

EXAMINING THE SKIN AND WORKPLACE MICROBIOME
FOLLOWING THE RETURN TO THE UNIVERSITY OF NORTH
TEXAS HEALTH SCIENCE CENTER AFTER SELF-ISOLATION

THESIS

Presented to the Graduate Council of the
Graduate School of Biomedical Sciences
University of North Texas
Health Science Center at Fort Worth

in Partial Fulfillment of the Requirements

For the Degree of

MASTER OF SCIENCE

By

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Fort Worth, TX

July 2021

ACKNOWLEDGEMENTS

First and foremost, I am grateful for my major professor, Dr. Michael Allen for his invaluable advice, continuous support, and patience. Although joining the lab during stay-at-home orders (due to the coronavirus pandemic) was a difficult transition for me, you made me feel welcomed. Thank you for giving me a seat at the virtual table. I would also like to thank my committee members: Dr. Yan Zhang and Dr. Roxanne Zascavage for their support and feedback throughout this process. Thank you to our lab members Megan Williams and Rebecca Kilgore for helping me with DNA extractions, resolving any technical issues that arose, and always willing to answer my questions. A special thank you to my husband Shubham Khichi. Without your continuous support and sacrifices, earning my master's would not have been possible. You kept me motivated and focused on the big picture. Thank you to my brother-in-law for helping me navigate through the bioinformatic pipeline. Lastly, I would like to thank my parents for their unconditional support throughout my education. It takes village & I thank you all for being a part of mine!

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CHAPTER I

INTRODUCTION

Background on the Human Skin Microbiome

A microbiome is a habitat comprising the community of microorganisms associated with a particular environment or host (Davenport et al.). The human microbiome consists of trillions of microbes (viruses, bacteria, archaea, and fungi) that colonize the human body. Different sites on and within the body harbor unique assemblages of microbes. For example, the largest and most diverse microbial communities are within the colon. Microbial communities can also be found in other body regions, such as the skin, or lung. Microbial communities associated with these sites differ from one another due to the specific biochemical conditions associated with each site.

The skin is the largest organ of the human body, which serves as a physical barrier to prevent pathogen invasion. When the barrier breaks, skin disease, and even systemic disease can occur (Byrd et al.). As stated, the skin is also populated by a diverse assemblage of microbes. This skin microbiome not only serves to protect against pathogens but also help educate the immune system, and aid in the breakdown of natural products (Grice et al., 2015). The skin comprises two distinct layers: the epidermis and the dermis, each containing a specific microbial niche. The skin microbiota can also be categorized as either residential or transient microorganisms. Residential microorganisms (known as the core microbiota) are often found on the skin that re-establish themselves after disruption or dysbiosis. The core microbiota is

considered to be commensal, meaning these microorganisms are typically harmless and provide some benefit to the host. Transient microorganisms do not establish permanent residence but arise from the environment and may persist for hours to days before disappearing (Dreno et al.).

Each external body site provides a unique microenvironment that varies in characteristics such as pH, temperature, moisture, sebum content, and topography (Grice et al., 2011). These are divided into three main categories based on their characteristics: sebaceous or oily (i.e., face and back), moist (i.e., bend of forearm and back of the knee), and dry (i.e., volar forearm and palm). Appendages such as sweat glands, hair follicles, and sebaceous glands influence the skin site's environment. Sweat glands are essential for thermoregulation, and lead to acidification of the skin, making growth and colonization unfavorable for numerous microorganisms. Sweat also contains antimicrobial molecules such as free fatty acids and antimicrobial peptides that inhibit microbial colonization. Sebaceous glands connected to hair follicles secrete lipid-rich sebum that provides an additional antibacterial shield to hair and skin (Gallo et al.).

The site-specific microbial communities' composition is dependent mainly on the skin site's physiology. Changes in the relative abundance of bacterial taxa are associated with moist, dry, and sebaceous microenvironments. Moist regions harbor mostly *Staphylococcus* and *Corynebacterium* species. Sebaceous sites have a higher abundance of lipophilic species such as *Propionibacterium*. The dry sites host *Staphylococcus*, *Propionibacterium*, and *Streptococcus* species predominantly (Oh et al.).

Initial Colonization

After birth, a newborns' skin microbiome correlates strongly with delivery mode. The microbiome of infants delivered vaginally is similar to the mother's birth canal, and infants born by Cesarean resemble the mother's skin flora. Skin colonization by commensal skin microorganisms continues during breastfeeding (Dominguez-Bello et al.). Simultaneously, microorganisms from the environment colonize the skin to build a healthy relationship with the host's skin. The infant's microbiota composition and function are also influenced by antibiotic exposure and early-life feeding practices. During early infancy (i.e. birth to one year of age), the most crucial influence on the microbiome's development is skin contact with the parents. By the age of three, the infant microbiome achieves a more complex structure, resembling adults (Dominguez-Bello et al.). As cognition and the immune system develop during early childhood, the microbiome is the most dynamic. The microbiome reaches homeostasis beginning at early adolescence, influenced heavily by antibiotic use and the built environment (Langdon et al.).

Human Microbiome and the Built Environment

The built environment includes all human-made structures, including buildings, transportation systems, workplaces, schools, hospitals, and vehicles. These spaces are where people spend most of their time indoors, and they harbor a unique microbiome. The built environment's microbiome is unlike most microbial communities found on Earth's outside environments, such as trails, streets, parks, and trees (Gilbert, 2018). The built environment harbors diverse microbial populations, including viruses, bacteria, fungi, and protozoa. Humans are continually interacting with the built environment's microbiome by touched objects and air circulation. Common bacterial genera in indoor environments include *Pseudomonas*,

Acinetobacter, *Staphylococcus*, *Corynebacterium*, and *Clostridium* (Adams et al.). The built environment's microbiome differs considerably in environments with different functions such as homes, schools, and offices (Kembel et al.). While researchers are not sure of all the factors correlating to this variation, it is believed to be due to differences in layout, structural components such as ventilation and windows, and variations in the types of human interaction both with and within the building. The microbiome of the built environment has profound impacts on human health. High occupancy increases human-associated microorganisms and microbial transmission potential via direct or indirect contact with surfaces. Direct human contact can occur by touching a surface or object with their hands, emission of bioaerosols, and resuspending indoor dust containing human-emitted microbes (Meadow et al.). Building layouts directly affect individuals' movement and occupancy, affecting how occupant-associated microbes are dispersed throughout different building types. Although there has been tremendous progress in characterizing the microbiome of the built environment, significant gaps have been identified within the field, including (1) characterization of the built environment's microbiome at a higher resolution to understand the dynamics of the microbial communities that reside in different buildings with different functions; (2) lack of efficient tools to monitor the patterns of indoor microbiomes that are present as a function of occupancy; and (3) lack of approaches to integrating data from the built environment, occupants, and microbiomes to identify transmission of pathogenic species (Li et al.).

Meadow et al. found that bacterial communities on classroom surfaces vary with human contact. Samples were collected from the same classroom at the Lillis Business Complex at the University of Oregon. Researchers sampled a total of fifty-eight chairs, desks, floors, and walls of the same classroom. All samples represented approximately 4,000 bacterial operational

taxonomic units (OTUs). The four surface types harbored significantly different communities ($P < 0.001$). Their results indicated that site-specific factors (i.e., habitat selection or dispersal from a specific body site) are more important than distribution among bacterial community assembly sites in the built environment. Desk surfaces were significantly associated with several taxa from the human body, including *Streptococcus* and *Cyanobacteria*. Walls, the surfaces with the least contact with humans, were found to contain bacteria related to *Sphingomonas* and *Alicyclobacillus*, which are not commonly associated with human skin. Evidence to date suggested that microbial communities on indoor surfaces are likely primarily human dispersal-driven via surface contact. Meadow et al. suggested the microbial communities detected on different body-sites can be transferred to indoor surfaces following contact.

Ross et al. studied the microbial biogeography of a university campus by swabbing the entrance door handle from each of the sixty-five buildings at the University of Waterloo at three-time points during an academic term. Microbial communities assembled coincided with building use and whether those communities were temporally stable. Samples were collected by swabbing the left and right handles and classified by building, faculty, building use, estimated human throughput, handle size, building age, and the number of rooms. Across all door handles, the dominant phyla were *Proteobacteria*, *Firmicutes*, *Actinobacteria*, and *Bacteroidetes*, which accounted for 89% of all total reads. These dominant phyla have been previously associated with built environment studies of homes, gyms, and public restroom surfaces. Although inter-handle variability was high, several individual building entrances harbored distinct microbial communities that were consistent over time. Dead skin, oils from the hand, and other organic matter supply nutrients and moisture for microorganisms to form stable communities on entrance

handles. The study demonstrated highly variable microbial communities associated with frequently contacted door handles on a university campus (Ross et al.).

The Microbiome of Fomites

Fomites are inanimate objects that become colonized with microbes and serve as potential intermediates for transmission to and from humans. A review article by Stephens et al. summarized fomite contamination, microbial survival in the built environment, and transmission between fomites and humans. In buildings, the microbial communities are formed by skin shedding in the indoor air and onto building surfaces. Human occupancy and activity, the outdoor environment, and building design can all influence the abundance and diversity of microbes in the indoor microbiome. Not all microbes that are found on indoor surfaces are pathogenic. Bacterial communities in the built environment with higher occupancies have been shown to have high abundances of skin-associated bacteria such as *Streptococcus* and *Corynebacterium*. Lax et al. showed that humans deposit their microbial clouds on indoor surfaces via shedding and touch. Individuals occupying a space can emit their own distinct personal microbial cloud leaving upwards of 10^6 biological particles per hour that can transmit pathogens to other individuals and indoor surfaces (Meadow et al.). The microbial communities tend to remain inactive or dormant until being transferred to other host locations. Greene et al. demonstrated microbes could physically transfer between fomite surfaces and humans via touching. Still, the transfer's efficiency depends on the surface material, hand covering, and moisture content of contact surfaces.

Greene et al. studied the transfer efficiency of *Acinetobacter baumannii*, a gram-negative, multidrug-resistant bacterium with and without latex gloves. They reported that it was easily

transferred via fomites and difficult to eradicate from the environment. Fomite-to-fingerpad transfer efficiency was determined for six different materials: glass, stainless steel, porcelain, polypropylene, and rubber. For *A. baumannii*, the fomite-to-fingerpad transfer efficiency was statistically significant regardless of glove use. Greene et al. found no significant differences in transfer efficiencies by material type except for rubber, which resulted in higher transfer efficiencies. Fomite-to-fingerpad transfer efficiency was not equal to fingerpad-to-fomite transfer efficiency when the two contact surfaces were not identical (i.e., fomite-skin transfer or fomite-glove transfer). It was found that the fomite-to-fingerpad was four times greater than the overall fingerpad-to-fomite transfer efficiency. Latex gloves reduced the fomite-to-fingerpad transfer efficiency from 55.9% to 47.1%. Although the transfer of pathogens between surfaces and latex gloves is reduced, there is still a transfer.

Species of the human microbiome have been shown to transfer between cohabitating couples, family members, pets, and students sharing dormitory rooms, as well as by both direct and indirect mechanisms between non-cohabitating individuals' hands (Neckovic et al.). The microbial cloud (via skin-shedding) can be indirectly deposited into the built environment. Studies have assessed human microbiomes' direct transfer and applied it in linking individuals to personal effects, office equipment, and shared spaces/surfaces within homes. Still, the persistence of transferred microbial members has not been fully understood over time. Some studies suggest microbial signatures (or microbial fingerprints) may persist on items within an office or home environment over a short period (Park et al.). Other studies indicate microbes rapidly decay from surfaces once the environment is no longer occupied (Prussin et al.). This inconsistency may be due to how different surface types affect individual species (Neckovic et al.).

Fierer et al. demonstrated that the human skin harbors a large number of bacteria that can readily be transferred to surfaces upon touching. Skin-associated bacteria are highly individualized and link touched surfaces to specific individuals. Fierer et al. compared bacterial communities on individual keys of three computer keyboards to the communities found on the keyboard owners' fingers. They linked objects to specific individuals by comparing the bacteria on their computer mice against a database containing bacterial community information for more than 250 hand surfaces, including the owner's hand. Their findings indicated that bacterial communities on the fingertips for a given individual's keyboard were more similar to each other than to fingertips or keyboards from other individuals. Bacterial communities on the fingers of the owner of each keyboard resembled the communities on the owner's keyboard, which suggests that the direct transfer of fingertip bacteria causes differences in keyboard-associated communities. The computer's mouse was also significantly more similar to the microbial communities of the owner's hands than to those of other hands in the database in all nine cases. These results demonstrated the potential use of skin-associated bacteria persistent on objects for forensic identification.

As stated, microbial deposits from humans to the built environment have been used to match individuals to objects they have touched. The microbiomes of various home surfaces have shown that microbial signatures of a family can be highly predictive of an individual's microbiome. Lax et al. performed a longitudinal characterization on personal mobile phones and examined if microbial communities associated with an individual's shoes were determined by the floor microbiome correlated with walking. They found that microbial community structure was determined by surface type and participant. This study used supervised machine learning analysis that assessed which bacterial taxa were most connected with different surface types.

Random forest models, trained at the genus level, determined whether a sample was taken from a phone, shoe, or floor with an error ratio of 3.6. Genera such as *Propionibacterium*, *Streptococcus*, and *Corynebacterium* often found on human skin were highly enriched on phone samples relative to shoe samples, again indicating that the skin microbiome interacts with the built environment. A Bayesian source tracking approach was employed to determine the extent to which the shoe has interacted with the floor to test whether individual shoe and floor time series could be matched based on similarity. Their results demonstrated the similarity between shoe and floor microbial communities could be used to infer where someone has recently walked (Lax et al.).

Challenges in Investigating the Human Skin Microbiome

The skin microbiome's composition depends on a plethora of factors both intrinsic and extrinsic. Intrinsic factors include skin site, intra- and interpersonal variability, ethnicity, gender, and aging. Extrinsic factors include mode of delivery, lifestyle, hygiene routine, and use of cosmetics, as well as antibiotic use and certain diseases (Skowron et al). These factors form a complex network that newer, massively parallel DNA sequencing technologies allow researchers to better understand. However, due to multiple platforms for sequencing, various DNA extraction kits and culture tools, and different sampling methods, standardization in the field has not been achieved. Presently, studying the skin microbiome is at a turning point by utilizing 3D models that investigate the microbe-skin relationship and transplantation of the skin microbiome which could provide a therapeutic avenue for the treatment of diseases such as atopic dermatitis (Boxberger et al.). Wilkens et al. noted that taxa on both skin and surface sites appear to have a diurnal variation. Time of day was a notable contributor to variance at the community level with

significant differences between morning and evening samples. Taken together, a number of factors can influence the skin microbiome and its study poses many challenges for researchers.

Research Significance

The Covid-19 pandemic led to widespread measures to control the spread of the disease, including closing of US schools and business beginning in March 2020. As a result, many individuals began to work and learn from home. Additionally, education campaigns to increase hand washing and sanitizing were widely implemented. It is currently unknown how skin bacterial communities were impacted by these efforts. In this work it was hypothesized that as individuals returned to work following extended absence, there would be changes in the **intra**individual, **inter**individual, and fomite microbiomes. As a surrogate for pandemic-related absence from work, individuals away for two to three weeks over the winter holiday break were swabbed upon returning to work to assess their skin microbiome. Participants self-swabbed their dominant hand, corresponding forearm, and an object chosen from their campus laboratory or office space at selected time points over a one-month period. After all samples were collected, DNA was extracted and the V4 region of the 16S rRNA gene was amplified and sequenced on an Illumina MiSeq. The data produced from this study were analyzed using the Quantitative Insights Into Microbial Ecology 2 (QIIME 2) pipeline. The information generated from this study can help researchers better understand how bacterial communities shift as a result of behavioral changes such as quarantining or increased sanitation procedures, and how those changes may ultimately affect human health. This research may also help scientists better understand how prevention methods impact the skin microbiome. Furthermore, microbial deposits from humans to the built environment have been used to match individuals with high

accuracy to objects they have recently touched, such as keyboards, doorknobs, and phones, and the data generated here may add to the growing application of microbiology to forensic science.

CHAPTER II

MATERIALS & METHODS

Experimental Design

The purpose of this research focused on investigating the impact of returning to work at UNTHSC on the intraindividual, interindividual, and workplace fomite's microbiome. Participants swabbed their dominant hand, the forearm of their dominant hand, and an object from either their laboratories or office spaces to determine if and how the skin and workplace microbiome shifts in bacterial communities after staying away from campus for at least two weeks. This was tested through four stages. The first stage was subject recruitment and sample collection. The second stage involved DNA extraction. The third stage required library preparations and performing next-generation sequencing (NGS) of the prepared libraries using Illumina's MiSeq System. In the fourth and final stage, data analysis & interpretation were performed to determine how an individual's skin microbiome changed. Stage four results were also used to evaluating the changes in the fomite's microbiome as well as compare individuals' skin microbiomes against each other to determine if individuals have become more like each other since returning to work in the same building (CBH). Fomites are considered as inanimate object that, when contaminated with an infectious organism, can serve as a means of transferring disease-causing agents to a human host. The most important fomites for contamination and transmission tend to be found in the built environment and those that humans frequently come into direct contacts with, such as doorknobs, mobile phones, and keyboards (Stephens et al.).

Phase I: Subject recruitment and sample collection

The study population consisted of UNTHSC employees (faculty, staff, and students). Individuals needed to be between the ages of 18-90 and current employees of UNTHSC whose office space or laboratory (or both) is located on the 2nd, 3rd, 4th, or 5th floor of the CBH building. The first floor of CBH was excluded from the study due to ongoing construction and outpatient services. The sixth floor (last floor) was excluded from the study because it is dedicated to the UNT Center for Human Identification laboratories, where human remains, and DNA are often tested. Including the first and sixth floors would have increased the possibility of receiving contaminated samples. A sample size of fifteen individuals was determined using the G*Power software with an alpha of 0.05 and an effect size of 0.7. Potential subjects were recruited through an advertisement in the Daily News (campus news outlet) and emails sent out to individuals identified as likely subjects. Twelve subjects were enrolled in the study (four males, eight females). From the twelve subjects, only eight (four males, four females) participant's DNA were used in downstream analysis because not all the extracted DNA samples were successfully amplified (discussed further in the results section). The total number of enrolled participants was less than expected (fifteen), possibly because the inclusion criteria were restricted to one building. Additionally, many individuals continued to work from home and were not sure when they would return to campus due to the COVID-19 global pandemic and social distancing guidelines.

Characteristics	n	Male	Female
		4	4
Age range:	25-32	1	2
	33-40	1	2
	49-56	1	0
	57-63	1	0
Object location:	Laboratory	2	3
	Office	2	1
Object:	Computer mouse	3	2
	Keyboard	1	0
	Fridge door	0	1
	Arm of chair	0	1
CBH floor number	2	1	1
	3	2	2
	4	1	1

Table 1. Participant characteristics

Samples were collected from twelve individuals who swabbed their dominant hand, the forearm of their dominant hand, and an object from either their laboratory or office space according to an approved protocol by the North Texas Regional Institutional Review Board

(Appendix A). Although multiple methods have been accepted for skin sampling, each varying in biomass yield, human DNA contribution, sampling depth, and discomfort, moistened swabs were chosen because it is the most established and least invasive collection method (Ogai et al.). Dry swabbing is not as widely used due to reduced biomass collection. All samples were collected using sterile nylon flocked Puritan specimen collection swabs with a 30 mm breakpoint and sterile water.

Each participant received a brown bag labeled with their sample ID number. Within each brown bag, individuals received twenty-three swabs and twenty-three 1.5-mL microcentrifuge tubes to store and transport their samples. Their sample collection materials were divided into eight Ziplock bags. The first Ziplock bag (corresponding to $t=0$) contained two swabs and two collection tubes: one for the dominant hand and the second for the forearm. Subjects did not swab the fomite from their laboratory or office on $t=0$ since these swabs were taken one day before they returned to work. Participants were instructed to freeze their $t=0$ samples until they could return their samples the next day. The remainder of the seven Ziplock bags (corresponding to days $t=1, 3, 5, 7, 14, 21,$ and 28) each contained three swabs and three tubes: one for the dominant hand, another for the forearm, and a third for the fomite. Each subject labeled their tubes with their sample ID, collection date, and body part/item sampled. Subjects used RH to indicate the right hand, RHFA for the right-hand forearm, LH for the left-hand, and LHFA to indicate the left-hand forearm on the collection tubes. On the fomite's collection tubes, subjects wrote either office or laboratory to identify where the sample was collected from and the object's name to indicate which item was used (i.e., office/mouse or laboratory/pipette). Individuals used the same fomite throughout the study. Shortly after participants picked up their study materials, they received an email from a member of the research team, which included documents such as a

guide on how to swab their skin and fomite, a list that contained commonly found objects in laboratories and offices to swab, and a questionnaire to be filled out throughout the study (Appendix B, Appendix C, Appendix D).

To adhere to social distancing guidelines, participants swabbed themselves and their chosen object. Before each sample collection, participants moistened their swabs with sterile water provided in 2-mL microfuge tubes. Subjects swabbed their dominant hand by creating a T-shape, starting from the middle bottom of their palm, slowly rotating the swab as they move up (vertically) further away from their wrist and stopping once they reached the base of their ring finger. Next, participants placed the swab on the bottom of their index finger, slowly rotating the swab as they move horizontally across the index, middle, ring, and pinky finger. To swab the dominant hand's forearm, participants placed the swab on the median cubital fossa (inside of the bend of the elbow), slowly rotating the swab as they moved down the forearm towards their wrist. To collect the surface swab from the laboratory or office's fomite, participants will swab a 10 cm X 10 cm area (4 in. x 4 in.) on the object of choice in a zigzag formation, moving first horizontally then vertically. If their chosen object was small (such as a pen), participants were instructed to swab the item in its entirety.

Study participants coordinated with a member of the research team via email to determine a time to drop off their samples on each collection day to a box outside of the Allen lab (CBH 303). Receiving samples from subjects on each collection day kept subjects accountable for swabbing their samples on their specified days. Not all twelve participants began the study at the same time. Therefore, each sample drop-off date depended on when they began the study. However, all samples were collected during the study period from early January 2021 to late February 2021. This collection system ensured social distancing between participants and

members of the research team. It maintained the subject's anonymity to other participants as no two participants were allowed to drop off their samples simultaneously. After each sample drop-off, a member of the research team collected the samples and checked each tube to ensure the appropriate information was written and stored in the freezer. The collected samples remained in a -80°C freezer prior to extraction.

Phase 2: DNA extraction

The workflow for isolating DNA using the MagMax™ DNA Multi-Sample Ultra Kit protocol (ThermoFisher) included disrupting the samples, performing DNA extraction, collection, and elution. It is important to note that this protocol was used to perform automated DNA extraction using the KingFisher™ Duo Prime. This specific protocol was downloaded to the KingFisher™ Duo Prime via the BindIt software. After downloading the protocol (A25597_Blood_Buccal) to the BindIt software, it was modified to carry out the heated elution step and final elution in row A of the 96-well plate instead of the elution strips in the KingFisher. This modification was performed to reduce plastic waste, and a previous member of the lab was able to carry out the elution steps of a different protocol in row A of the 96-well plates.

Before the first use of the kit, 25 mL of isopropanol was added to Wash Solution 1 Concentrate mix, and 132 mL of ethanol was added to Wash Solution 2 Concentrate mix. The solutions were stored at room temperature. Before each use of the kit, a dry bath was preheated to 65°C, and DNA Binding Bead Mix was prepared using 16 µL of DNA Binding Beads and 24 µL of nuclease-free water provided with the kit. Instead of transferring the collected swabs to the 96-well plate used for the KingFisher™ Duo Prime to be prepared for DNA extraction as stated by the protocol, it was decided to carry out DNA extraction and purification steps in the swab's original collection tube. The first step was to digest the samples with a Proteinase K (PK) mix.

