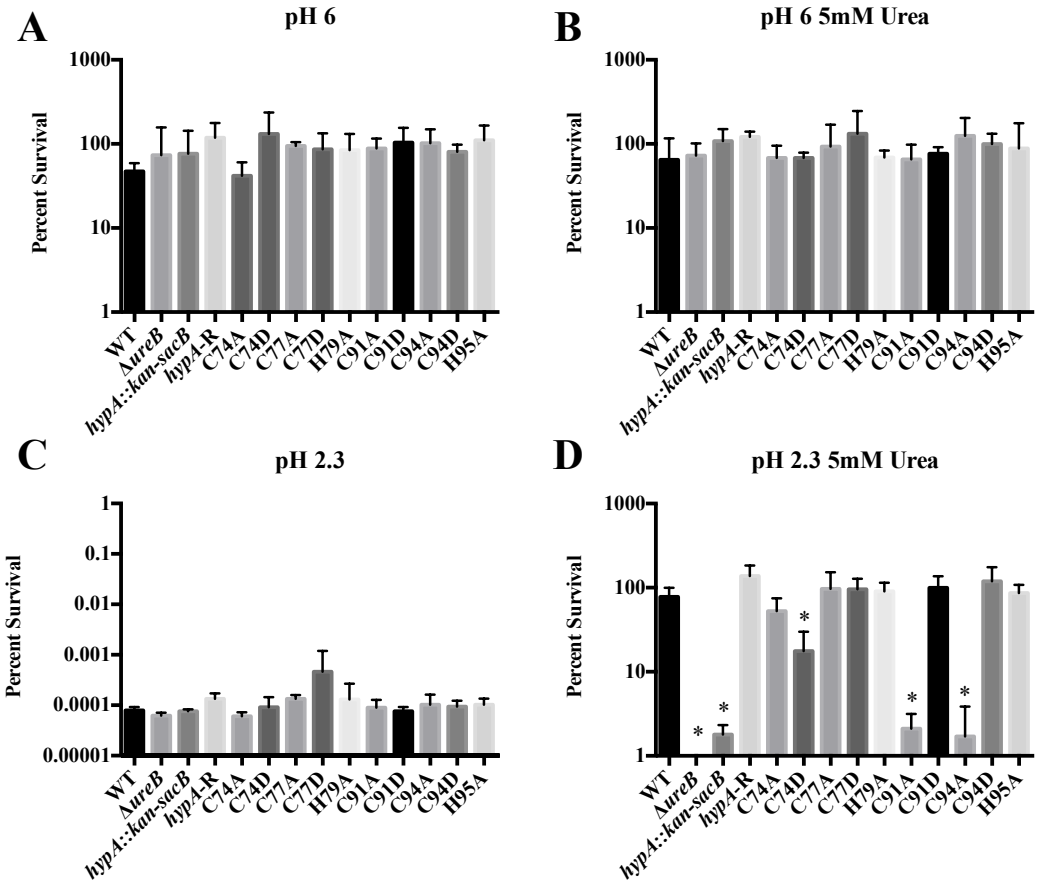

Figure 16. Specific amino acid mutations within the zinc-binding site of the HypA protein in *Helicobacter pylori* result in decreased acid resistance.
The ten *hypA* mutants, as well as the wild type (WT), *ureB* knockout (Δ*ureB*), *hypA* interrupted mutant (*hypA*::*kan-sacB*), and the *hypA*-restorant (*hypA*-R) were exposed to various environments for 1 hour: pH 6 (A), pH 6 containing 5mM urea (B), pH 2.3 (C), and pH 2.3 containing 5mM urea (D). Percent survival was calculated for each strain. Data represent mean ± standard deviation. * = Acid resistance was significantly reduced when compared to wild type ($p < 0.01$, one-way ANOVA followed by Dunnett's test for multiple comparisons).

resistance. Conversely, significant decreases in acid resistance, as compared to the wild type strain, were observed for the C74D, C91A, and C94A mutant strains: 17.6%, 2.1% and 1.7% average survival, respectively. This finding suggests that these zinc-binding site residues play a critical role in acid viability, presumably by affecting the ability of HypA to provide nickel to the urease maturation pathway.

Mutation to HypA Zn-binding sites impacts urease activity

The acid survival data suggested that the C74, C91 and C94 residues play a critical role in the ability of HypA to facilitate urease maturation (4; 17; 18). We next directly investigated urease activity in each of the ten Zn-binding site mutants of *hypA*, as well as in the *ΔureB*, the *hypA::kan-sacB*, the *hypA*-restorant and the wild type strains. The *hypA*-restorant showed three-fold less urease activity than wild type *H. pylori*, which may be a consequence of genetic manipulation. Consequently, urease activities were normalized to the *hypA*-restorant strain. Since the *ΔureB* strain of *H. pylori* is missing the nickel-containing β subunit of the urease enzyme and should have no urease activity, the average urease activity of the *ΔureB* strain was subtracted from measurements of all strains to correct for any background levels of ammonia present in whole cell extract.

As shown in Figure 17, we identified two classes of mutations of the HypA structural zinc site, those that had no effect on urease activity (WT-like), and those that decreased urease activity. This later class can be subdivided into moderately deficient and severely deficient (*ΔhypA*-like) subclasses. Mutations of His residues (H79A and H95A) flanking the HypA CXXC motifs, resulted in strains that retained WT-like activity, suggesting that these His residues are not important for urease maturation. In

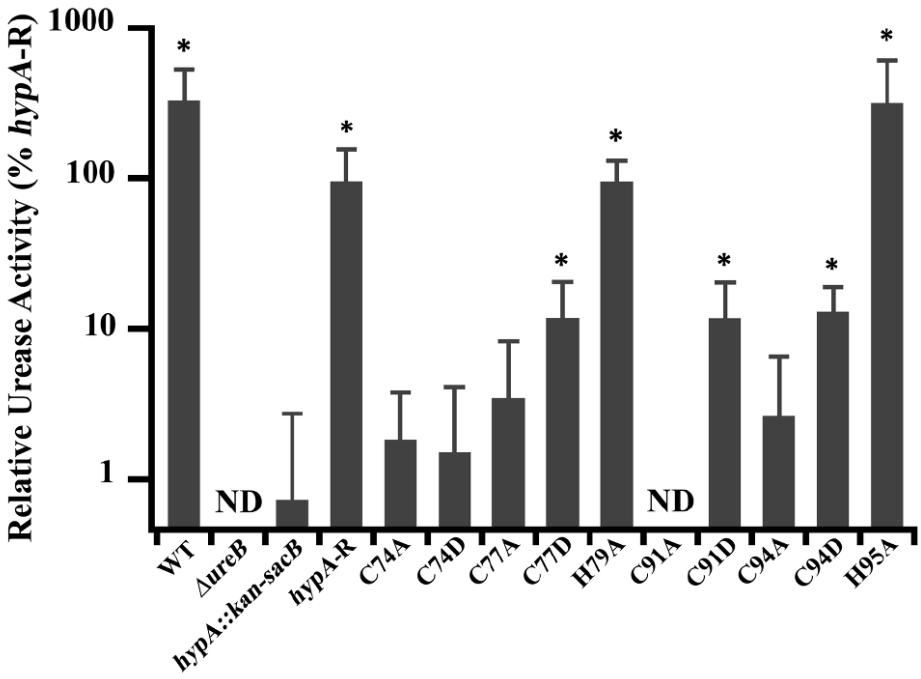

Figure 17. Zn-site mutations of *hypA* in *H. pylori* lead to deficiencies in urease activity. Soluble whole cell extracts were obtained from lysis of ten *hypA* Zn-site mutants strains, as well as the wild type (WT), *ureB* knockout (Δ*ureB*), *hypA* interrupted mutant (*hypA*::*kan-sacB*), and the *hypA*-restorant (*hypA*-R) strains. The phenol-hypochlorite method was used to assay the ammonia production (urease activity) of the strains. Amount of ammonia produced was quantified by comparison with a standard curve constructed with known amount of ammonium chloride. The *ΔureB* strain activity was subtracted from each strain as background ammonia in cell extracts and all activity was normalized to *hypA*-R strain. * = Urease activity was significantly different from the *hypA::kan-sacB* strain ($p < 0.05$). ND = none detected.

contrast, all of the mutations involving Cys residues in the HypA CXXC motifs were deficient in urease activity to some extent (less than 15% compared with the *hypA*-restorant strain), indicating the importance of the Cys residues in the proper function of HypA in the urease maturation pathway. Comparisons of the urease activities in the Cys mutant strains with the *ΔhypA* stain revealed more subtle phenotypes. The activity of C77D, C91D, and C94D were statistically different ($p < 0.05$) from the *ΔhypA* strain (12 – 13% compared with the *hypA*-restorant strain) constituting a moderately deficient phenotype (Figure 17). The remaining Cys mutants, C74A, C74D, C77A, C91A, and C94A, showed activity levels similar to the *ΔhypA* strain (> 4% compared with *hypA*-restorant strain). These urease activity results corroborate the acid survival phenotypes, where C74D, C91A, and C94A mutants were found to be both acid-sensitive and severely deficient in urease activity. Contrary to the acid survival results, C74A and C77A mutants were not acid sensitive under our test conditions, but were found to be severely deficient in urease activity. These findings suggest that, although all of the Cys residues in the CXXC motifs are important for proper HypA function in the urease maturation pathway, there is a position-dependent gradient of importance based on the residue position as well as the type of mutation.

DISCUSSION

The *H. pylori* HypA protein is a putative nickel metallochaperone that is involved in both hydrogenase maturation (as are all HypA proteins) and urease maturation, a function that is unique to *H. pylori*. NMR structural studies of a monomeric construct of *H. pylori* HypA revealed that it contains a structural zinc site associated with two

rigorously conserved CXXC motifs in addition to a nickel-binding site associated with the N-terminus (24). The amino acid sequence of *H. pylori* reveals that the zinc-binding CXXC motifs are unique among other HypA proteins in that each is flanked by a His residue (11). The structural Zn-sites of HypA were previously shown to change coordination in a pH and nickel-dependent manner, adopting a $Zn(Cys)_4$ conformation at neutral pH (7.2), and a $Zn(Cys)_2(His)_2$ conformation at more acidic pH (6.3) (Figure 15) in the presence of Ni(II) (11; 14). These two structures were correlated with other physical properties of dimeric HypA, including nickel binding stoichiometry and thermal stability, with the lower pH form associated with greater thermal stability (11). Mutagenesis studies revealed that altering any Cys residue in the two CXXC motifs (to Ala or Asp) resulted in adoption of the acidic conformation ($Zn(Cys)_2(His_2)$), and any mutation of the flanking His residues resulted in the neutral conformation ($Zn(Cys)_4$), in the presence of Ni(II) at both pH values, as determined by EXAFS analysis of data collected at ~ 50K (11). These pH-insensitive and structure-locking mutants of HypA were important tools employed in the present study to probe the role of HypA in urease maturation and acid viability *in vivo*.