Each sample tube received 192 μL of PK buffer and 8 μL of Proteinase K for a total of 200 μL . The samples were then vortexed at speed 5 (approx. 900-950 rpm) for five minutes and incubated at 65°C for twenty minutes. The second step was to disrupt the samples by adding 200 μL of Multi-Sample DNA Lysis Buffer to each sample tube and vortexed at speed 5 for five minutes. Finally, 240 μL of isopropanol (not included in the kit) was added to each sample tube and vortexed at speed 5 for five minutes. After taking the samples off from the vortex adaptors, the swabs were removed from the tubes using forceps that were rinsed in 80% ethanol between samples to avoid cross-contamination. The binding beads were moderately vortexed, and 40 μL were added to each well of row H in the 96-well plate. The total volume of 640 μL per tube was transferred to the wells of row H of the 96-well plate. 150 μL of Wash solution 1 was added to each well of row G of the 96-well plate. 150 μL of Wash Solution 2 was added to each well of row E & D of the 96-well plate. The tip comb for the 12-pin magnetic head was placed in row B. Row A was used for the heated elution step using 12.5 μL of Elution Buffer 1 followed by an additional non-heated elution step using 12.5 μL of Elution Buffer 2. The wells in row C and F remained empty. Due to low DNA yields, the amount of Elution Buffer 1 and Elution Buffer 2 was altered from 50 μL (as stated by the protocol) to 12.5 μL which allowed for a more concentrated eluant. Since the first elution step is heated to 74°C in the KingFisher, all 12.5 μL of Elution Buffer 1 evaporated out. The second elution step is not heated, and ergo, the final volume after extraction is 12.5 μL .

12.5 μL of the eluant were removed from the 96-well plate and placed in a new collection tube that was labeled with the sample ID number, specific time point, and where that sample was collected from (dominant hand, forearm, or object).

Sample ID 1-6 were all extracted via the KingFisher™ Duo Prime and sample ID 7-12 were manually extracted using magnetic beads (provided with the kit). The KingFisher™ Duo Prime stopped working during step one (DNA binding) while trying to extract sample ID 7. The machine required maintenance and could not to be used until the issues were resolved. After manual extraction of sample ID 7, it was decided to continue manually extracting the remainder of the samples because the DNA yield was similar, but the total eluant increased from 12.5 µL (automated extraction) to 25 µL. The difference in elution volume was attributed to the incubation period of the manual extractions. The samples remained capped which did not allow Elution Buffer 1 to evaporate. In the automated extractions, the 96-well plate was not covered which allowed Elution Buffer 1 to evaporate. To reduce contamination from the environment for the manually extracted samples, the tubes remained capped.

To make sure the manual extractions closely resembled the automated extractions, all reagents were used in the same quantity and order. Each sample tube contained 200 µL of PK mix, 200 µL of Multi-Sample DNA Lysis buffer, and 240 µL of isopropanol. The first step of the manual extraction protocol was to add 40 µL of DNA binding beads to each tube and to pulse vortex to allow the DNA to bind. Next, the tubes were placed on a magnetic stand. Once the solution cleared and the beads pelleted against the magnet, the supernatant was discarded, and the tubes were removed from the stand. Then 150 µL of Wash 1 was added, vortexed, and placed back on the magnetic stand. Once the solution cleared and the beads pelleted against the magnet, the supernatant was discarded, and the tubes were removed from the stand. Next, 150 µL of Wash Solution 2 was added, vortexed, and placed back on the magnetic stand. Once the solution cleared and the beads pelleted against the magnet, the supernatant was discarded, and the tubes were removed from the stand. Then, a second wash was performed by adding 150 µL of Wash

Solution 2. Next, the samples were air-dried (uncapped) for three minutes on the magnetic stand. After drying, 12.5 μL of Elution Buffer 1 was added to samples, vortexed, and incubated at 70°C for five minutes. After incubation, 12.5 μL of Elution Buffer 2 was added to each sample, vortexed, and placed on the magnetic stand until the solution cleared and the beads pelleted against the magnet. The resulting elution contained the purified DNA and was transferred to a new 2-mL tube.

Following all DNA extractions, the samples were quantified using the Qubit™ Assay (Invitrogen, Carlsbad, CA). The Qubit™ Working solution was prepared by diluting the Qubit™ reagent 1:200 in Qubit™ buffer. 1 μL of the extracted DNA sample was added to 199 μL of the working solution in the Qubit™ assay tubes. Each tube was vortexed for three seconds, followed by a two-minute incubation period at room temperature. The tubes were inserted in the Qubit™ 2.0 Fluorometer and the dilution calculator feature was used to determine the stock DNA concentration of the original sample. DNA yields ranged from 0.1 $\text{ng}/\mu\text{l}$ to 2.52 $\text{ng}/\mu\text{l}$. It is important to note that the Qubit™ Assay cannot differentiate between human and non-human DNA.

Phase 3: Library preparation

Metagenomic studies are commonly performed by analyzing the prokaryotic 16S ribosomal RNA gene (16S rRNA), which is approximately 1,500 base pairs long and contains nine variable regions interspersed between conserved regions. The variable regions of 16S rRNA are used in phylogenetic classification, such as genus or species in microbial population analyses. The library preparation workflow (Fig. 1) included amplification of the V4 region of the 16S rRNA gene, using thirty cycles of polymerase chain reaction (PCR), PCR clean-up,

adding Illumina sequencing adaptors and dual indices to the amplicon target and a final clean-up step. The gene-specific sequences used were selected from Klindworth et al. and are detailed in Table 2. Amplification of the V4 region's DNA sample used specific primers with specific overhang adaptors attached according to the 16S Metagenomics Sequencing Library Preparation protocol, which allowed the V4 region to be targeted. Overhang adaptor sequences had to be added to the gene-specific primers to ensure multiplexing indices can be attached during PCR indexing.

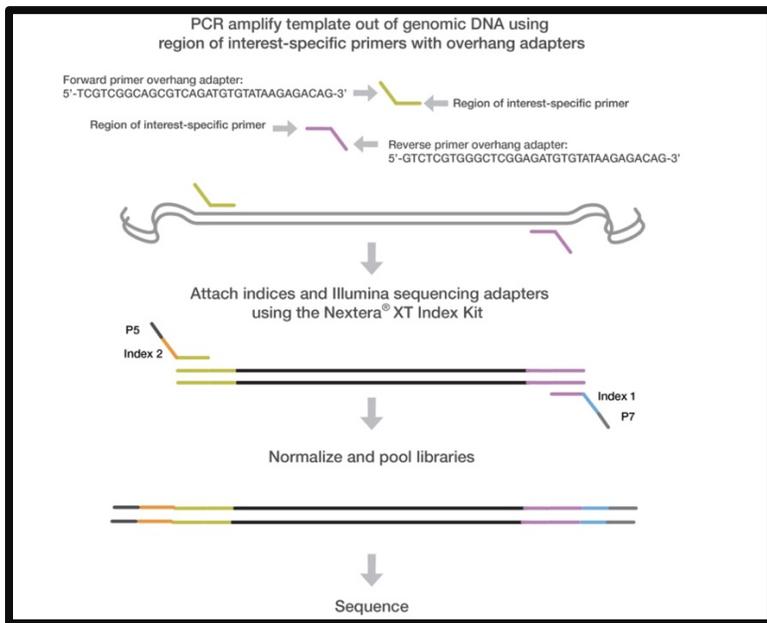


Figure 1. 16S V4 Amplicon Workflow (Amplicon, P. C. R., Clean-Up, P. C. R., & Index, P. C. R. (2013). Forward and reverse primers that are complementary upstream and downstream of the region of interest are designed with overhang adapters and used to amplify templates from genomic DNA. A subsequent limited-cycle amplification step is performed to add multiplexing indices and Illumina sequencing adapters. Libraries are normalized and pooled and sequenced on the MiSeq system. 16S metagenomic sequencing library preparation. (Used under license from Illumina, Inc. All Rights Reserved.)

Forward Primer	
Name	Amplicon PCR Forward Primer
Sequence Structure	5`-(forward adapter overhang)-forward primer-3`
Forward Adapter Overhang and Primer Sequence	5'(TCGTCGGCAGCGTCAGATGTGTATAAAGAGACAG)-GTGCCAGCMGCCGCGGTAA-3'
Reverse Primer	
Name	Amplicon PCR Reverse Primer
Sequence Structure	5`-(reverse adapter overhang)-forward primer-3`
Reverse Adapter Overhang and Primer Sequence	5`-(GTCTCGTGGGCTCGGAGATGTGTATAAAGAGACAG)-GGACTACHVGGGTWTCTAAT-3`

Table 2. Amplicon Primers and Overhang Adapter Sequences used to Target the V4

Region of 16S rRNA gene. (Amplicon, P. C. R., Clean-Up, P. C. R., & Index, P. C. R. (2013)).

To clean-up the PCR products, 32 μ L of AMPure XP beads (at room temperature) were added to each well of the PCR plate to 40 μ L of the pooled duplicates. The entire volume was gently pipetted up and down ten times and incubated at room temperature without mixing for five minutes. Then, the plate was paced on a magnetic stand until the supernatant cleared. While on the magnetic stand, the supernatant was discarded, and 200 μ L of freshly prepared 80% ethanol was added to each sample well. After thirty seconds, the supernatant was removed and discarded. A second wash was performed using 200 μ L of 80% ethanol and incubated for thirty seconds. The supernatant was removed and discarded. A P20 multichannel pipette was used to remove excess ethanol as it inhibits PCR. While on the magnetic stand, the beads air-dried for ten minutes. After drying, the plate was removed from the magnetic stand and 52.5 μ L of 10 mM Tris pH 8.5 was added to each sample well, gently mixed up and down ten times, and incubated

at room temperature for two minutes. Next, the PCR plate was returned to the magnetic stand until the supernatant cleared. Using a multichannel pipette, 50 μL of the supernatant from the Amplicon PCR plate was transferred to a new 96-well PCR plate.

The index PCR step attached dual indices and Illumina sequencing adapters using the Nextera XT Index kit. 5 μL from each well was transferred into a new 96-well plate. The remainder of the 45 μL is not used in the protocol and was stored for other uses. Index 1 primer tubes were arranged on the TruSeq Index Plate fixture horizontally, aligned with columns 1 through 12. Index 2 primer tubes were vertically aligned with rows A through H. The 96-well PCR plate produced was placed in the TruSeq Index Plate Fixture, as shown in Fig 2. Each well received 5 μL of Index 1 primer and Index 2 primer, an Accuprime Taq DNA polymerase (25 μL) and 10 μL of PCR Grade water for a total volume of 50 μL . The reaction mixture was gently pipetted up and down ten times to mix. The plate was then covered with Microseal' A' and centrifuged at 1,000 x g at 20°C for one minute. PCR was performed on a thermal cycler using the following program: 95°C for 3 minutes, eight cycles of 95°C for thirty seconds, 55°C for thirty seconds, 72°C for thirty seconds followed by 72°C for five minutes and a final hold at 4°C.

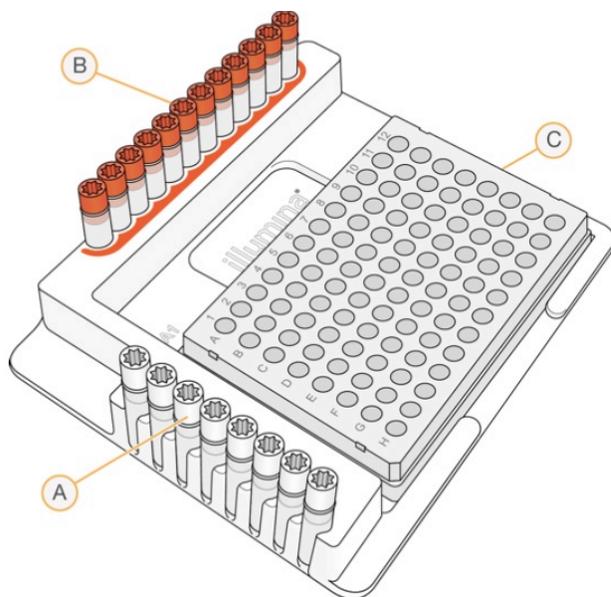


Figure 2. TruSeq Index Plate Fixture: (A) Index 2 primers (white caps). (B) Index 1 primers (orange caps). (C). 96-well plate (Amplicon, P. C. R., Clean-Up, P. C. R., & Index, P. C. R. (2013). 16s metagenomic sequencing library preparation. Used under license from Illumina, Inc. All Rights Reserved.)

A second PCR clean up using the AMPure XP beads was used to clean up the final library before sequencing. The Index PCR plate was centrifuged at 280 x g for 20°C for one minute to collect condensation—50 μ L was transferred out using a multichannel pipette and placed on the MIDI plate. The AMPure XP beads were vortexed for thirty seconds to make sure the beads were evenly dispersed. Next, 56 μ L of AMPure XP beads were added to each well of the Index PCR plate, shaken at 1000 rpm for one minute, and incubated at room temperature (without shaking) for five minutes. The plate was placed on a magnetic stand for two minutes, or until allow the supernatant to clear. A multichannel pipette was used to discard the supernatant with the Index PCR plate on the magnetic stand. The beads were washed twice using 200 μ L of

freshly prepared 80% ethanol and incubated for thirty seconds with the Index PCR plate on the magnetic stand. The beads were allowed to air-dry for ten minutes with the Index PCR plate on the magnetic stand. The Index PCR plate was removed from the magnetic stand, 27.5 μL of 10 mM Tris pH 8.5 was added to each well of the Index PCR plate, shaken at 1000 rpm for one minute, and left to incubate at room temperature for two minutes. The Index PCR plate was then placed on the magnetic stand for two minutes to clear the supernatant. Next, 25 μL of the supernatant from the Index PCR plate was transferred to a new 96-well PCR plate for sequencing. The Index PCR amplicons were quantified using the Qubit™ Assay in ng/ μL .

After quantification, the libraries were pooled together. Equimolar calculations were used to determine how much volume to add from each sample towards the library. After all volumes were added, the pooled library was quantified using the Qubit™ Assay in ng/ μL . The equation provided in the 16S Metagenomics Sequencing Library Preparation protocol was used to determine the concentration in nM (pg. 16). To dilute the final library concentration of 13.98 nM down to 4 nM, 10 μL of the pooled sample was added to 25 μL of Tris pH 8.5.

In preparation for sequencing, pooled libraries were denatured with NaOH, diluted with a hybridization buffer (HT1), and then heat denatured before MiSeq sequencing. To denature the DNA, 5 μL of 0.2 N NaOH was added to 5 μL of the pooled library. To mix the samples, the solution was briefly vortexed, centrifuged, and followed by a five-minute incubation period at room temperature. This allowed the DNA to denature into single strands. 990 μL of HT1 was added to the 10 μL of the denatured DNA resulting in a 20 pM denatured library in 1 mM NaOH. To dilute the denatured DNA down to 10 pM, 300 μL of the 20 pM denatured library was added to 300 μL of HT1. The diluted denatured DNA solution was inverted several times to mix and placed on ice. Each run on the MiSeq must contain a minimum of 5% PhiX to serve as

an internal control. 2 μL of 10 nM PhiX library was combined with 3 μL of Tris pH 8.5, which diluted the PhiX library to 4 nM. Next, 5 μL of NaOH was added to the PhiX library and briefly vortexed to mix. The solution was left to incubate at room temperature for five minutes, which allowed the PhiX library to denature into single strands. 990 μL of pre-chilled HT1 was added to the denatured PhiX library resulting in a 20 pM PhiX library. The PhiX library was diluted to the same loading concentration as the amplicon library (10 pM) by adding 300 μL of pre-chilled HT1 to 300 μL of the denatured PhiX library. The solution was inverted several times to mix and placed on ice. The heat denaturation step was done immediately before loading the library into the MiSeq reagent cartridge, ensuring efficient template loading on the MiSeq flow cell. The denatured and diluted PhiX control (30 μL) was combined with the denatured and diluted Amplicon library (570 μL). The combined solution was then incubated on a heating block set to 96 °C for two minutes. After incubation, the solution was inverted two times to mix, vortexed & centrifuged, then loaded into the MiSeq reagent cartridge.

Phase 4: Bioinformatics analysis

During the sequencing run, real-time analysis generated data files in the form of FASTQ files. Quantitative Insights into Microbial Ecology (QIIME) is an open-source bioinformatics pipeline for performing microbiome analysis from raw DNA sequencing data produced on Illumina and other platforms (Bolyen et al.). QIIME 2 (version 2021.4) workflow includes demultiplexing, quality filtering, denoising and clustering, generation of feature tables, as well as taxonomy classification and analysis (Fig 3).

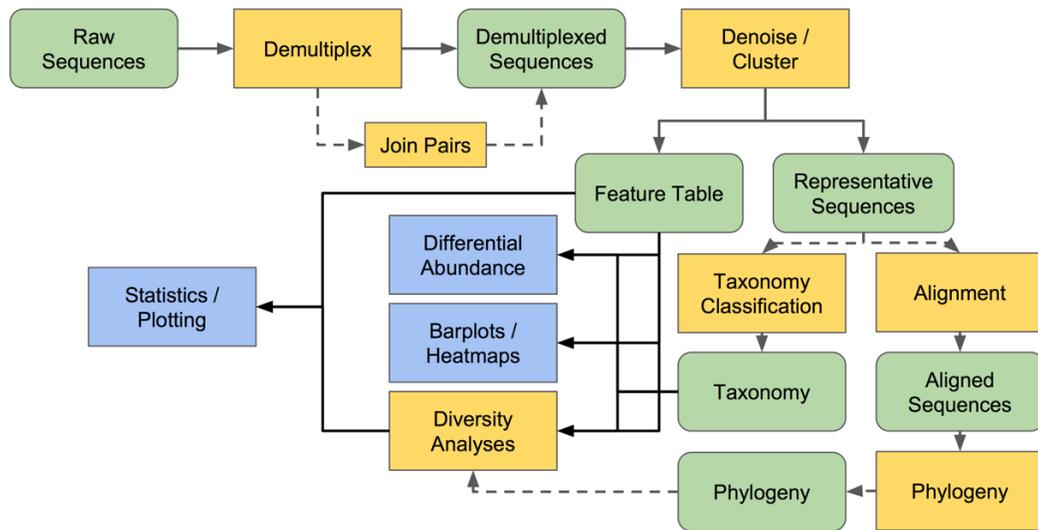


Figure 3. Conceptual Overview of QIIME 2. Key conceptual overview of the possible workflows for examining amplicon sequence data. The edges and nodes in this overview represent conceptual categories (i.e., basic types of data or analytical goals) in an experiment.

Demultiplexing reads determined and binned each read to its appropriate sample. Then, reads are denoised into amplicon sequence variants (ASVs) which aided in reducing sequence errors as well as dereplicating sequences. The resulting feature table was a matrix of ASVs that was observed in each sample. From the feature table, common analysis was conducted such as taxonomic classification (what species are present?) and beta diversity (how similar are samples?).

A package called DADA2, a plug-in of QIIME (2021.4) was used as the starting point data analysis. DADA2 contains the demultiplexed FASTQ files with the barcodes and adapters removed, which were generated during the sequencing runs. The FASTQ files' names were read, and string manipulation was performed to get matched lists of the forward and reverse FASTQ

files. The forward reads were visualized to inspect read quality profiles, first, then the reverse reads. A gray-scale heat map was generated for the forward reads, which were of good quality (Appendix F). The last few nucleotides were trimmed to avoid less controlled errors that potentially arise later. The reverse reads produced a gray-scale heat map that tends to be significantly worse quality at the end, common to Illumina sequencing. The FASTQ files were filtered and trimmed using standard parameters. Next, the forward and reverse reads were merged to obtain the full denoised sequence. After the merger, an amplicon sequence variance (ASV) table was constructed. ASV records the number of times each exact amplicon sequence variant was observed in each sample. As a final check of progress, the number of reads to make it through each step in the pipeline was assessed. Next, the Bayesian classifier method was used to assign taxonomy. Alpha diversity metrics (observed features and Shannon index) and beta diversity metrics (weighted UniFrac) were then assessed.

CHAPTER III

RESULTS AND DISCUSSION

Overview of Automated and Manual DNA Extractions:

This research study began with twelve different participants swabbing their dominant hand, forearm of their dominant hand, and a chosen object from either their laboratory or office across eight different timepoints (0, 1, 3, 5, 7, 14, 21, and 28 days). Each participant contributed twenty-three samples for a total of 276 samples. Participant numbers 1-6 were extracted using the KingFisher Duo Prime while participant numbers 7-12 were extracted manually with magnetic beads. At the end of the KingFisher run, 12.5 μL of eluted sample remained and after quantification, it was discovered that the samples contained low amounts of DNA. As stated in the methods section, the Qubit Assay cannot differentiate between human and microbial DNA. To confirm whether or not amplification (in duplicates) of the 16S rRNA gene was successful, gel electrophoresis was used. Unfortunately, not all samples were able to amplify at 2 μL , 3 μL , 5 μL , or even 6 μL of template. Since the elution output was 12.5 μL , the highest amount of template used was 6 μL . While the KingFisher was down for maintenance, it was discovered that manual extraction of DNA resulted in greater elution volume (25 μL) and about the same DNA yield (sample ID 7-12). Since there was more sample available for use, it was decided to use 10 μL of template, in duplicate which resulted in most samples failing to amplify. Only three total samples from Sample ID 7-12 successfully amplified. It is inferred that most of the DNA detected by the Qubit from the manual extractions are human. In addition, pulse vortexing the

samples was possibly insufficient to break open all cells. In total, sixty-nine samples successfully amplified and were carried into sequencing.

Overview of QIIME 2 (2021.4) Data Analysis

QIIME 2 was used to perform alpha and beta analyses of the human skin microbiome and workplace environment. The data discussed were obtained by sequencing on Illumina's MiSeq platform using the hypervariable region 4 (V4) of the 16S rRNA gene. QIIME 2's diversity analysis was available through the q2-diversity plugin which supported computing alpha and beta diversity metrics, applying related statistical tests, and generating interactive visualizations. Alpha diversity refers to the diversity within a particular sample while beta diversity refers to how samples vary against each other. The diversity metrics used take into account two aspects of a microbial community: the number of different organisms in a sample, and the range of abundances for each one. QIIME 2 supports a variety of alpha diversity metrics but the ones used for this study include Shannon's diversity index (quantitative measure of community richness), observed features (qualitative measure of community richness) and Faith's Phylogenetic Diversity (a qualitative measure of community richness that incorporates phylogenetic relationships between the features). The beta diversity metrics used include Bray-Curtis distance (quantitative measure of community dissimilarity), unweighted UniFrac distance (qualitative measure of community dissimilarity that incorporates phylogenetic relationships between the features), and weighted UniFrac distance (quantitative measure of community dissimilarity that incorporates phylogenetic relationships between the features). Lastly, the overall taxonomic composition of samples was examined to determine if individual's microbiomes became more similar to each others after returning to work in the same building. A total of 69 samples

(including the negative control) were processed on the MiSeq with over 8,000 features observed over 7.5 million times across all samples after denoising/quality control (Table 3; Fig. 4).

Table summary

Metric	Sample
Number of samples	69
Number of features	8,215
Total frequency	7,597,043

Frequency per sample

	Frequency
Minimum frequency	87.0
1st quartile	36,119.0
Median frequency	119,234.0
3rd quartile	145,172.0
Maximum frequency	484,798.0
Mean frequency	110,102.07246376811

Table 3. Summary and frequency per sample.