In vivo urease activities of *H. pylori hypA* Zn site variant strains correlate well with previous *in vitro* studies employing addition of purified HypA proteins to whole cell extract from a *ΔhypA* mutant of *H. pylori* (11). Results of the *in vitro* studies show a general decrease in urease activity upon addition of the zinc site variants relative to addition of wild type HypA protein, and a generally greater effect associated with Cys mutants as compared to His mutants (11). The *in vivo* studies presented here reveal two distinct phenotypes: WT-like urease activity, represented by His mutants, and urease-

deficient strains associated with Cys-mutants. These two classes of mutants correspond to the $Zn(Cys)_4$ or $Zn(Cys)_2(His)_2$ conformations, respectively. Our data suggest that the all the Cys residues in the HypA Zn site are important in the maturation of urease in *H. pylori*, a result that is consistent with a model in which the conformation associated with $Zn(Cys)_2(His)_2$ sites, or in which access to the $Zn(Cys)_4$ structure is inhibited in a dynamic sense, leads to lower levels of urease activation. Among the Cys mutations, there were two levels of urease activity observed, a moderate decrease associated with C77D, C91D, and C94D, all Cys → Asp mutations, and a severely deficient level associated primarily with Cys → Ala mutations, which have activity levels similar to the *ΔhypA* strain (C74A, C74D, C77A, C91A, and C94A). With the exception of C74D, Cys→Asp mutations to give rise to more active variants than Cys→Ala mutations, suggests that at least part of the difference lies in coordination of the CXXC motifs. A Cys → Ala mutation results in a loss of a ligand in the CXXC motif, while a Cys→Asp mutation results in the potential substitution of a Cys thiolate ligand by a carboxylate ligand. The latter, although uniformly deleterious, appears to preserve greater HypA activity, presumably by providing a mechanism to access a $Zn(Cys)_3$Asp site that resembles the wild type-like $Zn(Cys)_4$ conformation. A similar trend can be discerned in the study of acid viability: His mutations have no effect, whereas C91A and C94A mutations are associated with low acid survival (comparable to the *ΔhypA* strain), and C91D and C94D have wild type survival under the assay conditions employed. Interestingly, mutations in the more N-terminal CXXC motif lead to strains that are significantly less acid sensitive. Taken together with the urease activity assays, this suggests that the ability of HypA to deliver Ni to the urease maturation pathway may lie

with the dynamic nature of the structural zinc sites. While no clear reason is apparent for the functional differences observed for the two CXXC motifs, it is noteworthy that two Cys residues are substituted by His at low pH, whereas two are retained and anchor the Zn site. This pair-wise difference in function is one possible explanation for the differences between the more N- and C- terminal CXXC sequences. Further elucidation of this difference awaits structural studies of the low pH form of HypA.

It is clear from both the urease assay data and acid viability data that Cys74 is a special position among the Cys variants. It is the only position where the Cys → Asp mutation results in a less acid viable strain than the Cys →Ala mutation, and the only position where urease activity is not higher for the Asp variant than for the Ala variant. Examination of the NMR structure (Figure 15) shows that the Zn site is formed by a loop that begins with Cys74 and ends with Cys94. However, the terminal Cys residues differ in that Cys94 is flanked by a His residue and Cys74 is not. In the HypA dimer crystal structure from *Thermococcus kodakorensis KOD1* (PDB ID: 3A44) (21), Cys74 and 94 have a similar relationship, though these residues are now derived from different monomers in the strand-swap dimer (21). The lack of an alternative ligand could make Cys74 a more vulnerable position, particularly if it plays an anchoring role, the loss of which may result in a more severe phenotype due to destabilization of the entire structural zinc site.

HypA and HypB are accessory proteins that are generally associated with hydrogenase maturation, but in *H. pylori* have been shown to be important for the maturation of both NiFe-hydrogenase (17; 18) and urease (4; 17; 18). In addition to interacting with HypB (17; 25), HypA has also been shown to interact directly with the

urease-specific Ni metallochaperone, UreE (3; 4; 26). Interaction of HypA with both HypB (25) and UreE (26) has been demonstrated to involve the N-terminal Ni-binding domain of HypA and Ni-transfer between proteins. In this study we demonstrated that altering the HypA structural zinc site can also severely affect acid viability and urease maturation *in vivo*. These findings suggest that protein structural dynamics, reflected in the HypA zinc site structure, may result in subtle alterations of the overall HypA fold and differential interactions between HypA and partnering proteins, ultimately leading to a gradient in urease and hydrogenase enzymatic activities that is a function of cellular pH and nickel availability.

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APPENDIX B: Fur-Dependent Activation of Two Divergently Transcribed Genes (*HpG27_51* and *HpG27_52*) in *Helicobacter pylori*

Ryan C. Johnson, Oscar Q. Pich, and D. Scott Merrell.

The work presented in this chapter is the sole work of R.C. Johnson with the following exceptions: O.Q. Pich created strains DSM1180 and DSM1182.

ABSTRACT

The human bacterial pathogen, *Helicobacter pylori*, colonizes the gastric mucosa of approximately one-half of the world's population. In order to survive such a harsh environment, *H. pylori* is equipped with numerous regulatory pathways that allow the microbe to adapt to external stimuli such as iron deprivation and low pH. One *H. pylori* master regulatory protein that is required for *in vivo* adaptation is the ferric uptake regulator (Fur). In *H. pylori*, Fur has been shown to both activate and repress gene transcription in both its iron-bound and iron-free (*apo*) form. This occurs via DNA binding at specific nucleotide sequences known as Fur boxes. Conserved and semi-conserved Fur boxes are found throughout the *H. pylori* genome; those located in the promoter region may suggest direct Fur regulation of the corresponding gene. In this study, we characterize two divergently transcribed genes (*HpG27_51* and *HpG27_52*) that contain numerous intergenic Fur boxes. While gene *HpG27_51* encodes the *putA* homologue of *H. pylori*, which is important for proline utilization, gene *HpG27_52* encodes a hypothetical protein that we show harbors urease enhancing properties. At the

transcriptional level, both genes were up regulated in response to iron chelation in a manner that suggests *apo*-Fur activation. Preliminary animal studies suggest that gene *HpG27_52* is also important for proper colonization of the gastric mucosa. These findings further expand our ever-growing knowledge of the *H. pylori* Fur regulon and suggest additional ways in which *H. pylori* senses and responds to its fluctuating environment.

INTRODUCTION

The Gram-negative bacterium *Helicobacter pylori* is considered by some to be the most successful pathogen in human history; nearly 50% of the world's population is currently colonized (15; 26). This translates to nearly 3.5 billion individuals that are at increased risk for the development of severe gastric maladies such as gastric cancer (15). Indeed, over 60% of new gastric cancer cases can be directly attributed to *H. pylori* colonization (45). Despite the enormous impact on human health, it wasn't until 1982 that "S-shaped bacilli" were initially observed in gastric biopsy specimens (38). At the time, the noxious environment of the human stomach was considered a sterile body site. However, it is now clear that despite the low pH and limited nutrients available in this niche, *H. pylori* not only survives, but thrives within the human stomach.

To combat the harsh conditions of the human stomach, *H. pylori* is equipped with a vast array of regulatory networks that are called upon in response to environmental cues (18). One cue, of particular interest, is iron availability. Iron is essential to *H. pylori* physiology as it is a common cofactor required by numerous proteins (25; 48; 56).

Conversely, too much iron results in free radical formation through the Fenton and Haber-Weiss reactions (43; 60). To ensure proper uptake and utilization of iron, *H. pylori* has evolved a complex iron-responsive regulon that is centralized around the master regulatory protein known as the ferric uptake regulator (Fur) (59). Classically, in response to high levels of iron, iron-cofactored Fur will bind the promoter region of a gene and repress transcription via RNA polymerase (RNAP) interference (20). In *H. pylori,* Fur has also been shown to bind up stream of the promoter and to activate expression of some genes (20; 29). Additionally, upon iron limitation, iron-free (*apo*) Fur has been shown to both activate and repress expression of different sets of genes (3; 21; 25). Interestingly, while some bacteria possess a Fur homologue that performs multiple regulatory functions, *H. pylori* harbors the only documented Fur protein that can both activate and repress gene expression in both its iron-bound and *apo* forms (10). Additionally, not only is *H. pylori* Fur required for iron uptake, but it also responds to a wide array of environmental stresses including acid, osmototic, oxidative, and nitrosative stresses (4; 12; 25; 28; 49).

In order to define Fur regulated genes in *H. pylori,* we previously characterized the DNA sequences that are crucial for Fur-DNA binding (Fur boxes) (8; 47). A whole genome search revealed the presence of conserved and semi-conserved variants of the iron-bound Fur box (5'-TAATAATnATTATTA-3') that were interspersed throughout the *H. pylori* genome (47). Of particular interest was a semi-conserved Fur box (5'-TAATAATGCTTTTTA-3') located in the intergenic region between the two divergently transcribed genes *HpG27_51* and *HpG27_52*. While gene *HpG27_51* is believed to be involved in proline utilization (*putA*) (2), gene *HpG27_52* encodes a small hypothetical

protein of unknown function. The region containing the Fur box was confirmed to be bound by iron-bound Fur by electrophoretic mobility shift assays (EMSA) (47). In addition to the iron-bound Fur box, DNA sequences that are involved in *apo*-Fur binding (5'-AAATGA-3') were also identified within the *HpG27_51-HpG27_52* intergenic region (8). We therefore hypothesized that Fur binds to the Fur box(es) located in the promoter regions of genes *HpG27_51* and *HpG27_52* and alters gene expression in response to iron availability.

In this study, we show that expression of both *HpG27_51* and *HpG27_52* is influenced by iron availability in a Fur-dependent manner. However, initial analysis suggests that this occurs independent of the identified predicted Fur-binding site; Fur-dependent regulation still occurs when the Fur box is mutated. We also provide preliminary biological characterization of gene *HpG27_52* both *in vitro* and *in vivo*. The data provided herein will help investigators better understand the ever-growing complexity of the Fur regulon in *H. pylori*. Given Fur's importance to *H. pylori* adaptation *in vivo* (42) and the fact that it is a bacterial specific protein, Fur may be an attractive target for future drug development (11).

MATERIALS AND METHODS

Bacterial strains and growth conditions

All strains, plasmids, and primers utilized in this study are listed in Table 15. Wild-type *H. pylori* strain G27 (DSM1), a common laboratory strain originally isolated

Table 15. Strains, plasmids, and primers used in this study

Strains	Description	Reference
DSM1	G27 WT	(2; 14)
DSM43	G27 Δ*ureB*::*kan* Kan^R	(32)
DSM46	J166 WT	(53)
DSM48	7.13 WT	(27)
DSM300	G27 Δ*fur*::*cat* Cm^R	(9)
DSM343	G27 Δ*fur*::*cat* (pDSM340) Cm^R	(9)
DSM1139	DH5α (pHP8080) Cm^R	(39)
DSM1180	G27 Δ*HpG27_52::kan* Kan^R	This study
DSM1182	DH5α (pHP8080 + pBS:: *HpG27_52*) Cm^R Amp^R	This study
DSM1228	7.13 Δ*VD16_RS08305::kan* Kan^R	This study
DSM1271	G27 Δ*HpG27_51::kan* Kan^R	This study
DSM1302	G27 Δ*HpG27_52::kan* complement Kan^R Cm^R	This study
DSM1369	7.13 Δ*VD16_RS08305::kan* complement Kan^R Cm^R	This study
DSM1396	DH5α (pHP8080 + pBS) Cm^R Amp^R	This study
DSM1412	DH5α (pHP8080 + pUEF1004) Cm^R Amp^R	(39)
DSM1413	DH5α (pHP8080 + pUEF1004-511) Cm^R Amp^R	(39)
DSM1435	J166 Δ*EG65_00320::kan* Kan^R	This study
DSM1436	J166 Δ*EG65_00320::kan* complement Kan^R Cm^R	This study
DSM1437	G27 ΔP_{52}*::kan-sacB* Kan^R Suc^S	This study
DSM1438	G27 Δ*fur* $\Delta P_{HpG27\ 52}$*::kan-sacB* Cm^R Kan^R Suc^S	This study
DSM1439	G27 $\Delta P_{HpG27\ 52}$::scrambled iron-bound Fur Box	This study
DSM1440	G27 Δ*fur* P_{HpG27_52}::scrambled iron-bound Fur Box Cm^R	This study
DSM1444	G27 $\Delta P_{HpG27\ 52}$::scrambled *apo* Fur Box	This study
DSM1445	G27 Δ*fur* $P_{HpG27\ 52.:}$scrambled *apo* Fur Box Cm^R	This study

Plasmids	Description	Reference
pDSM3	pKSF-II	(13)
pDSM101	pUC18k-2	(40)
pDSM324	pRDX-C	(16)
pDSM340	p199::*fur*	(9)
pDSM745	pKJMSH	(33)
pDSM775	pBluescript (pBS) modified MCS (EcoRV only)	This study
pDSM1139	pHP8080	(39)

Primers	Sequence (5'-3')*	Reference
51_upF	CAATATGAGTGCCACTCATAAG	This study
51_upR	GTTAGTCACCCGGGTACCGAGCTCGGCTTGATTGTAGCATGT TTTAAG	This study
51_dnF	CCTCTAGAGTCGACCTGCAGGCACACAAATCATGCTGTGCTG	This study
51_dnR	GCGCTCATCATCAAAAGCC	This study
52_upF	GGTTACTGATGCTATCTTGC	This study
52_upR	GTTAGTCACCCGGGTACCGAGCTCGAGTGTGCCAATCATAAT ACC	This study
52_dnF	CCTCTAGAGTCGACCTGCAGGCCAAATTAGAAGACCTTGAAC CC	This study
52_dnR	GTTTTTTCTGTGGTTAGCGC	This study
Kan_F	GAGCTCGGTACCCGGGTGACTAAC	(40)
Kan_R	TGCCTGCAGGTCGACTCTAGAGG	(40)
51confirmF	GGGTAGAAGCAGTCGTTCTTG	This study
51confirmR	CGACTACGCTAGAGCCTTGC	This study
52confirmF	CTCAATCATTTCAAAGCGGGC	This study
52confirmR	GTTGATAGCGCTGTGGTTAGG	This study
52_upF_J166	CCGATCCATAAGCTCTATGAGC	This study
52_upR_J166	GTTAGTCACCCGGGTACCGAGCTCCCTTTGTTTTGTAAAATTT GTTATAAATCC	This study
52_dnF_J166	CCTCTAGAGTCGACCTGCAGGCACGGAGATATTCTTATGAGTG GCACTC	This study
52_dnR_J166	CTTGCTGAGATTGTTCTAACTC	This study
52confirmF_J166	GCGGGCTTTATTGTCTAGGC	This study

52confirmR_J166	CGGCTAGCTTTTGATTTTCTCC	This study
52compF	CGCGCGGATCCGTAGCATGTTTTAAGCGGG	This study
52compR	CGCGCCTGCAGGCCCCCTCTTTATAAACCCC	This study
HP0203-F	GATTGACTTGGGGTTCAGCGTTGGTG	(33)
HP0204-R	GTTTGAGCTTGCTAATGATAAGCGG	(33)
P52_Up_F	GACCATAGCTTTCGTGTCG	This study
P52_Up_R	TCTAGAAGCTTGCGATCGCTCGAGGACCGCTTAAAAACCCGC	This study
P52_Dn_F	CTCGAGCGATCGCAAGCTTCTAGAGTGGTAAGTATTTACCGCT TAAAAC	This study
P52_Dn_R	CCCTCTTTATAAACCCCTAGAATG	This study
Kan_SacB_F	GTGCTCGAGCCCGGGCGAACCATTTGAGGTGA	This study
Kan_SacB_R	GCTCTAGACCCGGGTATAAGCCCATTTTCATGC	This study
P52_Confirm_F	CCGCTCTCTTAATTGGCTC	This study
P52_Confirm_R	GAGTGCCACTCATAAGAATATCTCC	This study
P52_Up_R1	CAATTTTAATAATTAAATCGCGCGAGTATGAAAACAACCAC	This study
P52_Dn_F1	GTGGTTGTTTTCATACTCCGCCGATTTAATTATTAAAATTG	This study
51_RT_PCR_F	CGCCGGTATTGTGTTGCAAGC	This study
51_RT_PCR_R	CTTCGCTCTCCATGTTCGCTCC	This study
52_RT_PCR_F	ATTATGATTGGCACACTCGG	This study
52_RT_PCR_R	AGAATGTAGAATCCCAGTGG	This study
52_seq_F	GTGGTAAGTATTTACCGCTTAAAAC	This study
52_seq_R	GCCCTTAGGCATGTATTGCG	This study
52_P.ext	CTGAGTATCAAAGCTAGAACAACC	This study
52_RBS_F	CAAACAAAGGATATAAAATG	This study
52_RBS_R	ATAAACCCCTAGAATGTAGA	This study

*XhoI and XbaI restriction sites are underlined

by gastric biopsy from Grosseto Hospital (Tuscany, Italy) (2; 14), was used for all molecular experiments in this study. Additionally, the animal adapted *H. pylori* strains 7.13 (DSM48) and J166 (DSM46) were used for *in vivo* colonization studies (27; 53). All *H. pylori* strains were maintained at -80°C in brain heart infusion broth (Becton Dickinson) supplemented with 10% fetal bovine serum (FBS, Gibco) and 20% glycerol and were routinely cultivated on horse blood agar (HBA) containing 4% Colombia agar base (Neogen Corp), 5% defibrinated horse blood (HemoStat Laboratories, Dixon, CA), 0.2% β-cyclodextrin (Sigma), 10 μg/mL of vancomycin (Amresco), 2.5 U/mL of polymyxin B (Sigma), 5 μg/mL of trimethoprim (Sigma), and 5 μg/mL of amphotericin B (Amresco). When required, 5% sucrose was added to the HBA medium. Liquid *H. pylori* cultures were grown in brucella broth (Neogen Corp) containing 10% FBS and 10 μg/mL of vancomycin with shaking at 115 rpm. All *H. pylori* cultures were grown under microaerobic conditions (5% O_2, 10% CO_2, 85% N_2) at 37°C. *Escherichia coli* strains were maintained at -80°C in LB broth (MO BIO laboratories Inc.) containing 40% glycerol and were grown at 37°C on 1.5% LB agar or in LB broth with shaking at 225 rpm. When necessary, bacterial selection was performed using the following antibiotics: kanamycin (Kan) (25 μg/mL), ampicillin (Amp) (100 μg/mL), and chloramphenicol (Cm) (25 μg/mL).

Mutant construction

Deletion of the *fur* gene in *H. pylori* G27 (DSM300) and plasmid complementation of the Δ*fur* mutant (DSM343) were previously performed in our laboratory (9). Deletion of gene *HpG27_51* in *H. pylori* was accomplished through

splicing by overlap extension (SOE) mutagenesis (31). Briefly, the 51_upF/51_upR and 51_dnF/51_dnR primer pairs were used to PCR amplify the up stream and down stream regions of the *HpG27_51* coding region, respectively; note the 51_upR and 51_dnF primers were designed with regions of homology to the non-polar kanamycin resistance cassette. The up stream and down stream regions were then sequentially fused to the kanamycin resistance cassette originally PCR amplified from pDSM101 using the Kan_F and Kan_R primers. The "up stream-kanamycin-down stream" SOE construct was then integrated into the chromosome of wild-type *H. pylori* by natural transformation. Mutant selection was performed on HBA Kan. Successful replacement of the *HpG27_51* gene was confirmed by PCR and sequencing using the 51confirmF and 51confirmR primers. Replacement of *HpG27_52* in strain G27 and the *HpG27_52* homologue *VD16_RS08305* in strain 7.13 with the kanamycin cassette was performed in a similar fashion using the 52_upF and 52_upR and 52_dnF and 52_dnR SOE primers followed by confirmation using the 52confirmF and 52confirmR primers. The G27 Δ*HpG27_51* and Δ*HpG27_52* mutant strains were named DSM1271 and DSM1180, respectively. The 7.13 Δ*VD16_RS08305* mutant was named DSM1228.

Since it was determined by sequencing that the *HpG27_52* up stream region was not conserved between the G27 and J166 strains, new SOE primers were designed for gene replacement of the *HpG27_52* homologue *EG65_00320* in J166: 52_upF_J166 and 52_upR_J166 and 52_dnF_J166 and 52_dnR_J166. SOE was conducted as described above. The resulting J166 Δ*EG65_00320* mutant strain was confirmed by PCR and sequencing (primers: 52confirmF_J166 and 52confirmR_J166) and was named DSM1435.

Complementation of the Δ*HpG27_52* mutation in G27 and the Δ*VD16_RS08305* mutation in 7.13 was accomplished via chromosomal insertion of the *HpG27_52* or *VD16_RS08305* gene into an intergenic region of their respective mutant genomes as previously described (33). The gene coding region and endogenous promoter were PCR amplified (primers: 52compF and 52compR) and were individually cloned into the pDSM745 vector after digestion of both the vector and insert with BamHI and PstI. The resulting vectors were transformed into Top10 *E. coli* and transformants were selected on LB Cm. Successful insertion of the genes into pDSM745 was confirmed by PCR (primers: 52compF and 52compR). The confirmed vectors were then transformed into the G27 Δ*HpG27_52* and 7.13 Δ*VD16_RS08305* mutants (DSM1180 and DSM1228, respectively) and transformants were selected for on Cm. Complemented mutant strains were confirmed by PCR and sequencing using the HP0203-F and HP0204-R primers. The G27 Δ*HpG27_52* and 7.13 Δ*VD16_RS08305* complementation strains were named DSM1302 and DSM1369, respectively.

The J166 Δ*EG65_00320* mutant was complemented via chromosomal insertion of the *EG65_00320* gene into the *rdxA* locus (52). The J166 *EG65_00320* coding region and endogenous promoter were PCR amplified (primers: 52compF and 52compR), digested with BamHI and PstI, and inserted into the similarly digested pDSM324 plasmid. Vector confirmation and transformation into strain DSM1435 were performed as described above. Successful insertion of the *EG65_00320* gene into the *rdxA* locus was confirmed by PCR and sequencing.

DNA mutagenesis of Fur-binding sites

Markerless mutations of either the iron-bound or *apo*-Fur putative DNA-binding regions (Fur boxes) were created by sequential insertion (selection) and replacement (counter selection) of the *kan-sacB* cassette by DNA fragments containing the desired mutated Fur boxes. Briefly, DNA regions flanking the iron-bound and *apo*-Fur box #2 (Figure 18) were PCR amplified and spliced together using SOE (primers: P52_UpF and P52_UpR and P52_DnF and P52_DnR). The resulting construct was then cloned into the pGEM-T easy vector (Promega) and transformed into *E. coli* Top10 cells. Importantly, the spliced construct was designed to contain centralized XhoI and XbaI restriction enzyme sites. The *kan-sacB* cassette, which confers resistance to kanamycin and sensitivity to sucrose, was next amplified from pDSM3 using the Kan_SacB_F and Kan_SacB_R primers. The *kan-sacB* cassette was then inserted between the two spliced DNA fragments following digestion of both insert and vector by XhoI and XbaI. The resulting construct was transformed into wild-type G27 (DSM1) and G27 Δ*fur* (DSM300) strains and transformants were selected on HBA Kan. Chromosomal insertion of the *kan-sacB* cassette was confirmed by PCR and sequencing (primers: P52_Confirm_F and P52_Confirm_R). The wild-type and Δ*fur* P_{52}::*kan-sacB* mutant strains were named DSM1437 and DSM1438, respectively.