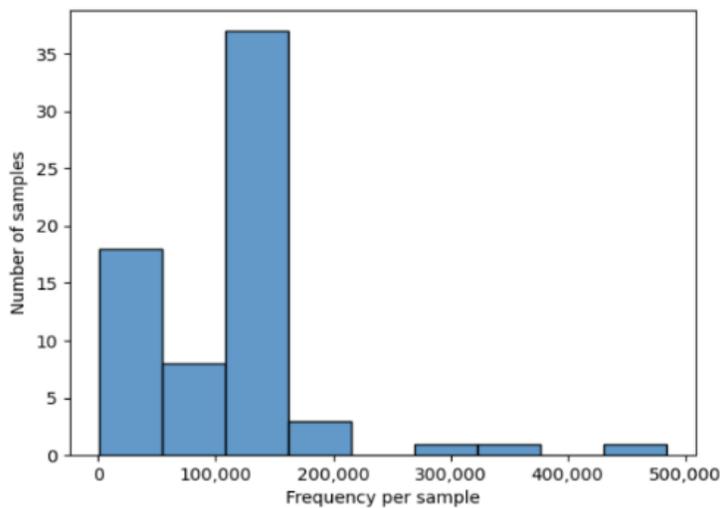
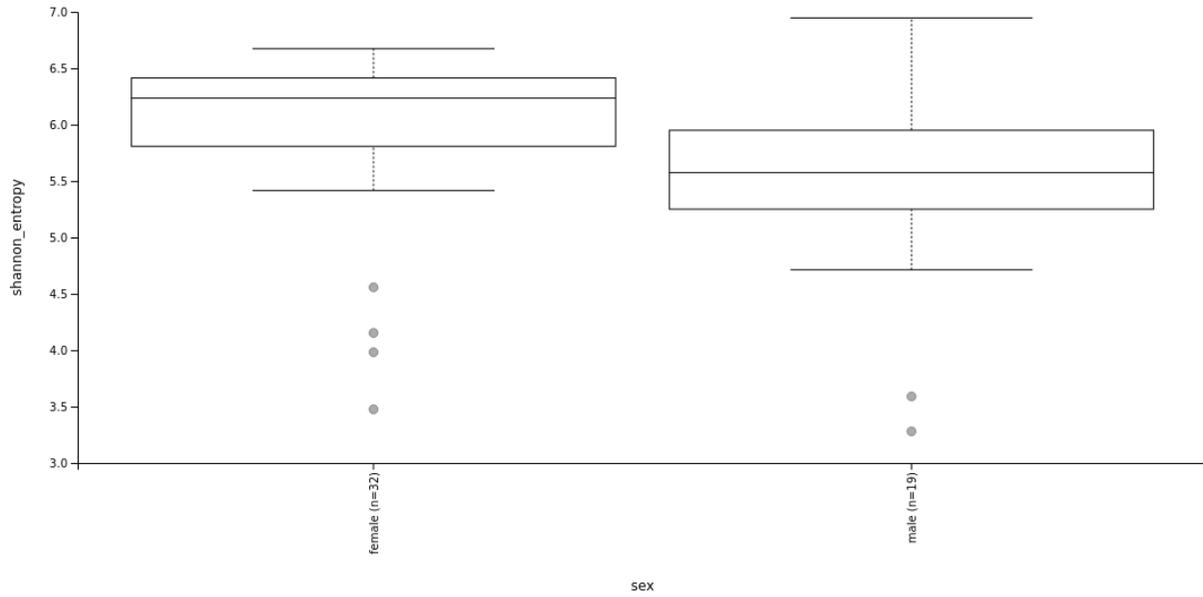


Figure 4. Frequency per sample. The total frequency distribution of the features per sample.

Alpha Diversity

The alpha diversity analysis did not include CBH floor, time since last handwashed, and timepoint because they did not contain categorical data. Furthermore, handedness was omitted due to all the study participants being right-handed. Kruskal-Wallis (KW) and KW pairwise tests were used for statistical analysis. The H-value reported is the test statistic for KW. A p-value of less than 0.05 is statistically significant and determines there is a difference between the medians of the groups but does not inform us where the difference lies when there are more than two groups. The post-hoc test for KW is the KW-pairwise test which finds which pairs of the groups were significantly different, if any. The q-value reported is the Benjamini-Hochberg false discovery rate (FDR) which is used to adjust the p-values to account for multiple testing (Benjamini & Hochberg, 1995). The categories which alpha diversity metrics were applied to include sex, subjects, age range, body site, workplace environment, and object (Appendix F). Shannon's index determined there was a statistically significant difference between the two sexes, indicating that females had more richness than males which was expected (Figure 5, Ying et al.). Faith's PD deemed all categories as statistically insignificant.



Kruskal-Wallis (all groups)

	Result
H	4.932692307692321
p-value	0.026353228732016228

Figure 5. Kruskal-Wallis test of Shannon Diversity results for sex differences. The Kruskal-Wallis (KW) test was applied to the sex category. The H-value represents the KW test statistic. A p-value of < 0.05 denotes statistical significance. Females have greater specie richness than males which is a result of biochemical differences as well as product application (Ying et al.).

Beta Diversity: Bray-Curtis Dissimilarity

Bray-Curtis dissimilarity is a statistical measure used to quantify the compositional dissimilarity between samples. Samples that cluster more closely to each other are more similar in composition than those that show clear separation. In Fig. 6, the samples were plotted by sampleID (only to include those samples from the right hand) and shaped by time since last handwashed. Each sampleID begins with the subject number, followed by RH to indicate it is a right-hand skin swab, and a timepoint represented by T. (i.e., T3 refers to the third timepoint in the study). Open circles represent those samples from subjects that washed their hands less than one hour before collection. Squares represent those samples from subjects that washed their hands two-to-four hours before collection. On the far-left side of the plot, subjectID 1 and 5 (red and yellow-green hues, respectively) cluster closely together, indicating their sample compositions are similar to one another but differ from the other participants. On the top-right side, subjectID 3 (orange hues) cluster with sampleID 2 (lighter reds). Finally, most of sampleID 6's sample cluster alone towards the bottom right. Since each sample has an associated timepoint attached, visually, there are shifts in the intraindividual microbial composition across the timepoints.

In Fig. 7, the samples were plotted by object and shaped by CBH floor number. The second floor of CBH is represented by diamonds, the third floor by open circles, and the fourth floor by squares. Although, the majority of the chosen objects were from a computer mouse, there are differences in microbial composition based on which floor of CBH the object was swabbed. Most of the second-floor objects (bottom right) cluster together as opposed to those from the third and fourth floors. Interestingly, one sample from a computer mouse on the third floor, is dissimilar from the other two, indicating that there are variances within a floor. Since

only thirteen objects successfully amplified, there is insufficient data to determine if there are differences in the fomite's microbiome.

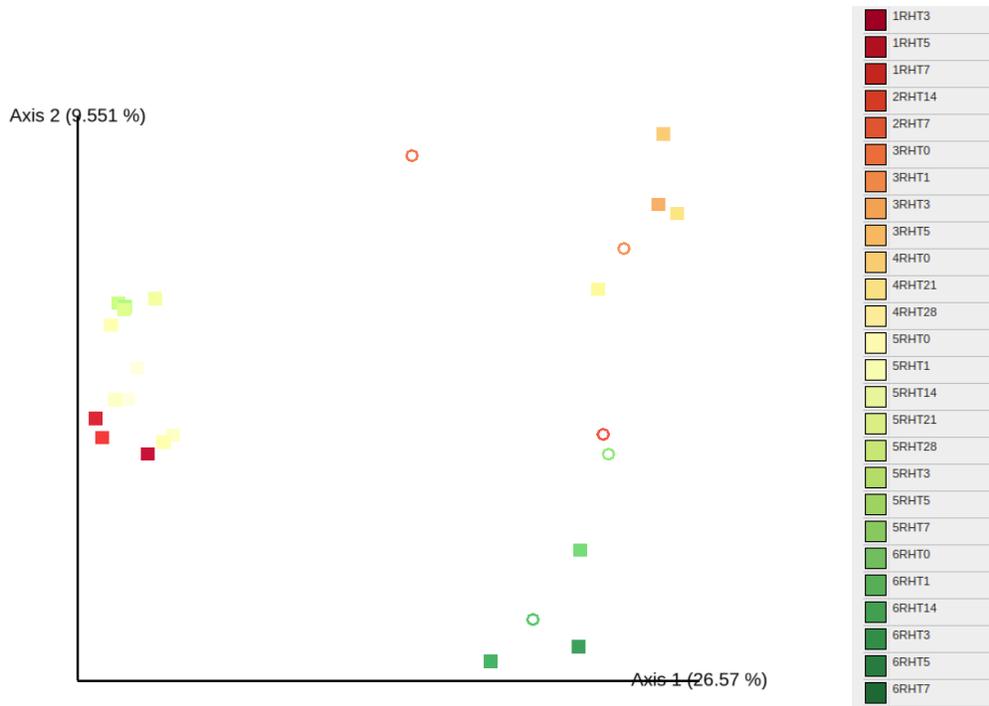


Figure 6. Bray Curtis Dissimilarity: SampleID vs time since last hand washed. Samples are color coded by SampleID. The first number indicates the participant ID, RH stands for right hand, T represents the timepoint followed by a number that represents the number of days since returning to work. Circles indicates those samples which were taken <1 hour after handwashing while squares represent sample collection 2-4 hours after handwashing.

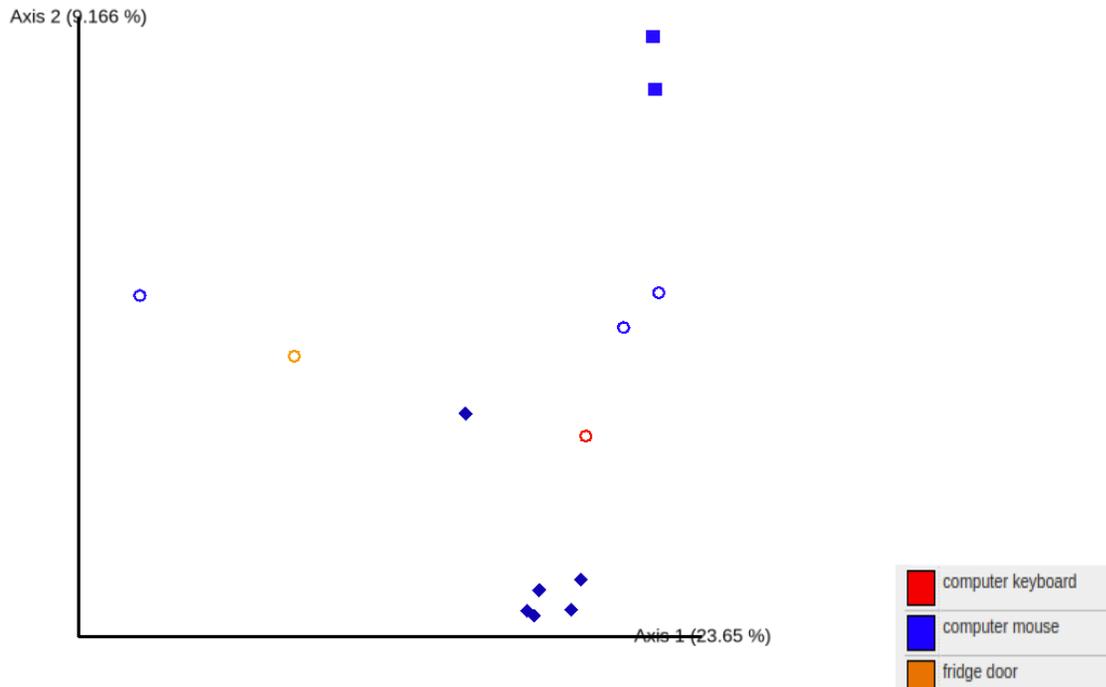


Figure 7. Bray Curtis Dissimilarity: Object vs CBH floor. Samples are color coded by object type. Diamonds represents samples from the 2nd floor of CBH. Circles indicate samples from the 3rd floor of CBH. Squares represent samples from the 4th floor of CBH. Samples separate based on floor level.

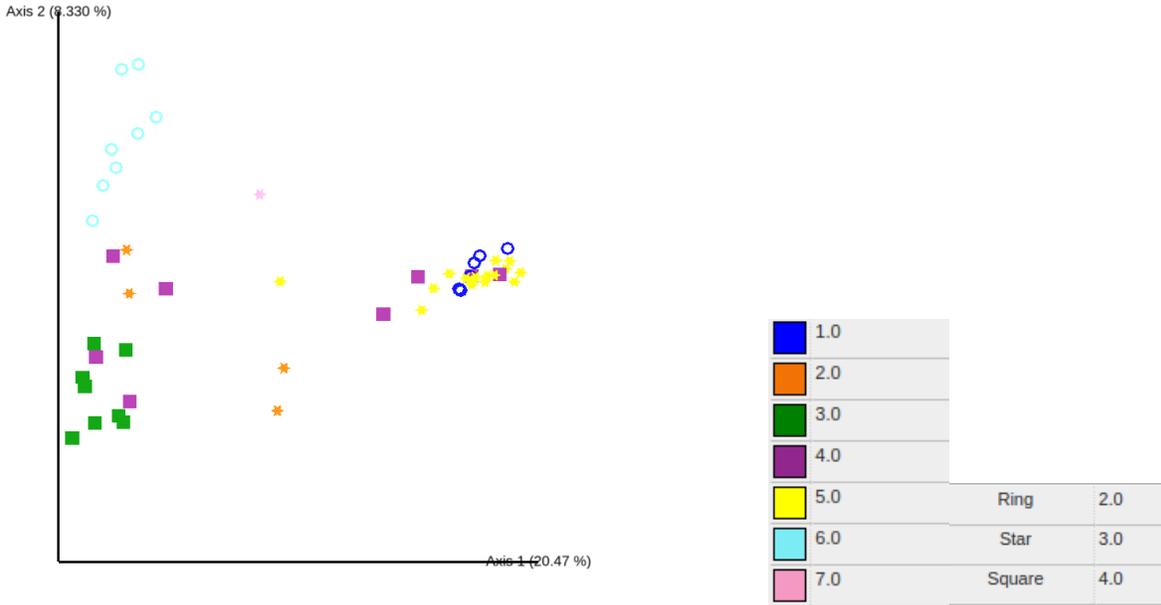


Figure 8. Bray-Curtis Dissimilarity: SampleID vs CBH floor level. Samples are color coded by participant ID and shaped by CBH floor level. Participant ID one (blue) and six (light blue) work in CBH floor 2 (ring) while participant IDs two (orange), five (yellow), and seven (pink), work in CBH floor 3 (star). Lastly, participant ID three (green) and four (purple) work in CBH floor 4 (square).

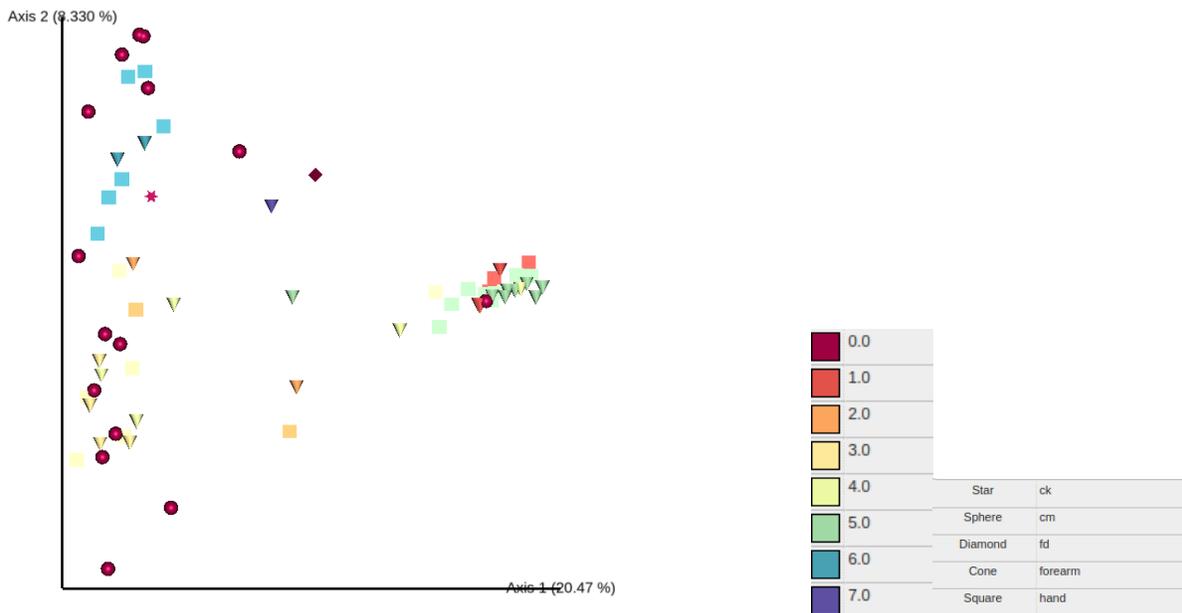


Figure 9A. Bray-Curtis Dissimilarity: SubjectID and Sample Type. Participant ID 0 (dark red) is not an individual but rather includes all thirteen objects. Actual study participants are numbered one through seven. Shapes represent the sample type, either computer keyboard (ck), computer mouse (cm), fridge door (fd), forearms, or hands.

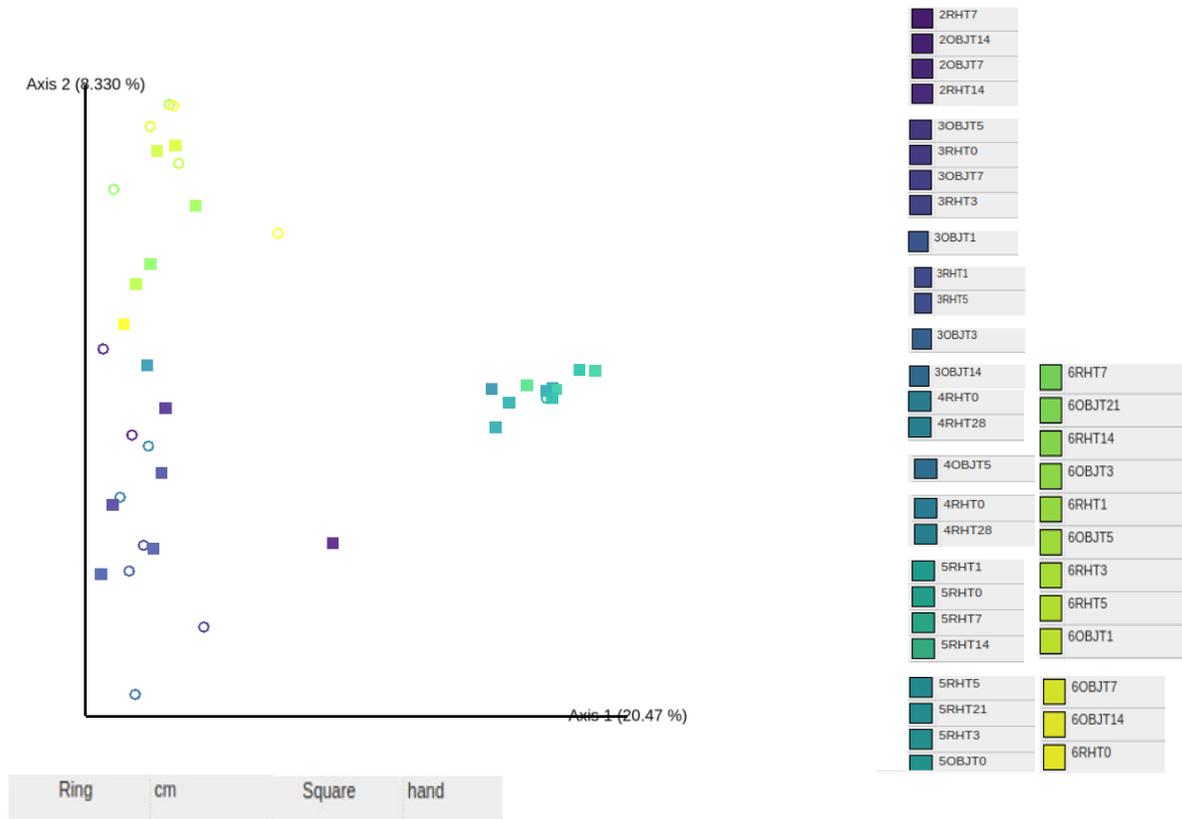


Figure 9B. PCoA plot of participants, objects, and right hands. Participants are color coded while objects (computer mouse) are shown in circles and the samples from the hands are shown in squares. The objects (fridge door and computer keyboard) from participant IDs seven and ten, respectively, have been omitted because there were no right-hand samples from either participant to compare.

In Fig. 9B, Participant IDs three and six (light purple and yellow-green, respectively) hand samples and objects cluster more closely together than all other participants. This observation is because participant three had four objects and five hand samples successfully amplify. Participant ID six had an equal number of objects (six) and hand (six) samples successfully amplify. Based on this, the intrapersonal microbiomes of the hands can be linked to participant ID three and six's objects. The remaining participants could not be linked to their objects from their hand microbiome due to insufficient data on their fomites.

Beta Diversity: Unweighted UniFrac and Weighted UniFrac

An unweighted UniFrac is a distance metric used for comparing biological communities and incorporates information on the relative relatedness of community members by incorporating phylogenetic distances between observed organisms but does not take into account abundance (Lozupone et al.). Weighted UniFrac, on the other hand takes into account abundance and relatedness of community members. In this study, participants swabbed their forearm of their dominant hand as a control. Since both forearms and hands are dry areas, their microbial composition is expected to be similar. Although in Fig.10A (unweighted), there is slight separation between right forearms and right hands, the overall trend indicates the microbial communities on the forearms and the hands are similarly related to one another. The forearms were used as a control for the study since the forearms are in close proximity to the hands and are the same microenvironment (dry), their microbiomes are expected to be similar. In Fig.10B(weighted), there is less separation between the hands and forearms as compared to 10A.

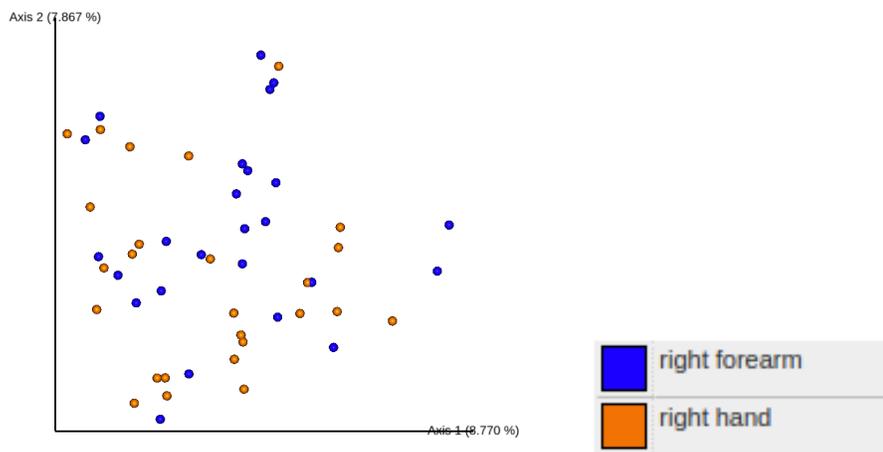


Figure 10A. Unweighted UniFrac distance between right forearms and right hands shows no clustering by body site. A UniFrac is a distance metric used for comparing biological communities. The principal component analysis plot of an unweighted (qualitative) UniFrac

considers only the presence or absence of observed organisms on the right hand and right forearm. The percentage in the parenthesis is the percent variance for each axis.