Next, the *kan-sacB* cassette was replaced with DNA fragments that harbored scrambled Fur DNA-binding sequences. For both the iron-bound and *apo*-Fur boxes, the sequences were mutated to a run of alternating guanines and cytosines. We utilized G-Block technology (Integrated DNA Technologies) to synthesize a 909 base pair DNA fragment that contained the mutated iron-bound Fur box in the center (Figure 18). The G-Block was transformed into DSM1437 and DSM1438 and homologous recombination

Figure 18. Key regulatory elements found within the intergenic region of genes *HpG27_51* and *HpG27_52*.
The sequence shown was extracted from the *Helicobacter pylori* G27 genome (NC_011333.1) beginning at nucleotide position 62,140 and ending at position 63,048. The green and blue DNA sequences correspond to the coding region of genes *HpG27_51* and *HpG27_52*, respectively. The arrows indicate the transcriptional start sites (TSS) and the -10 sequences are shown in red. The various putative *apo*-Fur boxes are underlined and numbered (1-4). The putative iron-bound Fur box is underlined with the dashed line. The sequence shown is identical to the G-block used to mutate the iron-bound Fur box except with TAATAATGCTTTTTA changed to GCGCGCGCGCGCGCG.

events were selected for on HBA sucrose plates. Sucrose resistant colonies were subsequently screened for Kan sensitivity on HBA Kan. Colonies that were sucrose resistant as well as kanamycin sensitive were confirmed by PCR and sequencing (primers: P52_Confirm_F and P52_Confirm_R) to contain the mutated version of the iron-bound Fur box. The scrambled iron-bound Fur box strains were named DSM1439 (wild-type) and DSM1440 (Δ*fur*). For the *apo*-Fur box, the mutated DNA fragment was created by SOE. Briefly, DNA regions up stream and down stream of *apo*-Fur box #2 (Figure 18) were amplified with the following primer pairs: P52_Up_F and P52_Up_R1 and P52_Dn_F1 and P52_Dn_R. Of note, the P52_Up_R1 and P52_Dn_F1 primers contain overlapping DNA sequences that encompass the mutated *apo*-Fur box. The two DNA fragments were spliced together (SOE) and subsequently transformed into DSM1437 and DSM1438 strains. Selection and confirmation of the mutant strains were performed in a similar fashion as described above. The wild-type and Δ*fur* scrambled *apo*-Fur box strains were named DSM1444 and DSM1445, respectively.

Cell harvesting, RNA extraction, and RT-PCR

Overnight liquid starter cultures of *H. pylori* were used to inoculate a 25 mL culture to an OD_{600} of 0.05 in 125 mL flasks. Cultures were grown for various times ranging from 6 hours (early exponential growth phase) to 31 hours (stationary phase). 10 mLs was removed from the culture and harvested by vacuum filtration onto a 0.45 μm nitrocellulose filter and immediately snap-frozen in liquid nitrogen. Another 10 mLs was simultaneously removed from the 25 mL culture and added to a fresh 125 mL flask. Iron chelation of the medium was then performed by the addition of 200 μM 2, 2'-Bipyridyl

(DPP, Sigma). The chelated culture was incubated for 1 hour at 37°C under microaerobic conditions with shaking (115 rpm). The chelated cultures were then harvested onto nitrocellulose filters and snap-frozen as described above. TRIzol (Invitrogen) mediated extraction of RNA was performed as previously described (7). Next, approximately 500 ng of purified RNA per sample was converted into cDNA using the Quantitect reverse transcription kit (Qiagen). For each reverse transcription (RT) reaction, a corresponding tube lacking the reverse transcriptase enzyme was included (NoRT) to assess genomic DNA contamination. A 1 µl aliquot of the RT or NoRT reaction was added to a 20 µL real-time PCR (RT-PCR) reaction consisting of 1X SYBR Green RT-PCR master mix (Qiagen) and 3 pmol of each primer. All RT-PCR primers are listed in Table 15. The RT-PCR reactions underwent an initial activation step for 5 minutes at 95°C and were then subjected to 35 cycles of 95°C for 5 seconds followed by 50°C for 10 seconds using a Roto-gene Q thermocylcer (Qiagen). RT-PCR primers were tested for specificity by single DNA band detection using DNA gel electrophoresis (2% agarose gel) as well as post RT-PCR melt curve analysis. Fold change in gene expression was calculated using the $2^{-(\Delta\Delta Ct)}$ method with the 16S rRNA gene as the internal control. All RT-PCR reactions were performed minimally in triplicate.

Primer extension and 5' transcriptional start site (TSS) mapping

A 375 base pair region encompassing the promoter region of gene *HpG27_52* in *H. pylori* G27 was PCR amplified using the 52_seq_F and 52_seq_R primers. This PCR fragment served as template for dideoxy sequencing reactions using the Sequenase PCR product sequencing kit v2.0 (USB) according to the manufacturer's recommendation.

Additionally, approximately 2.5 μg of total RNA served as template for primer extension analysis using the AMV reverse transcription kit (Promega). An additional NoRT control was performed in a similar manner as mentioned above. Sequencing and primer extension reactions were initiated from the same genomic location using the 52_P.ext γ-^{32}P-labeled DNA primer and resolved by urea polyacrylamide gel electrophoresis. The gels were subsequently exposed to phosphor screens overnight and scanned using a Storm 860 scanner (Molecular Dynamics). Gel images were analyzed using ImageQuant TL Software (GE). 5' TSS mapping was performed in triplicate with comparable results.

Urease activity analysis

To test the ability of gene *HpG27_52* to enhance urease activity in *H. pylori,* we utilized a colorimetric assay to measure ammonia production in both *H. pylori* as well as in a previously documented surrogate *E. coli* model (39). A fragment of DNA containing the *HpG27_52* ribosomal binding site (RBS) and coding region from *H. pylori* G27 were PCR amplified (primers: 52_RBS_F and 52_RBS_R) and cloned into the EcoRV digested pDSM775 vector. The pBS::*HpG27_52* construct was then transformed into strain DSM1139, which carries the pHP8080 vector that expresses the entire urease gene cluster (*ureABIEFGH*). An empty pBS vector (DSM1396) as well as two pBS vectors that each contained known urease enhancing factors (pUEF1004 (DSM1412) and pUEF1004-511 (DSM1413)) were included as negative and positive controls, respectively. All *E. coli* strains were grown overnight from a single colony in 1.5 mLs of M9 minimal medium-1X M9 salts, 0.4% glucose, 1 mM $MgSO_4$, 0.1 mM $CaCl_2$, 1.68 μM thiamine-HCl, 0.5% Casamino Acids, 1% L broth, and 1 μM $NiCl_2$ (39) containing either

Cm or Cm plus Amp to ensure plasmid retention. The following day, the bacteria were pelleted via centrifugation at 12,000 x g for 2 minutes at 4°C. The cells were washed twice with 50 mM HEPES buffer pH 7.5 and subsequently resuspended in 1 mL of the HEPES buffer in 1.5 mL eppendorf tubes. The resuspended bacteria were lysed on ice by sonication (3 x 20 second pulses at 40% intensity). Cytosolic proteins (supernatant) were separated from the cell debris (pellet) by centrifugation at 12,000 x g for 10 minutes at 4°C. The protein concentration in the supernatant was measured using the Pierce BCA protein assay (Life Technologies). 50 μgs of protein was then added to urease buffer (50mM HEPES, 25mM urea, pH 7.5) to a final volume of 1.5 mLs and incubated at 37°C for 20 minutes. 100 μLs of the reaction was then stopped by the addition of 1.5 mLs of solution A (10 g/liter phenol, 50 mg/liter sodium nitroprusside). An equal volume of solution B (5 g/liter NaOH, 0.044% NaClO) was added, vortexed, and incubated for 30 minutes at 37°C. Color development was measured by absorbance at 625 nm using a Genesys 20 spectrophotometer (Thermo Scientific). A standard curve of ammonium chloride ranging from 0 to 2.5 mM was implemented to quantify ammonia production. All data was normalized to DSM1139 (pHP8080).

A modified protocol was used to directly assess urease activity in *H. pylori*. For all strains of *H. pylori* used, 25 mL cultures were initially inoculated to an OD_{600} of 0.05 and grown for 6 hrs. 1 mL was removed from the culture, pelleted, and washed 2X in HEPES buffer as described above. The *H. pylori* cells were then resuspended in 750 μLs of buffer containing HEPES (50 mM), pH 7, 1 mM phenylmethanesulfonyl fluoride (PMSF) (Sigma) and protease inhibitor cocktail tablets (Roche) and lysed on ice by sonication (6 x 2 second pules at 70% intensity). Cell debris was removed by

centrifugation (15,000 x g for 10 minutes at 4°C) and the supernatant was collected. 10 μgs of total protein from the supernatant was added to the urease buffer (50 mM HEPES, 25 mM urea, pH 7) to a final volume of 1.5 mLs and incubated at 37°C for 20 minutes. 50 μLs of the reaction was removed and added to solution A (same recipe as above) to a final volume of 1.5 mLs. Addition of solution B, incubation, and quantification of ammonia was performed as described above. A previously created G27 Δ*ureB* mutant (DSM43) served as a negative control to compensate for any background ammonia production. Ammonia production for the various *H. pylori* mutant strains was normalized to wild-type G27.

Competitive animal infections

H. pylori infection of Mongolian gerbils (6-12 week-old male) was performed using the 7.13 and J166 *H. pylori* strain backgrounds. Wild-type *H. pylori* was mixed with mutant bacteria or the complementation strain in a 1:1 ratio. Gerbils were fasted for 12 hours and then infected with approximately 10^9 total colony forming units (CFUs) of the bacterial mixture via oral gavage. Animals were sacrificed at 1, 2, and 3 weeks post infection and the glandular portion of the stomachs were excised, cleared of food bits, and weighed. After mechanical homogenization of the stomach (Bullet Blender 5, Next Advance), a portion was plated onto HBA containing nalidixic acid (10 μg/mL) (Sigma), bacitracin (100 μg/mL) (USB), and vancomycin (5 μg/mL) (Amresco) and an equal portion was plated on HBA containing Kan and/or Cm to select for mutant strain growth. Wild-type colonization levels were determined by subtracting the number of antibiotic resistant colonies from the total number of colonies that grew on plain HBA medium.

Competitive index (CI) values were calculated by dividing the ratio of mutant to wild-type bacteria recovered from the gerbil's stomach by the inoculum mutant to wild type ratio. A total of 5 animals were included in each coinfection group.

Statistical analysis

Differences in gene expression between the various strains for the RT-PCR experiments were calculated using the Student's *t* test on $\log_{10}$-transformed fold change ratios. Additionally, the Student's *t* test was used to compute differences in ammonia production between the various strains tested for the urease activity assays.

RESULTS

HpG27_51-HpG27_52 intergenic region contains Fur-binding sequences

Previously, we identified a putative semi-conserved iron-bound Fur box located in the intergenic region between the divergently transcribed genes *HpG27_51* and *HpG27_52* in *H. pylori* G27 (47). A detailed diagram of this intergenic region is depicted in Figure 18. The Fur box contains two mismatches as compared to the canonical *H. pylori* iron-bound Fur box (5'-TAATAATGCTTTTTA-3'). Through the use of electrophoretic mobility shift assays (EMSA), it was previously determined that Fur does bind the fragment of DNA containing the predicted iron-bound Fur box (47). Additional analysis revealed four potential *apo*-Fur boxes (5'-AATGA-3') dispersed throughout the *HpG27_51-HpG27_52* intergenic region. We utilized *H. pylori* transcriptome data to identify the transcriptional start sites (TSS) for genes *HpG27_51* and *HpG27_52* (50).