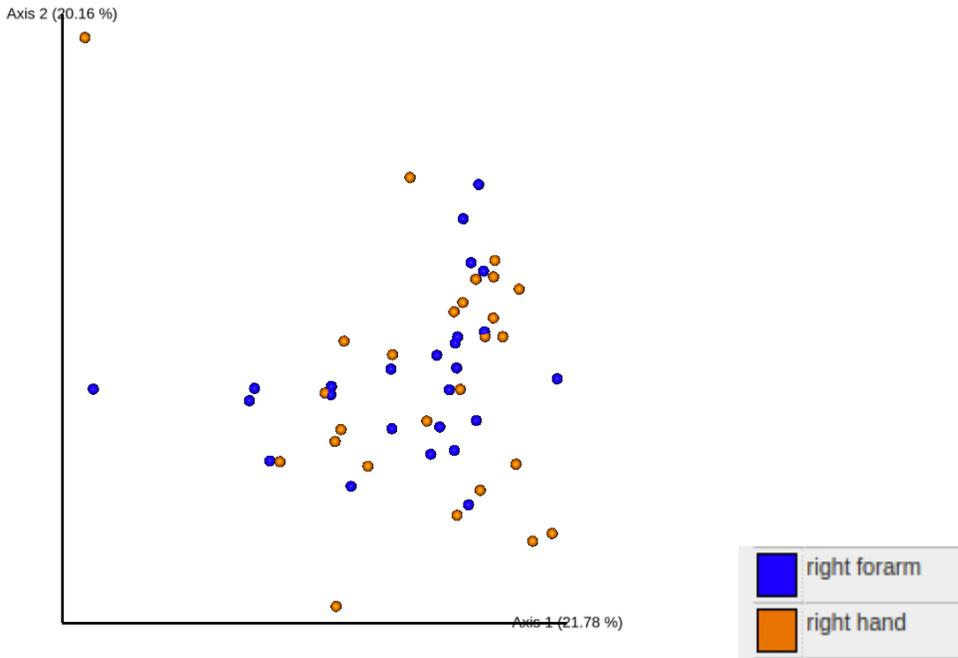


Figure 10B. Weighted UniFrac distance between right forearms and right hands shows no clustering by body site. The principal coordinate analysis plot of the weighted (qualitative) UniFrac accounts for abundance of observed organisms on the right hand and right forearm. There is a higher percent variance in 10B as opposed to 10A.

Taxonomic Analysis: Bar Plots

To explore the taxonomic compositions of the samples, taxonomy was assigned to the sequences by using a pre-trained Naïve Bayes classifier and the q2-feature-classifier plugin.

QIIME 2's classifier was trained on the Greengenes 13_8 99% OTUs where the sequences were trimmed to only include 250 bases from the V4 region of the 16S rRNA gene (515F/806R primer pair). This classifier was applied to the sequences which generated taxonomic bar plots. Fig. 11A depicts the overall composition of bacterial communities with their relative frequencies plotted on the y-axis with the top ten taxonomic abundances listed below (full legend can be found in Appendix H). Genus *Corynebacterium* was found to be present on all sample (including objects) with as little as 5% abundance to as high as 44% across all samples, followed by *Streptococcus* and *Pseudomonas*. Fig. 11B is sorted by the right-hand samples and time since last hand washed where 1 indicates less than or equal to one hour and 2.4 indicates a sample collected two-to-four hours after handwashing. The general trend, visually, for most bacterial communities on the hands is that those hands that were washed two to four hours before sample collection had a greater abundance of bacteria than those washed one hour before collection. The greater abundance can be attributed to individual's having more time to interact with the built environment as microbes transfer from fomites to the hands. Fig. 12 (A-B), samples are sorted by object and sampleID on the left-hand side and only by sampleID on the right side. From Fig. 12B, objects generally have a greater abundance of *Staphylococcus* than all other sample types. In Fig. 13, the samples were sorted by subject number and timepoint. Slight shifts in microbial abundance can be seen when comparing an individual to themselves overtime, but that same pattern is not observed when comparing an individual's microbial composition to against each other. As individuals returned back to work in CBH, it was expected that their microbial profiles would be more similar to each other. One reason for this result could be explained by individual's keeping their distance from each other even after returning to work.

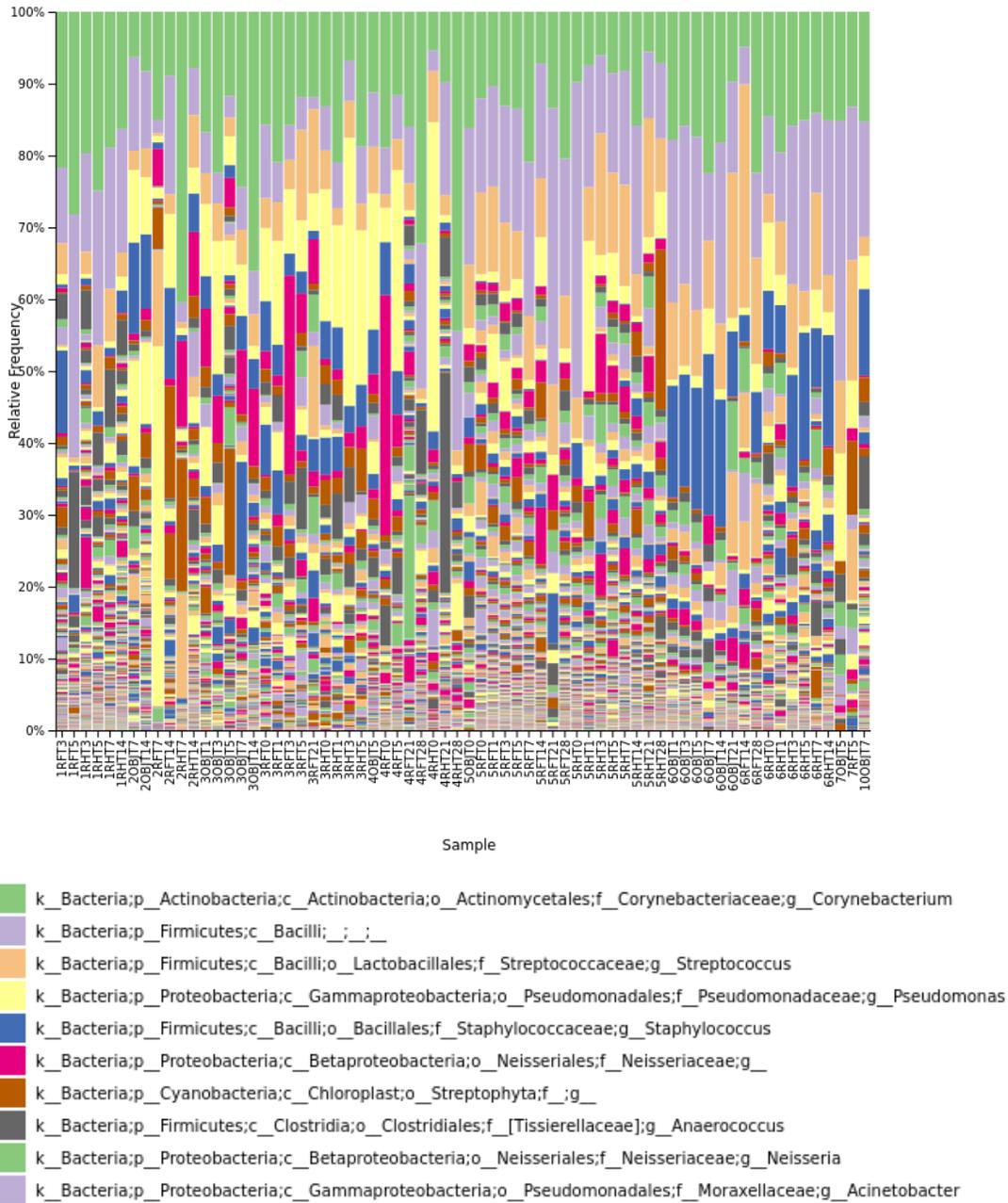


Figure 11A. Level 6 (genus) taxonomic classification of all samples. The overall taxonomic bar plots for all samples with the top ten bacterial communities indicated by the legend (full legend can be found in Appendix H). The first number indicates the participant's ID followed by RH (right hand), RF (right forearm), obj (object), T for timepoint and a number that indicates the specific timepoint in the study.

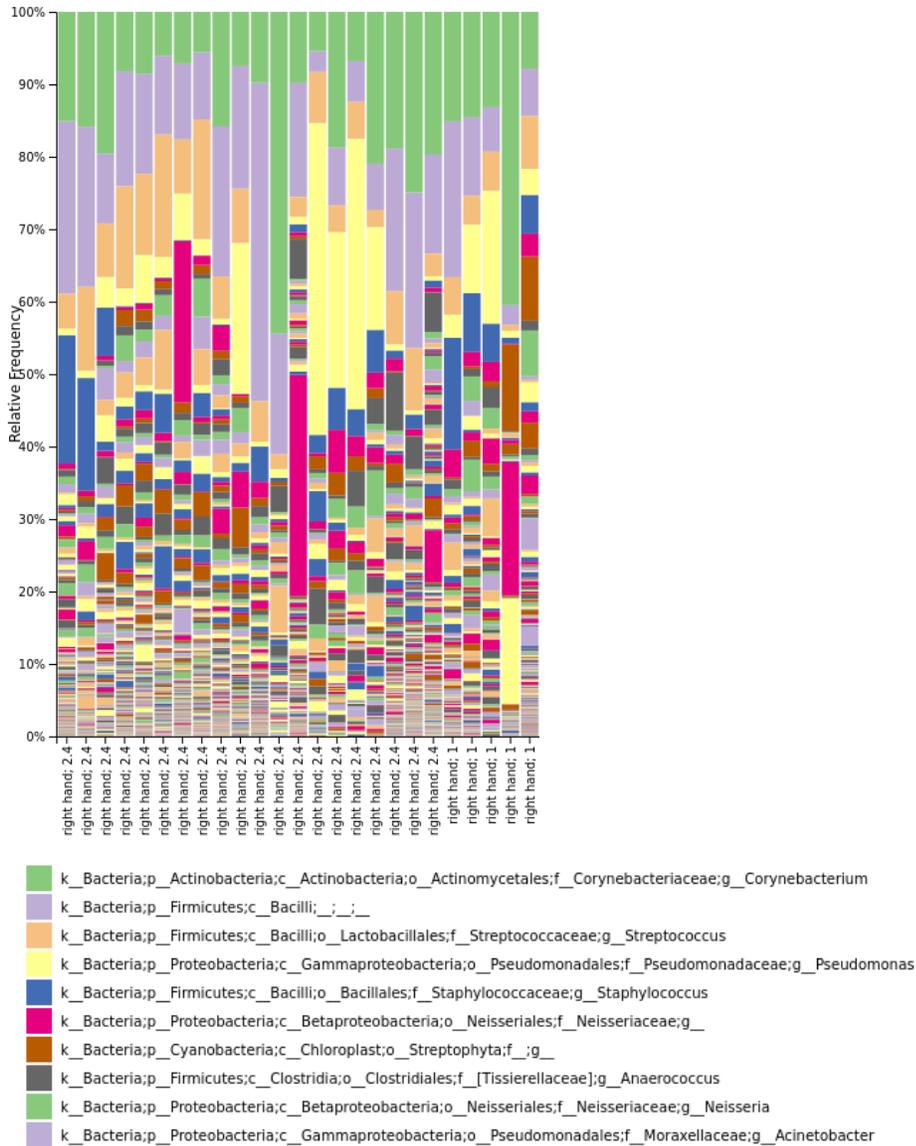


Figure 11B. Level 6 taxonomic classification on right hands by time since last handwashed.

The x-axis represents the right-hand samples that were sampled < 1 hour after handwashing (indicated by a 1) or two-four hours after handwashing (represented by 2.4). The Y-axis represents the relative frequency. The top ten bacteria shown in the legend (full legend can be found in Appendix H).

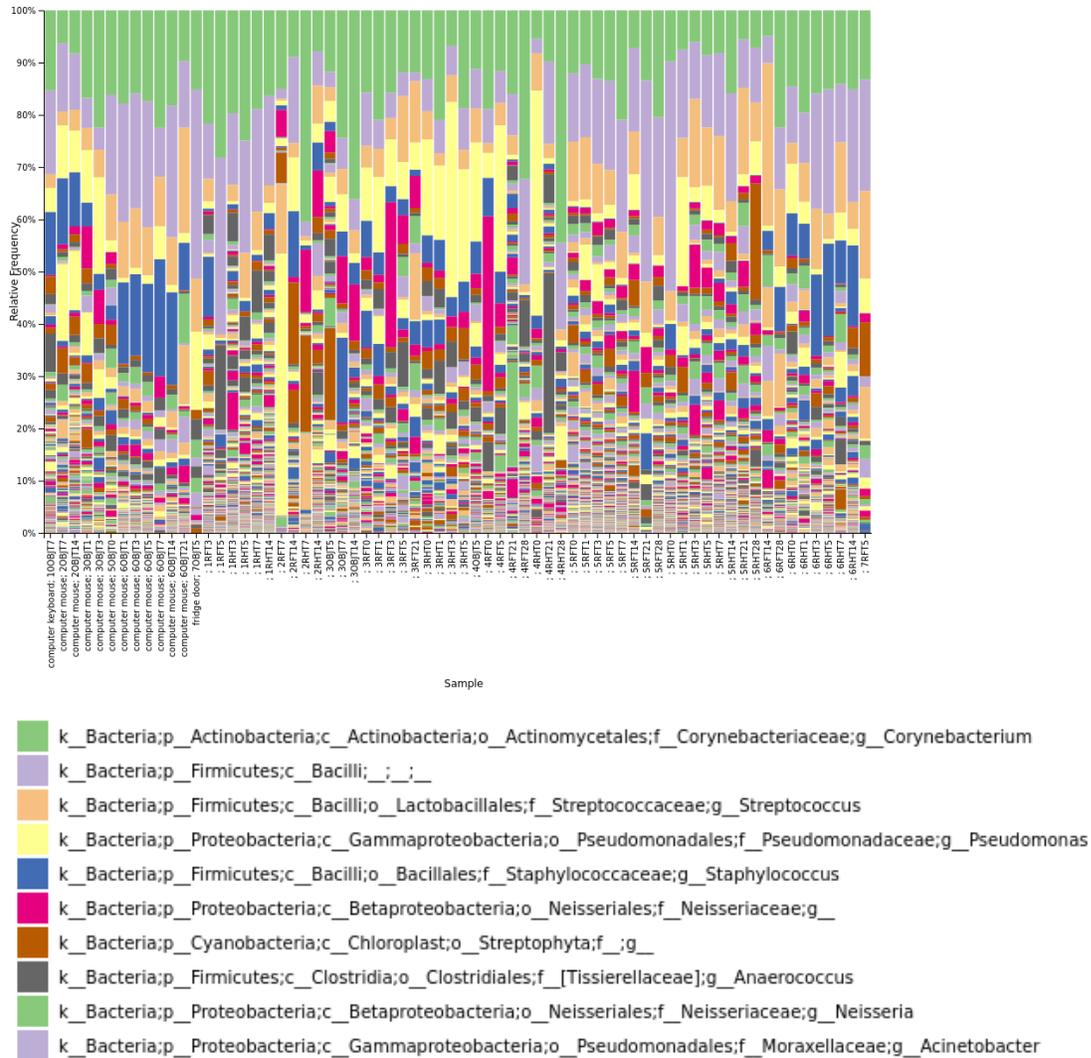


Figure 12A Object microbiome vs. all other samples. The overall view of the taxonomic bar plots sorted by objects followed by sample index. The top ten bacteria are shown in the legend (full legend can be found in Appendix H).

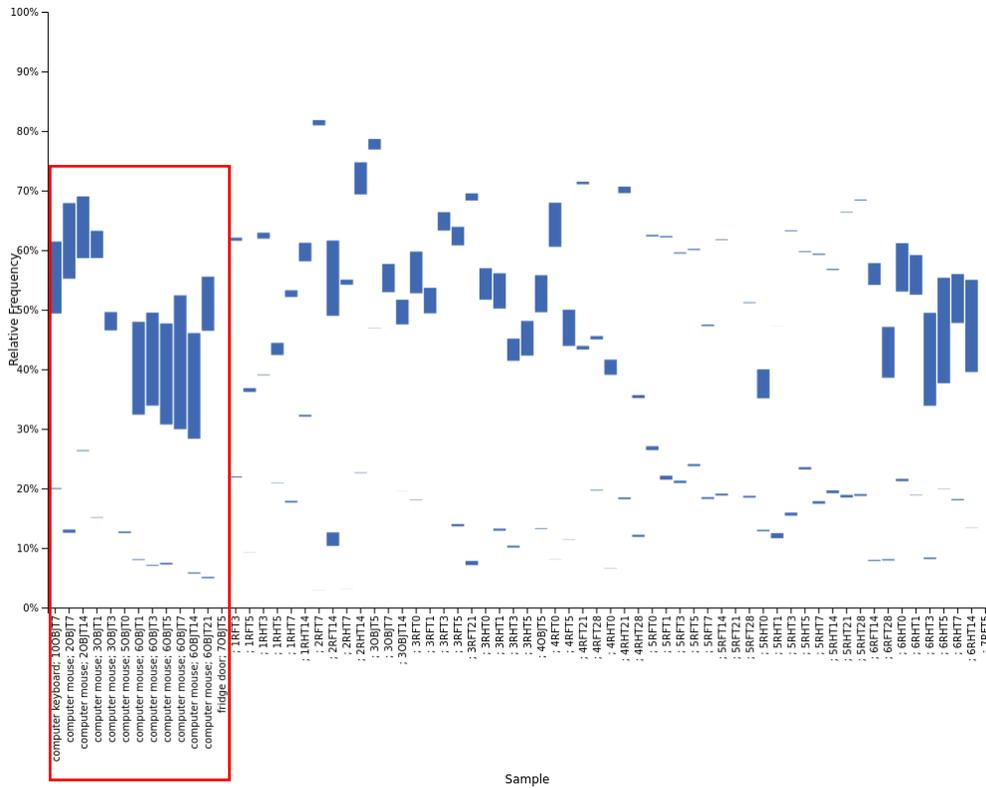
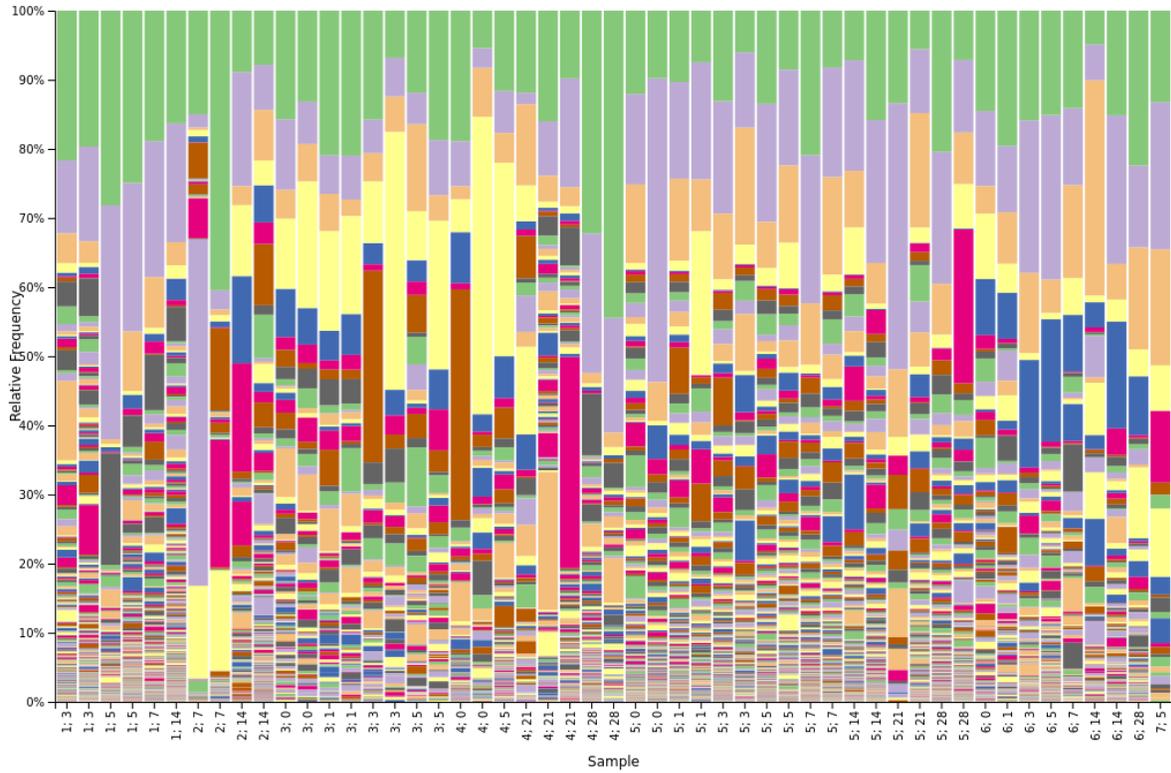


Figure 12B. *Staphylococcus* on objects (red box) vs all other samples. The samples contained in the red box are the thirteen total objects in the study (11 computer mouse, 1 fridge door, and 1 computer keyboard). The samples to the right of the red box include all the right hand and right forearm samples. The objects have a higher relative abundance of *Staphylococcus* than those of the forearms and hands.

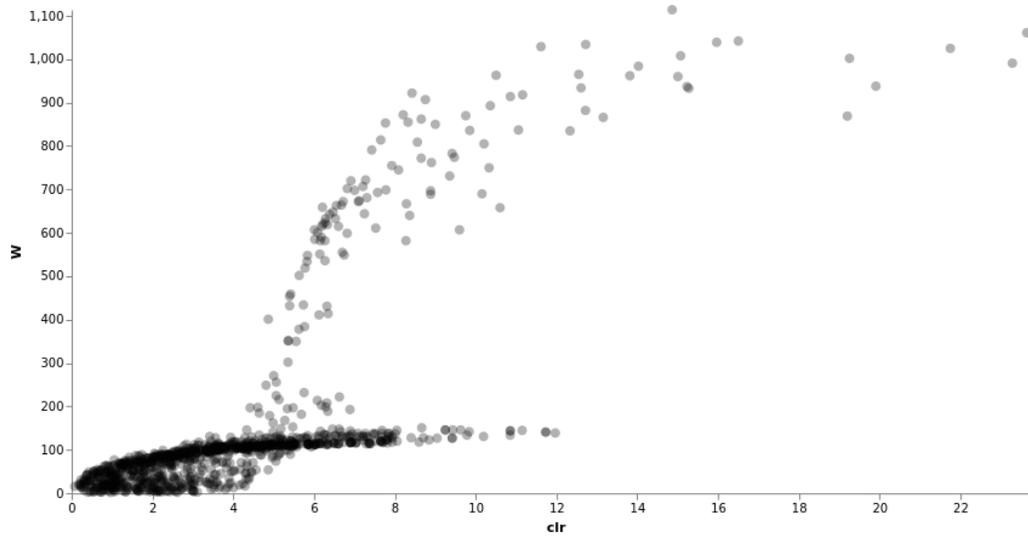


- k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Corynebacteriaceae;g_Corynebacterium
- k_Bacteria;p_Firmicutes;c_Bacilli;_ ; _
- k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus
- k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas
- k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus
- k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Neisseriales;f_Neisseriaceae;g_
- k_Bacteria;p_Cyanobacteria;c_Chloroplast;o_Streptophyta;f_ ;g_
- k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Tissierellaceae];g_Anaerococcus
- k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Neisseriales;f_Neisseriaceae;g_Neisseria
- k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter

Figure 13. Subjects and timepoints. The first number indicated is the participant ID followed by the specific timepoint in the study. The top ten bacteria are shown in the legend (full legend can be found in Appendix H). Visually examining individuals separately, changes in the relative frequency of bacteria can be seen over the course of the study.

Taxonomic Analysis: ANCOM

Analysis of composition of microbiomes (ANCOM) test assesses out differential abundance of bacteria between groups. ANCOM is a strong tool as it makes no assumptions about independence between features. However, ANCOM makes a few assumptions about the distribution of ASVs: (1) assumes that there are less than 25% species changing, and (2) there are no zeros in the data set. ANCOM's strategy is to run tests on the log ratios across ASVs instead of on the ASVs themselves. Using log ratios is ideal for detecting large relative changes and are ideal for normalizing sequence depth. Since ANCOM raises a problem for zeros, pseudo counts were introduced that added a value of 1 to all zero counts. The x-axis summarizes the effect size difference of the given features between subjects and the y-axis represents the strength W , the ANCOM test statistic. The W -value is a count of the number of sub-hypotheses that have passed for a given species (Estaki et al.). The differentially abundant features will be those ASVs with high values on both the x and y axes (points that are closer to the top right or top left corners). ANCOM determined nine features that differs across subjects. This result is significant because of its medical relevance. *Staphylococcus* was identified by ANCOM and there are approximately thirty different species which includes the opportunistic pathogen, *S. aureus*, which causes skin infections (Becker et al.).



ANCOM statistical results

	W
k_Bacteria;p_Firmicutes;c_Bacilli;o_Gemellales;f_Gemellaceae;g__	1114
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus	1114
k_Bacteria;p_Tenericutes;c_Mollicutes;o_Mycoplasmatales;f_Mycoplasmataceae;g_Mycoplasma	1061
k_Bacteria;p_Fusobacteria;c_Fusobacteriia;o_Fusobacteriales;f_Fusobacteriaceae;__	1042
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Jeotgalicoccus	1039
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Bifidobacteriales;f_Bifidobacteriaceae;g_Gardnerella	1034
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g__	1029
k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_[Weeksellaceae];g_Bergeyella	1025
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Mogibacteriaceae];__	1008

Figure 14. ANCOM L6 Volcano Results. Analysis of compositions of microbiomes; the clr (centered log ratio) transformed the ASV table at the genus level that was modified to adjust 0 values to 1 was used. The W value represents the number of times of the null hypothesis (average abundance of a given species in a group is equal to that in the other group) was rejected for a given species. The x-axis represents the clr transformed mean difference in species. ANCOM determined nine species of bacteria that was abundantly different across all subjects.

CHAPTER IV

CONCLUSIONS

The focus of this research study was to examine the skin and workplace environment's microbiome following the return to work after being away from campus for at least two weeks. The aims of this study were to investigate the interpersonal, intrapersonal, and fomite differences, and to see if individual's microbiomes became more similar as people returned to work in the same building. DNA amplification of the V4 region of the 16S rRNA gene in sixty-nine samples were sequenced on Illumina's MiSeq platform. QIIME2, a next-generation microbiome bioinformatics pipeline, was used to perform alpha and beta analyses as well as the generation of taxonomic bar plots to visualize the overall microbial composition.

Alpha diversity analysis used included Shannon's index and Faith's PD. Shannon's Index determined there were differences between sexes, with females having higher richness than males. However, Faith's PD did not find any categories significantly different. Beta diversity metrics included Bray-Curtis Dissimilarity, unweighted and weighted UniFrac distance matrices. Considering all beta diversity metrics together, it was found that over time, the intrapersonal microbial composition shifted, but the interpersonal microbiome did not become more similar to each other after returning to work in the same building. One explanation could be that individuals continued to practice social distancing at work and were not as interactive with each other. Another reason why the interpersonal shift was not observed could be due to increased

cleaning in CBH. Furthermore, this study was able to link the hand microbiome to the object's microbiome for participant ID three and six. One explanation to why this study was unable to link all hands to objects is due to insufficient data. There was not an equal number of hand samples to objects for all participants. Interestingly, an ANCOM test revealed nine features that differed across subjects, including five from phylum Firmicutes, and one each from phyla Tenericutes, Fusobacteria, Actinobacteria, and Bacteroidetes. Although, there was no definitive trend in the microbiomes of the fomites due to limited samples (n=13), generally objects had a greater abundance in *Staphylococcus* than all other sample types. This finding is of particular health relevance since *Staphylococcus* member *S. aureus* is a major cause of nosocomial infection and a frequently of concern for its antimicrobial resistance.

Although only 25% of the samples successfully amplified and were able to be carried into sequencing and analysis, this research is significant because it allows researchers to explore how hygiene practices such as handwashing and social distancing impact the skin microbiome. The information generated from this semi-quantitative study can help researchers better understand how bacterial communities shift as a result of behavioral changes. Furthermore, this research study can be a steppingstone to investigating if changes in microbial communities makes individuals more susceptible to diseases. It is imperative to continue to examine the human skin microbiome because these studies have the potential to improve our understanding of host-microbial interactions and their implications for disease transmission and health.

APPENDIX

-A-



DATE: October 29, 2020

3500 Camp Bowie Blvd Fort Worth, TX 76107
NorthTexRegIRB@unthsc.edu
(817) 735-0409

TO: Micheal Allen

FROM: North Texas Regional Institutional Review Board

PROJECT TITLE: [1632598-1] Investigating the Skin Microbiome During Times of
Self-Isolation REFERENCE #: 2020-080
SUBMISSION TYPE: New Project

ACTION: APPROVED

APPROVAL DATE: October 29,
2020

REVIEW CATEGORY: Expedited review categories # 3 & 7

Thank you for your submission of New Project materials for this project. The North Texas Regional Institutional Review Board has APPROVED your submission. This approval is based on an appropriate risk/ benefit ratio and a project design wherein the risks have been minimized. All research must be conducted in accordance with this approved submission.

This submission has received Expedited Review based on applicable federal regulations (45 CFR 46). The IRB Chair concluded that the study meets the regulatory safeguards appropriate to qualify as Expedited category research under the provisions of 45 CFR 46.110(b)(1)(i) per the

following categories:

- **(3)** Prospective collection of biological specimens for research purposes by noninvasive means
- **(7)** Research on individual or group characteristics or behavior (including, but not limited to, research on perception, cognition, motivation, identity, language, communication, cultural beliefs or practices, and social behavior) or research employing survey, interview, oral history, focus group, program evaluation, human factors evaluation, or quality assurance methodologies.

The following items have been approved with your submission:

- Protocol synopsis
- Consent Form
- Recruitment email
- Questionnaire
- Eligibility Checklist
- Documents related to sample collection including collection instructions and object list

Please remember that informed consent is a process beginning with a description of the project and insurance of participant understanding followed by a signed consent form. Informed consent must continue throughout the project via a dialogue between the researcher and research participant. Federal regulations require that each participant receives a copy of the consent document.

You may ONLY use documents that have been IRB-approved and display IRB approval verification (print-stamping).

Please note that any revision to previously approved materials must be approved by the IRB prior to initiation. Please use the appropriate revision procedures for this activity.

This project has been determined to be a MINIMAL RISK project. Based on the Revised Common Rule (2018 Requirements), no annual review of this project is required. However, please seek review and approval of ANY changes, even if minor including changes in research personnel, made to the protocol prior to implementation, and notify the IRB when the study has been completed.

All UNANTICIPATED PROBLEMS involving risks to subjects or others (UPIRSOs) and SERIOUS and UNEXPECTED adverse events must be reported promptly to this office. Please use the appropriate reporting forms for this procedure. All FDA and sponsor reporting requirements should also be followed.

All NON-COMPLIANCE issues or COMPLAINTS regarding this project must be reported promptly to this office within 10 business days of identifying the issue / complaint.

In addition, the Principal Investigator must notify the IRB immediately if any new potential Conflict of Interest arises.

Any research / key personnel involved in the study are also responsible for maintaining appropriate humansubject protection educational training current.

If you have any questions, please contact Jessica Bird at 817-735-2081 or jessica.bird@unthsc.edu. Please include your project title and reference number in all correspondence with this committee.

This letter has been electronically signed in accordance with all applicable regulations, and a copy is retained within North Texas Regional Institutional Review Board's records.

-B-

Please read these instructions carefully before collecting your sample. When swabbing your dominant hand, forearm, and workplace object, you will use a different swab, sterile water tube, and transport tube. You must wait until Ophelia has contacted you informing you to begin your baseline collection before you collect ANY specimens.

1. Partially peel open the swab package as shown in diagram 1. Remove the swab. Do not touch the soft tip or lay the swab down. If the soft tip is touched, the swab is laid down, or the swab is dropped, request a new swab.
2. Hold the swab in your non-dominant hand as shown in diagram 2. Placing your thumb & forefinger in the middle of the swab shaft covering the score line. Do not hold the swab shaft below the score line.
3. While holding the swab in the same hand, unscrew the cap from your sterile water as shown in diagram 4. NOTE: this is no diagram 3 shown here.
4. Carefully insert the swab into the tube of sterile water. Do not spill the contents of the tube. If the tube contents are spilled, discard and request a new tube contain sterile water. Do not use any other water besides sterile water. Your swab must be wet prior to collecting your specimens.
5. To collect your sample from your dominant hand, start swabbing from the middle bottom of your palm, slowly rotating the swab as you move up (vertically) from the palm (i.e. further away from your wrist). Stop once you've reached the base of your ring finger. Lift your swab. Place your swab on the base of your index finger and move the swab (while rotating the swab) horizontally across your index finger, middle finger, ring finger, and pinky.
6. After swabbing your dominant hand, immediately place the swab into the transport tube so that the score line is at the top of the tube as shown in diagram 5.
7. Carefully break the swab shaft at the score line against the side of the tube as shown in diagram 6.
8. Immediately discard the top portion of the swab shaft as shown in diagram 7.

9. Tightly screw the cap onto the tube as shown in diagram 8. Using a permanent marker please write on the tube your assigned number for the study, and RH or LF to indicate right hand or left hand and the date.
10. Repeat steps 1-4 to begin swabbing your forearm.
11. After completing step 4, extend your forearm of your dominant hand (i.e. if you're righthanded, extend the forearm of your right arm).
12. Place the swab on the middle of the crevasse of your elbow, begin moving the swab downwards towards your wrist making sure to slowly rotate the swab until you reach the middle of your wrist.
13. Repeat steps 6-9.
14. In order to swab an object from either your laboratory or office space, please pick one object from the list provided to you. This object is to be used throughout the duration of the study. If your object breaks, needs repair, or is no longer usable, inform the research staff. You will then be allowed to pick another item from the same space (i.e. if you chose an object from your lab, you must choose another item from your lab).
15. Repeat steps 1-4.
16. To collect your surface swab, use any 4 in x 4 in area on your object. To ensure that a representative sample is collected, please use the guidelines illustrated in figure 1

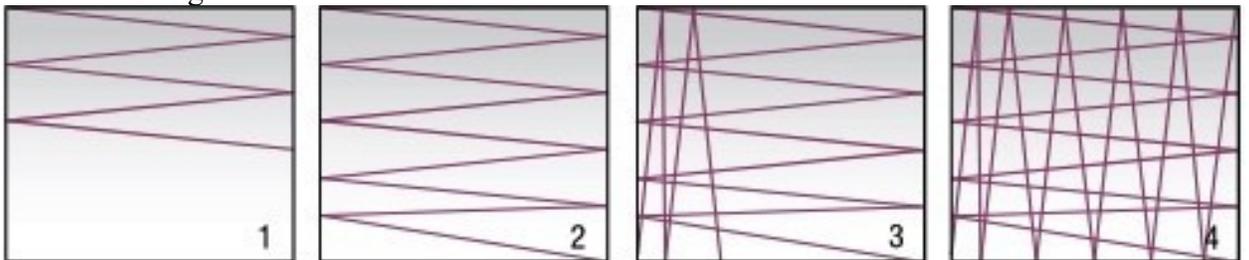
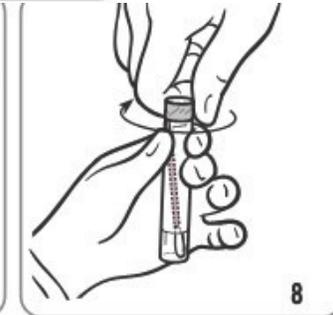
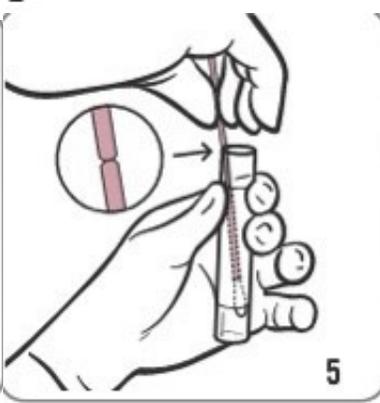
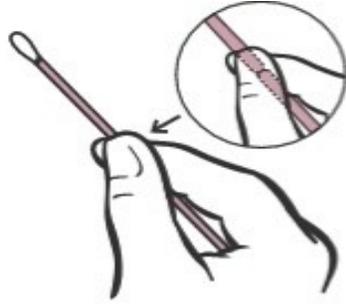
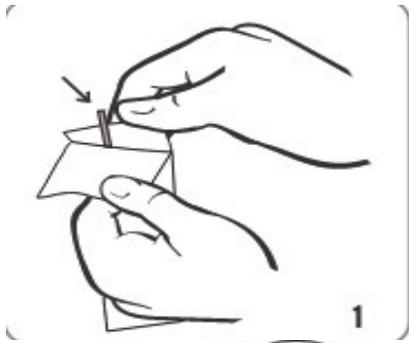


Figure 1.

17. Once you have collected your sample from your object repeat steps 6-9.
18. After all samples have been collected please contact Ophelia (by text or email) to arrange a time for specimen drop off to the bin posted in front of the Allen lab (CBH 303). You must return your samples the same day you collected them with the exception of your baseline (t=0).



INSTRUCTIONS: From this list, please select one object you will be swabbing from either your office or laboratory for the duration of the study. Do not change the object you will be swabbing. If the object of choice happens to break or no longer is usable, inform the researchers. You will swab this object at the same frequency you are swabbing your hand and forearm (daily for week 1, weekly for weeks 2-6, and every other week for weeks 7-12). Place your swab in a separate tube from your hand and forearm tubes. Label it as either office or laboratory/object name (EX: office/keyboard). Once you have collected your samples from your office/laboratory, hand, and forearm on the specified frequencies, make an appointment with Ophelia at opheliakhichi@my.unthsc.edu for specimen drop-off.

- Keyboard
- Doorknob/handle on the inside of office or lab
- Light switch
- Portion of a desk
- Computer mouse/trackpad
- Computer monitor
- Desk calendar
- Filing cabinet
- Arm of a chair
- Printer
- Office phones
- Pen
- Balance/scale
- Microscopes
- Pipettes
- Test tube racks
- Permanent markers
- Rulers
- Laboratory coats
- Centrifuge
- Hot plates
- Floor of your office or laboratory
- Glass wear- flasks, cylinders
- Timers
- Vortexers

- Pumps
- Incubators
- pH meters
- Sequencing instruments

INSTRUCTIONS: Use this document throughout the course of the study. Please fill out this questionnaire by **bolding** and/or typing your response. If you're ambidextrous, bold ambidextrous as well as either left or right to indicate which hand you will be using for this study. Use the same hand throughout the study. Please note that phase I reopening is defined as on or after June 15, 2020 through July 05, 2020. Phase II reopening is defined as on or after July 06, 2020. Do not include your name on this document. At the end of the study, you may drop off the document to Dr. Allen's office (CBH 363) or email opheliakhichi@my.unthsc.edu

What is your sample ID?	
Are you male or female?	Male Female
Which age range do you fall into	18-25 25-32 33-40 41-48 49-56 57-63 64-71 72-79 80-90
When was the first day you returned back to campus since the lockdown/stay-at-home orders? Please indicate whether you were able to return to campus during phase 1 or phase 2 and include the first day you returned to campus.	I reopening: mm/dd/yr Or Phase II reopening: mm/dd/yr
Are you left-handed, right-handed or ambidextrous?	Left Right Ambidextrous
How long has it been since you washed your hands or used hand-sanitizer? Please indicate your answers below starting from day 0.	Less than 1 hour ago 2-4 hours ago 5+ hours ago
Will you be swabbing an object from your laboratory or office space?	Laboratory Office space
What floor of CBH is your laboratory or office space located on?	2 nd 3 rd 4 th 5 th

Please indicate below (after the colon symbol) how long has it been since you washed your hands or used hand-sanitizer from the following options: Less than 1 hour ago, 2-4 hours ago or 5+ hours ago. Please type your answer in the space provided.

Day 0: Day 1: Day 3:
 Day 5: Day 7: Day 14:
 Day 21: Day 28:

Parties

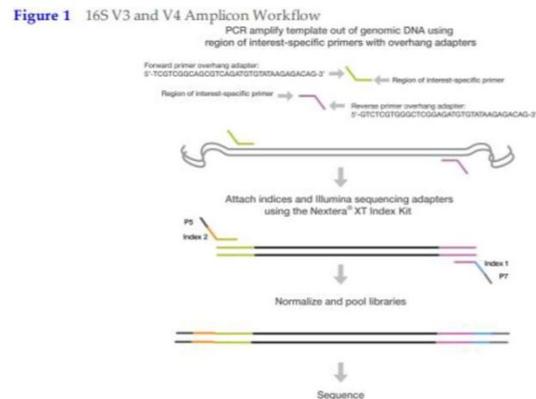
<p>Illumina</p>	<p>Illumina, Inc. 5200 Illumina Way, San Diego, CA 92122, US</p>
<p>Requestor</p>	<p>Ophelia Khichi MS Candidate Department of Microbiology, Immunology, & Genetics UNT Health Science Center 3500 Camp Bowie Blvd, Fort Worth, TX 76107</p>

Start Date & Term

<p>Start Date</p>	<p>5/04/21</p>
<p>Term</p>	<p>N/A</p>

Permitted Content

Requestor wants to use the images below from the 16S Metagenomic Sequencing Library Preparation protocol:



User-defined forward and reverse primers that are complementary upstream and downstream of the region of interest are designed with overhang adapters, and used to amplify templates from genomic DNA. A subsequent limited-cycle amplification step is performed to add multiplexing indices and Illumina sequencing adapters. Libraries are normalized and pooled, and sequenced on the MiSeq system using v3 reagents.

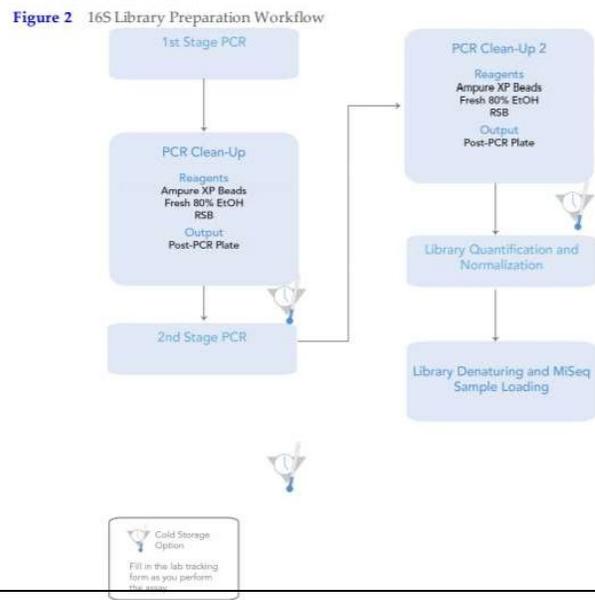
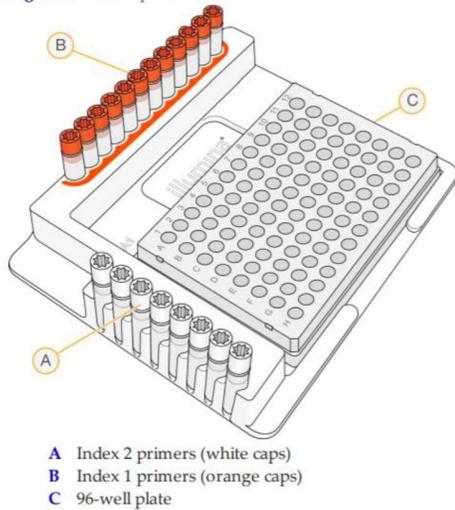


Figure 4 TruSeq Index Plate Fixture



- A Index 2 primers (white caps)
- B Index 1 primers (orange caps)
- C 96-well plate

Permitted Territory/ Use

Requestor wants to use the Illumina images in her thesis titled: Examining the Skin and Workplace Microbiome Following the Return to the University of North Texas Health Science Center After Self-Isolation.