Because the original transcriptome analysis was performed in the 26695 strain background, we experimentally verified the TSS in G27 for gene *HpG27_52* by 5'TSS mapping (Figure 19). As shown in Figure 18, the iron-bound Fur box lies 47 base pairs up stream of gene *HpG27_51*'s TSS and 161 base pairs up stream of gene *HpG27_52*'s TSS. Additionally, the first two identified *apo*-Fur boxes appear to flank the iron-bound Fur box and are in close proximity to the *HpG27_51* promoter region (40 and 83 base pairs up stream of the *HpG27_51* TSS, respectively). The other two predicted *apo*-Fur boxes are farther up stream of the *HpG27_51* promoter but are in the direct vicinity of the *HpG27_52* promoter (19 and 38 base pairs up stream of the *HpG27_52* TSS, respectively).

Fur regulation of genes *HpG27_51* and *HpG27_52*

Given the large number of potential Fur-binding sites, it stands to reason that these two genes may be directly regulated by Fur. To assess this, we utilized RT-PCR to measure transcript levels in response to iron chelation in the wild-type and Δ*fur* backgrounds. We initially performed a time course analysis to determine at which growth phase the *HpG27_51* and *HpG27_52* genes were most responsive to iron chelation. As shown in Figure 20, at 6 hours of growth, we saw a significant increase in both *HpG27_51* and *HpG27_52* expression in wild-type G27 after iron chelation; a similar increase was not observed in the Δ*fur* mutant ($p < 0.004$). Of note, the increase in expression was more pronounced for the *HpG27_52* gene (16.76 versus 3.75 average fold increase for *HpG27_51*, $p = 0.0011$). We also detected an increase in expression in the Δ*fur* complemented strain compared to the Δ*fur* mutant (Figure 21), thus

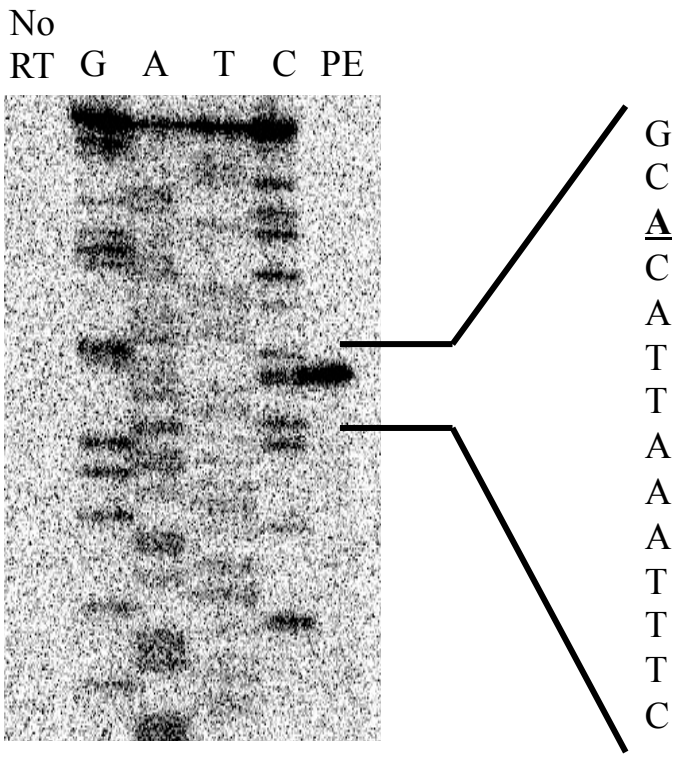

Figure 19. 5' Transcriptional start site (TSS) mapping of gene *HpG27_52*. Primer extension (PE) was performed on wild-type G27 RNA and the single DNA band is shown on the right hand side of the gel. A similar reaction in which no reverse transcriptase was added to the primer extension reaction (NoRT) was simultaneously performed and ran on the left hand side of the gel to control for any genomic DNA contamination. The DNA sequence surrounding the PE product is shown to the right of the gel. The nucleotide that aligns to the PE product (TSS) is underlined and in bold.

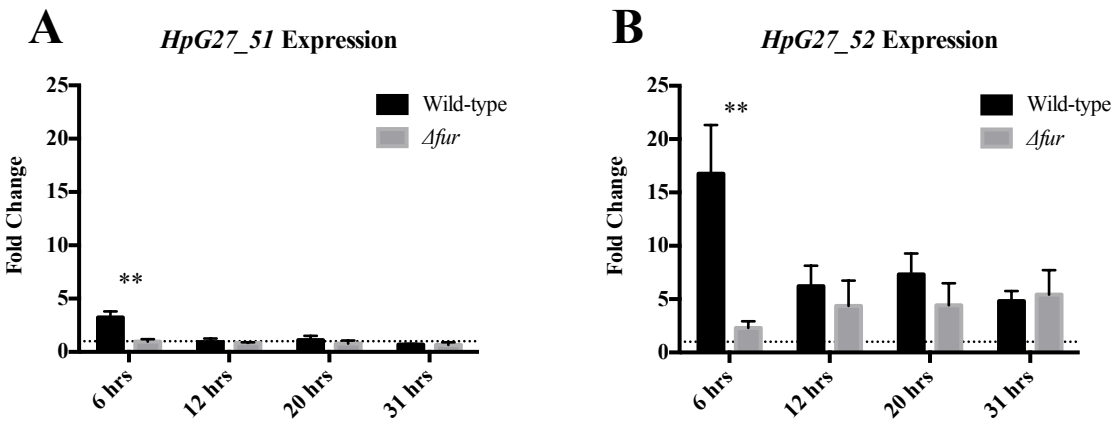

Figure 20. Fold change in gene expression after 1 hour iron chelation as assessed via RT-PCR.

Iron chelation was performed on wild-type (black) and Δ*fur* (gray) cultures that were grown for 6, 12, 20 and 31 hours. Changes in expression were determined for genes *HpG27_51* (A) and *HpG27_52* (B). Double asterisk denotes significant differences in fold change between wild-type and Δ*fur* ($p < 0.005$) as determined by Student's *t* test. Each bar corresponds to the mean fold change with the error bars representing the standard deviation. The dotted line at y=1 indicates no change in gene expression. 3 biological replicates were performed for each sample.

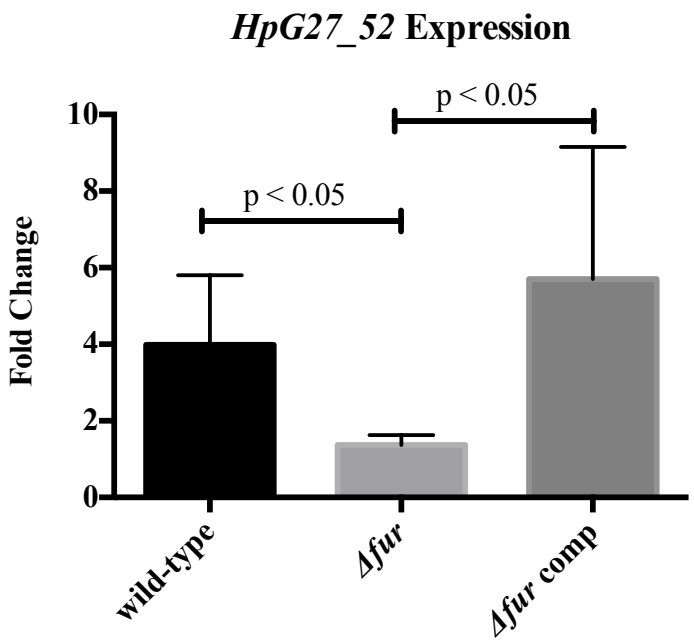

Figure 21. Fold change in *HpG27_52* expression after 1 hour iron chelation for wild-type, Δ*fur*, and the complemented Δ*fur H. pylori* G27 strains.
RNA was extracted from cultures grown to early stationary phase (18-22 hours). Each bar represents the mean of 3 biologically independent experiments. Error bars represent the standard deviation. Statistical comparisons were conducted using the Student's *t* test.

confirming that the increase in *HpG27_52* expression was a Fur-dependent phenomenon.

To determine if the increase in *HpG27_51* and *HpG27_52* transcripts was a product of Fur activation or de-repression, we compared the ratio of transcripts in the Δ*fur* strain to the wild-type before and after iron chelation (Figure 22). For both *HpG27_51* and *HpG27_52*, gene expression in wild-type and Δ*fur* was similar prior to iron chelation at 6 hours. However, post iron chelation, transcripts levels were more abundant in the wild-type as compared to the Δ*fur* mutant at 6 hours. Together, these data suggest that in early exponential growth phase (6 hours), iron chelation results in *apo*-Fur activation of expression of *HpG27_51* and *HpG27_52*. Of note, this phenomenon was exquisitely growth phase dependent since similar results were not seen at any other timepoints.

Fur box contribution to *HpG27_51* and *HpG27_52* expression

As mentioned previously, Fur typically influences gene expression via direct DNA binding at specific locations known as Fur boxes. To assess the contribution of the various putative Fur boxes identified in the promoter regions of *HpG27_51* and *HpG27_52*, we mutated the 15 nucleotide iron-bound Fur box as well as the 6 nucleotide *apo*-Fur box #2 (Figure 18) to a series of repeating guanines and cytosines. Fur box mutations were created in both wild-type G27 as well as the Δ*fur* mutant. Despite evidence that Fur directly binds the iron-bound Fur box (47), we did not detect any significant differences in *HpG27_51* or *HpG27_52* expression between wild-type and the scrambled iron-bound Fur box counterpart (Figure 23). Additionally, disruption of *apo*-

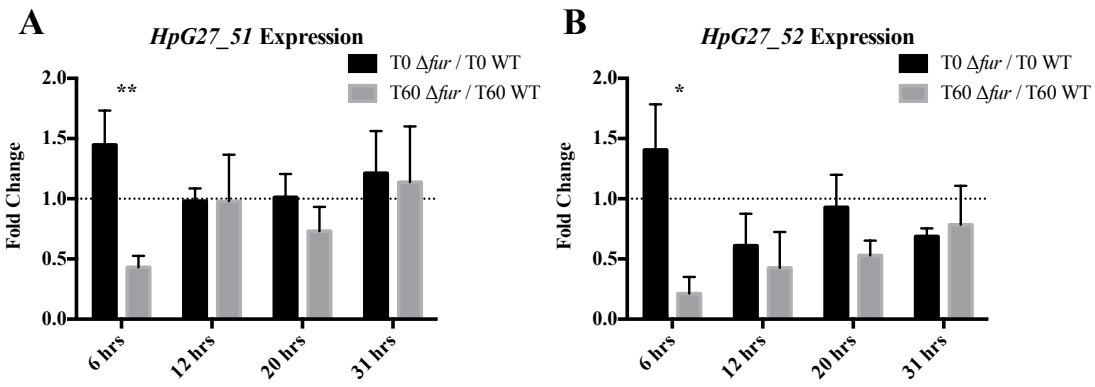

Figure 22. Expression of genes *HpG27_51* (A) and *HpG27_52* (B) in the Δ*fur* mutant compared to wild-type either before (T0, black) or after (T60, gray) 1 hour iron chelation.

Ratios were computed for cultures grown for 6, 12, 20, and 31 hours. The dotted line at y=1 represents equal transcript levels in the Δ*fur* and wild-type strains. Bars represent the mean of 3 biologically independent experiments. Error bars correspond to standard deviation. * = $p<0.05$, ** = $p<0.01$.