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Relationship Managers

Illumina	none
Requestor	Khichi, Ophelia < OpheliaKhichi@my.unthsc.edu >

The parties each agree to be bound by this Agreement which shall come into effect on the date of the last signature below

Illumina, Inc. Signed: *R. Schwillinski*
 Name: Roland Schwillinski Title: VP
 Global IP & Litigation Date: May 7,
 2021

Ophelia Khichi,
 Signed: 
 Date: 05/07/2021

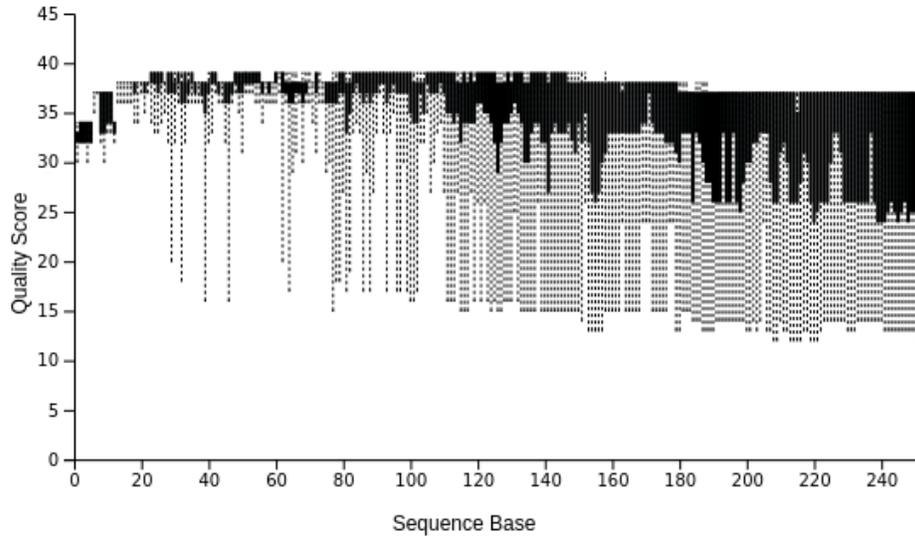
**REVIEWED BY
ILLUMINA LEGAL**

**Nichola
Jamotillo**

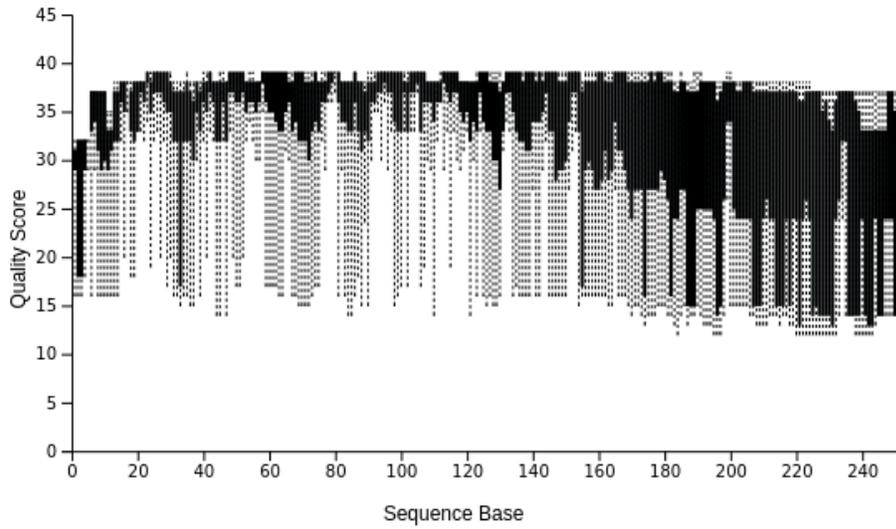
Digitally signed by Nichola Jamotillo
 DN: cn=Nichola Jamotillo, o=illumina,
 ou=Legal,
 email=njamotillo@illumina.com, c=US
 Date: 2021.05.04 15:13:45 -07'00'

-F-

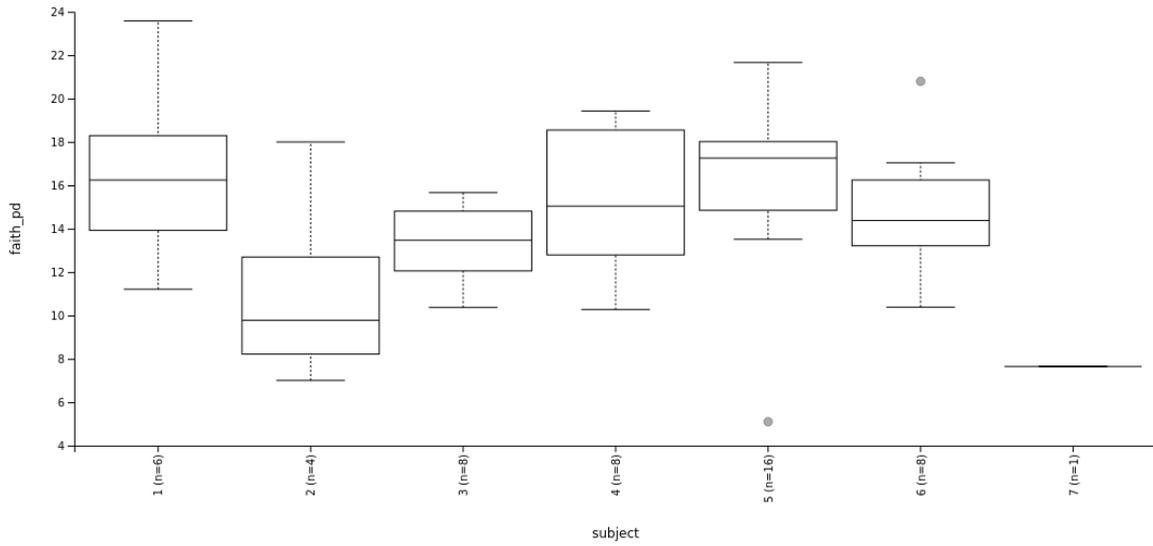
Forward Reads



Reverse Reads



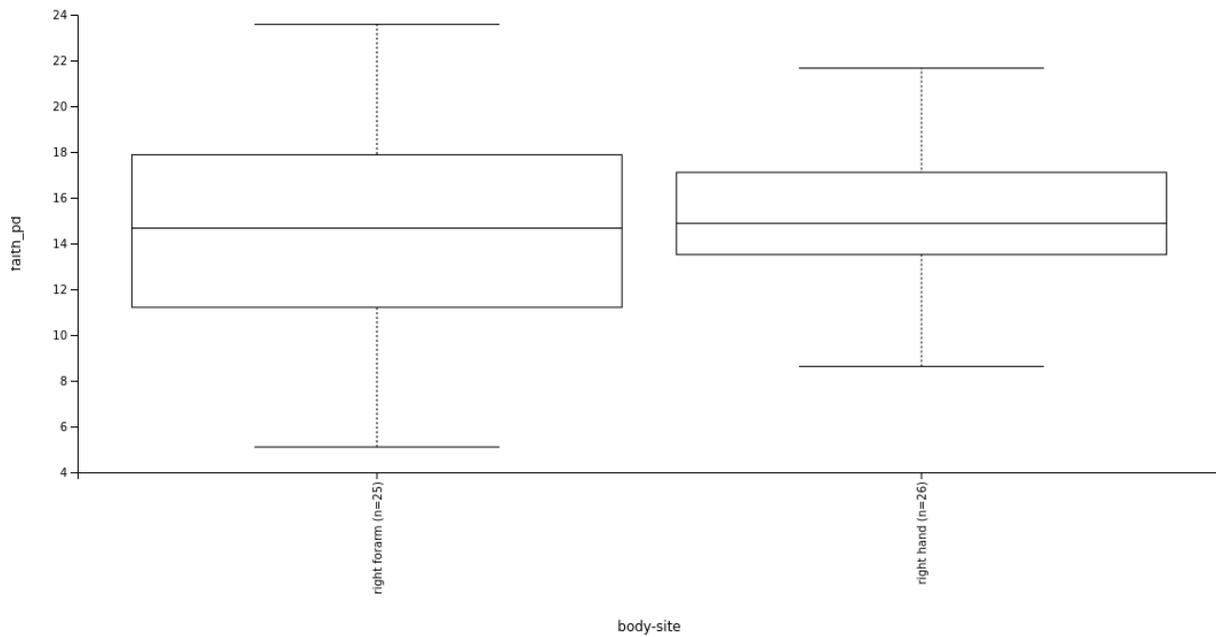
-G-



Kruskal-Wallis (all groups)

Result

H	10.930052790346934
p-value	0.09056244164832113



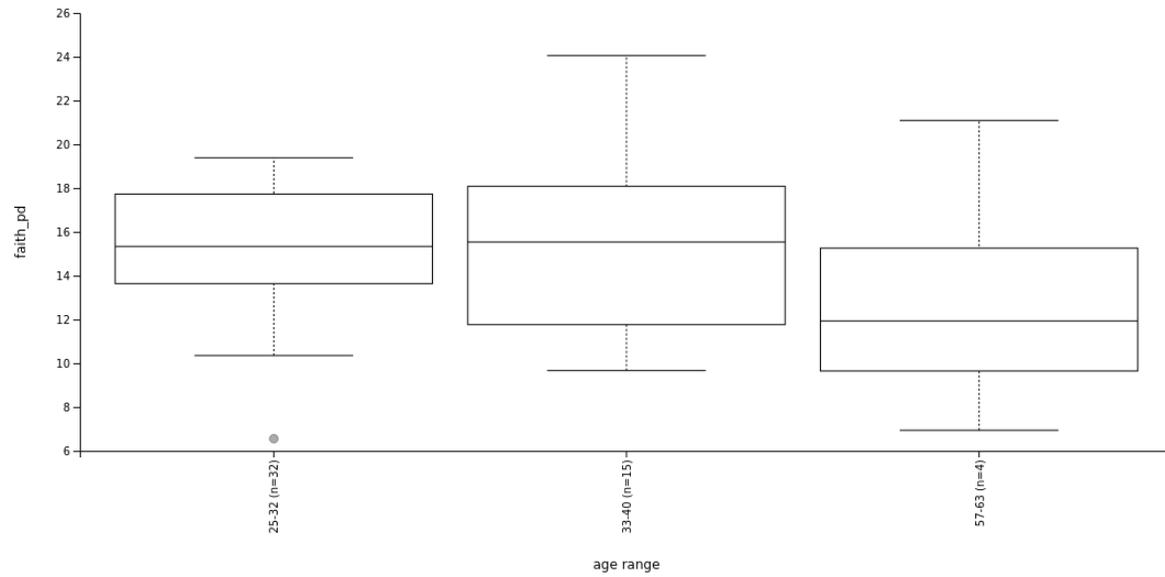
Result

H

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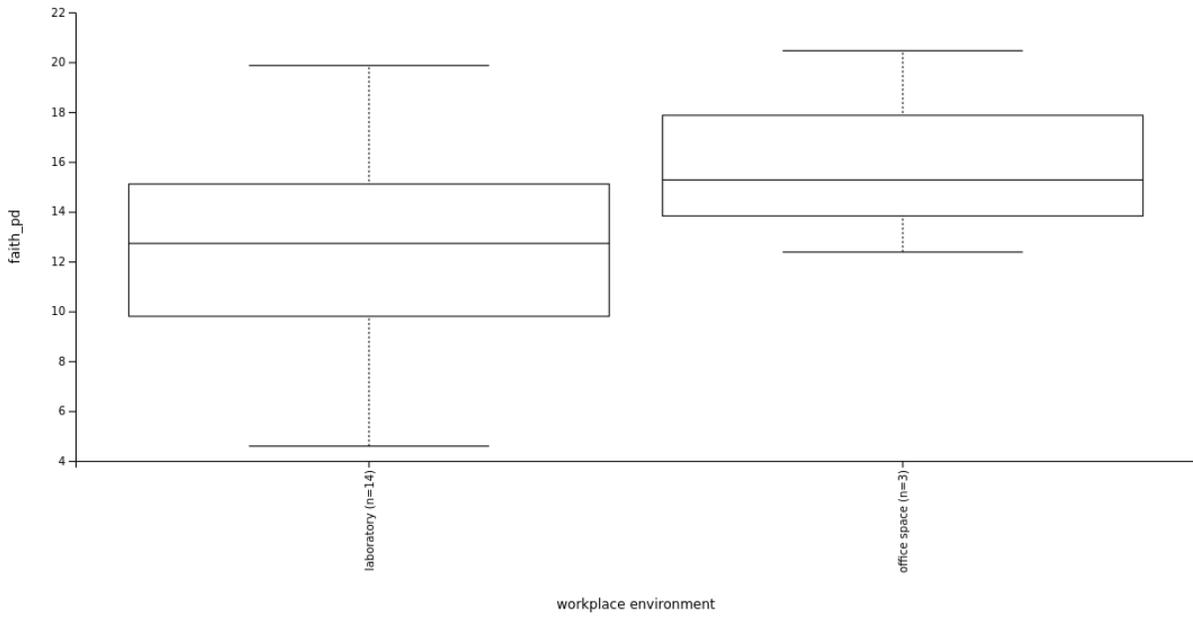
p-value

0.7630518071602646



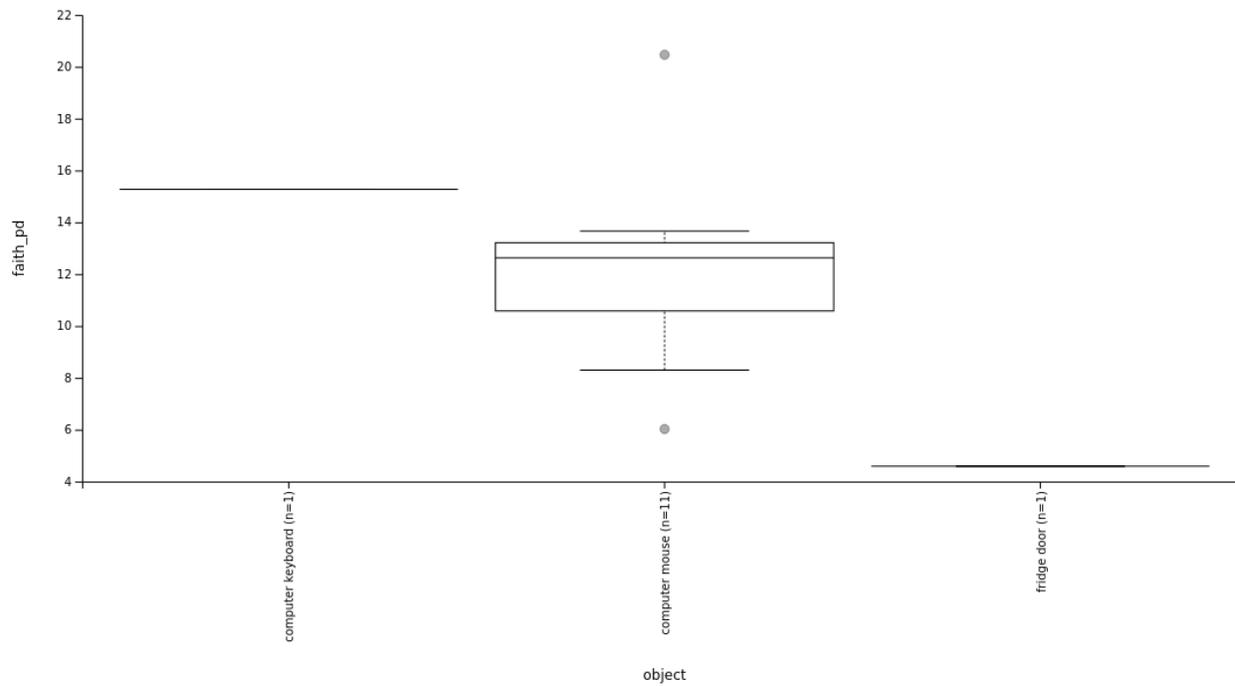
Kruskal-Wallis (all groups)

	Result
H	1.2689950980392268
p-value	0.5302018218273787



Kruskal-Wallis (all groups)

	Result
H	1.0158730158730194
p-value	0.31349994558358435



Kruskal-Wallis (all groups)

	Result
H	4.027972027972034
p-value	0.13345565695137443

-H-

k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Corynebacteriaceae;g_Corynebacterium
 k_Bacteria;p_Firmicutes;c_Bacilli;_:_;
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas
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 k_Bacteria;p_Cyanobacteria;c_Chloroplast;o_Streptophyta;f_:_g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Tissierellaceae];g_Anaerococcus
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Neisseriales;f_Neisseriaceae;g_Neisseria
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococcaceae;g_Rothia
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Propionibacteriaceae;g_Propionibacterium
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Shigella
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g_Prevotella
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;_
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 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Veillonella
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;_:_;
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Gemellales;f_Gemellaceae;_
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 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pasteurellales;f_Pasteurellaceae;g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Enhydrobacter
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 k_Bacteria;p_Firmicutes;c_Bacilli;o_Gemellales;f_Gemellaceae;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus
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 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_Roseomonas
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;_:_;
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Lactococcus
 k_Bacteria;p_Bacteroidetes;c_Flavobacteria;o_Flavobacteriales;f_Flavobacteriaceae;g_Capnocytophaga
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Aerococcaceae;g_Abiotrophia
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococcaceae;g_Kocuria
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pasteurellales;f_Pasteurellaceae;_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Lautropia

k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Neisseriales;f_Neisseriaceae;_
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Massilia
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Dialister
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiales;f_mitochondria;g_Raphanus
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas
 k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_Flavobacteriaceae;_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Faecalibacterium
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Roseburia
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Tissierellaceae];g_WAL_1855D
 k_Bacteria;p_Proteobacteria;c_Epsilonproteobacteria;o_Campylobacteriales;f_Campylobacteraceae;g_Campylobacter
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Selenomonas
 k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_[Weeksellaceae];g_
 k_Bacteria;p_Spirochaetes;c_Spirochaetes;o_Spirochaetales;f_Spirochaetaceae;g_Treponema
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Leuconostocaceae;g_Leuconostoc
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Aerococcaceae;g_Facklamia
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Macrococcus
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Dermacoccaceae;g_Dermacoccus
 k_Bacteria;p_Fusobacteria;c_Fusobacteriia;o_Fusobacteriales;f_Fusobacteriaceae;g_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Psychrobacter
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_Hymenobacter
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylobacteriaceae;g_Methylobacterium
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Tissierellaceae];g_1-68
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae;g_Photobacterium
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_Aeromonas
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales; ;_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales; ;_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Blautia
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Stenotrophomonas
 k_Bacteria;p_[Thermi];c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_Deinococcus
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria; ; ;_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Tissierellaceae];g_Parvimonas
 k_Bacteria;p_TM7;c_TM7-3;o_f ;g_
 k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_[Weeksellaceae];g_Wautersiella
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Ruminococcus
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Jonesiaceae;g_Jonesia
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Clostridium
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f ;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae;g_Peptostreptococcus
 k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_Flavobacteriaceae;g_Flavobacterium
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Mogibacteriaceae];g_
 k_Bacteria;p_Fusobacteria;c_Fusobacteriia;o_Fusobacteriales;f_Fusobacteriaceae;_

k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Bacillus
 k_Bacteria;p_SR1;c_o_f_g_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Lampropedia
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Tissierellaceae];g_Gallicola
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Rhizobium
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Lysobacter
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardioidaceae;g_Nocardioides
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Agrobacterium
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Cardiobacteriales;f_Cardiobacteriaceae;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Geodermatophilaceae;g_Blastococcus
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Jeotgalicoccus
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococcaceae;g_Arthrobacter
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Mycobacteriaceae;g_Mycobacterium
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacteriales;f_Caulobacteraceae;g_Brevundimonas
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Intrasporangiaceae;_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardiaceae;g_Rhodococcus
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Pseudonocardiaceae;g_Actinomycetospora
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae;g_Clostridium
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Bifidobacteriales;f_Bifidobacteriaceae;g_Bifidobacterium
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Dermabacteraceae;g_Brachybacterium
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Cardiobacteriales;f_Cardiobacteriaceae;g_Cardiobacterium
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Varibaculum
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Enterococcus
 k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Bulleidia
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Mogibacteriaceae];g_Mogibacterium
 k_Bacteria;p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Atopobium
 k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_[Weeksellaceae];g_Bergeyella
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;_:_;
 k_Bacteria;p_Acidobacteria;c_[Chloracidobacteria];o_RB41;f_Ellin6075;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;_:_;
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pasteurellales;f_Pasteurellaceae;g_Aggregatibacter
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae;g_
 k_Bacteria;p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Oribacterium
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Moryella
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Lachnoanaerobaculum
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Aerococcaceae;_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Coproccoccus
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyrimonadaceae;g_Tannerella
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Tissierellaceae];g_ph2
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Dermabacteraceae;g_Dermabacter
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Neisseriales;f_Neisseriaceae;g_Kingella
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae;g_Filifactor

k_Bacteria;p_Bacteroidetes;c_Sphingobacteriia;o_Sphingobacteriales;f_Sphingobacteriaceae;g_Mucilagibacter
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Variovorax
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pasteurellales;f_Pasteurellaceae;g_Actinobacillus
 k_Bacteria;p_GN02;c_BD1-5;o_ ;f_ ;g_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Aerococcaceae;g_Marinilactibacillus
 k_Bacteria;p_Bacteroidetes;c_Sphingobacteriia;o_Sphingobacteriales;f_Sphingobacteriaceae;g_Sphingobacterium
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales; ;_
 k_Bacteria;p_Actinobacteria;c_Thermoleophila;o_Solirubrobacterales;f_ ;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Acidaminobacteraceae];g_Fusibacter
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylobacteriaceae;_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Kineosporiaceae;g_Kineococcus
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Gordoniaceae;g_Gordonia
 k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_[Weeksellaceae];g_Cloacibacterium
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Megasphaera
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Bifidobacteriales;f_Bifidobacteriaceae;g_Gardnerella
 k_Bacteria;p_Bacteroidetes;c_[Saprosirae];o_[Saprosirales];f_Chitinophagaceae;_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_[Ruminococcus]
 k_Bacteria;p_Tenericutes;c_Mollicutes;o_Mycoplasmatales;f_Mycoplasmataceae;g_Mycoplasma
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pasteurellales;f_Pasteurellaceae;g_Pasteurella
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Mogibacteriaceae];_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Peptococcus
 k_Bacteria;p_Actinobacteria;c_Thermoleophila;o_Gaiellales;f_Gaiellaceae;g_
 k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_Ardenscatenales;f_Ardenscatenaceae;g_Ardenscatena
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Buchnera
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_ ;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Aurantimonadaceae;g_Aurantimonas
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Turicibacterales;f_Turicibacteraceae;g_Turicibacter
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Tissierellaceae];g_Helcococcus
 k_Bacteria;p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Olsenella
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;_
 k_Bacteria;p_Fusobacteria;c_Fusobacteriia;o_Fusobacteriales;f_Leptotrichiaceae;g_
 k_Archaea;p_Crenarchaeota;c_Thaumarchaeota;o_Nitrososphaerales;f_Nitrososphaeraceae;g_Candidatus Nitrososphaera
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Dorea
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Tepidimonas
 k_Bacteria;p_Acidobacteria;c_Acidobacteria-6;o_iii1-15;f_ ;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiales;f_mitochondria;g_Phytophthora
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_Spirosoma
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Catonella
 k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_[Weeksellaceae];_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Geodermatophilaceae;_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae;g_Proteocatella
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;_
 k_Bacteria;p_Synergistetes;c_Synergistia;o_Synergistales;f_Dethiosulfovibrionaceae;g_TG5
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria; ; ;_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Rubellimicrobium

k_Bacteria;p_Actinobacteria;c_Rubrobacteria;o_Rubrobacterales;f_Rubrobacteraceae;g_Rubrobacter
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Skermanella
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_Dyadobacter
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradyrhizobiaceae;g_Balneimonas
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Xanthomonas
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Pseudonocardiaceae;g_Pseudonocardia
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Pseudoclavibacter
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Gemellales;f_Gemellaceae;g_Gemella
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_
 k_Bacteria;p_Bacteroidetes;c_[Saprospirae];o_[Saprospirales];f_Chitinophagaceae;g_Flavisolibacter
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_Shewanellaceae;g_Shewanella
 k_Bacteria;p_Actinobacteria;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Planococcaceae;_
 k_Bacteria;p_Acidobacteria;c_Acidobacteria-6;o_f_;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Geodermatophilaceae;g_Actinotelluria
 k_Bacteria;p_Bacteroidetes;c_[Saprospirae];o_[Saprospirales];f_Chitinophagaceae;g_
 k_Bacteria;p_Bacteroidetes;c_Sphingobacteria;o_Sphingobacteriales;f_Sphingobacteriaceae;g_Pedobacter
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Megamonas
 k_Bacteria;p_Chlorobi;c_OPB56;o_f_;g_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Alicyclobacillaceae;g_Alicyclobacillus
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Neisseriales;f_Neisseriaceae;g_Eikenella
 k_Bacteria;p_Chloroflexi;c_Ellin6529;o_f_;g_
 k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Holdemania
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Dermatophilaceae;_
 k_Bacteria;p_Bacteroidetes; ; ; ;_
 k_Bacteria;p_Proteobacteria;c_Epsilonproteobacteria;o_Campylobacterales;f_Helicobacteraceae;g_Wolinella
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfomicrobiaceae;g_Desulfomicrobium
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Gemmiger
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Brucellaceae;_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Paenibacillaceae;g_Paenibacillus
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Aerococcaceae;g_Aerococcus
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococcaceae;_
 k_Bacteria;p_TM7;c_TM7-3;o_CW040;f_;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Tissierellaceae];g_GW-34
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Alkanindiges
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Ruminococcus
 k_Bacteria;p_Proteobacteria; ; ; ;_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Acidovorax
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylobacteriaceae;g_
 k_Bacteria;p_[Thermi];c_Deinococci;o_Deinococcales;f_Trueperaceae;g_Truepera
 k_Bacteria;p_Proteobacteria;c_Epsilonproteobacteria;o_Campylobacterales;f_Helicobacteraceae;g_Helicobacter
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Sporichthyaceae;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardiodaceae;g_Aeromicrobium
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales; ; ;_
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacterales;f_Syntrophobacteraceae;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Williamsiaceae;g_Williamsia
 k_Bacteria;p_Chloroflexi;c_Thermomicrobia;o_JG30-KF-CM45;f_;g_

k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae;_
 k_Bacteria;p_Actinobacteria;c_Nitriliruptoria;o_Euzebyales;f_Euzebyaceae;g_Euzebya
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Paenibacillaceae;_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_[Chromatiaceae];g_Rheinheimera
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_Larkinella
 k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Tatumella
 k_Bacteria;p_Actinobacteria;c_Acidimicrobiia;o_Acidimicrobiales;f_;g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Sinobacteraceae;g_
 k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_[Eubacterium]
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Kaistobacter
 k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Catenibacterium
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Devosia
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Salinarimonas
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Mobiluncus
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Dietziaceae;g_Dietzia
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Streptomycetaceae;g_Streptomyces
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;_
 k_Bacteria;p_Acidobacteria;c_Acidobacteria-6;o_iii1-15;f_mb2424;g_
 k_Bacteria;p_Cyanobacteria;c_Oscillatoriohyphycideae;o_Chroococcales;f_Xenococcaceae;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradyrhizobiaceae;_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Brucellaceae;g_Ochrobactrum
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_[Exiguobacteraceae];g_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Oligella
 k_Bacteria;p_Cyanobacteria;_:_;_
 k_Bacteria;p_Acidobacteria;c_[Chloracidobacteria];o_RB41;f_;g_
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_Adhaeribacter
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Burkholderia
 k_Bacteria;p_Gemmatimonadetes;c_Gemm-3;o_;f_;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micromonosporaceae;_
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Spirobacillales;f_;g_
 k_Bacteria;p_Planctomycetes;c_Phycisphaerae;o_WD2101;f_;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Cellulomonadaceae;g_Cellulomonas
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Pediococcus
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Bifidobacteriales;f_Bifidobacteriaceae;g_Scardovia
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_;g_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Leuconostocaceae;g_Weissella
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_
 Unassigned;_:_;_:_;_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;_
 k_Bacteria;p_Actinobacteria;c_Thermoleophilia;o_Solirubrobacterales;f_Patulibacteraceae;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Acidaminobacteraceae];g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Nitrobacteria
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Xanthobacter

k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_[Paraprevotellaceae];g_
 k_Bacteria;p_Gemmatimonadetes;c_Gemmatimonadetes;o_Gemmatimonadales;f_;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bartonellaceae;g_
 k_Bacteria;p_Acidobacteria;c_Solibacteres;o_Solibacterales;f_;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Pseudonocardiaceae;_
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_[Paraprevotellaceae];_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Erythrobacteraceae;_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Lachnospira
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Oceanicella
 k_Bacteria;p_Cyanobacteria;c_Synechococcophycideae;o_Pseudanabaenales;f_Pseudanabaenaceae;g_Leptolyngbya
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardiodaceae;g_Marmoricola
 k_Bacteria;p_Bacteroidetes;c_[Saprospirae];o_[Saprospirales];f_Chitinophagaceae;g_Trachelomonas
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Geodermatophilaceae;g_Geodermatophilus
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Dietziaceae;g_
 k_Bacteria;p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;_
 k_Bacteria;p_Bacteroidetes;c_Sphingobacteriia;o_Sphingobacteriales;f_Sphingobacteriaceae;_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Streptomycetaceae;_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Intrasporangiaceae;g_Knoellia
 k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_p-75-a5
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingobium
 k_Bacteria;p_Actinobacteria;c_Thermoleophila;o_Solirubrobacterales;_;_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Haematobacter
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococcaceae;g_Nesterenkonia
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Schwartzia
 k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Gemmataceae;g_
 k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Isosphaeraceae;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Kineosporiaceae;g_Kineosporia
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Cystobacterineae;g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Sinobacteraceae;g_Steroidobacter
 k_Bacteria;p_Proteobacteria;c_Epsilonproteobacteria;o_Campylobacteriales;f_Campylobacteraceae;g_Arcobacter
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_SC-I-84;f_;g_
 k_Bacteria;p_Actinobacteria;c_Thermoleophila;o_Solirubrobacterales;f_Solirubrobacteraceae;_
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Bdellovibrionales;f_Bacteriovoracaceae;g_Peredibacter
 k_Bacteria;p_Synergistetes;c_Synergistia;o_Synergistales;f_Dethiosulfovibrionaceae;g_Jonquetella
 k_Bacteria;p_Bacteroidetes;c_Sphingobacteriia;o_Sphingobacteriales;f_Sphingobacteriaceae;g_Olivibacter
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes
 k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Gemmataceae;g_Gemmata
 k_Bacteria;p_Cyanobacteria;c_Oscillatoriothycideae;o_Chroococcales;f_Xenococcaceae;g_Chroococciopsis
 k_Bacteria;p_Cyanobacteria;c_Chloroplast;o_Stramenopiles;f_;g_
 k_Bacteria;p_Actinobacteria;c_Thermoleophila;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Solirubrobacter
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;_;_
 k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Pirellulales;f_Pirellulaceae;g_
 k_Bacteria;p_Bacteroidetes;c_Sphingobacteriia;o_Sphingobacteriales;f_Sphingobacteriaceae;g_Cytophagales
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_

k_Bacteria;p_Verrucomicrobia;c_[Spartobacteria];o_[Chthoniobacteriales];f_[Chthoniobacteraceae];g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Phascalartobacterium
 k_Bacteria;p_Chloroflexi;c_Gitt-GS-136;o_f_g_
 k_Bacteria;p_Acidobacteria;c_Acidobacteria-6;_:_;_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Clostridium
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Enterobacter
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococcaceae;g_Microbispora
 k_Bacteria;p_Cyanobacteria;c_Chloroplast;o_Chlorophyta;f_Trebouxiophyceae;g_Chloroidium
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;_
 k_Bacteria;p_Bacteroidetes;c_[Saprosirae];o_[Saprosirales];f_Chitinophagaceae;g_Segetibacter
 k_Bacteria;p_FBP;c_o_f_g_
 k_Bacteria;p_Firmicutes;_:_;_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micromonosporaceae;g_Actinoplanes
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Rhodoplanes
 k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Clostridium
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Pseudorhodofera
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;_
 k_Bacteria;p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_
 k_Bacteria;p_Actinobacteria;c_MB-A2-108;o_0319-7L14;f_g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Intrasporangiaceae;g_Kytococcus
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Kineosporiaceae;_
 k_Bacteria;p_Tenericutes;c_Mollicutes;o_Mycoplasmatales;f_Mycoplasmataceae;g_Ureaplasma
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyrimonadaceae;g_Parabacteroides
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacteriales;f_Caulobacteraceae;g_Caulobacter
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Methylibium
 k_Bacteria;p_Armatimonadetes;c_[Fimbrilimonadia];o_[Fimbrilimonadales];f_[Fimbrilimonadaceae];g_Fimbrilimonas
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_[Chromatiaceae];g_Alishewanella
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Mogibacteriaceae];g_Anaerovorax
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;_
 k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Allobaculum
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_Alteromonadaceae;g_Cellvibrio
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Beutenbergiaceae;g_Salana
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae;g_[Clostridium]
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Hydrogenophaga
 k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_[Weeksellaceae];g_Riemerella
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Ancylobacter
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardiodaceae;_
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_MIZ46;f_g_
 k_Bacteria;p_Cyanobacteria;c_Nostocophycideae;o_Stigonematales;f_Rivulariaceae;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinobaculum
 k_Bacteria;p_Gemmatimonadetes;c_Gemmatimonadetes;o_f_g_
 k_Bacteria;p_Verrucomicrobia;c_Verruco-5;o_WCHB1-41;f_RFP12;g_
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Cystobacteraceae;_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Arcanobacterium
 k_Bacteria;p_Acidobacteria;c_Sva0725;o_Sva0725;f_g_
 k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Planctomycetales;f_Planctomycetaceae;g_Planctomyces
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_Bilophila

k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_Blattabacteriaceae;g_Blattabacterium
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylocystaceae;g_Methylopila
 k_Bacteria;p_Fusobacteria;c_Fusobacteriia;o_Fusobacteriales;f_Leptotrichiaceae;g_Streptobacillus
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Flammeovirgaceae;_
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_Rhodocytophaga
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Azospirillum
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_SMB53
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Robinsoniella
 k_Bacteria;p_Cyanobacteria;c_Chloroplast;o_Chlorophyta;f_g_
 k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Verrucomicrobiaceae;g_Luteolibacter
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Kineosporiaceae;g_Quadrisphaera
 k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Isosphaeraceae;_
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales; ;_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Intrasporangiaceae;g_Serinicoccus
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Sutterella
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Shuttleworthia
 k_Bacteria;p_Actinobacteria;c_Thermoleophilla;o_Solirubrobacterales;f_Patulibacteraceae;g_Patulibacter
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_Desulfovibrio
 k_Bacteria;p_Actinobacteria;c_Acidimicrobiia;o_Acidimicrobiales; ;_
 k_Bacteria;p_Nitrospirae;c_Nitrospira;o_Nitrospirales;f_Nitrospiraceae;g_Nitrospira
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Bdellovibrionales;f_Bdellovibrionaceae;g_Bdellovibrio
 k_Bacteria;p_Chloroflexi;c_Chloroflexi;o_AKIW781;f_g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Pseudonocardiaceae;g_Saccharopolyspora
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Paenibacillaceae;g_Brevibacillus
 k_Bacteria;p_Verrucomicrobia;c_[Spartobacteria];o_[Chthoniobacterales];f_[Chthoniobacteraceae];g_Ellin506
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Butyricoccus
 k_Bacteria;p_Cyanobacteria;c_Chloroplast; ; ;_
 k_Bacteria;p_Proteobacteria;c_Zetaproteobacteria;o_Mariprofundales;f_Mariprofundaceae;g_
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Haliangiaceae;g_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Comamonas
 k_Bacteria;p_Actinobacteria;c_Thermoleophilla;o_Gaiellales;f_Gaiellaceae;g_Gaiella
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Kineosporiaceae;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradyrhizobiaceae;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Phyllobacteriaceae;_
 k_Bacteria;p_Gemmatimonadetes;c_Gemm-1;o_f_g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Coxiellaceae;g_Rickettsiella
 k_Bacteria;p_Verrucomicrobia;c_[Spartobacteria];o_[Chthoniobacterales];f_[Chthoniobacteraceae];g_DA101
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Tissierellaceae;g_
 k_Bacteria;p_Acidobacteria;c_Acidobacteria-6;o_iii1-15;f_RB40;g_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;g_Petrobacter
 k_Bacteria;p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Slackia
 k_Bacteria;p_Cyanobacteria;c_Oscillatoriothycideae;o_Chroococcales;f_Xenococcaceae;_
 k_Bacteria;p_Bacteroidetes;c_Sphingobacteriia;o_Sphingobacteriales;f_g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Thiotrichales;f_Piscirickettsiaceae;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Beijerinckia
 k_Bacteria;p_Verrucomicrobia;c_Opitutae;o_Opitutales;f_Opitutaceae;g_Opitutus
 k_Bacteria;p_Acidobacteria;c_Acidobacteriia;o_Acidobacteriales;f_Acidobacteriaceae;g_Granulicella

k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Polyangiaceae;_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Thermicanaceae;g_Thermicanus
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Microbacterium
 k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_Flavobacteriaceae;g_Aquimarina
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Paenibacillaceae;g_Ammoniphilus
 k_Bacteria;p_Tenericutes;c_Mollicutes;o_Acholeplasmatales;f_Acholeplasmataceae;g_Acholeplasma
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_MND1;f_g_
 k_Bacteria;p_Actinobacteria;c_Thermoleophilia;o_Solirubrobacterales;f_Conexibacteraceae;g_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Janthinobacterium
 k_Bacteria;p_Acidobacteria;c_iii1-8;o_DS-18;f_g_
 k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_SBR1031;f_A4b;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Johnsonella
 k_Bacteria;p_Chloroflexi;c_Thermomicrobia;o_f_g_
 k_Archaea;p_Crenarchaeota;c_Thaumarchaeota;o_Nitrososphaerales;f_Nitrososphaeraceae;g_
 k_Bacteria;p_Acidobacteria;c_Solibacteres;o_Solibacterales;_;
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Aurantimonadaceae;_
 k_Bacteria;p_Thermi;c_Deinococci;o_Thermales;f_Thermaceae;g_Thermus
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Planococcaceae;g_Bacillus
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Arthrospira
 k_Bacteria;p_Cyanobacteria;c_Oscillatoriothycideae;o_Oscillatoriales;f_Phormidiaceae;g_Phormidium
 k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Verrucomicrobiaceae;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_Acetobacter
 k_Bacteria;p_TM7;c_TM7-3;o_CW040;f_F16;g_
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Barnesiellaceae;g_Barnesiella
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nakamurellaceae;g_Nakamurella
 k_Bacteria;p_TM7;c_TM7-1;o_f_g_
 k_Bacteria;p_Cyanobacteria;c_Nostocophycideae;o_Nostocales;f_Nostocaceae;g_Tolypothrix
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Arenimonas
 k_Bacteria;p_Verrucomicrobia;c_[Spartobacteria];o_[Chthoniobacterales];f_[Chthoniobacteraceae];g_Candidatus Xiphinema
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Geodermatophilaceae;g_Modestobacter
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Aerococcaceae;g_Granulicatella
 k_Bacteria;p_Cyanobacteria;c_ML635J-21;o_f_g_
 k_Bacteria;p_Bacteroidetes;c_[Saprosipirae];o_[Saprosipirales];f_Chitinophagaceae;g_Parasegitibacter
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Promicromonosporaceae;g_Cellulosimicrobium
 k_Bacteria;p_Actinobacteria;c_Acidimicrobiia;o_Acidimicrobiales;f_Iamiaceae;g_Iamia
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_f_g_
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;_;
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Frankiaceae;_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardiodaceae;g_Friedmanniella
 k_Bacteria;p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Adlercreutzia
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Mycoplana
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Bdellovibrionales;f_Bacteriovoraceae;g_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Neisseriales;f_Neisseriaceae;g_Gulbenkiania
 k_Bacteria;p_Cyanobacteria;c_Oscillatoriothycideae;_;
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_Rudanella
 k_Bacteria;p_Cyanobacteria;c_Synechococcophycideae;o_Synechococcales;f_Synechococcaceae;g_Synechococcus
 k_Bacteria;p_Actinobacteria;c_Acidimicrobiia;o_Acidimicrobiales;f_AKIW874;g_

k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Sarcina
 k_Bacteria;p_Actinobacteria;_:_;_:_
 k_Bacteria;p_Actinobacteria;c_Acidimicrobia;o_Acidimicrobiales;f_EB1017;g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Thermomonas
 k_Bacteria;p_Elusimicrobia;c_Elusimicrobia;o_MVP-88;f_;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Ethanoligenes
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Coxiellaceae;g_
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Nannocystaceae;g_Nannocystis
 k_Bacteria;p_Verrucomicrobia;c_[Pedosphaerae];o_[Pedosphaerales];f_Ellin517;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Butyriovibrio
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Christensenellaceae;g_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Methylophilales;f_Methylophilaceae;g_Methylotenera
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_Roseococcus
 k_Bacteria;p_Actinobacteria;c_Acidimicrobia;o_Acidimicrobiales;f_C111;g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Coxiellaceae;g_Aquicella
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Novispirillum
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinosynnemataceae;_
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_Emticicia
 k_Bacteria;p_TM7;c_TM7-3;o_I025;f_Rs-045;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Dermabacteraceae;g_Devriesea
 k_Bacteria;p_Acidobacteria;c_[Chloracidobacteria];o_DS-100;f_;g_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Marinococcus
 k_Bacteria;p_Cyanobacteria;c_Nostocophycideae;o_Nostocales;f_Nostocaceae;_
 k_Bacteria;p_Chloroflexi;c_TK10;o_AKYG885;f_Dolo_23;g_
 k_Bacteria;p_Nitrospirae;c_Nitrospira;o_Nitrospirales;f_0319-6A21;g_
 k_Bacteria;p_Tenericutes;c_Mollicutes;o_RF39;f_;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Cellulomonadaceae;_
 k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Pirellulales;f_Pirellulaceae;_
 k_Bacteria;p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Eggerthella
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Subdoligranulum
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Terribacillus
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_;f_;g_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Vagococcus
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_Belnapia
 k_Bacteria;p_Armatimonadetes;c_Armatimonadia;o_Armatimonadales;f_Armatimonadaceae;g_
 k_Bacteria;p_Spirochaetes;c_Spirochaetes;o_;f_;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingopyxis
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Nocardia
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_
 k_Bacteria;p_Gemmatimonadetes;c_Gemmatimonadetes;_:_;_:_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;_:_;_:_
 k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;_:_;_:_
 k_Bacteria;p_Armatimonadetes;c_0319-6E2;o_;f_;g_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Thermoactinomycetaceae;g_Thermoactinomyces
 k_Bacteria;p_Actinobacteria;c_Thermoleophilia;o_Gaiellales;f_AK1AB1_02E;g_
 k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Pirellulales;f_Pirellulaceae;g_Pirellula
 k_Bacteria;p_TM7;c_TM7-3;o_I025;f_;g_

k_Bacteria;p_Acidobacteria;c_Acidobacteria-5;o_f_g_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;g_Hydrogenophilus
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_ACK-M1;g_Planktophila
 k_Bacteria;p_OD1;_:_:_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Carnobacteriaceae;g_Desemzia
 k_Bacteria;p_TM6;c_SJA-4;o_f_g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Trueperella
 k_Bacteria;p_Bacteroidetes;c_[Saprosirae];o_[Saprosirales];f_Chitinophagaceae;g_Ferruginibacter
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Legionellaceae;g_Legionella
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_Pontibacter
 k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;f_Anaerolinaceae;g_SHD-231
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_[Odoribacteraceae];g_Odoribacter
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Pedomicrobium
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Curvibacter
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Aerococcaceae;g_Atopostipes
 k_Bacteria;p_Chlamydiae;c_Chlamydia;o_Chlamydiales;f_Parachlamydiaceae;g_Candidatus Protochlamydia
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyrimonadaceae;g_Paludibacter
 k_Bacteria;p_Gemmatimonadetes;c_Gemmatimonadetes;o_Gemmatimonadales;f_Gemmatimonadaceae;g_Gemmatimonas
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardiopepsaceae;g_Nocardiopepsis
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Lachnobacterium
 k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_Flavobacteriaceae;g_Myroides
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;_
 k_Bacteria;p_Acidobacteria;c_Acidobacteriia;o_Acidobacteriales;f_Acidobacteriaceae;g_Edaphobacter
 k_Bacteria;p_Actinobacteria;c_Thermoleophilia;o_Gaiellales;f_g_
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cyclobacteriaceae;_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Achromobacter
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Anaerostipes
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Promicromonosporaceae;g_Promicromonospora
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Azohydromonas
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiales;f_mitochondria;g_Pythium
 k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Verrucomicrobiaceae;g_Roseibacillus
 k_Bacteria;p_Tenericutes;c_Mollicutes;o_Entomoplasmatales;f_Entomoplasmataceae;_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Propionibacteriaceae;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacteriales;f_Caulobacteraceae;g_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Polynucleobacter
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Shinella
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Azomonas
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Legionellaceae;_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_Gluconacetobacter
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiales;f_mitochondria;g_Acanthamoeba
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Azotobacter
 k_Bacteria;p_Fusobacteria;c_Fusobacteriia;o_Fusobacteriales;f_Leptotrichiaceae;g_Sneathia
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Thermoactinomycetaceae;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micromonosporaceae;g_Micromonospora
 k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Verrucomicrobiaceae;g_Akkermansia
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Thermoactinomycetaceae;_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Leucobacter

k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Luteibacter
 k_Bacteria;p_Verrucomicrobia;c_[Pedosphaerae];o_[Pedosphaerales];f_;g_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;g_Dechloromonas
 k_Bacteria;p_;c_;o_;f_;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiales;f_mitochondria;g_Trebouxia
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_N09
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_[Entotheonellales];f_[Entotheonellaceae];g_
 k_Bacteria;p_Bacteroidetes;c_[Saprosirae];o_[Saprosirales];f_Chitinophagaceae;g_Chitinophaga
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_[Paraprevotellaceae];g_CF231
 k_Bacteria;p_Actinobacteria;c_Thermoleophilia;o_Solirubrobacterales;f_Conexibacteraceae;g_Conexibacter
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiales;f_;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiales;f_mitochondria;g_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Ellin6067;f_;g_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Bordetella
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Oceanospirillaceae;g_Marinomonas
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Paenibacillaceae;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Bifidobacteriales;f_Bifidobacteriaceae;g_Alloscardovia
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Thermoactinomycetaceae;g_Shimazuella
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Proteus
 k_Bacteria;p_TM7;c_TM7-3;_;_;_
 k_Bacteria;p_Acidobacteria;c_Acidobacteriia;o_Acidobacteriales;f_Acidobacteriaceae;_
 k_Bacteria;p_WPS-2;c_;o_;f_;g_
 k_Bacteria;p_Chloroflexi;c_Chloroflexi;o_Chloroflexales;f_Chloroflexaceae;g_Chloronema
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Beutenbergiaceae;_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Frankiaceae;g_
 k_Bacteria;p_Cyanobacteria;c_Synechococcophycideae;o_Pseudanabaenales;f_Pseudanabaenaceae;g_Pseudanabaena
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Erythrobacteraceae;g_
 k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_Caldilineales;f_Caldilineaceae;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Yaniellaceae;g_Yaniella
 k_Bacteria;p_Actinobacteria;c_Rubrobacteria;o_Rubrobacterales;f_Rubrobacteraceae;g_
 k_Bacteria;p_Cyanobacteria;c_;o_;f_;g_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;_
 k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Isosphaeraceae;g_Nostocoida
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Planococcaceae;g_Viridibacillus
 k_Bacteria;p_Tenericutes;c_Mollicutes;_;_;_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Paenibacillaceae;g_Cohnella
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Thermoactinomycetaceae;g_Planifilum
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Polyangiaceae;g_Byssovorax
 k_Bacteria;p_Bacteroidetes;c_[Rhodothermi];o_[Rhodothermales];f_Rhodothermaceae;g_Rubricoccus
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyrimonadaceae;_
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_BS11;g_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Pelomonas
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae;g_Tepidibacter
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingosinicella
 k_Bacteria;p_Cyanobacteria;c_Chloroplast;o_;f_;g_
 k_Bacteria;p_Cyanobacteria;c_Nostocophycideae;o_Stigonematales;f_Rivulariaceae;g_Calothrix

k_Bacteria;p_Chloroflexi;c_TK10;o_B07_WMSP1;f_g_
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Bdellovibrionales;f_Bdellovibrionaceae;g_
 k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Pirellulales;f_Pirellulaceae;g_A17
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Hermiimonas
 k_Bacteria;p_Verrucomicrobia;c_Verruco-5;o_WCHB1-41;f_g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Agromyces
 k_Bacteria;p_Proteobacteria;c_TA18;o_PHOS-HD29;f_g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Halanaerobiales;f_Halanaerobiaceae;g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Haererehalobacter
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Glycomycetaceae;g_Glycomyces
 k_Bacteria;p_Acidobacteria;c_S035;o_f_g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Cryptosporangiaceae;g_Cryptosporangium
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Listeriaceae;g_Listeria
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Ramlibacter
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Rhodanobacter
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Succinivibrionaceae;g_Succinivibrio
 k_Bacteria;p_Acidobacteria;c_[Chloracidobacteria];o_PK29;f_g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nakamurellaceae;g_
 k_Bacteria;p_Verrucomicrobia;c_[Pedosphaerae];o_[Pedosphaerales];f_[Pedosphaeraceae];g_Pedosphaera
 k_Bacteria;p_Chlamydiae;c_Chlamydia;o_Chlamydiales;f_g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Labrys
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Pandora
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Erythrobacteraceae;g_Porphryobacter
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Azorhizobium
 k_Bacteria;p_Chloroflexi;c_C0119;o_f_g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Serratia
 k_Bacteria;p_Planctomycetes;c_vadinHA49;o_DH61;f_g_
 k_Bacteria;p_Gemmatimonadetes;c_Gemmatimonadetes;o_Gemmatimonadales;f_Ellin5301;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_Acidisphaera
 k_Bacteria;p_Bacteroidetes;c_[Saprospirae];o_[Saprospirales];f_Chitinophagaceae;g_Niabella
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bartonellaceae;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micromonosporaceae;g_Catenuloplanes
 k_Bacteria;p_Verrucomicrobia;c_[Spartobacteria];o_[Chthoniobacteriales];f_g_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Carnobacteriaceae;g_Carnobacterium
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_BD7-3;f_g_
 k_Bacteria;p_Fibrobacteres;c_Fibrobacteria;o_258ds10;f_g_
 k_Bacteria;p_Acidobacteria;c_Solibacteres;o_Solibacterales;f_Solibacteraceae;g_
 k_Archaea;p_Crenarchaeota;c_Thaumarchaeota;o_Nitrososphaerales;f_Nitrososphaeraceae;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nakamurellaceae;g_
 k_Bacteria;p_Actinobacteria;c_Nitriliruptoria;o_Nitriliruptorales;f_Nitriliruptoraceae;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Reyranella
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Brevibacteriaceae;g_
 k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;f_Anaerolinaceae;g_Anaerolinea
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardiaceae;g_Nocardia
 k_Bacteria;p_Actinobacteria;c_OPB41;o_f_g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylocystaceae;g_Pleomorphomonas
 k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Gemmataceae;g_
 k_Bacteria;p_Acidobacteria;c_Acidobacteriia;o_Acidobacteriales;f_Acidobacteriaceae;g_Terriglobus