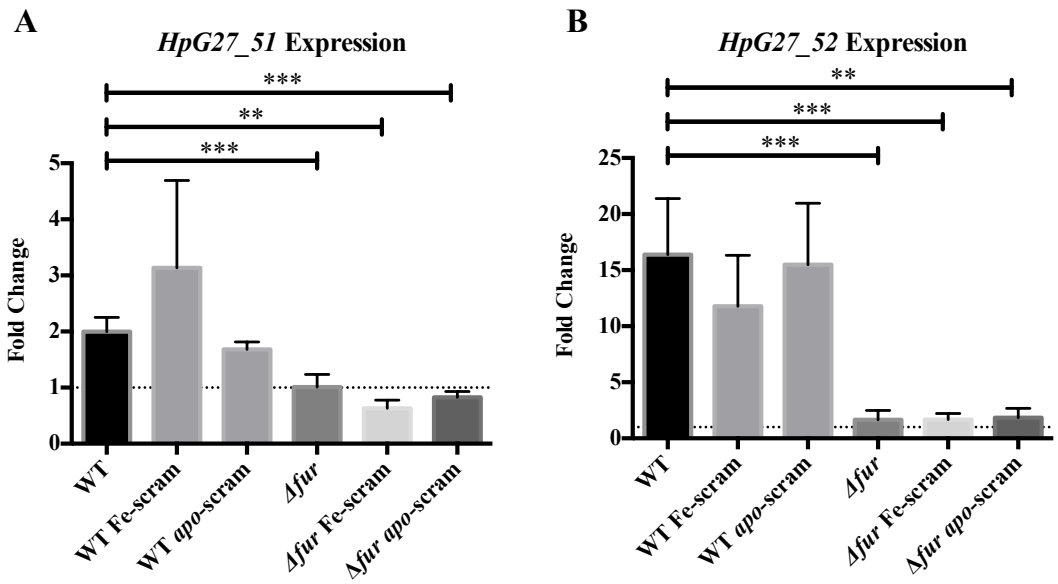

Figure 23. Fold change in gene *HpG27_51* (A) and *HpG27_52* expression after 1 hour iron chelation for the various Fur box mutants.
Both the iron-bound (Fe-scram) and *apo* Fur box (*apo*-scram) mutants were generated in the wild-type (WT) and Δ*fur* strain backgrounds. RNA used for cDNA synthesis was extracted from cultures grown for 6 hours. The dotted line at y=1 indicates no change in gene expression. Bars represent the mean of 3 biologically independent experiments. Error bars correspond to standard deviation. No significant differences among the various wild-type or Δ*fur* strains were detected for either gene *HpG27_51* or *HpG27_52* as determined by the Student's *t* test. ** =$p<0.01$, *** = $p<0.001$.

Fur box #2 did not alter either gene's expression pattern after iron chelation. This was true in both wild-type and Δ*fur* strains.

When transcript levels were compared between the various Fur box mutant strains prior to iron chelation, we found that mutation of the iron-bound Fur box resulted in a significant reduction in *HpG27_51* transcript levels as compared to the non-mutated Fur box strains (Figure 24). Because this effect was observed both in the wild-type and Δ*fur* mutant strains, it is likely a product of promoter-structure disruption rather than actual Fur regulation.

HpG27_52 encodes a potential urease enhancing factor

According to the annotated *H. pylori* G27 genome (NC_011333.1), *HpG27_51* encodes an enzyme involved in proline utilization (proline/delta1-pyrroline-5-carboxylate dehydrogenase). On the other hand, *HpG27_52* encodes a hypothetical protein of unknown function. To associate a function to the protein encoded by *HpG27_52*, we searched the *H. pylori* G27 genome for potential gene paralogs using the Basic Local Alignment Search Tool (BLAST). We found that the amino acid sequence of *HpG27_52* showed high similarity to a known urease enhancing factor (UEF) (*HpG27_469*) (43% amino acid identity, 58% similarity). We therefore utilized a previously described *E. coli* surrogate colorimetric assay to test the ability of *HpG27_52* to enhance urease activity. As shown in Figure 25A, when the *HpG27_52* gene was introduced into an *E. coli* strain expressing *H. pylori* urease, a significant increase in ammonia production was seen as compared to the same strain containing an empty pBS vector. While the increase in

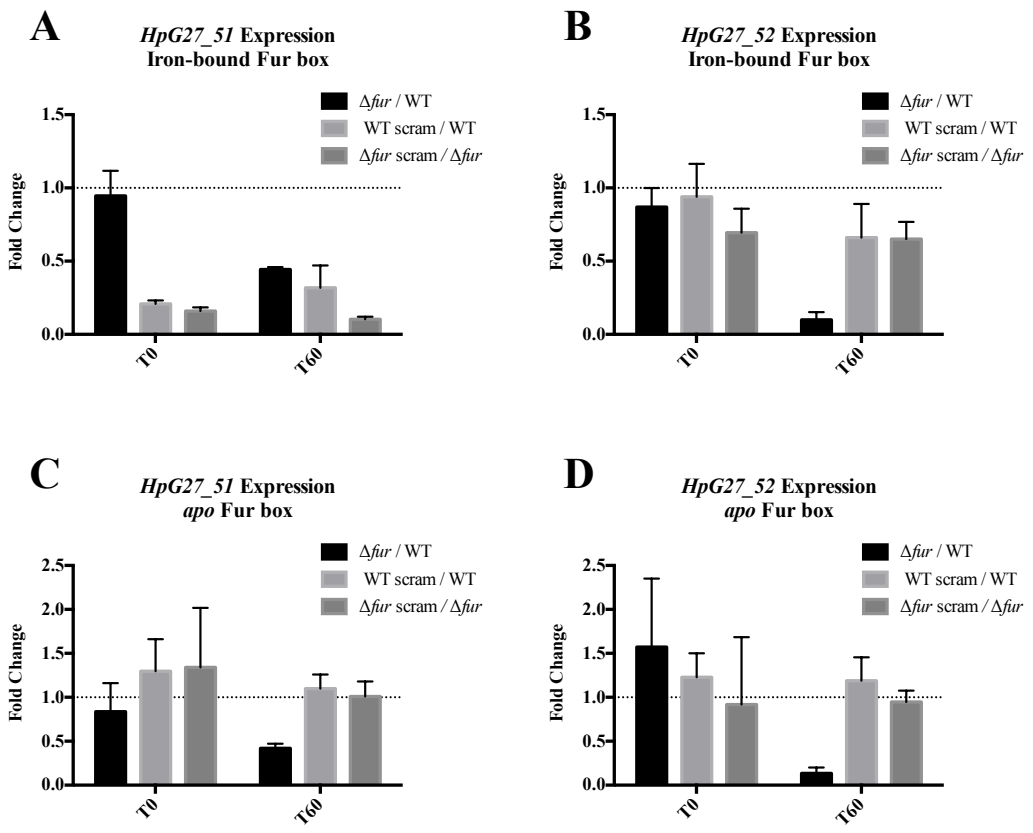

Figure 24. Expression of genes *HpG27_51* (panels A and C) and *HpG27_52* (panels B and D) in the scrambled Fur box mutant strains compared to wild-type or Δ*fur* either before (T0) or after (T60) 1 hour iron chelation.
Fold change data was calculated for the iron-bound Fur box mutants (top panels, A and B) as well as the *apo* Fur box mutants (bottom panels, C and D) at 6 hours. Fur box mutations were created in both wild-type (WT scram) as well as Δ*fur* (Δ*fur* scram). The dotted line at y=1 represents equal transcript levels between the two strains. Bars represent the mean of 3 biologically independent experiments. Error bars correspond to standard deviation.

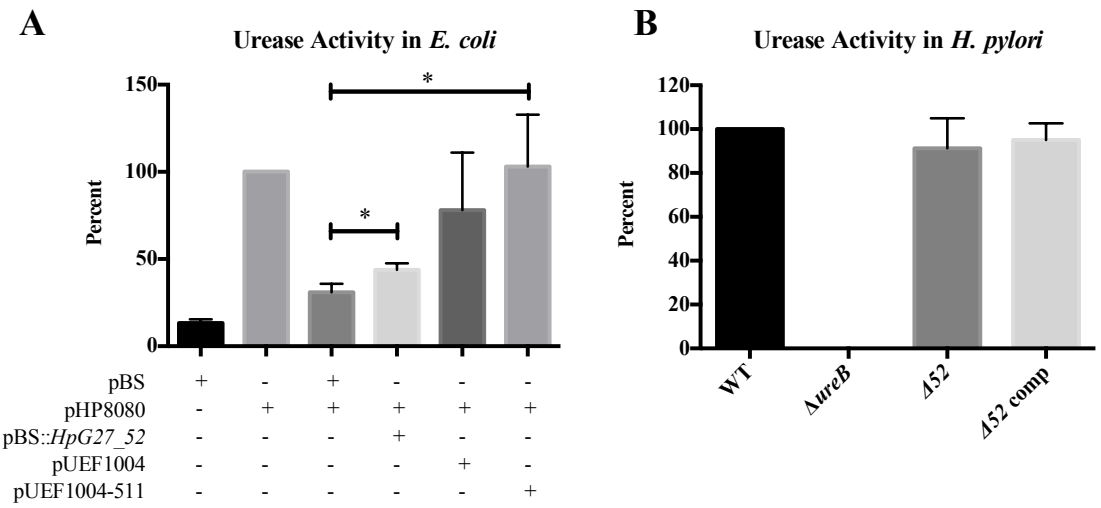

Figure 25. Urease enhancing activity of gene *HpG27_52*.

The ability of gene *HpG27_52* to enhance urease activity was measured in a surrogate *E. coli* model (A) as well as in *H. pylori* G27 (B). For the various *E. coli* strains tested in panel A, the plus symbol (+) indicates the presence of the listed plasmid. Data is normalized to pHP8080 in panel A and wild-type (WT) in panel B. As a negative control, a Δ*ureB* strain was included to detect background ammonia levels. Bars represent the mean of 3 biologically independent experiments. Error bars correspond to standard deviation. Statistical differences were determined using the Student's *t* test (* = $p < 0.05$).

ammonia production was smaller than with other known UEFs (pUEF1004-511), these data support the notion that *HpG27_52* has a role in urease function.

Although the *E. coli* system is an accepted model for measuring urease activity (39), we felt it necessary to directly assess urease activity in *H. pylori*. To this end, we used a similar protocol to measure ammonia production in wild-type *H. pylori* as well the Δ*HpG27_52* mutant and its respective complemented strain. Additionally, we included a urease-deficient strain of *H. pylori* (Δ*ureB*) as a means to assess background ammonia levels produced by other systems in the cell. With the exception of Δ*ureb*, We did not detect any differences in ammonia production among the various strains tested (Figure 25B), which suggests that within the context of *H. pylori, HpG27_52* has little to no detectable urease enhancing activity in the conditions tested.

HpG27_52 homologues in 7.13 and J166 may contribute to *in vivo* colonization

While elucidation of the molecular function of *HpG27_52* is important, we also wished to ascertain any role gene *HpG27_52* may play in *in vivo* colonization. This was accomplished through competitive animal infections using the 7.13 and J166 gerbil adapted *H. pylori* strains. For our model, we infected male Mongolian gerbils with a 1:1 mixture of wild-type and mutant bacteria via oral gavage. The bacteria were allowed to colonize the stomach for up to three weeks before euthanasia and subsequent recovery of *H. pylori*. As shown in Figure 26, for both 7.13 and J166, the mutant strain was dramatically outcompeted by wild-type for all time points tested. In fact, the mutant strain was cleared from the stomach in the vast majority of infected animals. Unfortunately, the complemented strains were also outcompeted by wild-type at two

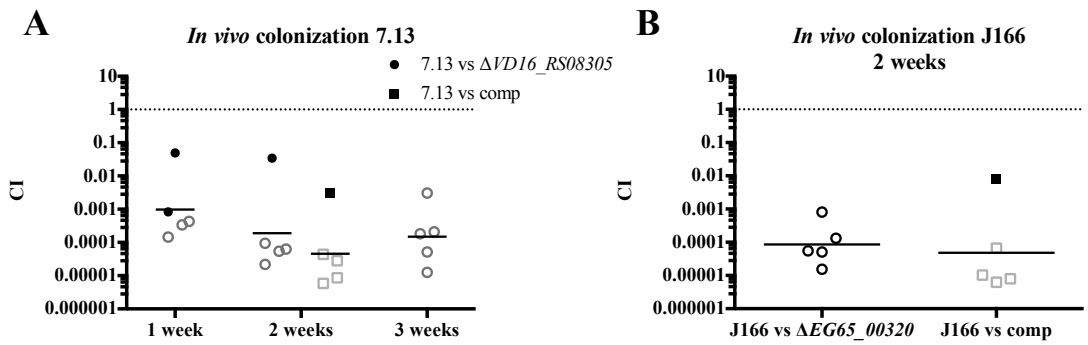

Figure 26. Competitive index (CI) of the various *HpG27_52* homologue mutant strains (Δ*VD16_RS08305* and Δ*EG65_00320*) and complemented strains (comp) versus wild-type *H. pylori*.
(A) CI of wild-type 7.13 versus Δ*VD16_RS08305* (circles) and wild-type versus the complemented Δ*VD16_RS08305* mutant (squares) after 1, 2, and 3 weeks post infection. (B) CI of wild-type J166 versus Δ*EG65_00320* (circles) and wild-type versus the complemented Δ*EG65_00320* mutant (squares) after 2 weeks post infection. Mongolian gerbils in which no mutant bacteria were recovered are depicted as open symbols. Lines represent geometric mean. Dotted line indicates no colonization advantage for either strain (CI = 1).

weeks post infection. Thus, there appears to be a secondary mutation affecting these results. *In vivo* competition analyses between the mutant and its complement are currently planned in order to elucidate any role of the *HpG27_52* gene homologues in colonization.

DISCUSSION

Helicobacter pylori is a unique bacterial pathogen for numerous reasons. First, *H. pylori* is capable of surviving within the harsh environment of the human stomach and, if left untreated, can persist in the stomach for decades (36). Secondly, the genome of *H. pylori* is relatively small (~1.7 Mb) and encodes surprisingly few regulatory proteins (55). In fact, of the 1,590 open reading frames identified in the *H. pylori* 26695 genome, only four encode proteins with a perfect helix-turn-helix DNA-binding motif (55). Lastly, of the few regulatory proteins encoded by *H. pylori*, many have evolved multiple regulatory functions that influence expression of numerous genes throughout the genome (24; 37; 44). In support of these three unique bacterial facets, the *H. pylori* Fur protein is a master regulatory protein that is not only important for *in vivo* survival (42), but also influences an impressively large number of genes that span an array of physiological functions that range from iron acquisition and storage to oxidative stress response (4; 12; 24; 28; 49). Further elucidation of the Fur regulon is imperative as it may reveal susceptibilities in the microbe that can be exploited for development of antimicrobial compounds. Despite numerous reports that have characterized portions of the Fur regulon (4; 24; 28; 48; 59), significant work still remains. To this end, we characterize a set of

two divergently transcribed genes, *HpG27_51* and *HpG27_52*, that are regulated by Fur in response to iron availability.

According to the annotated G27 genome, *HpG27_51* encodes and enzyme involved in proline utilization (*putA)* (proline/delta1-pyrroline-5-carboxylate dehydrogenase). For most organisms, proline is converted to glutamate via a two-step oxidation process that requires two distinct enzymes: initial oxidation of proline to delta1-pyrroline-5-carboxylate (P5C) via proline dehydrogenase followed by NAD+-dependent oxidation of P5C to glutamate through P5C dehydrogenase activity (41). In certain Gram-negative bacteria, including *H. pylori*, this dual enzymatic activity is coupled into a single protein known as PutA (1; 34; 41; 54). In regards to *Helicobacter* physiology, PutA oxidation of proline generates reactive oxygen species as a bi-product that can be harmful to the cell (35). In fact, high levels of proline were shown to be toxic to wild-type *H. hepaticus* (35). Interestingly, Fur has been shown to directly regulate the expression of antioxidant genes that are responsible for combating oxidative stress (12). In our study, we show that expression of the *HpG27_51* gene is influenced by Fur (Figure 20). Thus, the balance between proline utilization and antioxidant production is likely controlled by Fur. Alternatively, as pointed out by Pich and Merrell (48), the reduced flavins generated by PutA may also be used to convert extracellular ferrous iron to ferric iron via iron reductases, a process also influenced by Fur (61). Thus, by placing *putA* expression under the control of Fur, *H. pylori* can efficiently modulate both proline and iron metabolism within the cell.

HpG27_52 is predicted to encode a protein of unknown function. Initial characterization of the gene revealed a high similarity to a known urease enhancing factor

(UEF) in *H. pylori* (*HpG27_469*). While the ability of *HpG27_52* to enhance urease activity in *H. pylori* was undetectable, the gene did possess UEF qualities when tested in *E. coli* (Figure 25). Urease is essential for *H. pylori* survival within the human stomach as it hydrolyzes urea to ammonia, thus neutralizing the surrounding gastric acid (22; 23). Besides urease, Fur is also involved in acid tolerance in *H. pylori* (4) as well as in other bacterial pathogens (30). In fact, mutation of the *fur* gene in *H. pylori* results in diminished acid-responsive induction of the two major subunits of the urease enzyme, UreA and UreB (58). Given that *HpG27_52* was also shown to be Fur-regulated (Figure 20), it is possible that *H. pylori* can further fine tune urease activity via levels of UEFs in the cell. Preliminary data in our lab suggests no survival defect at low pH for the *HpG27_52* mutant, however, additional experiments need to be conducted. We also acknowledge that multiple UEF's may exist within the *H. pylori* genome (39) and that deletion of one UEF may be compensated for by redundancy or by overexpression of additional UEFs. This may explain why we did not detect differences in urease activity between the wild-type and Δ*HpG27_52* mutant strain in *H. pylori*. Regardless, these data reveal additional facets of the Fur regulon that warrant further investigation.

While both *HpG27_51* and *HpG27_52* are up regulated in response to iron chelation in a Fur dependent manner, the nature of the interaction of Fur with the promoter regions remains unclear. It is not entirely surprising that mutations in the iron-bound Fur box did not alter either *HpG27_51* or *HpG27_52*'s iron-responsive Fur regulation (Figure 23) as both genes have regulatory profiles indicative of *apo*-Fur activation. Subsequent mutation of an *apo*-Fur box in the promoter regions also did not elicit changes in iron responsiveness. We do note, however, that three additional *apo*-Fur

boxes were identified in the intergenic region and may contribute to *apo*-Fur activation of *HpG27_51* and *HpG27_52*. Mutational studies to address this possibility are currently underway. We are also in the process of conducting DNA footprinting assays under iron-deplete and replete conditions to ascertain where Fur binds.

In addition, we also must consider the possibility that Fur may not be the only regulatory protein at play, especially in regards to *HpG27_52* gene regulation. *HpG27_52* was demonstrated to enhance urease activity and thus, may have a direct role in *H. pylori*'s response to acid stress. In addition to Fur, the metal-dependent regulatory protein, NikR, and the two-component signal transduction system, ArsRS, are both involved in regulation of genes important for acid tolerance, including urease (6; 46; 58). Previous reports have shown that some Fur regulated genes in the *H. pylori* genome are co-regulated by NikR and/or ArsR (17; 19; 46). We hypothesize that *HpG27_52* transcription is likely up regulated in response to low pH, however, this possibility and the role of the three acid-responsive regulators (Fur, ArsRS, and NikR) would need to be investigated to determine if this is in fact the case.

If *HpG27_52* is pH responsive, this could be important for *in vivo* colonization of the gastric mucosa (Figure 26). Logically, we can hypothesize that in the acidic environment of the stomach, *H. pylori* up regulates *HpG27_52*, which in turn increases urease activity. Proper urease activity has long been known to be required for gastric colonization (23; 51; 57). Unfortunately, we were unable to restore the colonization defect in the 7.13 and J166 mutant strains upon chromosomal reintroduction of the *HpG27_52* gene homologue (Figure 26). While we expect that mutant complementation with the gene coding region and its endogenous promoter would yield wild-type

transcript levels, it is possible that genomic location may also affect gene transcription. A recent study found that in *E. coli*, gene location on the bacterial chromosome can alter gene expression as much as 300 fold (5). While we can test *HpG27_52* expression *in vitro*, we currently have no way to assess transcript levels while the bacterium actively colonizes the gastric mucosa.

In summary, we demonstrate that two genes, one involved in proline utilization (gene *HpG27_51*), and another involved in urease activity (gene *HpG27_52*), are activated in response to iron limited conditions in a Fur-dependent fashion. This activation did not appear to be the result of Fur binding to the iron-bound or one of the tested *apo*-Fur boxes identified in the intergenic/promoter regions of *HpG27_51* and *HpG27_52*. Lastly, through *in vivo* competitive index studies, we show that *HpG27_52* may be necessary for proper colonization of the gastric mucosa. Significant work yet remains in order to tease out the details regarding the exact role of Fur in this system and how it may influence *H. pylori* physiology.

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APPENDIX C: Identification of additional conserved Fur binding sites on the *Helicobacter pylori* chromosome

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The work presented in this chapter is the sole work of R.C. Johnson.

The ferric uptake regulator, Fur, is a bacterial specific regulatory protein that controls expression of key iron-homeostasis genes in response to fluctuating iron levels (4; 12; 16). When iron levels are elevated, iron-cofactored Fur will bind to the promoter region of iron acquisition genes and repress their expression (4; 12; 16). When iron levels decrease, this repression is alleviated and transcription is restored. The region of DNA that is bound by Fur (Fur box) appears to be sequence specific and has been defined for numerous organisms (1; 7; 9; 11). While some Fur boxes are structured as hexameric repeats (9; 11), others consist of two AT-rich inverted repeats separated by a single nucleotide in a 7-1-7 or 9-1-9 pattern (1; 7; 13). Post elucidation of the Fur box sequence, subsequent bacterial genome searches for this consensus sequence have led to the identification of additional genes that may be directly regulated by Fur (1; 13; 15). For example, in the Gram-negative gastric pathogen *Helicobacter pylori*, a total of 33 semi-conserved Fur boxes were previously identified. These Fur boxes were interspersed throughout the genome, and some were located upstream of transcriptional start sites, which is indicative of direct Fur regulation (13). Of the various potential Fur regulated genes identified in *H. pylori*, some are predicted to be involved in iron metabolism: *fecA1* and *frpB1*. Interestingly, Fur boxes were also found upstream of genes involved in non-

iron related processes including virulence (*cagA*), proline utilization (*putA*), and pyridoxine synthesis (*pdxJ*). The Fur regulon in *H. pylori* is exceptionally complex (4; 6; 8; 14), and despite years of research and numerous published studies (2; 3; 5; 10), our current understanding of Fur regulation in *H. pylori* likely encompasses only the "tip" of the regulatory iceberg.