k_Bacteria;p_WS3;c_PRR-12;o_Sediment-1;f_g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micromonosporaceae;g_Virgisporangium
 k_Bacteria;p_Cyanobacteria;c_4C0d-2;o_MLE1-12;f_g_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Brachymonas
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Camellimonas
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micromonosporaceae;g_Phytohabitans
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Thermomonosporaceae;g_Actinoallomurus
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_[Paraprevotellaceae];g_Paraprevotella
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Perlucidibaca
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pasteurellales;f_Pasteurellaceae;g_Necropsobacter
 k_Bacteria;p_Gemmatimonadetes;c_Gemm-5;o_f_g_
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Pelistega
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Xenorhabdus
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_FAC87;f_g_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Sporolactobacillaceae;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Phyllobacteriaceae;g_Chelativorans
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;g_Azospira
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Acidaminococcus
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Elстера
 k_Bacteria;p_Elusimicrobia;c_Elusimicrobia;o_FAC88;f_g_
 k_Bacteria;p_Chlamydiae;c_Chlamydiai;o_Chlamydiales;f_g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_
 k_Bacteria;p_Acidobacteria;c_Acidobacteria-6;o_CCU21;f_g_
 k_Bacteria;p_Chloroflexi;c_TK10;o_B07_WMSP1;f_FFCH4570;g_
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Myxococcaceae;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Promicromonosporaceae;g_
 k_Bacteria;p_Chlamydiae;c_Chlamydiai;o_Chlamydiales;f_Parachlamydiaceae;_
 k_Bacteria;p_Actinobacteria;c_Acidimicrobiai;o_Acidimicrobiales;f_Microthrixaceae;g_
 k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_[Weeksellaceae];g_Elizabethkingia
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;_
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_OM27;g_
 k_Bacteria;p_Actinobacteria;c_Thermoleophila;o_Gaiellales;f_Gaiellaceae;_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Hespellia
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Salinispora
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Hyphomonadaceae;g_Woodsholea
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinopolysporaceae;g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Pantoea
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;g_Z-35
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Tetragenococcus
 k_Bacteria;p_Acidobacteria;c_[Chloracidobacteria];o_11-24;f_g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Rhodobacter
 k_Bacteria;p_Actinobacteria;c_Acidimicrobiai;o_Acidimicrobiales;f_TK06;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiales;f_Rickettsiaceae;g_Rickettsia
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiales;f_mitochondria;g_Citrullus
 k_Archaea;p_Euryarchaeota;c_Methanobacteria;o_Methanobacteriales;f_Methanobacteriaceae;g_Methanobrevibacter

k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Erythrobacteraceae;g_Lutibacterium
 k_Bacteria;p_Chloroflexi;c_Chloroflexi;o_Herpetosiphonales;f_g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Intrasporangiaceae;g_Arsenicicoccus
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_Acidocella
 k_Bacteria;p_Firmicutes;c_Clostridia;o_OPB54;f_g_
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_Leadbetterella
 k_Bacteria;p_Verrucomicrobia;c_[Spartobacteria];o_[Chthoniobacteriales];f_[Chthoniobacteraceae];_
 k_Bacteria;p_Bacteroidetes;c_[Saprospirae];o_[Saprospirales];f_Chitinophagaceae;g_Sediminibacterium
 k_Bacteria;p_BRC1;c_PRR-11;o_f_g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Thermoanaerobacterium
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;_
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyrimonadaceae;g_Dysgonomonas
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Agrococcus
 k_Bacteria;p_Synergistetes;c_Synergistia;o_Synergistales;f_Synergistaceae;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiales;f_mitochondria;g_Saprolegnia
 k_Bacteria;p_Chloroflexi;c_Chloroflexi;o_[Roseiflexales];f_[Kouleothrixaceae];g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Cohaesibacteraceae;g_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micromonosporaceae;g_Dactylosporangium
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Streptomycetaceae;g_Streptacidiphilus
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Stella
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Dyella
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Caloramator
 k_Bacteria;p_WWE1;c_[Cloacamonae];o_[Cloacamonales];f_[Cloacamonaceae];_
 k_Bacteria;p_Verrucomicrobia;c_[Pedosphaerae];o_[Pedosphaerales];_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Sinobacteraceae;g_Panacagrionas
 k_Bacteria;p_Chloroflexi;c_Chloroflexi;o_Chloroflexales;f_FFCH7168;g_
 k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Verrucomicrobiaceae;g_Prosthecoacter
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Phyllobacteriaceae;g_Mesorhizobium
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Dokdonella
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Bifidobacteriales;f_Bifidobacteriaceae;_
 k_Bacteria;p_Cyanobacteria;c_4C0d-2;o_YS2;f_g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_Rhodovarius
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Blastomonas
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Pseudonocardiaceae;g_Saccharomonospora
 k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_PSB-M-3
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Methylophilales;f_Methylophilaceae;g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_[Chromatiaceae];_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Inhella
 k_Bacteria;p_Acidobacteria;c_Acidobacteriia;o_Acidobacteriales;f_Koribacteraceae;g_Candidatus_Koribacter
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Cystobacteraceae;g_Cystobacter
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_
 k_Bacteria;p_Verrucomicrobia;c_[Spartobacteria];o_[Chthoniobacteriales];f_01D2Z36;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Marvinbryantia
 k_Bacteria;p_Gemmatimonadetes;c_Gemmatimonadetes;o_Ellin5290;f_g_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Tetrathioabacter

k_Bacteria;p_[Thermi];c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_R18-435
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Intrasporangiaceae;g_Phycococcus
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Polyangiaceae;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Epuloiscium
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Pseudonocardiaaceae;g_Amycolatopsis
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Aerococcaceae;g_Alkalibacterium
 k_Bacteria;p_Actinobacteria;c_Acidimicrobia;o_Acidimicrobiales;f_Iamiaceae;_
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_0319-6G20;g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_211ds20;g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Acidithiobacillales;f_;g_
 k_Bacteria;p_Bacteroidetes;c_[Saprospirae];o_[Saprospirales];f_Chitinophagaceae;g_Terrimonas
 k_Bacteria;p_Acidobacteria;c_Solibacteres;o_Solibacterales;f_Solibacteraceae;g_Candidatus Solibacter
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinosynnemataceae;g_Saccharothrix
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Neisseriales;f_Neisseriaceae;g_Vitreoscilla
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Dermabacteraceae;g_Helicobacillus
 k_Bacteria;p_Chlamydiae;c_Chlamydia;o_Chlamydiales;f_Rhabdochlamydiaceae;g_Candidatus Rhabdochlamydia
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Serpens
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Thermoactinomycetaceae;g_Laceyella
 k_Bacteria;p_Gemmatimonadetes;c_;o_;f_;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Thermomonosporaceae;g_Actinomadura
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinosynnemataceae;g_Lentzea
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyrimonadaceae;g_Proteiniphilum
 k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_Flavobacteriaceae;g_Sufflavibacter
 k_Bacteria;p_Chloroflexi;c_5085;o_;f_;g_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Paenibacillaceae;g_Saccharibacillus
 k_Bacteria;p_Elusimicrobia;c_Endomicrobia;o_;f_;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micromonosporaceae;g_Pilimelia
 k_Bacteria;p_Verrucomicrobia;c_[Spartobacteria];o_[Chthoniobacteriales];f_[Chthoniobacteraceae];g_OR-59
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Tremblayales;f_Tremblayaceae;g_Carsonella
 k_Bacteria;p_Planctomycetes;c_OM190;o_CL500-15;f_;g_
 k_Bacteria;p_TM7;c_TM7-3;o_EW055;f_;g_
 k_Bacteria;p_Tenericutes;c_Mollicutes;o_Entomoplasmatales;f_Entomoplasmataceae;g_Mycoplasma
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Streptosporangiaceae;g_Nonomuraea
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_Siphonobacter
 k_Bacteria;p_Bacteroidetes;c_[Saprospirae];o_[Saprospirales];f_Chitinophagaceae;g_Flavihumibacter
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardiodaceae;g_Pimelobacter
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_Paracraurococcus
 k_Bacteria;p_TM7;c_;o_;f_;g_
 k_Bacteria;p_Planctomycetes;c_OM190;o_agg27;f_;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Beutenbergiaceae;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Mitsuokella
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_RF16;g_
 k_Bacteria;p_Bacteroidetes;c_[Rhodothermi];o_[Rhodothermales];f_Rhodothermaceae;g_
 k_Bacteria;p_Verrucomicrobia;c_Opitutae;o_Opitutales;f_Opitutaceae;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Christensenellaceae;g_Christensenella
 k_Bacteria;p_Bacteroidetes;c_[Saprospirae];o_[Saprospirales];f_Saprospiraceae;g_
 k_Bacteria;p_Chloroflexi;c_;o_;f_;g_

k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyrimonadaceae;g_Petrimonas
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Neisseriales;f_Neisseriaceae;g_Vogesella
 k_Bacteria;p_Elusimicrobia;c_Elusimicrobia;o_Illb;f_;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Propionibacteriaceae;g_Microlunatus
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_IS-44;f_;g_
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Bdellovibrionales;f_Bacteriovoraceae;_
 k_Bacteria;p_Armatimonadetes;c_Armatimonadia;o_Armatimonadales;f_Armatimonadaceae;_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Erythrobacteraceae;g_Altererythrobacter
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Leifsonia
 k_Bacteria;p_Cyanobacteria;c_Chloroplast;o_Chlorophyta;f_Chlamydomonadaceae;_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;g_C39
 k_Bacteria;p_Chloroflexi;c_Thermomicrobia;_;_;_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Frankiaceae;g_Kaistibacter
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Ralstonia
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_Granulibacter
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiales;f_Rickettsiaceae;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiales;f_mitochondria;g_Cucurbita
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Geobacillus
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nakamurellaceae;g_Humicoccus
 k_Bacteria;p_Planctomycetes;c_Planctomycetia;_;_;_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Phyllobacteriaceae;g_Aminobacter
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Halomonas
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Legionellaceae;g_Tatlockia
 k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_Cryomorphaceae;g_Fluviicola
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Eubacteriaceae;g_Pseudoramibacter_Eubacterium
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Frondihabitans
 k_Bacteria;p_Verrucomicrobia;c_[Pedosphaerae];o_[Pedosphaerales];f_Ellin515;g_
 k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Coprobacillus
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_ACK-M1;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Promicromonosporaceae;g_Xylanimicrobium
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micromonosporaceae;g_Solwaraspora
 k_Bacteria;p_Planctomycetes;c_Phycisphaerae;o_Phycisphaerales;f_;g_
 k_Bacteria;p_Cyanobacteria;c_Synechococcophycideae;o_Pseudanabaenales;f_Pseudanabaenaceae;_
 k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Oceaniovalibus
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardoidaceae;g_Propionicimonas
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Pseudonocardaceae;g_Jiangella
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfuromonadales;f_Pelobacteraceae;g_Pelobacter
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Nannocystaceae;g_Plesiocystis
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Oceanobacillus
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Eubacteriaceae;g_Garciella
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Phyllobacteriaceae;g_Phyllobacterium
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Polyangiaceae;g_Sorangium
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Gracillbacteraceae;g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Ignatzschineria
 k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_AF12

k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nakamurellaceae;g_Saxeibacter
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Bifidobacteriales;f_g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;_;
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Polyangiaceae;g_Phaselicystis
 k_Bacteria;p_Cyanobacteria;c_Chloroplast;o_Chlorophyta;f_Trebouxiophyceae;_
 k_Bacteria;p_TM7;c_SC3;o_f_g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Magnetospirillum
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Ruegeria
 k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Isosphaeraceae;g_Singulisphaera
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Tsukamurellaceae;g_Tsukamurella
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_Acidomonas
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Nitrosomonadales;f_Nitrosomonadaceae;g_Nitrosovibrio
 k_Bacteria;p_Fusobacteria;c_Fusobacteria;o_Fusobacteriales;f_Leptotrichiaceae;g_Sealdella
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_HTCC2188;f_HTCC2089;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Phyllobacteriaceae;g_Pseudaminobacter
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Cryptosporangiaceae;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Starkeya
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Succinivibrionaceae;g_
 k_Bacteria;p_[Thermi];c_Deinococci;o_Thermales;f_Thermaceae;g_Meiothermus
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_Flectobacillus
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacteriales;f_Caulobacteraceae;g_Asticcacaulis
 k_Bacteria;p_Armatimonadetes;c_OPB50;o_f_g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Symbiobacteriaceae;g_Symbiobacterium
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Providencia
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Kaistia
 k_Bacteria;p_Chloroflexi;c_TK10;o_AKYG885;f_g_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Paenibacillaceae;g_Thermobacillus
 k_Bacteria;p_Bacteroidetes;c_At12OctB3;o_f_g_
 k_Bacteria;p_Acidobacteria;_;;_
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_[Entotheonellales];f_[Entotheonellaceae];_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Syntrophomonadaceae;g_Syntrophomonas
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;_;;_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Pseudonocardiaaceae;g_Actinophytocola
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Desulfotomaculum
 k_Bacteria;p_Thermotogae;c_Thermotogae;o_Thermotogales;f_Thermotogaceae;g_Fervidobacterium
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Castellaniella
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micromonosporaceae;g_Catellatospora
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Ellin329;f_g_
 k_Bacteria;p_GN02;c_GKS2-174;o_f_g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Chromatiales;f_Halothiobacillaceae;_
 k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_Cryomorphaceae;_
 k_Bacteria;p_Gemmatimonadetes;c_Gemmatimonadetes;o_N1423WL;f_g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Chelatococcus
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Aerococcaceae;g_Atopococcus
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Myxococcaceae;g_Myxococcus
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Methylococcales;f_Methylococcaceae;_
 k_Bacteria;p_Cyanobacteria;c_4C0d-2;o_SM1D11;f_g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Kushneria

k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Marinibacillus
 k_Bacteria;p_Chloroflexi;c_Thermomicrobia;o_AKYG1722;f_g_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Sphaerotilus
 k_Bacteria;p_Acidobacteria;c_iii1-8;o_32-20;f_g_
 k_Bacteria;p_Acidobacteria;c_PAUC37f;o_f_g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_Alteromonadaceae;_
 k_Bacteria;p_Armatimonadetes;c_[Fimbriimonadia];o_f_g_
 k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Pirellulales;f_Pirellulaceae;g_planctomycete
 k_Bacteria;p_Chloroflexi;c_TK10;o_f_g_
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Myxococcaceae;g_Anaeromyxobacter
 k_Bacteria;p_Proteobacteria;c_TA18;o_CV90;f_g_
 k_Bacteria;p_OD1;c_o_f_g_
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cyclobacteriaceae;g_Algoriphagus
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Salinicoccus
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Polyangiaceae;g_Polyangium
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_NB1;f_g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Pseudonocardiaceae;g_Sciscionella
 k_Bacteria;p_Chloroflexi;c_o_f_g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Succiniclasticum
 k_Bacteria;p_Verrucomicrobia;c_Opitutae;o_Opitutales;f_Opitutaceae;_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_
 k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_A31;f_S47;g_
 k_Bacteria;p_Acidobacteria;c_Acidobacteria-6;o_BPC015;f_g_
 k_Bacteria;p_Armatimonadetes;c_Chthonomonadetes;o_Chthonomonadales;f_Chthonomonadaceae;g_
 k_Bacteria;p_Verrucomicrobia;c_[Pedosphaerae];o_[Pedosphaerales];f_OPB35;g_
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfuromonadales;_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Salsuginibacillus
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacteriales;f_Syntrophobacteraceae;g_Desulforhabdus
 k_Bacteria;p_Actinobacteria;c_Acidimicrobiia;o_Acidimicrobiales;f_C111;g_Illumatobacter
 k_Bacteria;p_OP3;c_PBS-25;o_f_g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;_
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfuromonadales;f_Geobacteraceae;g_Geobacter
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Silanimonas
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;g_Zoogloea
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Thermoanaerobacteriales;f_g_
 k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Sharpea
 k_Bacteria;p_Cyanobacteria;c_Nostocophycideae;o_Nostocales;f_Scytonemataceae;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_f_g_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Neisseriales;f_Neisseriaceae;g_Aquaspirillum
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Pseudoburkholderia
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Cardiobacteriales;f_Cardiobacteriaceae;g_Suttonella
 k_Bacteria;p_Bacteroidetes;c_[Saprospirae];o_[Saprospirales];_
 k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_SBR1031;f_SHA-31;g_
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_Cytophaga
 k_Bacteria;p_Chlamydiae;c_Chlamydia;o_Chlamydiales;f_Parachlamydiaceae;g_Parachlamydia
 k_Bacteria;p_Acidobacteria;c_Acidobacteriia;o_Acidobacteriales;f_Koribacteraceae;g_
 k_Bacteria;p_Chloroflexi;c_TK17;o_f_g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Rathayibacter

k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_Blattabacteriaceae;g_Sulcia
 k_Bacteria;p_Cyanobacteria;c_Nostocophycideae;o_Nostocales;_;
 k_Bacteria;p_Chloroflexi;c_Chloroflexi;o_Roseiflexales;f_;g_
 k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Verrucomicrobiaceae;_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Nitrosomonadales;f_Nitrosomonadaceae;g_Nitrosospira
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Wohlfahrtiimonas
 k_Archaea;p_Euryarchaeota;c_Halobacteria;o_Halobacteriales;f_Halobacteriaceae;g_Halorubrum
 k_Bacteria;p_Chloroflexi;c_TK17;o_mle1-48;f_;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_
 k_Bacteria;p_Tenericutes;c_Mollicutes;o_Anaeroplasmatales;f_Anaeroplasmataceae;g_gut
 k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_Blattabacteriaceae;g_
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Haliangiaceae;g_Haliangium
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Candidatus Arthromitus
 k_Bacteria;p_Thermi;c_Deinococci;o_Deinococcales;f_Deinococcaceae;_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardiodiaceae;g_Kribbella
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradyrhizobiaceae;g_Nitrobacter
 k_Bacteria;p_Bacteroidetes;c_Saprosirae;o_Saprosirales;f_Saprosiraceae;g_Lewinella
 k_Bacteria;p_Acidobacteria;c_Acidobacteriia;o_Acidobacteriales;f_Acidobacteriaceae;g_
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;g_Denitromonas
 k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Verrucomicrobiaceae;g_Haloferula
 k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_B97;f_;g_
 k_Bacteria;p_Chlorobi;c_SJA-28;o_;f_;g_
 k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Verrucomicrobiaceae;g_Verrucomicrobium
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Tremblayales;f_Tremblayaceae;g_
 k_Bacteria;p_Chloroflexi;c_Chloroflexi;o_Chloroflexales;_;
 k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_H39;f_;g_
 k_Bacteria;p_MVP-21;c_;o_;f_;g_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Intrasporangiaceae;g_Omithinococcus
 k_Bacteria;p_Verrucomicrobia;c_Spartobacteria;o_Chthoniobacteriales;f_Chthoniobacteraceae;g_Chthoniobacter
 k_Bacteria;p_Armatimonadetes;c_Armatimonadia;o_Armatimonadales;f_Armatimonadaceae;g_CL0-1
 k_Bacteria;p_Verrucomicrobia;c_Pedosphaerae;o_Pedosphaerales;f_R4-41B;g_
 k_Bacteria;p_Tenericutes;c_Mollicutes;o_;f_;g_
 k_Bacteria;p_OP11;c_;o_;f_;g_
 k_Bacteria;p_Bacteroidetes;c_Rhodothermi;o_Rhodothermales;f_Rhodothermaceae;_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sandaracinobacter
 k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_Flavobacteriaceae;g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_34P16;f_;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_Swaminathania
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Propionibacteriaceae;_
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_;f_;g_
 k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_Sporocytophaga
 k_Bacteria;p_Nitrospirae;c_Nitrospira;o_Nitrospirales;f_FW;g_4-29
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_NB1-;f_NB1-i;g_
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Candidatus Portiera
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_Kozakia
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Sporolactobacillaceae;g_Sporolactobacillus
 k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Pusillimonas

k_Archaea;p_Crenarchaeota;c_Thaumarchaeota;o_Cenarchaeales;f_Cenarchaeaceae;g_
 k_Bacteria;p_Acidobacteria;c_BPC102;o_MVS-40;f_;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Alkaliphilus
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Phyllobacteriaceae;g_Hoeflea
 k_Bacteria;p_Cyanobacteria;c_Oscillatoriothycideae;o_Chroococcales;f_Xenococcaceae;g_Gloeocapsopsis
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Leuconostocaceae;g_Fructobacillus
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Rudaea
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Planococcaceae;g_Solibacillus
 k_Bacteria;p_Proteobacteria;c_Epsilonproteobacteria;o_Campylobacteriales;f_Campylobacteraceae;g_Sulfurospirillum
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Dehalobacteriaceae;g_Dehalobacterium
 k_Bacteria;p_Bacteroidetes;c_[Saprospirae];o_[Saprospirales];f_Chitinophagaceae;g_Niastella
 k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Intrasporangiaceae;g_Ornithinimicrobium
 k_Archaea;p_Euryarchaeota;c_Thermoplasmata;o_E2;f_;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_RF32;f_;g_
 k_Bacteria;p_[Thermi];c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_Deinobacterium
 k_Bacteria;p_Chloroflexi;c_Ktedonobacteria;o_Ktedonobacteriales;f_Ktedonobacteraceae;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Acidaminobacteraceae];g_Acidaminobacter
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_Saccharibacter
 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_Alteromonadaceae;g_Teredinibacter
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Tissierellaceae];g_Sporanaerobacter
 k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_WCHB1-50;f_;g_
 k_Bacteria;p_Bacteroidetes;c_[Saprospirae];o_[Saprospirales];f_;g_
 k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Isosphaeraceae;g_Isosphaera
 k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacteriales;f_Syntrophaceae;g_Syntrophus
 k_Bacteria;p_Planctomycetes;c_Pla3;o_;f_;g_
 k_Bacteria;p_Chloroflexi;c_Ktedonobacteria;_;_;g_
 k_Bacteria;p_Firmicutes;c_Clostridia;o_Natranaerobiales;f_Anaerobrancaceae;g_A55_D21
 k_Bacteria;p_OP3;c_koll11;o_;f_;g_
 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Methylovirgula
 k_Bacteria;p_Fusobacteria;c_Fusobacteria;o_Fusobacteriales;f_Leptotrichiaceae;_
 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Virgibacillus
 k_Bacteria;p_Firmicutes;c_AHT28;o_;f_;g_
 k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_GCA004;f_;g_

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