The iron-bound Fur box in *H. pylori*, as characterized by Pich *et al.*, is a 7-1-7 motif with dyad symmetry (5'-TAATAATnATTATTA-3') (13). Characterization of this Fur box, as mentioned previously, has been instrumental in the identification of additional Fur regulated genes on the *H. pylori* chromosome. However, given the palindromic nature of this Fur box, it is probable that Fur also binds the reverse complement sequence (5'-ATTATTAnTAATAAT-3'). Because this sequence was not originally considered in the search, the number of Fur boxes in the *H. pylori* genome may be vastly underestimated. Therefore, we set out to develop a computer program (Fur Box Finder) that could identify the 5'-TAATAATnATTATTA-3' sequence and it's reverse complement in the *H. pylori* genome. Additional Fur boxes identified by this program may reveal additional Fur regulated gene that would warrant further investigation.

The Fur Box Finder program was written in the Python programming language and executed using Python version 2.7.8 (www.python.org). The entire script is shown in Figure 27. The program can essentially be broken down into 3 segments: fasta sequence preparation, Fur box identification, and Fur box location reporting. To demonstrate the functionality of the Fur Box Finder program, we initially downloaded the *H. pylori* G27 genome fasta file (H. pylori_G27.fasta, GenBank: NC_011333.1) from the National Center for Biotechnology Information (NCBI, http://www.ncbi.nlm.nih.gov). As shown

```
import re
genome_seq = file("Hp_G27.fasta").readlines()
genome_seq = "".join(genome_seq[1:]).replace("\n", "")
file = open("Furboxes_in_Hp.txt", "w")
def compare(furbox):
        for N in range(0, (len(genome_seq)+1)):
                start = N
                stop = N + 15
                DNA_seq = genome_seq[start:stop]
                check_len = len(DNA_seq) == 15
                if check_len == True:
                        score = 0
                        for num in range(0, 7):
                                if DNA_seq[num] == furbox[num]:
                                        score = score + 1
                                else:
                                        score = score
                        for num1 in range(8, 15):
                                if DNA_seq[num1] == furbox[num1]:
                                        score = score + 1
                                else:
                                        score = score
                        if round(((score/14) * 100), 2) == 100:
                                match = re.search(DNA_seq, genome_seq)
                                print DNA_seq + " 0 mismatches at position " + str(match.start()+1)
                                file.write(DNA_seq + " 0 mismatches at position " + str(match.start()+1) + "\n")
                        elif round(((score/14) * 100), 2) == 92.86:
                                match = re.search(DNA_seq, genome_seq)
                                print DNA_seq + " 1 mismatch at position " + str(match.start()+1)
                                file.write(DNA_seq + " 1 mismatch at position " + str(match.start()+1) + "\n")
                        elif round(((score/14) * 100), 2) == 85.71:
                                match = re.search(DNA_seq, genome_seq)
                                print DNA_seq + " 2 mismatches at position " + str(match.start()+1)
                                file.write(DNA_seq + " 2 mismatches at position " + str(match.start()+1) + "\n")
                        else:
                                score = score
compare("TAATAATNATTATTA")
compare("ATTATTANTAATAAT")
file.close()
```

Figure 27. Fur Box Finder program written in Python.
The program is designed to search a single fasta file ("Hp_G27.fasta") for the presence of the iron-bound Fur box sequence (5'-TAATAATnATTATTA-3') and it's reverse complement. Output from the program include: identified Fur box sequence, number of mismatches from canonical Fur binding sequence, and location of Fur box within the fasta file.

in Figure 27, the initial step of the program converts the fasta sequence into a single line of nucleotide characters. This obviates any issues with “tab” or “return” characters located within the fasta sequence. The next step opens a blank text file (“Furboxes_in_Hp.txt”) that will be used later to document the various Fur boxes in the genome. In order to search the genome for potential Fur boxes (5’-TAATAATnATTATTA-3’ or 5’-ATTATTAnTAATAAT-3’), we utilized a 15 base pair “sliding-window” that begins at nucleotide position 1 and slides one base pair at a time until it reaches the end of the genome. For each 15 base pair segment located within the “sliding window”, the sequence was compared to the canonical *H. pylori* Fur box. Because the middle nucleotide is not specified (“n”), the program was designed to sequentially analyze the first and last 7 nucleotides within the window. For each comparison, a scoring variable was created that was initially set to 0. For each nucleotide that matches the known Fur box sequence, the score was increased by 1. For example, if a perfectly conserved Fur box sequence is located within the genome, it will be given a score of 14. A Fur box with one mismatch will have a score of 13. The score is then converted to a percentage that represents the percent of nucleotides that match the canonical Fur box sequence. Fur boxes with 0, 1, or 2 mismatches will have a percent match of 100%, 92.86% and 85.71%, respectively. The program was designed to extract Fur boxes that contain 2 or fewer nucleotide mismatches. As output, Fur Box Finder will print the exact sequence of the identified conserved/semi-conserved Fur box, the number of mismatches to the established Fur box sequence, along with the location of the Fur box on the *H. pylori* genome. The genomic location data can then be used to determine if the Fur box is located in close proximity to regulatory elements of genes. The results of the

Fur Box Finder program for *H. pylori* G27 using the 5'-ATTATTAnTAATAAT-3' sequence are shown in Table 16.

Fur Box Finder successfully identified 46 additional Fur boxes on the *H. pylori* chromosome. As shown in Table 16, 14 of the identified Fur boxes lie in the promoter region of genes. The vast majority of potentially Fur regulated genes identified encode proteins of unknown function. Additionally, for the genes with described functions, these genes span a wide array of molecular tasks including protein folding (*groEL/groES*), oxidative stress response (catalase), and DNA recombination. Validation of the Fur Box Finder program via transcriptional and Fur binding studies are currently underway and will hopefully further expand our current knowledge regarding Fur regulation in *H. pylori.*

Table 16. Additional Fur boxes identified in *Helicobacter pylori* G27

# of Mismatches[a]	Genomic Location[b]	Intergenic or Coding[c]	Coding Gene[c]	Flanking Gene 1[c]	Flanking Gene 2[c]
2	9020*	intergenic		*groEL**	*groES*
2	9023*	intergenic		*groEL**	*groES*
2	16927*	coding	hypothetical protein		
2	62565	intergenic		*putA**	hypothetical protein*
2	67486*	coding	hypothetical protein		
2	68318*	coding	hypothetical protein		
2	79017*	intergenic		*ureA**	*tRNA-Val*
2	135602*	intergenic		outer membrane protein	hypothetical protein*
2	218087*	coding	tRNA uridine		
2	222796	intergenic		hypothetical protein*	phospholipid-binding protein*
2	258822*	coding	outer membrane protein (*hopG*-1)		
1	264689	coding	type III adenine methyltransferase		
2	264940*	coding	type III adenine methyltransferase		
2	285743	coding	hypothetical protein		
2	290509*	coding	hypothetical protein		
2	306594	intergenic		para-aminobenzoate synthase	*amiE**
2	323622	coding	type II restriction enzyme		
2	389923*	coding	phosphatidyl serine synthase		
2	389926*	coding	phosphatidyl serine synthase		
2	389931	coding	phosphatidyl serine synthase		
2	430480	intergenic		*fur**	*rarA*
2	449319*	coding	type I restriction enzyme S protein		
2	477843	intergenic		catalase*	*hofC*
2	537753	coding	*cagM*		
2	545139	coding	*cagE*		
2	546269*	coding	*cagE*		
2	548097	intergenic		*cagB**	*cagA**
2	548095*	intergenic		*cagB**	*cagA**
2	548100	intergenic		*cagB**	*cagA**
2	579993*	coding	hypothetical protein		
1	588073	coding	amino deoxy chorismate lyase		
2	603954*	coding	multidrug resistance protein		
2	616318*	coding	*vacA* like protein		
2	636769*	intergenic		recombinant and DNA strand exchange inhibitor protein*	hypothetical protein

2	636770	intergenic		recombinant and DNA strand exchange inhibitor protein*	hypothetical protein
2	636773	intergenic		recombinant and DNA strand exchange inhibitor protein*	hypothetical protein
2	636776	intergenic		recombinant and DNA strand exchange inhibitor protein*	hypothetical protein
2	636781*	intergenic		recombinant and DNA strand exchange inhibitor protein*	hypothetical protein
2	669932*	intergenic		hypothetical protein	protective surface antigen D15*
1	703673	intergenic		*fecA1*	ligand gated channel*
2	728269	coding	*hopE*		
2	732049*	coding	*homB*		
2	732052*	coding	*homB*		
1	828366	intergenic		*ribBA**	*lex2B*
1	832471	intergenic		*facA2**	holo-ACP synthase
2	834782	intergenic		dihydroneopterin aldolase*	SAM-dependent methyltransferase
2	834777*	intergenic		hypothetical protein	hypothetical protein*
1	834780*	intergenic		hypothetical protein	hypothetical protein*
2	834782	intergenic		hypothetical protein	hypothetical protein*
2	834783*	intergenic		hypothetical protein	hypothetical protein*
1	834785	intergenic		hypothetical protein	hypothetical protein*
2	892111	intergenic		CDP-diacylglycerol pyrophosphatase*	hypothetical protein*
2	895819*	intergenic		catalase*	Iron-regulated outer membrane protein*
1	895824	intergenic		catalase*	Iron-regulated outer membrane protein*
2	897622	coding	*frpB1*		
2	930656*	intergenic		DNA-dependent ATPase	outer membrane protein*
2	930659*	intergenic		DNA-dependent ATPase	outer membrane protein*
2	950237*	coding	*vacA* like protein		
2	950240*	coding	*vacA* like protein		
2	980666	coding	hypothetical protein		
2	997324*	coding	cobalt-zinc-cadmium resistance protein		
2	1001033	coding	hypothetical protein		
2	1054951	coding	comB9-like protein		
2	1057322*	coding	competence protein		
0	1057325*	intergenic		competence protein	hypothetical protein
2	1058383	coding	virB11-like ATPase		
2	1067777	coding	adenine-specific DNA methyltransferase		
2	1074922*	coding	adenine specific methyltransferase		

2	1078502*	coding	hypothetical protein		
2	1079627*	coding	hypothetical protein		
2	1139462*	coding	UDP-glucose4-epimerase		
2	1169453	intergenic		*ggt**	*flgK*
2	1181050*	coding	FOF1 ATP synthase subunit gamma		
2	1209065*	coding	*hopL*		
2	1374701*	intergenic		ATP-binding protein	hypothetical protein
2	1447119*	coding	hypothetical protein		
2	1465943	intergenic		*rrnA* methyltransferase A*	*hpn2**
2	1535497*	coding	type II methylase		
2	1536879*	coding	type II adenine methyltransferase		
2	1536887	coding	type II adenine methyltransferase		
2	1571795*	intergenic		periplasmic competence protein	chromosomal replication initiation protein
2	1571800	intergenic		periplasmic competence protein	chromosomal replication initiation protein
2	1645025	intergenic		methicillin resistance protein*	*pdxJ**
2	1648219	intergenic		threonylcarbomyl-transferase	*flgG**

[a] Number of nucleotide mismatches from the canonical 5'-ATTATTAnTAATAAT-3' or 5'-TAATAATNATTATTA-3' Fur box sequence

[b] Newly identified Fur boxes are denoted with an asterisk (*). Previously identified Fur boxes were originally described in Pich *et al*. 2012 (13). The number corresponds to the genomic location of the first nucleotide of the Fur box.

[c] Location of Fur box with respect to gene coding regions. An asterisk (*) indicates that the Fur box is located within or upstream of the gene's promoter.

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